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Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^1] or the previous versions[^2] page to find documentation for the version you are using.

The following documentation is split into four parts. About Bio-Formats explains the goal of the software, discusses how it processes metadata, and provides other useful information such as version history and how to report bugs. User Information focuses on how to use Bio-Formats as a plugin for ImageJ and Fiji, and also gives details of other software packages which can use Bio-Formats to read and write microscopy formats. Developer Documentation covers more in-depth information on using Bio-Formats as a Java library and how to interface from non-Java codes. Finally, Formats is a guide to all the file formats currently supported by Bio-Formats.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^3] or the previous versions[^4] page to find documentation for the version you are using.

[^1]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^2]: http://www.openmicroscopy.org/site/support/legacy/
[^3]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^4]: http://www.openmicroscopy.org/site/support/legacy/
Part I

About Bio-Formats
Bio-Formats is a standalone Java library for reading and writing life sciences image file formats. It is capable of parsing both pixels and metadata for a large number of formats, as well as writing to several formats.

The primary goal of Bio-Formats is to facilitate the exchange of microscopy data between different software packages and organizations. It achieves this by converting proprietary microscopy data into an open standard called the OME data model\(^5\), particularly into the OME-TIFF\(^6\) file format.

We believe the standardization of microscopy metadata to a common structure is of vital importance to the community. You may find LOCI’s article on open source software in science\(^7\) of interest.

\(^5\)http://genomebiology.com/2005/6/5/R47
\(^6\)http://www.openmicroscopy.org/site/support/ome-model/ome-tiff
\(^7\)http://loci.wisc.edu/software/oss
There is a guide for reporting bugs here.

For help relating to opening images in ImageJ or FIJI or when using the command line tools, refer to the users documentation. You can also find tips on common issues with specific formats on the pages linked from the supported formats table.

Please contact us1 if you have any questions or problems with Bio-Formats not addressed by referring to the documentation.

Other places where questions are commonly asked and/or bugs are reported include:

- OME Trac2
- ome-devel mailing list3 (searchable using google with ‘site:lists.openmicroscopy.org.uk’)
- ome-users mailing list4 (searchable using google with ‘site:lists.openmicroscopy.org.uk’)
- ImageJ mailing list (for ImageJ/Fiji issues) forum archive5 and mailing list6
- ImageJ developer mailing list7
- Fiji Bugzilla (for ImageJ/Fiji issues)8
- Fiji developer google group9
- Confocal microscopy mailing list10

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1 http://www.openmicroscopy.org/site/community/mailing-lists
2 http://trac.openmicroscopy.org.uk/ome
3 http://lists.openmicroscopy.org.uk/pipermail/ome-devel
4 http://lists.openmicroscopy.org.uk/pipermail/ome-users
5 http://imagej.1557.n6.nabble.com/
6 http://imagej.nih.gov/ij/list.html
7 http://imagej.net/mailman/listinfo/imagej-devel
8 http://fiji.sc/cgi-bin/bugzilla/index.cgi
9 https://groups.google.com/forum/#!forum/fiji-devel
10 http://lists.umn.edu/cgi-bin/wa?A0=confocalmicroscopy
Bio-Formats is now decoupled from OMERO with its own release schedule rather than being updated whenever a new version of OMERO\(^1\) is released. We expect this to result in more frequent releases to get fixes out to the community faster.

The version number is three numbers separated by dots e.g. 4.0.0. See the version history for a list of major changes in each release.

\(^1\)http://www.openmicroscopy.org/site/support/omero5.1/
From a practical perspective, Bio-Formats is written in Java because it is cross-platform and widely used, with a vast array of libraries for handling common programming tasks. Java is one of the easiest languages from which to deploy cross-platform software. In contrast to C++, which has a large number of complex platform issues to consider, and Python, which leans heavily on C and C++ for many of its components (e.g., NumPy and SciPy), Java code is compiled one time into platform-independent byte code, which can be deployed as is to all supported platforms. And despite this enormous flexibility, Java manages to provide time performance nearly equal to C++, often better in the case of I/O operations (see further discussion on the comparative speed of Java on the LOCI site\(^1\)).

There are also historical reasons associated with the fact that the project grew out of work on the VisAD Java component library\(^2\). You can read more about the origins of Bio-Formats on the LOCI Bio-Formats homepage\(^3\).

\(^1\)http://loci.wisc.edu/faq/isnt-java-too-slow
\(^2\)http://visad.ssec.wisc.edu
\(^3\)http://loci.wisc.edu/software/bio-formats
CHAPTER
FOUR

BIO-FORMATS METADATA PROCESSING

Pixels in microscopy are almost always very straightforward, stored on evenly spaced rectangular grids. It is the metadata (details about the acquisition, experiment, user, and other information) that can be complex. Using the OME data model enables applications to support a single metadata format, rather than the multitude of proprietary formats available today.

Every file format has a distinct set of metadata, stored differently. Bio-Formats processes and converts each format’s metadata structures into a standard form called the OME data model\(^1\), according to the OME-XML\(^2\) specification. We have defined an open exchange format called OME-TIFF\(^3\) that stores its metadata as OME-XML. Any software package that supports OME-TIFF is also compatible with the dozens of formats listed on the Bio-Formats page, because Bio-Formats can convert your files to OME-TIFF format.

To facilitate support of OME-XML, we have created a library in Java\(^4\) for reading and writing OME-XML\(^5\) metadata.

There are three types of metadata in Bio-Formats, which we call core metadata, original metadata, and OME metadata.

1. **Core metadata** only includes things necessary to understand the basic structure of the pixels: image resolution; number of focal planes, time points, channels, and other dimensional axes; byte order; dimension order; color arrangement (RGB, indexed color or separate channels); and thumbnail resolution.

2. **Original metadata** is information specific to a particular file format. These fields are key/value pairs in the original format, with no guarantee of cross-format naming consistency or compatibility. Nomenclature often differs between formats, as each vendor is free to use their own terminology.

3. **OME metadata** is information from #1 and #2 converted by Bio-Formats into the OME data model. Performing this conversion is the primary purpose of Bio-Formats. Bio-Formats uses its ability to convert proprietary metadata into OME-XML as part of its integration with the OME and OMERO servers—essentially, they are able to populate their databases in a structured way because Bio-Formats sorts the metadata into the proper places. This conversion is nowhere near complete or bug free, but we are constantly working to improve it. We would greatly appreciate any and all input from users concerning missing or improperly converted metadata fields.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^6\) or the previous versions\(^7\) page to find documentation for the version you are using.

### 4.1 Reporting a bug

#### 4.1.1 Before filing a bug report

If you think you have found a bug in Bio-Formats, the first thing to do is update your version of Bio-Formats to the latest version to check if the problem has already been addressed. The Fiji updater will automatically do this for you, while in ImageJ you can select Plugins → Bio-Formats → Update Bio-Formats Plugins.

You can also download the latest version of Bio-Formats\(^8\). If you are not sure which version you need, select the latest build of the Bio-Formats package bundle from the components table.

---

\(^1\)http://genomebiology.com/2005/6/5/R47
\(^2\)http://www.openmicroscopy.org/site/support/ome-model/ome-xml
\(^3\)http://www.openmicroscopy.org/site/support/ome-model/ome-tiff
\(^4\)http://www.openmicroscopy.org/site/support/ome-model/ome-xml/ja-v-library.html
\(^5\)http://www.openmicroscopy.org/site/support/ome-model/ome-xml
\(^6\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^7\)http://www.openmicroscopy.org/site/support/legacy/
\(^8\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/
### 4.1.2 Common issues to check

- If your 12, 14 or 16-bit images look all black when you open them, typically the problem is that the pixel values are very, very small relative to the maximum possible pixel value (4095, 16383, and 65535, respectively), so when displayed the pixels are effectively black. In ImageJ/Fiji, this is fixable by checking the “Autoscale” option; with the command line tools, the “-autoscale-fast” options should work.

- If the file is very, very small (4096 bytes) and any exception is generated when reading the file, then make sure it is not a Mac OS X resource fork\(^9\). The ‘file’ command should tell you:

  ```sh
  $ file /path/to/suspicious-file
  suspicious-file: AppleDouble encoded Macintosh file
  ```

- If you get an OutOfMemory or NegativeArraySize error message when attempting to open an SVS or JPEG-2000 file then the amount of pixel data in a single image plane exceeds the amount of memory allocated to the JVM (Java Virtual Machine) or 2 GB, respectively. For the former, you can increase the amount of memory allocated; in the latter case, you will need to open the image in sections. If you are using Bio-Formats as a library, this means using the `openBytes(int, int, int, int)` method in `loci.formats.IFormatReader`. If you are using Bio-Formats within ImageJ, you can use the `Crop on import` option.

  Note that JPEG-2000 is a very efficient compression algorithm - thus the size of the file on disk will be substantially smaller than the amount of memory required to store the uncompressed pixel data. It is not uncommon for a JPEG-2000 or SVS file to occupy less than 200 MB on disk, and yet have over 2 GB of uncompressed pixel data.

### 4.1.3 Sending a bug report

If you can still reproduce the bug after updating to the latest version of Bio-Formats, and your issue does not relate to anything listed above or noted on the relevant file format page, please send a bug report to the OME Users mailing list\(^10\). You can upload files to our QA system\(^11\) or for large files (>2 GB), we can provide you with an FTP server address if you write to the mailing list.

To ensure that any inquiries you make are resolved promptly, please include the following information:

- **Exact error message.** Copy and paste any error messages into the text of your email. Alternatively, attach a screenshot of the relevant windows.

- **Version information.** Indicate which release of Bio-Formats, which operating system, and which version of Java you are using.

- **Non-working data.** If possible, please send a non-working file. This helps us ensure that the problem is fixed for next release and will not reappear in later releases. Note that any data provided is used for internal testing only; we do not make images publicly available unless given explicit permission to do so.

- **Metadata and screenshots.** If possible, include any additional information about your data. We are especially interested in the expected dimensions (width, height, number of channels, Z slices, and timepoints). Screenshots of the image being successfully opened in other software are also useful.

- **Format details.** If you are requesting support for a new format, we ask that you send as much data as you have regarding this format (sample files, specifications, vendor/manufacture information, etc.). This helps us to better support the format and ensures future versions of the format are also supported.

**Please be patient** - it may be a few days until you receive a response, but we reply to every email inquiry we receive.

---


\(^12\) [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)

\(^13\) [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
4.2 Version history

4.2.1 5.1.3 (2015 July 21)

• Native C++ updates:
  – Added cmake superbuild to build core dependencies (zlib, bzip2, png, icu, xerces, boost)
  – Progress on support for Windows

• Bug fixes, including:
  – Fixed segfault in the showinf tool used with the C++ bindings
  – Allow reading from https URLs
  – ImageJ
    * improved performance of displaying ROIs
  – Command line tools
    * fixed bfconvert to correctly create datasets with multiple files
  – Metamorph
    * improved detection of time series
    * fixed .nd datasets with variable Z and T counts in each channel
    * fixed .nd datasets that contain invalid TIFF/STK files
    * fixed dimensions when the number of planes does not match the recorded Z, C, and T sizes
  – SlideBook
    * improved native library detection (thanks to Richard Myers)
  – JPEG
    * fixed decompression of lossless files with multiple channels (thanks to Aaron Avery)
  – Inspector OBF
    * updated to support version 2 files (thanks to Bjoern Thiel)
  – Inspector MSR
    * improved detection of Z stacks
  – PerkinElmer Opera Flex
    * improved handling of multiple acquisitions of the same plate
  – Zeiss CZI
    * fixed error when opening single-file datasets whose names contained "(" and ")"
  – TIFF
    * improved speed of reading files with many tiles
  – AVI
    * updated to read frame index (idx1) tables
  – Nikon ND2
    * fixed channel counts for files with more than 3 channels
  – PNG
    * fixed decoding of interlaced images with a width or height that is not a multiple of 8
  – PSD
    * improved reading of compressed images
• Documentation improvements, including:
  – updated instructions for writing a new file format reader
  – updated usage information for command line tools
  – new Javadocs for the MetadataStore and MetadataRetrieve interfaces

4.2.2 5.1.2 (2015 May 28)

• Added OME-TIFF writing support to the native C++ implementation
• OME-TIFF export: switch to BigTIFF if .ome.tf2, .ome.tf8, or .ome.btf extensions are used
• Improved MATLAB developer documentation
• Added SlideBook reader that uses the SDK from 3I (thanks to Richard Myers and 3I - Intelligent Imaging Innovations)
• Preliminary work to make MATLAB toolbox work with Octave
• Many bug fixes, including:
  – ImageJ
    * fixed regression in getPlanePosition* macro extension methods
    * fixed display of composite color virtual stacks
  – Nikon ND2
    * improved parsing of plane position and timestamp data
  – TIFF
    * reduced memory required to read color lookup tables
  – Zeiss LSM
    * improved parsing of 16-bit color lookup tables
  – Zeiss CZI
    * fixed ordering of original metadata table
    * fixed reading of large pre-stitched tiled images
  – AIM
    * fixed handling of truncated files
  – Metamorph/MetaXpress TIFF
    * improved UIC1 metadata tag parsing

4.2.3 5.1.1 (2015 April 28)

• Add TIFF writing support to the native C++ implementation
• Fixed remaining functional differences between Windows and Mac/Linux
• Improved performance of ImageJ plugin when working with ROIs
• TIFF export: switch to BigTIFF if .tf2, .tf8, or .btf extensions are used
• Many bug fixes, including:
  – fixed upgrade checking to more accurately report when a new version is available
  – Zeiss CZI
    * fixed ordering of multiposition data
    * improved support for RGB and fused images

14https://www.intelligent-imaging.com
– Nikon ND2
  * improved ordering of multiposition data

– Leica LIF
  * improved metadata validity checks
  * improved excitation wavelength detection

– Metamorph STK/TIFF
  * record lens numerical aperture
  * fixed millisecond values in timestamps

– Gatan DM3
  * correctly detect signed pixel data

– Imaris HDF
  * fix channel count detection

– ICS export
  * fix writing of files larger than 2GB

4.2.4 5.1.0 (2015 April 2)

• Improvements to performance with network file systems
• Improvements to developer documentation
• Initial version of native C++ implementation
• Improved support for opening and saving ROI data with ImageJ
• Added support for CellH5 data (thanks to Christophe Sommer)
• Added support for Perkin Elmer Nuance data (thanks to Lee Kamentsky)
• Added support for Amnis FlowSight data (thanks to Lee Kamentsky and Sebastien Simard)
• Added support for Veeco AFM data
• Added support for Zeiss .lms data (not to be confused with .lsim)
• Added support for I2I data
• Added support for writing Vaa3D data (thanks to Brian Long)
• Updated to OME schema 2015-0115
• Update RandomAccessInputStream and RandomAccessOutputStream to read and write bits
• Many bug fixes, including:
  – Leica SCN
    * fix pixel data decompression
    * fix handling of files with multiple channels
    * parse magnification and physical pixel size data
  – Olympus/CellSens .vsi
    * more thorough parsing of metadata
    * improved reading of thumbnails and multi-resolution images
  – NDPI
    * fix reading of files larger than 4GB

* parse magnification data
  - **Zeiss CZI**
    * improve parsing of plane position coordinates
  - **Inveon**
    * fix reading of files larger than 2 GB
  - **Nikon ND2**
    * many improvements to dimension detection
    * many improvements to metadata parsing accuracy
    * update original metadata table to include PFS data
  - **Gatan DM3**
    * fix encoding when parsing metadata
    * fix physical pixel size parsing
  - **Metamorph**
    * fix off-by-one in metadata parsing
    * fix number parsing to be independent of the system locale
  - **JPEG**
    * parse EXIF data, if present (thanks to Paul Van Schayck)
  - **OME-XML/OME-TIFF**
    * fix handling of missing image data
  - **PrairieView**
    * improved support for version 5.2 data (thanks to Curtis Rueden)
  - **DICOM**
    * fix dimensions for multi-file datasets
    * fix pixel data decoding for files with multiple images
  - **PNG**
    * reduce memory required to read large images
  - **Inspector OBF**
    * fix support for version 5 data (thanks to Bjoern Thiel)
  - **PCORAW**
    * fix reading of files larger than 4 GB
  - **AIM**
    * fix reading of files larger than 4 GB
  - **MRC**
    * add support for signed 8-bit data
  - **Fix build errors in MIPAV plugin**
  - **ImageJ**
    * fix export from a script/macro
    * fix windowless export
    * allow exporting from any open image window
    * allow the “Group files with similar names” and “Swap dimensions” options to be used from a script/macro
  - **bfconvert**

4.2. **Version history**
* fix writing each channel, Z section, and/or timepoint to a separate file
* add options for configuring the tile size to be used when saving images

4.2.5 5.0.8 (2015 February 10)

- No changes - release to keep version numbers in sync with OMERO

4.2.6 5.0.7 (2015 February 5)

- Several bug fixes, including:
  - ND filter parsing for DeltaVision
  - Timepoint count and original metadata parsing for Metamorph
  - Build issues when Genshi or Git are missing
  - LZW image decoding

4.2.7 5.0.6 (2014 November 11)

- Several bug fixes, including:
  - Pixel sign for DICOM images
  - Image dimensions for Zeiss CZI and Nikon ND2
  - Support for Leica LIF files produced by LAS AF 4.0 and later

4.2.8 5.0.5 (2014 September 23)

- Documentation improvements
- Support for non-spectral Prairie 5.2 datasets

4.2.9 5.0.4 (2014 September 3)

- Fix compile and runtime errors under Java 1.8
- Improvements to Nikon .nd2 metadata parsing
- Added support for PicoQuant .bin files (thanks to Ian Munro)

4.2.10 5.0.3 (2014 August 7)

- Many bug fixes for Nikon .nd2 files
- Several other bug fixes, including:
  - LZW image decoding
  - Stage position parsing for Zeiss CZI
  - Exposure time units for ScanR
  - Physical pixel size units for DICOM
  - NDPI and Zeiss LSM files larger than 4GB
  - Z and T dimensions for InCell 6000 plates
  - Export of RGB images in ImageJ
- Improved metadata saving in MATLAB functions

4.2. Version history
4.2.11 5.0.2 (2014 May 28)

- Many bug fixes for Zeiss .czi files
- Several other bug fixes, including:
  - Gatan .dm3 units and step count parsing
  - Im inspector .msr 5D image support
  - DICOM reading of nested tags
- Update native-lib-loader version (to 2.0.1)
- Updates and improvements to user documentation

4.2.12 5.0.1 (2014 Apr 7)

- Added image pyramid support for CellSens .vsi data
- Several bug fixes, including:
  - Woolz import into OMERO
  - Cellomics file name parsing (thanks to Lee Kamentsky)
  - Olympus FV1000 timestamp support (thanks to Lewis Kraft and Patrick Riley)
  - (A)PNG large image support
  - Zeiss .czi dimension detection for SPIM datasets
- Performance improvements for Becker & Hickl .sdt file reading (thanks to Ian Munro)
- Performance improvements to directory listing over NFS
- Update slf4j and logback versions (to 1.7.6 and 1.1.1 respectively)
- Update jgoodies-forms version (to 1.7.2)

4.2.13 5.0.0 (2014 Feb 25)

- New bundled ‘bioformats_package.jar’ for ImageJ
- Now uses logback as the slf4j binding by default
- Updated component names, .jar file names, and Maven artifact names
- Fixed support for Becker & Hickl .sdt files with multiple blocks
- Fixed tiling support for TIFF, Hamamatsu .ndpi, JPEG, and Zeiss .czi files
- Improved continuous integration testing
- Updated command line documentation

4.2.14 5.0.0-RC1 (2013 Dec 19)

- Updated Maven build system and launched new Artifactory repository (http://artifacts.openmicroscopy.org)
- Added support for:
  - Bio-Rad SCN
  - Yokogawa CellVoyager (thanks to Jean-Yves Tinevez)
  - LaVision Inspector
  - PCORAW
  - Woolz (thanks to Bill Hill)
- Added support for populating and parsing ModuloAlong[Z, C, T] annotations for FLIM/SPIM data
• Updated netCDF and slf4j version requirements - netCDF 4.3.19 and slf4j 1.7.2 are now required
• Updated and improved MATLAB users and developers documentation
• Many bug fixes including for Nikon ND2, Zeiss CZI, and CellWorX formats

4.2.15 5.0.0-beta1 (2013 June 20)
• Updated to 2013-06 OME-XML schema\textsuperscript{16}
• Improved the performance in tiled formats
• Added caching of Reader metadata using http://code.google.com/p/kryo/
• Added support for:
  – Aperio AFI
  – Inveon
  – MPI-BPC Inspector
• Many bug fixes, including:
  – Add ZEN 2012/Lightsheet support to Zeiss CZI
  – Improved testing of autogenerated code
  – Moved OME-XML specification into Bio-Formats repository

4.2.16 4.4.10 (2014 Jan 15)
• Bug fixes including CellWorx, Metamorph and Zeiss CZI
• Updates to MATLAB documentation

4.2.17 4.4.9 (2013 Oct 16)
• Many bug fixes including improvements to support for ND2 format
• Java 1.6 is now the minimum supported version; Java 1.5 is no longer supported

4.2.18 4.4.8 (2013 May 2)
• No changes - release to keep version numbers in sync with OMERO

4.2.19 4.4.7 (2013 April 25)
• Many bug fixes to improve support for more than 20 formats
• Improved export to multi-file datasets
• Now uses slf4j for logging rather than using log4j directly, enabling other logging implementations to be used, for example when Bio-Formats is used as a component in other software using a different logging system.

4.2.20 4.4.6 (2013 February 11)
• Many bug fixes
• Further documentation improvements

\textsuperscript{16}http://www.openmicroscopy.org/site/support/ome-model/
4.2.21 4.4.5 (2012 November 13)

- Restructured and improved documentation
- Many bug fixes, including:
  - File grouping in many multi-file formats
  - Maven build fixes
  - ITK plugin fixes

4.2.22 4.4.4 (2012 September 24)

- Many bug fixes

4.2.23 4.4.2 (2012 August 22)

- Security fix for OMERO plugins for ImageJ

4.2.24 4.4.1 (2012 July 20)

- Fix a bug that prevented BigTIFF files from being read
- Fix a bug that prevented PerkinElmer .flex files from importing into OMERO

4.2.25 4.4.0 (2012 July 13)

- Many, many bug fixes
- Added support for:
  - .nd2 files from Nikon Elements version 4
  - PerkinElmer Operetta data
  - MJPEG-compressed AVIs
  - MicroManager datasets with multiple positions
  - Zeiss CZI data
  - IMOD data

4.2.26 4.3.3 (2011 October 18)

- Many bug fixes, including:
  - Speed improvements to HCImage/SimplePCI and Zeiss ZVI files
  - Reduce memory required by Leica LIF reader
  - More accurately populate metadata for Prairie TIFF datasets
  - Various fixes to improve the security of the OMERO plugin for ImageJ
  - Better dimension detection for Bruker MRI datasets
  - Better thumbnail generation for histology (SVS, NDPI) datasets
  - Fix stage position parsing for Metamorph TIFF datasets
  - Correctly populate the channel name for PerkinElmer Flex files
4.2.27 4.3.2 (2011 September 15)

- Many bug fixes, including:
  - Better support for Volocity datasets that contain compressed data
  - More accurate parsing of ICS metadata
  - More accurate parsing of cellSens .vsi files

- Added support for a few new formats
  - .inr
  - Canon DNG
  - Hitachi S-4800
  - Kodak .bip
  - JPX
  - Volocity Library Clipping (.acff)
  - Bruker MRI

- Updated Zeiss LSM reader to parse application tags
- Various performance improvements, particularly for reading/writing TIFFs
- Updated OMERO ImageJ plugin to work with OMERO 4.3.x

4.2.28 4.3.1 (2011 July 8)

- Several bug fixes, including:
  - Fixes for multi-position DeltaVision files
  - Fixes for MicroManager 1.4 data
  - Fixes for 12 and 14-bit JPEG-2000 data
  - Various fixes for reading Volocity .mvd2 datasets

- Added various options to the ‘showinf’ and ‘bfconvert’ command line tools
- Added better tests for OME-XML backwards compatibility
- Added the ability to roughly stitch tiles in a multi-position dataset

4.2.29 4.3.0 (2011 June 14)

- Many bug fixes, including:
  - Many fixes for reading and writing sub-images
  - Fixes for stage position parsing in the Zeiss formats
  - File type detection fixes

- Updated JPEG-2000 reading and writing support to be more flexible

- Added support for 9 new formats:
  - InCell 3000
  - Trestle
  - Hamamatsu .ndpi
  - Hamamatsu VMS
  - SPIDER
  - Volocity .mvd2
• Olympus SIS TIFF
• IMAGIC
• cellSens VSI
• Updated to 2011-06 OME-XML schema
• Minor speed improvements in many formats
• Switched version control system from SVN to Git
• Moved all Trac tickets into the OME Trac: http://trac.openmicroscopy.org.uk
• Improvements to testing frameworks
• Added Maven build system as an alternative to the existing Ant build system
• Added pre-compiled C++ bindings to the download page

4.2.30 4.2.2 (2010 December 6)

• Several bug fixes, notably:
  – Metadata parsing fixes for Zeiss LSM, Metamorph STK, and FV1000
  – Prevented leaked file handles when exporting to TIFF/OME-TIFF
  – Fixed how BufferedImages are converted to byte arrays
• Proper support for OME-XML XML annotations
• Added support for SCANCO Medical .aim files
• Minor improvements to ImageJ plugins
• Added support for reading JPEG-compressed AVI files

4.2.31 4.2.1 (2010 November 12)

• Many, many bug fixes
• Added support for 7 new formats:
  – CellWorX .pnl
  – ECAT7
  – Varian FDF
  – Perkin Elmer Densitometer
  – FEI TIFF
  – Compix/SimplePCI TIFF
  – Nikon Elements TIFF
• Updated Zeiss LSM metadata parsing, with generous assistance from Zeiss, FMI, and MPI-CBG
• Lots of work to ensure that converted OME-XML validates
• Improved file stitching functionality; non-numerical file patterns and limited regular expression-style patterns are now supported

4.2.32 4.2.0 (2010 July 9)

• Fixed many, many bugs in all aspects of Bio-Formats
• Reworked ImageJ plugins to be more user- and developer-friendly
• Added many new unit tests

4.2. Version history
• Added support for approximately 25 new file formats, primarily in the SPM domain
• Rewrote underlying I/O infrastructure to be thread-safe and based on Java NIO
• Rewrote OME-XML parsing/generation layer; OME-XML 2010-06 is now supported
• Improved support for exporting large images
• Improved support for exporting to multiple files
• Updated logging infrastructure to use slf4j and log4j

4.2.33 4.1.1 (2009 December 3)

• Fixed many bugs in popular file format readers
4.1 (2009 October 21):

• Fixed many bugs in most file format readers
• Significantly improved confocal and HCS metadata parsing
• Improved C++ bindings
• Eliminated references to Java AWT classes in core Bio-Formats packages
• Added support for reading Flex datasets from multiple servers
• Improved OME-XML generation; generated OME-XML is now valid
• Added support for Olympus ScanR data
• Added OSGi information to JARs
• Added support for Amira Mesh files
• Added support for LI-FLIM files
• Added more informative exceptions
• Added support for various types of ICS lifetime data
• Added support for Nikon EZ-C1 TIFFs
• Added support for Maia Scientific MIAS data

4.2.34 4.0.1 (2009 June 1)

• Lots of bug fixes in most format readers and writers
• Added support for Analyze 7.1 files
• Added support for Nifti files
• Added support for Cellomics .c01 files
• Refactored ImageJ plugins
• Bio-Formats, the common package, and the ImageJ plugins now require Java 1.5
• Eliminated native library dependency for reading lossless JPEGs
• Changed license from GPL v3 or later to GPL v2 or later
• Updated Olympus FV1000, Zeiss LSM, Zeiss ZVI and Nikon ND2 readers to parse ROI data
• Added option to ImageJ plugin for displaying ROIs parsed from the chosen dataset
• Fixed BufferedImage construction for signed data and unsigned int data
4.2.35 4.0.0 (2009 March 3)

- Improved OME data model population for Olympus FV1000, Nikon ND2, Metamorph STK, Leica LEI, Leica LIF, InCell 1000 and MicroManager
- Added TestNG tests for format writers
- Added option to ImageJ plugin to specify custom colors when customizing channels
- Added ability to upgrade the ImageJ plugin from within ImageJ
- Fixed bugs in Nikon ND2, Leica LIF, BioRad PIC, TIFF, PSD, and OME-TIFF
- Fixed bugs in Data Browser and Exporter plugins
- Added support for Axon Raw Format (ARF), courtesy of Johannes Schindelin
- Added preliminary support for IPLab-Mac file format

4.2.36 2008 December 29

- Improved metadata support for DeltaVision, Zeiss LSM, MicroManager, and Leica LEI
- Restructured code base/build system to be component-driven
- Added support for JPEG and JPEG-2000 codecs within TIFF, OME-TIFF and OME-XML
- Added support for 16-bit compressed Flex files
- Added support for writing JPEG-2000 files
- Added support for Minolta MRW format
- Added support for the 2008-09 release of OME-XML
- Removed dependency on JMagick
- Re-added caching support to data browser plugin
- Updated loci.formats.Codec API to be more user-friendly
- Expanded loci.formats.MetadataStore API to better represent the OME-XML model
- Improved support for Nikon NEF
- Improved support for TillVision files
- Improved ImageJ import options dialog
- Fixed bugs with Zeiss LSM files larger than 4 GB
- Fixed minor bugs in most readers
- Fixed bugs with exporting from an Image5D window
- Fixed several problems with virtual stacks in ImageJ

4.2.37 2008 August 30

- Fixed bugs in many file format readers
- Fixed several bugs with swapping dimensions
- Added support for Olympus CellR/APL files
- Added support for MINC MRI files
- Added support for Aperio SVS files compressed with JPEG 2000
- Added support for writing OME-XML files
- Added support for writing APNG files
- Added faster LZW codec
• Added drag and drop support to ImageJ shortcut window
• Re-integrated caching into the data browser plugin

4.2.38 2008 July 1

• Fixed bugs in most file format readers
• Fixed bugs in OME and OMERO download functionality
• Fixed bugs in OME server-side import
• Improved metadata storage/retrieval when uploading to and downloading from the OME Perl server
• Improved Bio-Formats ImageJ macro extensions
• Major updates to MetadataStore API
• Updated OME-XML generation to use 2008-02 schema by default
• Addressed time and memory performance issues in many readers
• Changed license from LGPL to GPL
• Added support for the FEI file format
• Added support for uncompressed Hamamatsu Aquacosmos NAF files
• Added support for Animated PNG files
• Added several new options to Bio-Formats ImageJ plugin
• Added support for writing ICS files

4.2.39 2008 April 17

• Fixed bugs in Slidebook, ND2, FV1000 OIB/OIF, Perkin Elmer, TIFF, Prairie, Openlab, Zeiss LSM, MNG, Molecular Dynamics GEL, and OMEO-TIFF
• Fixed bugs in OME and OMERO download functionality
• Fixed bugs in OME server-side import
• Fixed bugs in Data Browser
• Added support for downloading from OMERO 2.3 servers
• Added configuration plugin
• Updates to MetadataStore API
• Updates to OME-XML generation - 2007-06 schema used by default
• Added support for Li-Cor L2D format
• Major updates to TestNG testing framework
• Added support for writing multi-series OMEO-TIFF files
• Added support for writing BigTIFF files

4.2.40 2008 Feb 12

• Fixed bugs in QuickTime, SimplePCI and DICOM
• Fixed a bug in channel splitting logic
4.2.41 2008 Feb 8

- Many critical bugfixes in format readers and ImageJ plugins
- Newly reborn Data Browser for 5D image visualization
  - some combinations of import options do not work yet

4.2.42 2008 Feb 1

- Fixed bugs in Zeiss LSM, Metamorph STK, FV1000 OIB/OIF, Leica LEI, TIFF, Zeiss ZVI, ICS, Prairie, Openlab LIF, Gatan, DICOM, QuickTime
- Fixed bug in OME-TIFF writer
- Major changes to MetadataStore API
- Added support for JPEG-compressed TIFF files
- Added basic support for Aperio SVS files
  - JPEG2000 compression is still not supported
- Improved “crop on import” functionality
- Improvements to bfconvert and bfview
- Improved OME-XML population for several formats
- Added support for JPEG2000-compressed DICOM files
- EXIF data is now parsed from TIFF files

4.2.43 2007 Dec 28

- Fixed bugs in Leica LEI, Leica TCS, SDT, Leica LIF, Visitech, DICOM, Imaris 5.5 (HDF), and Slidebook readers
- Better parsing of comments in TIFF files exported from ImageJ
- Fixed problem with exporting 48-bit RGB data
- Added logic to read multi-series datasets spread across multiple files
- Improved channel merging in ImageJ - requires ImageJ 1.39l
- Support for hyperstacks and virtual stacks in ImageJ - requires ImageJ 1.39l
- Added API for reading directly from a byte array or InputStream
- Metadata key/value pairs are now stored in ImageJ’s “Info” property
- Improved OMERO download plugin - it is now much faster
- Added “open all series” option to ImageJ importer
- ND2 reader based on Nikon’s SDK now uses our own native bindings
- Fixed metadata saving bug in ImageJ
- Added sub-channel labels to ImageJ windows
- Major updates to 4D Data Browser
- Minor updates to automated testing suite
4.2.44 2007 Dec 1

- Updated OME plugin for ImageJ to support downloading from OMERO
- Fixed bug with floating point TIFFs
- Fixed bugs in Visitech, Zeiss LSM, Imaris 5.5 (HDF)
- Added alternate ND2 reader that uses Nikon’s native libraries
- Fixed calibration and series name settings in importer
- Added basic support for InCell 1000 datasets

4.2.45 2007 Nov 21

- Fixed bugs in ND2, Leica LIF, DICOM, Zeiss ZVI, Zeiss LSM, FV1000 OIB, FV1000 OIF, BMP, Evotec Flex, BioRad PIC, Slidebook, TIFF
- Added new ImageJ plugins to slice stacks and do “smart” RGB merging
- Added “windowless” importer plugin
  - uses import parameters from IJ_Prefs.txt, without prompting the user
- Improved stack slicing and colorizing logic in importer plugin
- Added support for DICOM files compressed with lossless JPEG
  - requires native libraries
- Added bugs with signed pixel data
- Added support for Imaris 5.5 (HDF) files
- Added 4 channel merging to importer plugin
- Added API methods for reading subimages
- Major updates to the 4D Data Browser

4.2.46 2007 Oct 17

- Critical OME-TIFF bugfixes
- Fixed bugs in Leica LIF, Zeiss ZVI, TIFF, DICOM, and AVI readers
- Added support for JPEG-compressed ZVI images
- Added support for BigTIFF
- Added importer plugin option to open each plane in a new window
- Added MS Video 1 codec for AVI

4.2.47 2007 Oct 1

- Added support for compressed DICOM images
- Added support for uncompressed LIM files
- Added support for Adobe Photoshop PSD files
- Fixed bugs in DICOM, OME-TIFF, Leica LIF, Zeiss ZVI, Visitech, PerkinElmer and Metamorph
- Improved indexed color support
- Addressed several efficiency issues
- Fixed how multiple series are handled in 4D data browser
- Added option to reorder stacks in importer plugin
• Added option to turn off autoscaling in importer plugin
• Additional metadata convenience methods

4.2.48 2007 Sept 11

• Major improvements to ND2 support; lossless compression now supported
• Support for indexed color images
• Added support for Simple-PCI .cxd files
• Command-line OME-XML validation
• Bugfixes in most readers, especially Zeiss ZVI, Metamorph, PerkinElmer and Leica LEI
• Initial version of Bio-Formats macro extensions for ImageJ

4.2.49 2007 Aug 1

• Added support for latest version of Leica LIF
• Fixed several issues with Leica LIF, Zeiss ZVI
• Better metadata mapping for Zeiss ZVI
• Added OME-TIFF writer
• Added MetadataRetrieve API for retrieving data from a MetadataStore
• Miscellaneous bugfixes

4.2.50 2007 July 16

• Fixed several issues with ImageJ plugins
• Better support for Improvision and Leica TCS TIFF files
• Minor improvements to Leica LIF, ICS, QuickTime and Zeiss ZVI readers
• Added searchable metadata window to ImageJ importer

4.2.51 2007 July 2

• Fixed issues with ND2, Openlab LIFF and Slidebook
• Added support for Visitech XYS
• Added composite stack support to ImageJ importer

4.2.52 2007 June 18

• Fixed issues with ICS, ND2, MicroManager, Leica LEI, and FV1000 OIF
• Added support for large (> 2 GB) ND2 files
• Added support for new version of ND2
• Minor enhancements to ImageJ importer
• Implemented more flexible logging
• Updated automated testing framework to use TestNG
• Added package for caching images produced by Bio-Formats

4.2. Version history
4.2.53 2007 June 6

- Fixed OME upload/download bugs
- Fixed issues with ND2, EPS, Leica LIF, and OIF
- Added support for Khoros XV
- Minor improvements to the importer

4.2.54 2007 May 24

- Better Slidebook support
- Added support for Quicktime RPZA
- Better Leica LIF metadata parsing
- Added support for BioRad PIC companion files
- Added support for bzip2-compressed files
- Improved ImageJ plugins
- Native support for FITS and PGM

4.2.55 2007 May 2

- Added support for NRRD
- Added support for Evotec Flex (requires LuraWave Java SDK with license code)
- Added support for gzip-compressed files
- Added support for compressed QuickTime headers
- Fixed QuickTime Motion JPEG-B support
- Fixed some memory issues (repeated small array allocations)
- Fixed issues reading large (> 2 GB) files
- Removed “ignore color table” logic, and replaced with Leica-specific solution
- Added status event reporting to readers
- Added API to toggle metadata collection
- Support for multiple dimensions rasterized into channels
- Deprecated reader and writer methods that accept the ‘id’ parameter
- Deprecated IFormatWriter.save in favor of saveImage and saveBytes
- Moved dimension swapping and min/max calculation logic to delegates
- Separate GUI logic into isolated lociformats.gui package
- Miscellaneous bugfixes and tweaks in most readers and writers
- Many other bugfixes and improvements

4.2.56 2007 Mar 16

- Fixed calibration bugs in importer plugin
- Enhanced metadata support for additional formats
- Fixed LSM bug
4.2.57 2007 Mar 7

- Added support for Micro-Manager file format
- Fixed several bugs – Leica LIF, Leica LEI, ICS, ND2, and others
- Enhanced metadata support for several formats
- Load series preview thumbnails in the background
- Better implementation of openBytes(String, int, byte[]) for most readers
- Expanded unit testing framework

4.2.58 2007 Feb 28

- Better series preview thumbnails
- Fixed bugs with multi-channel Leica LEI
- Fixed bugs with “ignore color tables” option in ImageJ plugin

4.2.59 2007 Feb 26

- Many bugfixes: Leica LEI, ICS, FV1000 OIB, OME-XML and others
- Better metadata parsing for BioRad PIC files
- Enhanced API for calculating channel minimum and maximum values
- Expanded MetadataStore API to include more semantic types
- Added thumbnails to series chooser in ImageJ plugin
- Fixed plugins that upload and download from an OME server

4.2.60 2007 Feb 7

- Added plugin for downloading images from OME server
- Improved HTTP import functionality
- Added metadata filtering – unreadable metadata is no longer shown
- Better metadata table for multi-series datasets
- Added support for calibration information in Gatan DM3
- Eliminated need to install JAI Image I/O Tools to read ND2 files
- Fixed ZVI bugs: metadata truncation, and other problems
- Fixed bugs in Leica LIF: incorrect calibration, first series labeling
- Fixed memory bug in Zeiss LSM
- Many bugfixes: PerkinElmer, DeltaVision, Leica LEI, LSM, ND2, and others
- IFormatReader.close(boolean) method to close files temporarily
- Replaced Compression utility class with extensible Compressor interface
- Improved testing framework to use .bioformats configuration files
4.2.61 2007 Jan 5

- Added support for Prairie TIFF
- Fixed bugs in Zeiss LSM, OIB, OIF, and ND2
- Improved API for writing files
- Added feature to read files over HTTP
- Fixed bugs in automated testing framework
- Miscellaneous bugfixes

4.2.62 2006 Dec 22

- Expanded ImageJ plug-in to optionally use Image5D or View5D
- Improved support for ND2 and JPEG-2000 files
- Added automated testing framework
- Fixed bugs in Zeiss ZVI reader
- Miscellaneous bugfixes

4.2.63 2006 Nov 30

- Added support for ND2/JPEG-2000
- Added support for MRC
- Added support for MNG
- Improved support for floating-point images
- Fixed problem with 2-channel Leica LIF data
- Minor tweaks and bugfixes in many readers
- Improved file stitching logic
- Allow ImageJ plug-in to be called from a macro

4.2.64 2006 Nov 2

- Bugfixes and improvements for Leica LIF, Zeiss LSM, OIF and OIB
- Colorize channels when they are split into separate windows
- Fixed a bug with 4-channel datasets

4.2.65 2006 Oct 31

- Added support for Imaris 5 files
- Added support for RGB ICS images

4.2.66 2006 Oct 30

- Added support for tiled TIFFs
- Fixed bugs in ICS reader
- Fixed importer plugin deadlock on some systems
4.2.67 2006 Oct 27

- Multi-series support for Slidebook
- Added support for Alicona AL3D
- Fixed plane ordering issue with FV1000 OIB
- Enhanced dimension detection in FV1000 OIF
- Added preliminary support for reading NEF images
- Added option to ignore color tables
- Fixed ImageJ GUI problems
- Fixed spatial calibration problem in ImageJ
- Fixed some lingering bugs in Zeiss ZVI support
- Fixed bugs in OME-XML reader
- Tweaked ICS floating-point logic
- Fixed memory leaks in all readers
- Better file stitching logic

4.2.68 2006 Oct 6

- Support for 3i SlideBook format (single series only for now)
- Support for 16-bit RGB palette TIFF
- Fixed bug preventing import of certain Metamorph STK files
- Fixed some bugs in PerkinElmer UltraView support
- Fixed some bugs in Leica LEI support
- Fixed a bug in Zeiss ZVI support
- Fixed bugs in Zeiss LSM support
- Fixed a bug causing slow identification of Leica datasets
- Fixed bugs in the channel merging logic
- Fixed memory leak for OIB format
- Better scaling of 48-bit RGB data to 24-bit RGB
- Fixed duplicate channels bug in “open each channel in a separate window”
- Fixed a bug preventing PICT import into ImageJ
- Better integration with HandleExtraFileTypes
- Better virtual stack support in Data Browser plugin
- Fixed bug in native QuickTime random access
- Keep aspect ratio for computed thumbnails
- Much faster file stitching logic

4.2.69 2006 Sep 27

- PerkinElmer: support for PE UltraView
- Openlab LIFF: support for Openlab v5
- Leica LEI: bugfixes, and support for multiple series
- ZVI, OIB, IPW: more robust handling of these formats (eliminated custom OLE parsing logic in favor of Apache POI)
• OIB: better metadata parsing (but maybe still not perfect?)
• LSM: fixed a bug preventing import of certain LSMS
• Metamorph STK: fixed a bug resulting in duplicate image planes
• User interface: use of system look & feel for file chooser dialog when available
• Better notification when JAR libraries are missing

4.2.70 2006 Sep 6

• Leica LIF: multiple distinct image series within a single file
• Zeiss ZVI: fixes and improvements contributed by Michel Boudinot
• Zeiss LSM: fixed bugs preventing the import of certain LSM files
• TIFF: fixed a bug preventing import of TIFFs created with Bio-Rad software

4.2.71 2006 Mar 31

• First release

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^\text{17}\) or the previous versions\(^\text{18}\) page to find documentation for the version you are using.

\(^{17}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{18}\)http://www.openmicroscopy.org/site/support/legacy/
Part II

User Information
CHAPTER FIVE

USING BIO-FORMATS WITH IMAGEJ AND FIJI

The following sections explain the features of Bio-Formats and how to use it within ImageJ and Fiji:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

5.1 ImageJ overview

ImageJ is an image processing and analysis application written in Java, widely used in the life sciences fields, with an extensible plugin infrastructure. You can use Bio-Formats as a plugin for ImageJ to read and write images in the formats it supports.

5.1.1 Installation

Download bioformats_package.jar and drop it into your ImageJ/plugins folder. Next time you run ImageJ, a new Bio-Formats submenu with several plugins will appear in the Plugins menu, including the Bio-FormatsImporter and Bio-FormatsExporter.

5.1.2 Usage

The Bio-FormatsImporter plugin can display image stacks in several ways:

- In a standard ImageJ window (including as a hyperstack)
- Using the LOCI Data Browser plugin (included)
- With Joachim Walter’s Image5D plugin (if installed)
- With Rainer Heintzmann’s View5D plugin (if installed)

ImageJ v1.37 and later automatically (via HandleExtraFileTypes) calls the Bio-Formats logic, if installed, as needed when a file is opened within ImageJ, i.e. when using File → Open instead of explicitly choosing Plugins → Bio-Formats → Bio-FormatsImporter from the menu.

For a more detailed description of each plugin, see the Bio-Formats page of the Fiji wiki.

5.1.3 Upgrading

To upgrade, just overwrite the old bioformats_package.jar with the latest one.

You may want to download the latest version of ImageJ first, to take advantage of new features and bug-fixes.

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1 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2 http://www.openmicroscopy.org/site/support/legacy/
3 http://rsb.info.nih.gov/ij/
4 http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/bioformats_package.jar
5 http://loci.wisc.edu/software/data-browser
6 http://developer.imagej.net/plugins/image5D
7 http://www.nanoimaging.de/View5D
8 http://fiji.sc/Bio-Formats
9 http://downloads.openmicroscopy.org/latest/bio-formats5.1/
As of the 4.0.0 release, you can also upgrade the Bio-Formats plugin directly from ImageJ. Select Plugins → Bio-Formats → Update Bio-Formats Plugins from the ImageJ menu, then select which release you would like to use. You will then need to restart ImageJ to complete the upgrade process.

5.1.4 Macros and plugins

Bio-Formats is fully scriptable in a macro, and callable from a plugin. To use in a macro, use the Macro Recorder to record a call to the Bio-Formats Importer with the desired options. You can also perform more targeted metadata queries using the Bio-Formats macro extensions.

Here are some example ImageJ macros and plugins that use Bio-Formats to get you started:

- basicMetadata.txt\(^{10}\) - A macro that uses the Bio-Formats macro extensions to print the chosen file’s basic dimensional parameters to the Log.
- planeTimings.txt\(^{11}\) - A macro that uses the Bio-Formats macro extensions to print the chosen file’s plane timings to the Log.
- recursiveTiffConvert.txt\(^{12}\) - A macro for recursively converting files to TIFF using Bio-Formats.
- bfOpenAsHyperstack.txt\(^{13}\) - This macro from Wayne Rasband opens a file as a hyperstack using only the Bio-Formats macro extensions (without calling the Bio-Formats Importer plugin).
- zvi2HyperStack.txt\(^{14}\) - This macro from Sebastien Huart reads in a ZVI file using Bio-Formats, synthesizes the LUT using emission wavelength metadata, and displays the result as a hyperstack.
- dvSplitTimePoints.txt\(^{15}\) - This macro from Sebastien Huart splits timepoints/channels on all DV files in a folder.
- batchTiffConvert.txt\(^{16}\) - This macro converts all files in a directory to TIFF using the Bio-Formats macro extensions.
- Read_Image\(^{17}\) - A simple plugin that demonstrates how to use Bio-Formats to read files into ImageJ.
- Mass_Importer\(^{18}\) - A simple plugin that demonstrates how to open all image files in a directory using Bio-Formats, grouping files with similar names to avoiding opening the same dataset more than once.

5.1.5 Usage tips

- “How do I make the options window go away?” is a common question. There are a few ways to do this:
  - To disable the options window only for files in a specific format, select Plugins → Bio-Formats → Bio-Formats Plugins Configuration, then pick the format from the list and make sure the “Windowless” option is checked.
  - To avoid the options window entirely, use the Plugins → Bio-Formats → Bio-Formats Windowless Importer menu item to import files.
  - Open files by calling the Bio-Formats importer plugin from a macro.

- A common cause of problems having multiple copies of bioformats_package.jar in your ImageJ plugins folder, or a copy of bioformats_package.jar and a copy of formats-gpl.jar. It is often difficult to determine for sure that this is the problem - the only error message that pretty much guarantees it is a NoSuchMethodException. If you downloaded the latest version and whatever error message or odd behavior you are seeing has been reported as fixed, it is worth removing all copies of bioformats_package.jar (and loci_tools.jar or any other Bio-Formats jars) and download a fresh version.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{19}\) or the previous versions\(^{20}\) page to find documentation for the version you are using.

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\(^{10}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/basicMetadata.txt

\(^{11}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/planetimings.txt

\(^{12}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/recursiveTiffConvert.txt

\(^{13}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/bfopenashyperstack.txt

\(^{14}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/zvi2hyperstack.txt

\(^{15}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/dvsplittimepoints.txt

\(^{16}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/macros/batchtiffconvert.txt

\(^{17}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/read_image.java

\(^{18}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/mass_importer.java

\(^{19}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{20}\)http://www.openmicroscopy.org/site/support/legacy/
5.2 Fiji overview

Fiji\textsuperscript{21} is an image processing package. It can be described as a distribution of \textit{ImageJ} together with Java, Java 3D and a lot of plugins organized into a coherent menu structure\textsuperscript{22}. Fiji compares to ImageJ as Ubuntu compares to Linux. Fiji works with Bio-Formats out of the box, because it comes bundled with the \textit{Bio-Formats ImageJ plugins}. For further details on Bio-Formats in Fiji, see the \textit{Bio-Formats Fiji wiki page}\textsuperscript{23}.

5.2.1 Upgrading

Upgrading Bio-Formats within Fiji is as simple as invoking the “Update Fiji” command from the Help menu. By default, Fiji even automatically checks for updates every time it is launched, so you will always be notified when new versions of Bio-Formats (or any other bundled plugin) are available.

Using Bio-Formats daily builds

Fiji currently shipping with the 5.1.x release versions of Bio-Formats. However, if you have encountered a bug which has been fixed by the Bio-Formats team but not yet released, you can use the Bio-Formats update site to access the daily build as described in the Fiji documentation\textsuperscript{24}.

\textbf{Warning:} These builds are not yet released and should be considered beta in quality. In particular, you should avoid exporting data using the Bio-Formats Exporter in case you write incompatible files which cannot be read by released versions of Bio-Formats or other OME-compliant tools. We recommend waiting for a fully tested release version of Bio-Formats if possible.

Manual upgrade

Manually updating your Fiji installation should not be necessary but if you need to do so, the steps are detailed below. Note that although we assume you will be upgrading to the latest release version, all previous versions of Bio-Formats are available from http://downloads.openmicroscopy.org/bio-formats/ so you can revert to an earlier version using this guide if you need to.

1. Fiji must first be fully updated
2. Close Fiji
3. Open the Fiji installation folder (typically named ‘Fiji.app’)
4. Remove bio-formats\_plugins.jar from the ‘plugins’ sub-folder
5. Remove all of the .jars from the ‘jars/bio-formats’ sub-folder:
   - jai\_imageio.jar
   - formats-gpl.jar
   - formats-common.jar
   - turbojpeg.jar
   - ome-xml.jar
   - formats-bsd.jar
   - ome-poi.jar
   - specification.jar
   - mdbtools-java.jar
   - metakit.jar

\textsuperscript{21}http://fiji.sc/
\textsuperscript{22}http://fiji.sc/Plugins\_Menu
\textsuperscript{23}http://fiji.sc/Bio-Formats
\textsuperscript{24}http://fiji.sc/Bio-Formats\#Daily\_builds
• download bio-formats_plugins.jar (from the latest release http://downloads.openmicroscopy.org/bio-formats/) and place it in the 'plugins' sub-folder

7. Download each of the following (from the latest release http://downloads.openmicroscopy.org/bio-formats/) and place them in the 'jars/bio-formats' sub-folder:
   • jai_imageio.jar
   • formats-gpl.jar
   • formats-common.jar
   • turbojpeg.jar
   • ome-xml.jar
   • formats-bsd.jar
   • ome-poi.jar
   • specification.jar
   • mdbtools-java.jar
   • metakit.jar
   • formats-api.jar

8. To Check Version of Bio-Formats Select Help > About Plugins > Bio-Formats Plugins... Check that the version of Bio-Formats matches the freshly downloaded version.


Note: It is vital to perform all of those steps in order; omitting even one will cause a problem. In particular, make sure that the old files are fully removed; it is not sufficient to add the new files to any sub-directory without removing the old files first.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[25] or the previous versions[26] page to find documentation for the version you are using.

5.3 Bio-Formats features in ImageJ and Fiji

When you select Bio-Formats under the Plugin menu, you will see the following features:

• The Bio-Formats Importer is a plugin for loading images into ImageJ or Fiji. It can read over 140 proprietary life sciences formats and standardizes their acquisition metadata into the common OME data model. It will also extract and set basic metadata values such as spatial calibration[27] if they are available in the file.

• The Bio-Formats Exporter is a plugin for exporting data to disk. It can save to the open OME-TIFF[28] file format, as well as several movie formats (e.g. QuickTime, AVI) and graphics formats (e.g. PNG, JPEG).

• The Bio-Formats Remote Importer is a plugin for importing data from a remote URL. It is likely to be less robust than working with files on disk, so we recommend downloading your data to disk and using the regular Bio-Formats Importer whenever possible.

• The Bio-Formats Windowless Importer is a version of the Bio-Formats Importer plugin that runs with the last used settings to avoid any additional dialogs beyond the file chooser. If you always use the same import settings, you may wish to use the windowless importer to save time (Learn more here).

• The Bio-Formats Macro Extensions plugin prints out the set of commands that can be used to create macro extensions. The commands and the instructions for using them are printed to the ImageJ log window.

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://fiji.sc/SpatialCalibration
http://www.openmicroscopy.org/site/support/ome-model/ome-tiff
• The **Stack Slicer** plugin is a helper plugin used by the Bio-Formats Importer. It can also be used to split a stack across channels, focal planes or time points.

• The **Bio-Formats Plugins Configuration** dialog is a useful way to configure the behavior of each file format. The Formats tab lists supported file formats and toggles each format on or off, which is useful if your file is detected as the wrong format. It also toggles whether each format bypasses the importer options dialog through the “Windowless” checkbox. You can also configure any specific option for each format. The Libraries tab provides a list of available helper libraries used by Bio-Formats.

• The **Bio-Formats Plugins Shortcut Window** opens a small window with a quick-launch button for each plugin. Dragging and dropping files onto the shortcut window opens them quickly using the **Bio-Formats Importer** plugin.

• The **Update Bio-Formats Plugins** command will check for updates to the plugins. We recommend you update to the newest Trunk build as soon as you think you may have discovered a bug.

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 5.4 Installing Bio-Formats in ImageJ

**Note:** Since FIJI is essentially ImageJ with plugins like Bio-Formats already built in, people who install Fiji can skip this section. If you are also using the OMERO plugin for ImageJ, you may find the set-up guide on the new user help site useful for getting you started with both plugins at the same time.

Once you download and install ImageJ, you can install the Bio-Formats plugin by going to the Bio-Formats download page.

For most end-users, we recommend downloading the **bioformats_package.jar** complete bundle.

However, you must decide which version of it you want to install. There are three primary versions of Bio-Formats: the latest builds, the daily builds, and the release versions. Which version you should download depends on your needs:

• The **latest build** is automatically updated every time any change is made to the source code on the main “dev_5_0” branch in Git, Bio-Formats’ software version control system. This build has the latest bug fixes, but it is not well tested and may have also introduced new bugs.

• The **daily build** is a compilation of that day’s changes that occurs daily around midnight. It is not any better tested than the latest build; but if you download it multiple times in a day, you can be sure you will get the same version each time.

• The **release** is thoroughly tested and has documentation to match. The list of supported formats on the Bio-Formats site corresponds to the most recent release. We do not add new formats to the list until a release containing support for that format has been completed. The release is less likely to contain bugs.

The release version is also more useful to programmers because they can link their software to a known, fixed version of Bio-Formats. Bio-Formats’ behavior will not be changing “out from under them” as they continue developing their own programs.

**Note:** There are currently two release version of Bio-Formats as we are maintaining support for the 4.4.x series while only actively developing the new 5.x series. Unless you are using Bio-Formats with the OMERO ImageJ plugin and an OMERO 4.4.x server, we recommend you use Bio-Formats 5. A new 4.4.x version will only be released if a major bug fix is required.

We often **recommend that most people simply use the latest build** for two reasons. First, it may contain bug-fixes or new features you want anyway; secondly, you will have to reproduce any bug you encounter in Bio-Formats against the latest build before submitting a bug report. Rather than using the release until you find a bug that requires you to upgrade and reproduce it, why not just use the latest build to begin with?

Once you decide which version you need, go to the Bio-Formats download page and save the appropriate **bioformats_package.jar** to the Plugins directory within ImageJ.

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29 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
30 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
33 [http://downloads.openmicroscopy.org/latest/bio-formats5.1/](http://downloads.openmicroscopy.org/latest/bio-formats5.1/)
34 [http://downloads.openmicroscopy.org/latest/bio-formats5.1/](http://downloads.openmicroscopy.org/latest/bio-formats5.1/)
Figure 5.1: Plugin Directory for ImageJ: Where in ImageJ’s file structure you should place the file once you downloaded it.

You may have to quit and restart ImageJ. Once you restart it, you will find Bio-Formats in the Bio-Formats option under the Plugins menu:

You are now ready to start using Bio-Formats.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

35 http://www.openmicroscopy.org/site/support/bio-formats5.0/
36 http://www.openmicroscopy.org/site/support/legacy/
5.5 Using Bio-Formats to load images into ImageJ

This section will explain how to use Bio-Formats to import files into ImageJ and how to use the settings on the Bio-Formats Import Options screen.

5.5.1 Opening files

There are three ways you can open a file using Bio-Formats:

1. Select the Bio-Formats Importer under the Bio-Formats plugins menu.
2. Drag and drop it onto the Bio-Formats Plugins Shortcut window.
3. Use the Open command in the File menu.

Unless you used the Bio-Formats Plugins Configuration dialog to open the file type windowlessly, you know you used Bio-Formats to open a file when you see a screen like this:

If you used the File > Open command and did not see the Bio-Formats Import Options screen, ImageJ/Fiji probably used another plugin instead of Bio-Formats to open the file. If this happens and you want to open a file using Bio-Formats, use one of the other two methods instead.

5.5.2 Opening files windowlessly

When you open a file with Bio-Formats, the Import Options Screen automatically recalls the settings you last used to open a file with that specific format (e.g. JPG, TIF, LSM, etc.). If you always choose the same options whenever you open files in a specific file format, you can save yourself time by bypassing the Bio-Formats Import Options screen. You can accomplish this two ways:

1. You can select the Bio-Formats Windowless Importer, located in the Bio-Formats menu under ImageJ’s Plugin menu. When you select this option, Bio-Formats will import the file using the same settings you used the last time you imported a file with the same format.

2. If you invariably use the same settings when you open files in a specific format, you can always bypass the Import Options Screen by changing the settings in the Bio-Formats Plugins Configuration option, which is also located in the Bio-Formats menu under ImageJ’s Plugin menu.

Once you select this option, select the file format you are interested in from the list on the left side of the screen. Check both the Enabled and Windowless boxes. Once you do this, whenever you open a file using the Bio-Formats Windowless Importer, the
Bio-Formats Importer, or the drag-and-drop method described in the previous section, the file will always open the same way using the last setting used.

Please note that if you want to change any of the import settings once you enable this windowless option, you will have to go back to the Bio-Formats Plugins Configuration screen, unselect the windowless option, open a file using the regular Bio-Formats Importer, select your settings, and re-select the windowless option.

5.5.3 Group files with similar names

One of the most important features of Bio-Formats is to combine multiple files from a dataset into one coherent, multi-dimensional image.

To demonstrate how to use the Group files with similar names feature, you can use the dub data set available under LOCI’s Sample Data page. You will notice that it is a large dataset: each of the 85 files shows the specimen at 33 optical sections along the z-plane at a specific time.

If you open just one file in ImageJ/Fiji using the Bio-Formats Importer, you will get an image incorporating three dimensions (x, y, z). However, if you select Group files with similar names from the Bio-Formats Import Options screen, you will be able to create a 4-D image (x, y, z, and t) incorporating the 85 files.

After clicking OK, you will see a screen like this:

This screen allows you to select which files within the 85-file cluster to use to create that 4-D image. Some information will be pre-populated in the fields. Unless you want to change the settings in that field, there is no need to change or delete it. If you click OK at this point, you will load all 85 files.

However, you can specify which files you want to open by adjusting the “axis information”, the file “name contains”, or the “pattern” sections. Even though there are three options, you only need to need to make changes to one of them. Since Bio-Format’s precedence for processing data is from top to bottom, only the uppermost section that you made changes to will be used. If you change multiple boxes, any information you enter into lower boxes will be ignored.

To return to the example involving the dub data set, suppose you want to open the first image and only every fifth image afterwards (i.e. dub01, dub06, dub11 . . . dub81). This would give you 17 images. There are different ways to accomplish this:

You can use the Axis Settings only when your files are numbered in sequential order and you want to open only a subset of the files that have similar names. Since the dub data set is numbered sequentially, you can use this feature.

**Axis 1 number of images** refers to the total number of images you want to open. Since you want to view 17 images, enter 17. **Axis 1 axis first image** specifies which image in the set you want to be the first. Since you want to start with dub01, enter 1 in that box. You also want to view only every fifth image, so enter 5 in the **Axis 1 axis increment** box.

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37http://loci.wisc.edu/sample-data/dub
38http://loci.wisc.edu/software/sample-data
The **File name contains** box should be used if all of the files that you want to open have common text. This is especially useful when the files are not numbered. For example, if you have “Image_Red.tif”, “Image_Green.tif”, and “Image_Blue.tif” you could enter “Image_” in the box to group them all.

To continue the example involving the dub data set, you cannot use the **file name contains** box to open every fifth image. However, if you only wanted to open dub10 thorough dub19, you could enter “dub1” in the **file name contains** box.

The **pattern** box can be used to do either of the options listed above or much more. This box can accept a single file name like “dub01.pic”. It can also contain a pattern that use “<” and “>” to specify what numbers or text the file names contain.

There are three basic forms to the “< >” blocks:

- **Text enumeration** - “Image_<Red,Green,Blue>.tif” is the pattern for Image_Red.tif, Image_Green.tif, Image_Blue.tif. (Note that the order you in which you enter the file names is the order in which they will be loaded.)
- **Number range** - “dub<1-85>.pic” is the pattern for “dub1.pic”, “dub2.pic”, “dub3.pic” . . . “dub85.pic”.
- **Number range with step** - “dub<1-85:5>.pic” is the pattern for “dub1.pic”, “dub6.pic”, “dub11.pic”, “dub16.pic” . . . “dub85.pic”.

It can also accept a **Java regular expression**\(^{39}\).

### 5.5.4 Autoscale

**Autoscale** helps increase the brightness and contrast of an image by adjusting the range of light intensity within an image to match the range of possible display values. Note that Autoscale does not change your data. It just changes how it is displayed.

Each pixel in an image has a numerical value ascribed to it to describe its intensity. The bit depth—the number of possible values—depends on the number of bits used in the image. Eight bits, for example, gives 256 values to express intensity where 0 is completely black, 255 is completely white, and 1 through 254 display increasingly lighter shades of grey.

ImageJ can collect the intensity information about each pixel from an image or stack and create a histogram (you can see it by selecting Histogram under the Analyze menu). Here is the histogram of a one particular image:

![Histogram of 15test.ome](image)

Notice that the histogram heavily skews right. Even though there are 256 possible values, only 0 thorough 125 are being used.

[^39]: http://download.oracle.com/javase/1.5.0/docs/api/java/util/regex/Pattern.html

**5.5. Using Bio-Formats to load images into ImageJ** 39
Autoscale adjusts the image so the smallest and largest number in that image or stack’s histogram become the darkest and brightest settings. For this image, pixels with the intensity of 125 will be displayed in pure white. The other values will be adjusted too to help show contrast between values that were too insignificant to see before.

Here is one image Bio-Formats imported with and without using Autoscale:

![Image with Autoscale](image1.png)

![Image without Autoscale](image2.png)

Autoscale readjusts the image based on the highest value in the entire data set. This means if the highest value in your dataset is close to maximum display value, Autoscale’s adjusting may be undetectable to the eye.

ImageJ/Fiji also has its own tools for adjusting the image, which are available by selecting Brightness/Contrast, which is under the Adjust option in the Image menu.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^40] or the previous versions[^41] page to find documentation for the version you are using.

[^40]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^41]: http://www.openmicroscopy.org/site/support/legacy/
5.6 Managing memory in ImageJ/Fiji using Bio-Formats

When dealing with a large stack of images, you may receive a warning like this:

![Image of memory warning]

This means the allotted memory is less than what Bio-Formats needs to load all the images. If you have a very large data set, you may have to:

- View your stack with Data Browser
- Crop the view area
- Open only a subset of images
- Use Virtual Stack
- Increase ImageJ/Fiji’s memory.

If your files contain JPEG or JPEG-2000 images, you may see this memory warning even if your file size is smaller than the amount of allocated memory. This is because compressed images like JPEG need to be decompressed into memory before being displayed and require more memory than their file size suggests. If you are having this issue, try utilizing one of the memory management tools below.

5.6.1 View your stack with Data Browser

Data Browser is another part of Bio-Formats that enables users to view large 3, 4, or 5-D datasets by caching a subset of all the images available. This enables users to view a stack that is bigger than the computer’s memory.

You can select Data Browser as an option for View stack with, the leftmost, uppermost option in the Bio-Formats Import Options screen.
Note that when you use Data Browser, other features like cropping and specifying range are not available. You can, however, adjust the size of the image cache in the Data Browser after you open the files. You can read more about it on LOCI’s Data Browser page.

5.6.2 Cropping the view area

Crop on Import is useful if your images are very large and you are only interested in one specific section of the stack you are importing. If you select this feature, you will see a screen where you can enter the height and width (in pixels) of the part of image you want to see. Note that these measurements are from the top left corner of the image.

5.6.3 Opening only a subset of images

The Specify Range for Each Series option is useful for viewing a portion of a data set where all the plane images are encapsulated into one file (e.g. the Zeiss LSM format). If your file has a large quantity of images, you can specify which channels, Z-planes, and times you want to load.

5.6.4 Use Virtual Stack

Virtual Stack conserves memory by not loading specific images until necessary. Note that unlike Data Browser, Virtual Stack does not contain a buffer and may produce choppy animations.

5.6.5 Increasing ImageJ/Fiji’s memory

Finally, you can also increase the amount of the computer memory devoted to ImageJ/Fiji by selecting Memory & Threads under the Edit menu.

---

Note: The referenced page 42 is not included in the text provided. For more information, visit http://loci.wisc.edu/software/data-browser
Generally, allocating more than 75% of the computer’s total memory will cause ImageJ/Fiji to become slow and unstable. **Please note** that unlike the other three features, ImageJ/Fiji itself provides this feature and not Bio-Formats. You can find out more about this feature by looking at ImageJ’s [documentation](http://rsbweb.nih.gov/ij/docs/menus/edit.html#options).

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43http://rsbweb.nih.gov/ij/docs/menus/edit.html#options
CHAPTER SIX

COMMAND LINE TOOLS

The Bio-Formats Command line tools (bftools.zip) provide a complete package for carrying out a variety of tasks:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^1\) or the previous versions\(^2\) page to find documentation for the version you are using.

6.1 Command line tools introduction

There are several scripts for using Bio-Formats on the command line.

6.1.1 Installation

Download bftools.zip\(^3\), unzip it into a new folder.

Note: As of Bio-Formats 5.0.0, this zip now contains the bundled jar and you no longer need to download loci_tools.jar or the new bioformats_package.jar separately.

The zip file contains both Unix scripts and Windows batch files.

6.1.2 Tools available

Currently available tools include:

- **showinf** Prints information about a given image file to the console, and displays the image itself in the Bio-Formats image viewer (see Displaying images and metadata for more information).
- **ijview** Displays the given image file in ImageJ using the Bio-Formats Importer plugin. See Display file in ImageJ for details.
- **bfconvert** Converts an image file from one format to another. Bio-Formats must support writing to the output file (see Converting a file to different format for more information).
- **formatlist** Displays a list of supported file formats in HTML, plaintext or XML. See List supported file formats for details.
- **xmlindent** A simple XML prettifier similar to **xmllint –format** but more robust in that it attempts to produce output regardless of syntax errors in the XML. See Format XML data for details.
- **xmlvalid** A command-line XML validation tool, useful for checking an OME-XML document for compliance with the OME-XML schema.
- **tiffcomment** Dumps the comment from the given TIFF file’s first IFD entry; useful for examining the OME-XML block in an OME-TIFF file (also see Editing XML in an OME-TIFF).
- **domainlist** Displays a list of imaging domains and the supported formats associated with each domain. See List formats by domain for more information.

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1. http://www.openmicroscopy.org/site/support/bio-formats5.0/
2. http://www.openmicroscopy.org/site/support/legacy/
**mkfake**  Creates a “fake” high-content screen with configurable dimensions. This is useful for testing how HCS metadata is handled, without requiring real image data from an acquired screen. See *Create a high-content screen for testing* for more information.

Some of these tools also work in combination, for example *Validating XML in an OME-TIFF* uses both `tiffcomment` and `xmlvalid`.

Running any of these commands without any arguments will print usage information to help you. When run with the `-version` argument, `showinf` and `bconvert` will display the version of Bio-Formats that is being used (version number, build date, and Git commit reference).

### 6.1.3 Using the tools directly from source

Firstly, obtain a copy of the sources and build them (see *Obtaining and building Bio-Formats*). You can configure the scripts to use your source tree instead of `bioformats_package.jar` in the same directory by following these steps:

1. Point your CLASSPATH to the checked-out directory and the JAR files in the `jar` folder.
   
   - E.g. on Windows with Java 1.6 or later, if you have checked out the source at `C:\code\bio-formats`, set your CLASSPATH environment variable to the value `C:\code\bio-formats\jar\*;C:\code\bio-formats`. You can access the environment variable configuration area by right-clicking on My Computer, choosing Properties, Advanced tab, Environment Variables button.

2. Compile the source with `ant compile`.

3. Set the `BF_DEVEL` environment variable to any value (the variable just needs to be defined).

### 6.1.4 Version checker

If you run bftools outside of the OMERO environment, you may encounter an issue with the automatic version checker causing a tool to crash when trying to connect to `upgrade.openmicroscopy.org.uk`. The error message will look something like this:

```plaintext
Failed to compare version numbers
java.io.IOException: Server returned HTTP response code: 400 for URL: http://upgrade.openmicroscopy.org.uk?version=4.4.8;os.name=Linux;os.version=2.6.32-358.6.2.el6.x86_64;os.arch=amd64;java.runtime.version=1.6.0_24-b24;java.vm.vendor=Sun Microsystems+Inc.;bioformats.caller=Bio-Formats+utilities
```

To avoid this issue, call the tool with the `-no-upgrade` parameter.

### 6.1.5 Profiling

For debugging errors or investigating performance issues, it can be useful to use profiling tools while running Bio-Formats. The command-line tools can invoke the HPROF\(^4\) agent library to profile Heap and CPU usage. Setting the `BF_PROFILE` environment variable allows to turn profiling on, e.g.:

```
BF_PROFILE=true showinf -nopix -no-upgrade myfile
```

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^5\) or the previous versions\(^6\) page to find documentation for the version you are using.

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\(^4\)http://docs.oracle.com/javase/7/docs/technotes/samples/hprof.html

\(^5\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^6\)http://www.openmicroscopy.org/site/support/legacy/
6.2 Displaying images and metadata

The `showinf` command line tool can be used to show the images and metadata contained in a file. If no options are specified, `showinf` displays a summary of available options.

To simply display images:

```
showinf /path/to/file
```

All of the images in the first ‘series’ (or 5 dimensional stack) will be opened and displayed in a simple image viewer. The number of series, image dimensions, and other basic metadata will be printed to the console.

- `series SERIES`
  Displays a different series, for example the second one:

```
showinf -series 1 /path/to/file
```

Note that series numbers begin with 0.

- `omexml`
  Displays the OME-XML metadata for a file on the console:

```
showinf -omexml /path/to/file
```

- `nopix`
  Image reading can be suppressed if only the metadata is needed:

```
showinf -nopix /path/to/file
```

- `range START END`
  A subset of images can also be opened instead of the entire stack, by specifying the start and end plane indices (inclusive):

```
showinf -range 0 0 /path/to/file
```

That opens only the first image in first series in the file.

- `crop X,Y,WIDTH,HEIGHT`
  For very large images, it may also be useful to open a small tile from the image instead of reading everything into memory. To open the upper-left-most 512x512 tile from the images:

```
showinf -crop 0,0,512,512 /path/to/file
```

The parameter to `crop` is of the format `x, y, width, height`. The `(x, y)` coordinate `(0, 0)` is the upper-left corner of the image; `x + width` must be less than or equal to the image width and `y + height` must be less than or equal to the image height.

- `no-upgrade`
  By default, `showinf` will check for a new version of Bio-Formats. This can take several seconds (especially on a slow internet connection); to save time, the update check can be disabled:

```
showinf -no-upgrade /path/to/file
```

- `no-valid`
  Similarly, if OME-XML is displayed then it will automatically be validated. On slow or missing internet connections, this can take some time, and so can be disabled:
showinf -novalid /path/to/file

-no-core
Most output can be suppressed:

showinf -nocore /path/to/file

-omexml-only
Displays the OME-XML alone:

showinf -omexml-only /path/to/file

This is particularly helpful when there are hundreds or thousands of series.

-debug
Enables debugging output if more information is needed:

showinf -debug /path/to/file

-fast
Displays an image as quickly as possible. This is achieved by converting the raw data into a 8 bit RGB image:

showinf -fast /path/to/file

Note: Due to the data conversion to a RGB image, using this option results in a loss of precision.

-autoscale
Adjusts the display range to the minimum and maximum pixel values:

showinf -autoscale /path/to/file

Note: This option automatically sets the -fast option and suffers from the same limitations.

-cache
Caches the reader under the same directory as the input file after initialization:

showinf -cache /path/to/file

-cache-dir DIR
Specifies the base directory under which the reader should be cached:

showinf -cache-dir /tmp/cachedir /path/to/file

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
6.3 Converting a file to different format

The `bfconvert` command line tool can be used to convert files between supported formats. `bfconvert` with no options displays a summary of available options.

To convert a file to single output file (e.g. TIFF):

```
bfconvert /path/to/input output.tiff
```

The output file format is determined by the extension of the output file, e.g. .tiff for TIFF files, .ome.tiff for OME-TIFF, .png for PNG.

- **-series** SERIES
  All images in the input file are converted by default. To convert only one series:

  ```
  bfconvert -series 0 /path/to/input output-first-series.tiff
  ```

- **-timepoint** TIMEPOINT
  To convert only one timepoint:

  ```
  bfconvert -timepoint 0 /path/to/input output-first-timepoint.tiff
  ```

- **-channel** CHANNEL
  To convert only one channel:

  ```
  bfconvert -channel 0 /path/to/input output-first-channel.tiff
  ```

- **-z** Z
  To convert only one Z section:

  ```
  bfconvert -z 0 /path/to/input output-first-z.tiff
  ```

- **-range** START END
  To convert images between certain indices (inclusive):

  ```
  bfconvert -range 0 2 /path/to/input output-first-3-images.tiff
  ```

- **-tilex** TILEX, **-tiley** TILEY
  All images larger than 4096x4096 will be saved as a set of tiles if the output format supports doing so. The default tile size is determined by the input format, and can be overridden like this:

  ```
  bfconvert -tilex 512 -tiley 512 /path/to/input output-512x512-tiles.tiff
  ```

  `-tilex` is the width in pixels of each tile; `-tiley` is the height in pixels of each tile. The last row and column of tiles may be slightly smaller if the image width and height are not multiples of the specified tile width and height. Note that specifying `-tilex` and `-tiley` will cause tiles to be written even if the image is smaller than 4096x4096.

  Also note that the specified tile size will affect performance. If large amounts of data are being processed, it is a good idea to try converting a single tile with a few different tile sizes using the `-crop` option. This gives an idea of what the most performant size will be.

Images can also be written to multiple files by specifying a pattern string in the output file. For example, to write one series, timepoint, channel, and Z section per file:
bfconvert /path/to/input output_series_%s_Z%z_C%c_T%t.tiff

%s is the series index, %z is the Z section index, %c is the channel index, and %t is the timepoint index (all indices begin at 0). For large images in particular, it can also be useful to write each tile to a separate file:

bfconvert -tilex 512 -tiley 512 /path/to/input output_tile_%x_%y_%m.jpg

%x is the row index of the tile, %y is the column index of the tile, and %m is the overall tile index. As above, all indices begin at 0. Note that if %x or %y is included in the file name pattern, then the other must be included too. The only exception is if %m was also included in the pattern.

**-compression**

By default, all images will be written uncompressed. Supported compression modes vary based upon the output format, but when multiple modes are available the compression can be changed using the `-compression` option. For example, to use LZW compression in a TIFF file:

bfconvert -compression LZW /path/to/input output-lzw.tiff

**-overwrite**

If the specified output file already exists, `bfconvert` will prompt to overwrite the file. When running `bfconvert` non-interactively, it may be useful to always allow `bfconvert` to overwrite the output file:

bfconvert -overwrite /path/to/input /path/to/output

**-nooverwrite**

To always exit without overwriting:

bfconvert -nooverwrite /path/to/input /path/to/output

**-bigtiff**

This option forces the writing of a BigTiff file:

bfconvert -bigtiff /path/to/input output.ome.tiff

New in version 5.1.2: The `-bigtiff` option is not necessary if a BigTiff extension is used for the output file, e.g.:

bfconvert /path/to/input output.ome.btf

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^9\) or the previous versions\(^10\) page to find documentation for the version you are using.

## 6.4 Validating XML in an OME-TIFF

The XML stored in an OME-TIFF file can be validated using the command line tools.

Both the `tiffcomment` and `xmlvalid` commands are used; `tiffcomment` extracts the XML from the file and `xmlvalid` validates the XML and prints any errors to the console.

For example:

\(^9\)\url{http://www.openmicroscopy.org/site/support/bio-formats5.0/}

\(^10\)\url{http://www.openmicroscopy.org/site/support/legacy/}
will perform the extraction and validation all at once.

Typical successful output is:

```
[~/Work/bftools]$ ./xmlvalid sample.ome
Parsing schema path
http://www.openmicroscopy.org/Schemas/OME/2010-06/ome.xsd
Validating sample.ome
No validation errors found.
[~/Work/bftools]$
```

If any errors are found they are reported. When correcting errors it is usually best to work from the top of the file as errors higher up can cause extra errors further down. In this example the output shows 3 errors but there are only 2 mistakes in the file:

```
[~/Work/bftools]$ ./xmlvalid broken.ome
Parsing schema path
http://www.openmicroscopy.org/Schemas/OME/2010-06/ome.xsd
Validating broken.ome
cvc-complex-type.4: Attribute ‘SizeY’ must appear on element ‘Pixels’.
cvc-enumeration-valid: Value ‘Non Zero’ is not facet-valid with respect
to enumeration ‘[EvenOdd, NonZero]’. It must be a value from the enumeration.
cvc-attribute.3: The value ‘Non Zero’ of attribute ‘FillRule’ on element
   ‘ROI:Shape’ is not valid with respect to its type, ‘null’.
Error validating document: 3 errors found
[~/Work/bftools]$
```

If the XML is found to have validation errors, the `tiffcomment` command can be used to overwrite the XML in the OME-TIFF file with corrected XML. The XML can be displayed in an editor window:

```
tiffcomment -edit /path/to/file.ome.tif
```

or the new XML can be read from a file:

```
tiffcomment -set new-comment.xml /path/to/file.ome.tif
```

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^1\) or the previous versions\(^2\) page to find documentation for the version you are using.

## 6.5 Editing XML in an OME-TIFF

To edit the XML in an OME-TIFF file you can use `tiffcomment`, one of the Bio-Formats tools.

To use the built in editor run:

```
tiffcomment -edit sample.ome.tif
```

To extract or view the XML run:

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^2\)http://www.openmicroscopy.org/site/support/legacy/
To inject replacement XML into a file run:

tiffcomment -set ‘newmetadata.xml’ sample.ome.tif

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{13}\) or the previous versions\(^{14}\) page to find documentation for the version you are using.

### 6.6 List formats by domain

Each supported file format has one or more imaging domains associated with it. To print the list of formats associated with each imaging domain:

```
domainlist
```

The command does not accept any arguments. The known image domains are defined by:

- **ASTRONOMY_DOMAIN**\(^{15}\)
- **EM_DOMAIN**\(^{16}\)
- **FLIM_DOMAIN**\(^{17}\)
- **GEL_DOMAIN**\(^{18}\)
- **GRAPHICS_DOMAIN**\(^{19}\)
- **HCS_DOMAIN**\(^{20}\)
- **HISTOLOGY_DOMAIN**\(^{21}\)
- **LM_DOMAIN**\(^{22}\)
- **MEDICAL_DOMAIN**\(^{23}\)
- **SEM_DOMAIN**\(^{24}\)
- **SPM_DOMAIN**\(^{25}\)
- **UNKNOWN_DOMAIN**\(^{26}\)

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{27}\) or the previous versions\(^{28}\) page to find documentation for the version you are using.

\(^{13}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{14}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{15}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#ASTRONOMY_DOMAIN
\(^{16}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#EM_DOMAIN
\(^{17}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#FLIM_DOMAIN
\(^{18}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#GEL_DOMAIN
\(^{19}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#GRAPHICS_DOMAIN
\(^{20}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#HCS_DOMAIN
\(^{21}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#HISTOLOGY_DOMAIN
\(^{22}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#LM_DOMAIN
\(^{23}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#MEDICAL_DOMAIN
\(^{24}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#SEM_DOMAIN
\(^{25}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#SPM_DOMAIN
\(^{26}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatTools.html#UNKNOWN_DOMAIN
\(^{27}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{28}\)http://www.openmicroscopy.org/site/support/legacy/
6.7 List supported file formats

A detailed list of supported formats can be displayed using the `formatlist` command.

The default behavior is to print a plain-text list of formats:

```
formatlist
```

- **-txt**
  Prints the list of formats as plain-text:
  ```
  formatlist -txt
  ```

- **-html**
  Prints the list of formats as HTML:
  ```
  formatlist -html
  ```

- **-xml**
  Prints the list of formats as XML:
  ```
  formatlist -xml
  ```

- **-help**
  Displays the usage information:
  ```
  formatlist -help
  ```

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{29}\) or the previous versions\(^{30}\) page to find documentation for the version you are using.

6.8 Display file in ImageJ

Files can be displayed from the command line in ImageJ. The Bio-Formats importer plugin for ImageJ is used to open the file.

The command takes a single argument:

```
ijview /file/to/open
```

If the input file is not specified, ImageJ will show a file chooser window.

The Bio-Formats import options window will then appear, after which the image(s) will be displayed.

If the `BF_DEVEL` environment variable is set, the ImageJ jar `<jars/ij.jar>` must be included in the classpath.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{31}\) or the previous versions\(^{32}\) page to find documentation for the version you are using.

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[^29]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^30]: http://www.openmicroscopy.org/site/support/legacy/
[^31]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^32]: http://www.openmicroscopy.org/site/support/legacy/
6.9 Format XML data

The **xmlindent** command formats and adds indenting to XML so that it is easier to read. Indenting is currently set to 3 spaces. If an XML file name is not specified, the XML to indent will be read from standard output. Otherwise, one or more file names can be specified:

```
xmlindent /path/to/xml
xmlindent /path/to/first-xml /path/to/second-xml
```

The formatted XML from each file will be printed in the order in which the files were specified.

By default, extra whitespace may be added to CDATA elements. To preserve the contents of CDATA elements:

```
xmlindent -valid /path/to/xml
```

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous versions page to find documentation for the version you are using.

6.10 Create a high-content screen for testing

The **mkfake** command creates a high-content screen for testing. The image data will be meaningless, but it allows testing of screen, plate, and well metadata without having to find appropriately-sized screens from real acquisitions.

If no arguments are specified, **mkfake** prints usage information.

To create a single screen with default plate dimensions:

```
mkfake default-screen.fake
```

This will create a directory that represents one screen with a single plate containing one well, one field, and one acquisition of the plate (see [PlateAcquisition](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID)).

---

**-plates** PLATES
To change the number of plates in the screen:

```
mkfake -plates 3 three-plates.fake
```

**-runs** RUNS
To change the number of acquisitions for each plate:

```
mkfake -runs 4 four-plate-acquisitions.fake
```

**-rows** ROWS
To change the number of rows of wells in each plate:

```
mkfake -rows 8 eight-row-plate.fake
```

**-columns** COLUMNS
To change the number of columns of wells in each plate:

---

33http://www.openmicroscopy.org/site/support/bio-formats5.0/
34http://www.openmicroscopy.org/site/support/legacy/
35http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID
mkfake -columns 12 twelve-column-plate.fake

**-fields FIELDS**

To change the number of fields per well:

mkfake -fields 2 two-field-plate.fake

It is often most useful to use the arguments together to create a realistic screen, for example:

mkfake -rows 16 -columns 24 -plates 2 -fields 3 two-384-well-plates.fake

**-debug DEBUG**

As with other command line tools, debugging output can be enabled if necessary:

mkfake -debug debug-screen.fake
OMERO 5 uses Bio-Formats to read original files from over 140 file formats. Please refer to the OMERO documentation\(^1\) for further information.

\(^1\)http://www.openmicroscopy.org/site/support/omero5.1/
IMAGE SERVER APPLICATIONS

8.1 BISQUE

The BISQUE\(^3\) (Bio-Image Semantic Query User Environment) Database, developed at the Center for Bio-Image Informatics at UCSB, was developed for the exchange and exploration of biological images. The Bisque system supports several areas useful for imaging researchers from image capture to image analysis and querying. The bisque system is centered around a database of images and metadata. Search and comparison of datasets by image data and content is supported. Novel semantic analyses are integrated into the system allowing high level semantic queries and comparison of image content.

Bisque integrates with Bio-Formats by calling the `showinf` command line tool.

8.2 OME Server

OME\(^6\) is a set of software that interacts with a database to manage images, image metadata, image analysis and analysis results. The OME system is capable of leveraging Bio-Formats to import files.

Please note - the OME server is no longer maintained and has now been superseded by the OMERO server\(^7\). Support for the OME server has been entirely removed in the 5.0.0 version of Bio-Formats; the following instructions can still be used with the 4.4.x versions.

8.2.1 Installation

For OME Perl v2.6.1\(^8\) and later, the command line installer automatically downloads the latest `loci_tools.jar` and places it in the proper location. This location is configurable, but is `/OME/java/loci_tools.jar` by default.

For a list of what was recognized for a particular import into the OME server, go to the Image details page in the web interface, and click the “Image import” link in the upper right hand box.

Bio-Formats is capable of parsing original metadata for supported formats, and standardizes what it can into the OME data model. For the rest, it expresses the metadata in OME terms as key/value pairs using an OriginalMetadata custom semantic type. However, this latter method of metadata representation is of limited utility, as it is not a full conversion into the OME data model.

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^2\)http://www.openmicroscopy.org/site/support/legacy/
\(^3\)http://www.bioimage.ucsb.edu/bisque
\(^4\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^5\)http://www.openmicroscopy.org/site/support/legacy/
\(^6\)http://openmicroscopy.org/site/support/ome-server
\(^7\)http://www.openmicroscopy.org/site/support/omero5.1/
\(^8\)http://downloads.openmicroscopy.org/ome/2.6.1/
Bio-Formats is enabled in OME v2.6.1 for all formats except:

- OME-TIFF
- Metamorph HTD
- Deltavision DV
- Metamorph STK
- Bio-Rad PIC
- Zeiss LSM
- TIFF
- BMP
- DICOM
- OME-XML

The above formats have their own Perl importers that override Bio-Formats, meaning that Bio-Formats is not used to process them by default. However, you can override this behavior (except for Metamorph HTD, which Bio-Formats does not support) by editing an OME database configuration value:

```sql
% psql ome
Toseethecurrentfileformatreaderlist:
```

```sql
ome=# select value from configuration where name='import_formats';
```

```sql
to remove extraneous readers from the list:
```

```sql
ome=# update configuration set value='[
  OME::ImportEngine::OMETIFFreader,
  OME::ImportEngine::MetamorphHTDFormat',
  OME::ImportEngine::DVreader',
  OME::ImportEngine::STKreader',
  OME::ImportEngine::BioradReader',
  OME::ImportEngine::LSMreader',
  OME::ImportEngine::TIFFreader',
  OME::ImportEngine::BMPreader',
  OME::ImportEngine::DICOMreader',
  OME::ImportEngine::XMLreader',
  OME::ImportEngine::BioFormats'
]'
(1 row)
```

To reset things back to how they were:

```sql
ome=# update configuration set value='[
  OME::ImportEngine::OMETIFFreader',
  OME::ImportEngine::MetamorphHTDFormat',
  OME::ImportEngine::DVreader',
  OME::ImportEngine::STKreader',
  OME::ImportEngine::BioradReader',
  OME::ImportEngine::LSMreader',
  OME::ImportEngine::TIFFreader',
  OME::ImportEngine::BMPreader',
  OME::ImportEngine::DICOMreader',
  OME::ImportEngine::XMLreader',
  OME::ImportEngine::BioFormats'
]'
(1 row)
```
Lastly, please note that Li-Cor L2D files cannot be imported into an OME server (see this Trac ticket\(^9\) for details). Since the OME perl server has been discontinued, we have no plans to fix this limitation.

### 8.2.2 Upgrading

You can upgrade your OME server installation to take advantage of a new Bio-Formats release\(^10\) by overwriting the old `loci_tools.jar` with the new one.

### 8.2.3 Source Code

The source code for the Bio-Formats integration with OME server spans three languages, using piped system calls in both directions to communicate, with imported pixels written to OMEIS pixels files. The relevant source files are:

- OmeISImporter.java\(^11\) – `omebf` Java command line tool
- BioFormats.pm\(^12\) – Perl module for OME Bio-Formats importer
- omeis.c\(^13\) – OMEIS C functions for Bio-Formats (search for “bioformats” case insensitively to find relevant sections)

---

\(^9\) [http://dev.loci.wisc.edu/trac/software/ticket/266](http://dev.loci.wisc.edu/trac/software/ticket/266)

\(^10\) [http://downloads.openmicroscopy.org/latest/bio-formats5.1/](http://downloads.openmicroscopy.org/latest/bio-formats5.1/)


\(^12\) [http://downloads.openmicroscopy.org/ome/code/BioFormats.pm](http://downloads.openmicroscopy.org/ome/code/BioFormats.pm)

\(^13\) [http://downloads.openmicroscopy.org/ome/code/omeis.c](http://downloads.openmicroscopy.org/ome/code/omeis.c)
CHAPTER NINE

LIBRARIES AND SCRIPTING APPLICATIONS

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^1\) or the previous versions\(^2\) page to find documentation for the version you are using.

9.1 FARSIGHT

FARSIGHT\(^3\) is a collection of modules for image analysis created by LOCI’s collaborators at the University of Houston\(^4\). These open source modules are built on the ITK library and thus can take advantage of ITK’s support for Bio-Formats to process otherwise unsupported image formats.

The principal FARSIGHT module that benefits from Bio-Formats is the Nucleus Editor\(^5\), though in principle any FARSIGHT-based code that reads image formats via the standard ITK mechanism will be able to leverage Bio-Formats.

See also:

FARSIGHT Downloads page\(^6\)
FARSIGHT HowToBuild tutorial\(^7\)

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^8\) or the previous versions\(^9\) page to find documentation for the version you are using.

9.2 i3dcare

i3dcare\(^10\), also known as the CBIA 3D image representation library, is a 3D image processing library developed at the Centre for Biomedical Image Analysis\(^11\). Together with i3dalgo\(^12\) and i4dcore\(^13\), i3dcare forms a continuously developed templated cross-platform C++ suite of libraries for multidimensional image processing and analysis.

i3dcare is capable of reading images with Bio-Formats using Java for C++\(^14\) (java4cpp).

See also:

Download i3dcare\(^15\)

\(^{1}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{2}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{3}\)http://www.farsight-toolkit.org/
\(^{4}\)http://www.uh.edu/
\(^{5}\)http://www.farsight-toolkit.org/wiki/NucleusEditor
\(^{6}\)http://www.farsight-toolkit.org/wiki/Special:FarsightDownloads
\(^{7}\)http://www.farsight-toolkit.org/wiki/FARSIGHT_HowToBuild
\(^{8}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{9}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{10}\)http://cbia.fi.muni.cz/user_dirs/i3dlib_doc/i3dcare/index.html
\(^{11}\)http://cbia.fi.muni.cz/software-development.html
\(^{12}\)http://cbia.fi.muni.cz/user_dirs/i3dlib_doc/i3dalgo/index.html
\(^{13}\)http://cbia.fi.muni.cz/user_dirs/of_doc/libi4d.html
\(^{14}\)http://java4cpp.kapott.org/
\(^{15}\)http://cbia.fi.muni.cz/user_dirs/i3dlib_doc/i3dcare/index.html#download
9.3 ImgLib

**ImgLib**\(^{19}\) is a multidimensional image processing library. It provides a general mechanism for writing image analysis algorithms, without writing case logic for **bit depth**\(^{20}\), or worrying about the source of the pixel data (arrays in memory, files on disk, etc.).

The **SCIFIO**\(^{21}\) project provides an **ImgOpener**\(^{22}\) utility class for reading data into ImgLib2 data structures using Bio-Formats.

---

9.4 ITK

The **Insight Toolkit**\(^{25}\) (ITK) is an open-source, cross-platform system that provides developers with an extensive suite of software tools for image analysis. Developed through extreme programming methodologies, ITK employs leading-edge algorithms for registering and segmenting multidimensional data.

ITK provides an ImageIO plug-in structure that works via discovery through a dependency injection scheme. This allows a program built on ITK to load plug-ins for reading and writing different image types without actually linking to the ImageIO libraries required for those types. Such encapsulation automatically grants two major boons: firstly, programs can be easily extended just by virtue of using ITK (developers do not have to specifically accommodate or anticipate what plug-ins may be used). Secondly, the architecture provides a distribution method for open source software, like Bio-Formats, which have licenses that might otherwise exclude them from being used with other software suites.

The **SCIFIO ImageIO**\(^{26}\) plugin provides an ITK imageIO base that uses Bio-Formats to read and write supported life sciences file formats. This plugin allows any program built on ITK to read any of the image types supported by Bio-Formats.

---

9.5 Qu for MATLAB

**Qu for MATLAB**\(^{29}\) is a MATLAB toolbox for the visualization and analysis of N-dimensional datasets targeted to the field of biomedical imaging, developed by Aaron Ponti.

- Uses Bio-Formats to read files
- Open source software available under the Mozilla Public License

\(^{16}\)http://cbia.fi.muni.cz/software-development.html
\(^{17}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{18}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{19}\)http://imglib2.net/
\(^{20}\)http://en.wikipedia.org/wiki/Color_depth
\(^{21}\)http://scif.io/
\(^{22}\)https://github.com/scifio/scifio/blob/master/src/main/java/io/scif/img/ImgOpener.java
\(^{23}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{24}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{25}\)http://itk.org/
\(^{26}\)https://github.com/scifio/scifio-imageio
\(^{27}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{28}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{29}\)http://www.scs2.net/home/index.php?option=com_content&view=article&id=46%3Aqu-for-matlab&catid=34%3Aqu&Itemid=55
Subimager is designed to be run as a subprocess of CellProfiler to provide CellProfiler with the capability to read and write a variety of image formats. It can be used as a stand-alone image server. It was developed by the Broad Institute to facilitate integration with their CellProfiler image analysis application.

---

**9.6 Subimager**

Subimager, the SUBprocess IMAGE servER, is an HTTP server that uses Bio-Formats as a back-end to serve .TIF images. Subimager is designed to be run as a subprocess of CellProfiler to provide CellProfiler with the capability to read and write a variety of image formats. It can be used as a stand-alone image server. It was developed by the Broad Institute to facilitate integration with their CellProfiler image analysis application.

---

30 http://www.scs2.net/home/index.php?option=com_content&view=article&id=46%3AQu-for-MATLAB&catid=34%3AQu&Itemid=55&limitstart=3
31 http://www.openmicroscopy.org/site/support/bio-formats5.0/
32 http://www.openmicroscopy.org/site/support/legacy/
33 https://github.com/CellProfiler/subimager
34 http://www.broadinstitute.org/
35 http://www.cellprofiler.org/
10.1 IDL

IDL\textsuperscript{3} (Interactive Data Language) is a popular data visualization and analysis platform used for interactive processing of large amounts of data including images.

IDL possesses the ability to interact with Java applications via its IDL-Java bridge. Karsten Rodenacker has written a script that uses Bio-Formats to read in image files to IDL.

10.1.1 Installation

Download the \texttt{ij\_read\_bio\_formats.pro}\textsuperscript{4} script from Karsten Rodenacker’s IDL goodies (?)\textsuperscript{5} web site. See the comments at the top of the script for installation instructions and caveats.

10.1.2 Upgrading

To use a newer version of Bio-Formats, overwrite the requisite JAR files with the newer version\textsuperscript{6} and restart IDL.

10.2 KNIME

KNIME\textsuperscript{9} (Konstanz Information Miner) is a user-friendly and comprehensive open-source data integration, processing, analysis, and exploration platform. KNIME supports image import using Bio-Formats using the KNIME Image Processing\textsuperscript{10} (a.k.a. KNIP) plugin.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{7} or the previous versions\textsuperscript{8} page to find documentation for the version you are using.

\begin{itemize}
  \item \textsuperscript{1}http://www.openmicroscopy.org/site/support/bio-formats5.0/
  \item \textsuperscript{2}http://www.openmicroscopy.org/site/support/legacy/
  \item \textsuperscript{3}http://www.exelisvis.com/ProductsServices/IDL.aspx
  \item \textsuperscript{4}http://karo03.bplaced.net/karo/IDL/_pro/ij\_read\_bio\_formats.pro
  \item \textsuperscript{5}http://karo03.bplaced.net/karo/ro\_embedded.php?file=IDL/index.html
  \item \textsuperscript{6}http://downloads.openmicroscopy.org/latest/bio-formats5.1/
  \item \textsuperscript{7}http://www.openmicroscopy.org/site/support/bio-formats5.0/
  \item \textsuperscript{8}http://www.openmicroscopy.org/site/support/legacy/
  \item \textsuperscript{9}http://www.knime.org/
  \item \textsuperscript{10}http://tech.knime.org/community/image-processing
  \item \textsuperscript{11}http://www.openmicroscopy.org/site/support/bio-formats5.0/
  \item \textsuperscript{12}http://www.openmicroscopy.org/site/support/legacy/
\end{itemize}
10.3 MATLAB

MATLAB\textsuperscript{13} is a high-level language and interactive environment that facilitates rapid development of algorithms for performing computationally intensive tasks.

Calling Bio-Formats from MATLAB is fairly straightforward, since MATLAB has built-in interoperability with Java. We have created a set of scripts\textsuperscript{14} for reading image files. Note the minimum supported MATLAB version is R2007b (7.5).

10.3.1 Installation

Download the MATLAB toolbox from the Bio-Formats downloads page\textsuperscript{15}. Unzip \texttt{bfmatlab.zip} and add the unzipped \texttt{bf-matlab} folder to your MATLAB path.

Note: As of Bio-Formats 5.0.0, this zip now contains the bundled jar and you no longer need to download \texttt{loci_tools.jar} or the new \texttt{bioformats_package.jar} separately.

10.3.2 Usage

Please see \textit{Using Bio-Formats in MATLAB} for usage instructions. If you intend to extend the existing .m files, please also see the developer page for more information on how to use Bio-Formats in general.

10.3.3 Performance

In our tests (MATLAB R14 vs. java 1.6.0_20), the script executes at approximately half the speed of our \texttt{showinf} command line tool, due to overhead from copying arrays.

10.3.4 Upgrading

To use a newer version of Bio-Formats, overwrite the content of the \texttt{bfmatlab} folder with the newer version\textsuperscript{16} of the toolbox and restart MATLAB.

10.3.5 Alternative scripts

Several other groups have developed their own MATLAB scripts that use Bio-Formats, including the following:

- \url{https://github.com/prakatmac/bf-tools/}
- \url{imread for multiple life science image file formats}\textsuperscript{17}

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{18} or the previous versions\textsuperscript{19} page to find documentation for the version you are using.

\textsuperscript{13}http://www.mathworks.com/products/matlab/
\textsuperscript{14}https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/formats-gpl/matlab
\textsuperscript{15}http://downloads.openmicroscopy.org/latest/bio-formats5.1/
\textsuperscript{16}http://downloads.openmicroscopy.org/latest/bio-formats5.1/
\textsuperscript{17}http://www.mathworks.com/matlabcentral/fileexchange/32920-imread-for-multiple-life-science-image-file-formats
\textsuperscript{18}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{19}http://www.openmicroscopy.org/site/support/legacy/
10.4 VisAD

The VisAD\textsuperscript{20} visualization toolkit is a Java component library for interactive and collaborative visualization and analysis of numerical data. VisAD uses Bio-Formats to read many image formats, notably TIFF.

10.4.1 Installation

The visad.jar file has Bio-Formats bundled inside, so no further installation is necessary.

10.4.2 Upgrading

It should be possible to use a newer version of Bio-Formats by putting the latest bioformats\_package.jar\textsuperscript{21} or formats-gpl.jar\textsuperscript{22} before visad.jar in the class path. Alternately, you can create a “VisAD Lite” using the make\_lite command from VisAD source, and use the resultant visad-lite.jar, which is a stripped down version of VisAD without sample applications or Bio-Formats bundled in.

\textsuperscript{20}http://www.ssec.wisc.edu/~billh/visad.html
\textsuperscript{21}http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/bioformats\_package.jar
\textsuperscript{22}http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/formats-gpl.jar
11.1 Bitplane Imaris

Imaris is Bitplane’s core scientific software module that delivers all the necessary functionality for data visualization, analysis, segmentation and interpretation of 3D and 4D microscopy datasets. Combining speed, precision and ease-of-use, Imaris provides a complete set of features for working with three- and four-dimensional multi-channel images of any size, from a few megabytes to multiple gigabytes in size.

As of version 7.2, Imaris integrates with Fiji overview, which includes Bio-Formats. See this page for a detailed list of Imaris’ features.

11.2 CellProfiler

CellProfiler—developed by the Broad Institute Imaging Platform—is free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically. CellProfiler uses Bio-Formats to read images from disk, as well as write movies.

11.2.1 Installation

The CellProfiler distribution comes with Bio-Formats included, so no further installation is necessary.

11.2.2 Upgrading

It should be possible to use a newer version of Bio-Formats by replacing the bundled loci_tools.jar with a newer version.

- For example, on Mac OS X, Ctrl+click the CellProfiler icon, choose Show Package Contents, and replace the following files:
  - Contents/Resources/bioformats/loci_tools.jar
11.3 Comstat2

Comstat2 is a Java-based computer program for the analysis and treatment of biofilm images in 3D. It is the Master’s project of Martin Vorregaard. Comstat2 uses the Bio-Formats Importer plugin for ImageJ to read files in TIFF and Leica LIF formats.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

11.4 Endrov

Endrov is a multi-purpose image analysis program developed by the Thomas Burglin group at Karolinska Institute, Department of Biosciences and Nutrition.

11.4.1 Installation

The EV distribution comes bundled with the core Bio-Formats library (bio-formats.jar), so no further installation is necessary.

11.4.2 Upgrading

It should be possible to use a newer version of Bio-Formats by downloading the latest formats-gpl.jar and putting it into the libs folder of the EV distribution, overwriting the old file.

You could also include some optional libraries, to add support for additional formats, if desired.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

References:

11.http://www.openmicroscopy.org/site/support/bio-formats5.0/
15.http://www.openmicroscopy.org/site/support/legacy/
17.http://www.biosci.ki.se/groups/tbu
18.http://www.ki.se/
20.http://www.openmicroscopy.org/site/support/bio-formats5.0/
11.5 FocalPoint

FocalPoint is an image browser, similar to Windows Explorer or other file manager application, specifically designed to work with more complex image types. FocalPoint uses Bio-Formats to generate thumbnails for some formats.

11.5.1 Installation

FocalPoint is bundled with Bio-Formats, so no further installation is necessary.

11.5.2 Upgrading

It should be possible to use a newer version of Bio-Formats by overwriting the old loci_tools.jar within the FocalPoint distribution. For Mac OS X, you will have to control click the FocalPoint program icon, choose “Show Package Contents” and navigate into Contents/Resources/Java to find the loci_tools.jar file.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

11.6 Graphic Converter

Graphic Converter is a Mac OS application for opening, editing, and organizing photos. Versions 6.4.1 and later use Bio-Formats to open all file formats supported by Bio-Formats.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

11.7 Icy

Icy is an open-source image analysis and visualization software package that combines a user-friendly graphical interface with the ability to write scripts and plugins that can be uploaded to a centralized website. It uses Bio-Formats internally to read images and acquisition metadata, so no further installation is necessary.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

11.8 imago

Mayachitra imago is an advanced desktop image management package that enables scientists to easily store, manage, search, and analyze 5D biological images and their analysis results. imago integrates flexible annotation and metadata management with advanced image analysis tools.
imago uses Bio-Formats to read files in some formats, including Bio-Rad PIC, Image-Pro Workspace, Metamorph TIFF, Leica LCS LEI, Olympus Fluoview FV1000, Nikon NIS-Elements ND2, and Zeiss LSM.

A free 30-day trial version of imago is available here\(^\text{35}\).

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^\text{36}\) or the previous versions\(^\text{37}\) page to find documentation for the version you are using.

## 11.9 Iqm

Iqm\(^\text{38}\) is an image processing application written in Java. It is mainly constructed around the Java JAI library and furthermore it incorporates the functionality of the popular ImageJ image processing software.

Because iqm integrates with ImageJ, it can take advantage of the **Bio-Formats ImageJ plugin** to read image data.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^\text{39}\) or the previous versions\(^\text{40}\) page to find documentation for the version you are using.

## 11.10 Macnification

Macnification\(^\text{41}\) is a Mac OS X application for organizing, editing, analyzing and annotating microscopic images, designed for ease of use. It is being developed by Orbicule\(^\text{42}\).

Macnification uses Bio-Formats to read files in some formats, including Gatan DM3, ICS, ImagePro SEQ, ImagePro IPW, Metamorph STK, OME-TIFF and Zeiss LSM.

**See also:**

Free trial download\(^\text{43}\)

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^\text{44}\) or the previous versions\(^\text{45}\) page to find documentation for the version you are using.

## 11.11 MIPAV

The **MIPAV**\(^\text{46}\) (Medical Image Processing, Analysis, and Visualization) application—developed at the Center for Information Technology\(^\text{47}\) at the National Institutes of Health\(^\text{48}\)—enables quantitative analysis and visualization of medical images of numerous modalities such as PET, MRI, CT, or microscopy. You can use Bio-Formats as a plugin for MIPAV to read images in the formats it supports.

### 11.11.1 Installation

Follow these steps to install the Bio-Formats plugin for MIPAV:

\(^\text{35}\)http://mayachitra.com/imago/download-trial.php
\(^\text{36}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^\text{37}\)http://www.openmicroscopy.org/site/support/legacy/
\(^\text{38}\)http://code.google.com/p/iqm/
\(^\text{39}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^\text{40}\)http://www.openmicroscopy.org/site/support/legacy/
\(^\text{41}\)http://www.orbicule.com/macnification/
\(^\text{42}\)http://www.orbicule.com
\(^\text{43}\)http://www.orbicule.com/macnification/download
\(^\text{44}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^\text{45}\)http://www.openmicroscopy.org/site/support/legacy/
\(^\text{46}\)http://mipav.cit.nih.gov/
\(^\text{47}\)http://cit.nih.gov/
\(^\text{48}\)http://nih.gov/
1. Download bioformats_package.jar\(^{49}\) and drop it into your MIPAV folder.

2. Download the plugin source code\(^{50}\) into your user "$\text{mipav}/\text{plugins}" folder.

3. From the command line, compile the plugin with:

   ```
cd mipav/plugins
javac -cp "$\text{MIPAV}:/text{MIPAV}/\text{bioformats\_package.jar}"
//PlugInBioFormatsImporter.java
```

4. where "$\text{MIPAV}" is the location of your MIPAV installation.

5. Add bioformats_package.jar to MIPAV’s class path:
   - How to do so depends on your platform.
   - E.g., in Mac OS X, edit the mipav.app/Contents/Info.plist file.


See the readme file\(^{51}\) for more information.

To upgrade, just overwrite the old bioformats_package.jar with the latest one\(^{52}\). You may want to download the latest version of MIPAV first, to take advantage of new features and bug-fixes.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{53}\) or the previous versions\(^{54}\) page to find documentation for the version you are using.

### 11.12 Vaa3D

Vaa3D\(^{55}\), developed by the Peng Lab\(^{56}\) at the HHMI Janelia Farm Research Campus\(^{57}\), is a handy, fast, and versatile 3D/4D/5D Image Visualization & Analysis System for Bioimages & Surface Objects.

Vaa3D can use Bio-Formats via the Bio-Formats C++ bindings\(^{58}\) to read images.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{59}\) or the previous versions\(^{60}\) page to find documentation for the version you are using.

### 11.13 VisBio

VisBio\(^{61}\) is a biological visualization tool designed for easy visualization and analysis of multidimensional image data. VisBio uses Bio-Formats to import files as the Bio-Formats library originally grew out of our efforts to continually expand the file format support within VisBio.

#### 11.13.1 Installation

VisBio is bundled with Bio-Formats, so no further installation is necessary.

\(^{49}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/bioformats_package.jar

\(^{50}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/utils/mipav/PlugInBioFormatsImporter.java

\(^{51}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/utils/mipav/readme.txt

\(^{52}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/

\(^{53}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{54}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{55}\)http://vaa3d.org

\(^{56}\)http://penglab.janelia.org/

\(^{57}\)http://www.hhmi.org/janelia/


\(^{59}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{60}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{61}\)http://loci.wisc.edu/software/visbio
11.13.2 Upgrading

It should be possible to use a newer version of Bio-Formats by overwriting the old `bio-formats.jar` and optional libraries within the VisBio distribution. For Mac OS X, you’ll have to control click the VisBio program icon, choose “Show Package Contents” and navigate into Contents/Resources/Java to find the JAR files.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

11.14 XuvTools

XuvTools is automated 3D stitching software for biomedical image data. As of release 1.8.0, XuvTools uses Bio-Formats to read image data.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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62 http://downloads.openmicroscopy.org/latest/bio-formats5.1/
63 http://www.openmicroscopy.org/site/support/bio-formats5.0/
64 http://www.openmicroscopy.org/site/support/legacy/
65 http://www.xuvtools.org
66 http://www.openmicroscopy.org/site/support/bio-formats5.0/
67 http://www.openmicroscopy.org/site/support/legacy/
Part III

Developer Documentation
The following sections describe various things that are useful to know when working with Bio-Formats. It is recommended that you obtain the Bio-Formats source by following the directions in the Source code section. Referring to the Javadocs as you read over these pages should help, as the notes will make more sense when you see the API.

For a complete list of supported formats, see the Bio-Formats supported formats table.

For a few working examples of how to use Bio-Formats, see these Github pages.

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68http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/
69https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/formats-gpl/utils
12.1 Overview for developers

From the rest of the Bio-Formats developer documentation one may piece together a correct and useful understanding of what Bio-Formats does and how it does it. This section gives a high-level tour of these technical details, for those new to working on Bio-Formats itself, making it easier to understand how the information from the other sections fits into the big picture.

12.1.1 Terms and concepts

Bio-Formats can read image data from files for many formats, and can write image data to files for some formats. An image may have many two-dimensional “planes” of pixel intensity values. Each pixel on a plane is identified by its x, y values. Planes within an image may be identified by various dimensions including z (third spatial dimension), c (channel, e.g. wavelength) or t (time). Planes may be divided into tiles, which are rectangular subsections of a plane; this is helpful in handling very large planes. A file (or set of related files) on disk may contain multiple images: each image is identified by a unique series number.

An image is more than a set of planes: it also has metadata. Bio-Formats distinguishes core metadata, such as the x, y, z, c, t dimensions of the image, from format-specific original metadata, e.g. information about the microscope and its settings, which is represented as a dictionary of values indexed by unique keys. Metadata apply to the image data as a whole, or separately to specific series within it.

Bio-Formats is able to translate the above metadata into a further form, OME metadata. The translation may be partial or incomplete, but remains very useful for allowing the metadata of images from different file formats to be used and compared in a common format defined by the OME data model.

12.1.2 Implementation

Bio-Formats is primarily a Java project. It can be used from MATLAB, and there are C++ bindings and an ongoing C++ implementation effort. The source code is available for download and sometimes the user community contributes code back into Bio-Formats by opening a pull request on GitHub. Bio-Formats is built from source with Ant or Maven and some of the Bio-Formats source code is generated from other files during the build process. The resulting JARs corresponding to official Bio-Formats releases are available for download.

Readers and writers for different image file formats are implemented in separate Java classes. Readers for related formats may reflect that relationship in the Java class hierarchy. Simple standalone command-line tools are provided with Bio-Formats, but it is more commonly used as a third-party library by other applications. Various examples show how one may use Bio-Formats in different ways in writing a new application that reads or writes image data. A common pattern is to initialize a reader based on the image data’s primary file, then query that reader for the metadata and planes of interest.

The set of readers is easily modified. The readers.txt file lists the readers to try in determining an image file’s format, and there are many useful classes and methods among the Bio-Formats Java code to assist in writing new readers and writers.

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1.http://www.openmicroscopy.org/site/support/bio-formats5.0/
2.http://www.openmicroscopy.org/site/support/legacy/
12.2 Obtaining and building Bio-Formats

12.2.1 Source code

The source code for this Bio-Formats release is available from the download page\(^6\). This release and the latest Bio-Formats source code are also available from the Git repository. This may be accessed using the repository path:

```
git@github.com:openmicroscopy/bioformats.git
```

More information about Git and client downloads are available from the Git project website\(^7\). You can also browse the Bio-Formats source on GitHub\(^8\).

**Note:** Windows users must set git to use `core.autocrlf=input` to ensure that Bio-Formats uses LF rather than CRLF line endings, otherwise the build will fail (Genshi can’t process code templates with CRLF line endings, leading to broken sources being generated). This can be set globally in the registry when installing `mysysgit` or by editing `etc/gitconfig` in the git installation directory. Annoyingly, these settings appear to override per-user and per-repository configuration values, requiring these to be set globally.

Lastly, you can browse the Bio-Formats Javadoc online\(^9\), or generate them yourself using the “docs” Ant target.

12.2.2 Source code structure

The Bio-Formats code is divided into several projects. Core components are located in subfolders of the `components`\(^10\) folder, with some components further classified into `components/forks`\(^11\) or `components/stubs`\(^12\), depending on the nature of the project. See the Component overview for more information, including associated build targets for each component.

Each project has a corresponding Maven POM file, which can be used to work with the project in your favorite IDE, or from the command line, once you have cloned the source.

12.2.3 Building from source

Instructions for several popular options follow. In all cases, make sure that the prerequisites are installed before you begin.

If you are interested in working on the Bio-Formats source code itself, you can load it into your favorite IDE, or develop with your favorite text editor.

**Prerequisites**

In addition to the Bio-Formats source code, the following programs and packages are also required:

- **Python**\(^13\), version 2.6 or later (note: not version 3)
- **Genshi**\(^14\) 0.5 or later (0.7 recommended)

\(^4\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^5\)http://www.openmicroscopy.org/site/support/legacy/
\(^6\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/
\(^7\)http://git-scm.com/
\(^8\)https://github.com/openmicroscopy/bioformats
\(^9\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/
\(^10\)https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/
\(^11\)https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/forks/
\(^12\)https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/stubs/
\(^13\)http://python.org
\(^14\)http://genshi.edgewall.org
Note: Genshi may be installed (in order of decreasing preference) with some Linux distributions’ package managers, pip (pip install genshi), by downloading a compatible .egg for your system from the Genshi download page[^15], or from source. If using a .egg, make sure it is added to your PYTHONPATH environment variable.

NetBeans

NetBeans comes with Maven support built in. To import the Bio-Formats source, perform the following steps:

1. Select File → Open Project from the menu - choose the top-level path to bioformats.git and click Open Project
2. In the ‘Projects’ tab on the left-hand side, expand the ‘Bio-Formats projects’ entry - you should now have a series of folders including ‘Other Sources’, ‘Modules’ and ‘Dependencies.’
3. Expand the ‘Modules’ folder to give a list of components and then double-click the desired project(s) to work with them.

Alternately, you can clone the source directly from NetBeans into a project by selecting Team → Git → Clone Other... from the menu.

Eclipse

Eclipse uses the “Maven Integration for Eclipse” (m2e) plugin to work with Maven projects. It is more flexible than Eclipse’s built-in project management because m2e transparently converts between project dependencies and JAR dependencies (stored in the Maven repository in ~/.m2/repository) on the build path, depending on which projects are currently open.

We recommend using Eclipse 4.3 (Kepler), specifically - “Eclipse IDE for Java developers”. It comes with m2e installed (http://eclipse.org/downloads/compare.php?release=kepler).

You can then import the Bio-Formats source by choosing File → Import → Existing Maven Projects from the menu and browsing to the top-level folder of your Bio-Formats working copy. Alternatively, run the Eclipse Maven target with mvn eclipse:eclipse to create the Eclipse project files, then use File → Import → Existing Projects into Workspace.

To remove post-import errors, either close the ome-xml project or run:

[^15]: http://genshi.edgewall.org/wiki/Download
ant jars & mvn generate-sources

See also:
[ome-devel] Importing source into eclipse

Command line

If you prefer developing code with a text editor such as vim or emacs, you can use the Ant or Maven command line tools to compile Bio-Formats. The Bio-Formats source tree provides parallel build systems for both Ant and Maven, so you can use either one to build the code.

For a list of Ant targets, run:

```bash
ant -p
```

In general, `ant jars` or `ant tools` is the correct command.

When using Maven, Bio-Formats is configured to run the “install” target by default, so all JARs will be copied into your local Maven repository in `~/.m2/repository`. Simply run:

```bash
mvn
```

With either Ant or Maven, you can use similar commands in any subproject folder to build just that component.

12.2.4 Using Gradle, Maven or Ivy

All released `.jar` artifacts may be obtained through the OME Artifactory server. The “Client Settings” section of the Artifactory main page provides example code snippets for inclusion into your Gradle, Maven or Ivy project, which will enable the use of this repository.

Example snippets for using the Bio-Formats `${release.major}.${release.minor}-SNAPSHOT formats-gpl` artifact are available for Gradle and for Maven. These may be copied into your project to enable the use of the Bio-Formats library components, and may be adjusted to use different components or different release or development versions of Bio-Formats.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

12.3 Component overview

The Bio-Formats code repository is divided up into separate components.

The Ant targets to build each component from the repository root are noted in the component descriptions below. Unless otherwise noted, each component can also be built with Maven by running `mvn` in the component’s subdirectory. The Maven module name for each component (as it is shown in most IDEs) is also noted in parenthesis.

12.3.1 Core components

The most commonly used and actively modified components.

- `formats-common`
12.3.2 Internal testing components

These components are used heavily during continuous integration testing, but are less relevant for active development work.

- `autogen`
- `test-suite`

12.3.3 Forks of existing projects

- `mdbtools`
- `jai`
- `turbojpeg`
- `poi`

12.3.4 All components

**autogen** (Bio-Formats code generator)\(^{20}\):

*Ant: jar-autogen*

Contains everything needed to automatically generate documentation for supported file formats. `format-pages.txt`\(^{21}\) should be updated for each new file format reader or writer, but otherwise manual changes should be unnecessary. The following Ant targets are used to regenerate the documentation for all formats:

- `gen-format-pages`
- `gen-meta-support`
- `gen-original-meta-support`

**bio-formats-plugins** (Bio-Formats Plugins for ImageJ)\(^{22}\):

*Ant: jar-bio-formats-plugins*

Everything pertaining to the Bio-Formats plugins for ImageJ lives in this component. Note that when built, this component produces `bio-formats_plugins.jar` (instead of `bio-formats-plugins.jar`) to be in keeping with ImageJ plugin naming conventions. `bio-formats-tools` (Bio-Formats command line tools)\(^{23}\):

*Ant: jar-bio-formats-tools*

The classes that implement the `showinf`, `bfconvert`, and `mkfake` command line tools are contained in this component. Note that this is built with the `jar-bio-formats-tools` Ant target, and not the `tools` target (which is the Ant equivalent of `bundles`). `bundles` (bioformats_package bundle, LOCI Tools bundle, OME Tools bundle)\(^{24}\):

*Ant: tools*

This is only needed by the Maven build system, and is used to aggregate all of the individual .jar files into `bioformats_package.jar`. There should not be any code here, just build system files. `forks/jai` (JAI Image I/O Tools)\(^{25}\):

\(^{20}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/autogen
\(^{21}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/autogen/src/format-pages.txt
\(^{22}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins
\(^{23}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-tools
\(^{24}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bundles
\(^{25}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/forks/jai
Ant: jar-jai

This is a fork of JAI ImageIO\textsuperscript{26} which adds support for decoding YCbCr JPEG-2000 data. This is primarily needed for reading images from histology/pathology formats in \textit{formats-gpl}. There are no dependencies on other components. forks/mdbtools (MDB Tools (Java port))\textsuperscript{27}:

Ant: jar-mdbtools

This is a fork of the mdbtools-java\textsuperscript{28} project. There are numerous bug fixes, as well as changes to reduce the memory required for large files. There are no dependencies on other components. forks/poi (Apache Jakarta POI)\textsuperscript{29}:

Ant: jar-ome-poi

This is a fork of Apache POI\textsuperscript{30}, which allows reading of Microsoft OLE document files. We have made substantial changes to support files larger than 2GB and reduce the amount of memory required to open a file. I/O is also handled by classes from \textit{formats-common}, which allows OLE files to be read from memory. forks/turbojpeg (libjpeg-turbo Java bindings)\textsuperscript{31}:

Ant: jar-turbojpeg

This is a fork of libjpeg-turbo\textsuperscript{32}. There are not any real code changes, but having this as a separate component allows us to package the libjpeg-turbo Java API together with all of the required binaries into a single .jar file using native-lib-loader\textsuperscript{33}. There are no dependencies on other components. \textit{formats-api} (Bio-Formats API)\textsuperscript{34}:

Ant: jar-formats-api

This defines all of the high level interfaces and abstract classes for reading and writing files. There are no file format readers or writers actually implemented in this component, but it does contain the majority of the API that defines Bio-Formats. \textit{formats-bsd} and \textit{formats-gpl} implement this API to provide file format readers and writers. \textit{formats-common} and \textit{ome-xml} are both required as part of the interface definitions. \textit{formats-common} (Common)\textsuperscript{35}:

Ant: jar-formats-common

Provides I/O classes that unify reading from files on disk, streams or files in memory, compressed streams, and non-file URLs. The primary entry points are Location\textsuperscript{36}, RandomAccessInputStream\textsuperscript{37} (for reading), and RandomAccessOutputStream\textsuperscript{38} (for writing).

In addition to I/O, there are several classes to assist in working with XML (XMLTools\textsuperscript{39}), date/timestamps (DateTools\textsuperscript{40}), logging configuration (DebugTools\textsuperscript{41}), and byte arithmetic (DataTools\textsuperscript{42}).

This does not depend on any other components, so can be used anywhere independent of the rest of the Bio-Formats API. \textit{formats-bsd} (BSD Bio-Formats readers and writers)\textsuperscript{43}:

Ant: jar-formats-bsd, jar-formats-bsd-tests

This contains readers and writers for formats which have a publicly available specification, e.g. TIFF. Everything in the component is BSD-licensed. \textit{formats-gpl} (Bio-Formats library)\textsuperscript{44}:

Ant: jar-formats-gpl

The majority of the file format readers and some file format writers are contained in this component. Everything in the component is GPL-licensed (in contrast with \textit{formats-bsd}). Most file formats represented in this component do not have a publicly available specification. metakit (Metakit)\textsuperscript{45}:

\begin{footnotesize}
\begin{enumerate}
\item[26]\url{http://java.net/projects/jai-imageio-core}
\item[27]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/forks/mdbtools}
\item[28]\url{http://mdbtools.cvs.sourceforge.net/viewvc/mdbtools/mdbtools-java}\n\item[29]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/forks/poi}
\item[30]\url{http://poi.apache.org}
\item[31]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/forks/turbojpeg}
\item[32]\url{http://libjpeg-turbo.virtualgl.org/}
\item[33]\url{http://github.com/scijava/native-lib-loader}
\item[34]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-api}
\item[35]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-common}
\item[36]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/Location.html}
\item[37]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/RandomAccessInputStream.html}
\item[38]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/RandomAccessOutputStream.html}
\item[39]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/XMLTools.html}
\item[40]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/DateTools.html}
\item[41]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/DebugTools.html}
\item[42]\url{http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/DataTools.html}
\item[43]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd}
\item[44]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl}
\item[45]\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/metakit}
\end{enumerate}
\end{footnotesize}
12.4 Reading files

12.4.1 Basic file reading

Bio-Formats provides several methods for retrieving data from files in an arbitrary (supported) format. These methods fall into three categories: raw pixels, core metadata, and format-specific metadata. All methods described here are present and documented in \texttt{loci.formats.IFormatReader}. In general, it is recommended that you read files using an instance of \texttt{loci.formats.ImageReader}. While it is possible to work with readers for a specific format, \texttt{ImageReader} contains additional logic to automatically detect the format of a file and delegate subsequent calls to the appropriate reader.
Prior to retrieving pixels or metadata, it is necessary to call `setId(java.lang.String)` on the reader instance, passing in the name of the file to read. Some formats allow multiple series (5D image stacks) per file; in this case you may wish to call `setSeries(int)` to change which series is being read.

Raw pixels are always retrieved one plane at a time. Planes are returned as raw byte arrays, using one of the openBytes methods.

Core metadata is the general term for anything that might be needed to work with the planes in a file. A list of core metadata fields is given in the table below together with the appropriate accessor method:

<table>
<thead>
<tr>
<th>Core metadata field</th>
<th>API method</th>
</tr>
</thead>
<tbody>
<tr>
<td>image width</td>
<td>getSizeX()</td>
</tr>
<tr>
<td>image height</td>
<td>getSizeY()</td>
</tr>
<tr>
<td>number of series per file</td>
<td>getSeriesCount()</td>
</tr>
<tr>
<td>total number of images per series</td>
<td>getImageCount()</td>
</tr>
<tr>
<td>number of slices in the current series</td>
<td>getSizeZ()</td>
</tr>
<tr>
<td>number of timepoints in the current series</td>
<td>getSizeT()</td>
</tr>
<tr>
<td>number of actual channels in the current series</td>
<td>getSizeC()</td>
</tr>
<tr>
<td>the ordering of the images within the current series</td>
<td>getDimensionOrder()</td>
</tr>
<tr>
<td>whether each image is RGB</td>
<td>isRGB()</td>
</tr>
<tr>
<td>whether the pixel bytes are in little-endian order</td>
<td>isLittleEndian()</td>
</tr>
<tr>
<td>whether the channels in an image are interleaved</td>
<td>isInterleaved()</td>
</tr>
<tr>
<td>the type of pixel data in this file</td>
<td>getPixelType()</td>
</tr>
</tbody>
</table>

All file formats are guaranteed to accurately report core metadata.

Format-specific metadata refers to any other data specified in the file - this includes acquisition and hardware parameters, among other things. This data is stored internally in a `java.util.Hashtable`, and can be accessed in one of two ways: individual values can be retrieved by calling `getMetadataValue(java.lang.String)`, which gets the value of the specified key. Note that the keys in this Hashtable are different for each format, hence the name “format-specific metadata”.

See Bio-Formats metadata processing for more information on the metadata capabilities that Bio-Formats provides.

See also:

IFormatReader Source code of the loci.formats.IFormatReader interface

### 12.4.2 File reading extras

The previous section described how to read pixels as they are stored in the file. However, the native format is not necessarily convenient, so Bio-Formats provides a few extras to make file reading more flexible.

- The `loci.formats.ReaderWrapper` API that implements `loci.formats.IFormatReader` allows to define “wrapper” readers that take a reader in the constructor, and manipulate the results somehow, for convenience. Using them is similar to the java.io InputStream/OutputStream model: just layer whichever functionality you need by nesting the wrappers.

The table below summarizes a few wrapper readers of interest:

60http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#setSeries(int)
61http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSizeX()
62http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSizeY()
63http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSeriesCount()
64http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getImageCount()
65http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSizeZ()
66http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSizeT()
67http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getSizeC()
68http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getRGBChannelCount()
69http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getDimensionOrder()
70http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isRGB()
71http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isLittleEndian()
72http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isInterleaved()
73http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getPixelType()
12.4.3 Troubleshooting

- Importing multi-file formats (Leica LEI, PerkinElmer, FV1000 OIF, ICS, and Prairie TIFF, to name a few) can fail if any of the files are renamed. There are “best guess” heuristics in these readers, but they are not guaranteed to work in general. So please do not rename files in these formats.
- If you are working on a Macintosh, make sure that the data and resource forks of your image files are stored together. Bio-Formats does not handle separated forks (the native QuickTime reader tries, but usually fails).
- Bio-Formats file readers are not thread-safe. If files are read within a parallelized environment, a new reader must be fully initialized in each parallel session. See Improving reading performance about ways to improve file reading performance in multi-threaded mode.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

12.5 Writing files

The loci.formats.IFormatWriter API is very similar to the reader API, in that files are written one plane at time (rather than all at once).

The file formats which can be written using Bio-Formats are marked in the supported formats table with a green tick in the ‘export’ column. These include, but are not limited to:

- TIFF (uncompressed, LZW, JPEG, or JPEG-2000)
- OME-TIFF (uncompressed, LZW, JPEG, or JPEG-2000)
- JPEG
- PNG
- AVI (uncompressed)
- QuickTime (uncompressed is supported natively; additional codecs use QTJava)
- Encapsulated PostScript (EPS)

---

79 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/ChannelSeparator.html
80 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/ChannelMerger.html
81 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/ChannelFiller.html
82 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/MinMaxCalculator.html
84 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/Memoizer.html
87 http://www.openmicroscopy.org/site/support/bio-formats5.0/
88 http://www.openmicroscopy.org/site/support/legacy/
• OME-XML (not recommended)

All writers allow the output file to be changed before the last plane has been written. This allows you to write to any number of output files using the same writer and output settings (compression, frames per second, etc.), and is especially useful for formats that do not support multiple images per file.

See also:

IFormatWriter\(^{90}\) Source code of the loci.formats.IFormatWriter interface

loci.formats.tools.ImageConverter\(^{91}\) Source code of the loci.formats.tools.ImageConverter class

*Further details on exporting raw pixel data to OME-TIFF files* Examples of OME-TIFF writing
13.1 Using Bio-Formats as a Java library

If you wish to make use of Bio-Formats within your own software, you can download formats-gpl.jar\(^3\) to use it as a library. Just add formats-gpl.jar to your CLASSPATH or build path. You will also need common.jar for common I/O functions, ome-xml.jar for metadata standardization, and SLF4J\(^4\) for logging.

There are also certain packages that if present will be utilized to provide additional functionality. To include one, just place it in the same folder.

<table>
<thead>
<tr>
<th>Package</th>
<th>Filename</th>
<th>License</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apache Jakarta POI(^5)</td>
<td>ome-poi.jar(^6)</td>
<td>Apache</td>
<td>OME fork; for OLE-based formats (zvi, oib, ipw, cxid)</td>
</tr>
<tr>
<td>MDB Tools(^2)</td>
<td>mdbtools-java.jar(^8)</td>
<td>LGPL</td>
<td>Java port, OME fork; for Olympus CellR and Zeiss LSM metadata (mdb)</td>
</tr>
<tr>
<td>JAI Image I/O Tools(^9)</td>
<td>jai_imageio.jar(^10)</td>
<td>BSD</td>
<td>Pure Java implementation, OME fork; for JPEG2000-based formats (nd2, jp2)</td>
</tr>
<tr>
<td>NetCDF(^11)</td>
<td>netcdf-4.3.19.jar(^12)</td>
<td>LGPL</td>
<td>Java library; for HDF5-based formats (Imaris 5.5, MINC MRI)</td>
</tr>
<tr>
<td>QuickTime for Java(^13)</td>
<td>QTJava.zip</td>
<td>Commercial</td>
<td>For additional QuickTime codecs</td>
</tr>
</tbody>
</table>

See the list in the Bio-Formats toplevel build file\(^14\) for a complete and up-to-date list of all optional libraries, which can all be found in our Git repository\(^15\).

13.1.1 Examples of usage

**MinimumWriter**\(^16\) - A command line utility demonstrating the minimum amount of metadata needed to write a file.

**ImageConverter**\(^17\) - A simple command line tool for converting between formats.

---

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^2\)http://www.openmicroscopy.org/site/support/legacy/
\(^3\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/formats-gpl.jar
\(^4\)http://slf4j.org/
\(^5\)http://jakarta.apache.org/poi/
\(^6\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/ome-poi.jar
\(^7\)http://sourceforge.net/projects/mdbtools
\(^8\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/mdbtools-java.jar
\(^9\)http://java.net/projects/jai-imageio
\(^10\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/jai_imageio.jar
\(^11\)http://www.unidata.ucar.edu/software/netcdf-java/
\(^12\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/artifacts/netcdf-4.3.19.jar
\(^13\)http://www.apple.com/quicktime/download/standalone.html
\(^14\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/build.xml
\(^15\)https://github.com/openmicroscopy/bioformats/tree/v5.1.3/jar
\(^16\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/utils/MinimumWriter.java
ImageInfo\(^{18}\) - A more involved command line utility for thoroughly reading an input file, printing some information about it, and displaying the pixels on screen using the Bio-Formats viewer.

PrintTimestamps\(^{19}\) - A command line example demonstrating how to extract timestamps from a file.

Simple_Read\(^{20}\) - A simple ImageJ plugin demonstrating how to use Bio-Formats to read files into ImageJ (see ImageJ overview).

Read_Image\(^{21}\) - An ImageJ plugin that uses Bio-Formats to build up an image stack, reading image planes one by one (see ImageJ overview).

Mass_Importer\(^{22}\) - A simple plugin for ImageJ that demonstrates how to open all image files in a directory using Bio-Formats, grouping files with similar names to avoiding opening the same dataset more than once (see ImageJ overview).

### 13.1.2 A Note on Java Web Start (bioformats_package.jar vs. formats-gpl.jar)

To use Bio-Formats with your Java Web Start application, we recommend using formats-gpl.jar rather than bioformats_package.jar—the latter is merely a bundle of formats-gpl.jar plus all its optional dependencies.

The bioformats_package.jar bundle is intended as a convenience (e.g. to simplify installation as an ImageJ plugin), but is by no means the only solution for developers. We recommend using formats-gpl.jar as a separate entity depending on your needs as a developer.

The bundle is quite large because we have added support for several formats that need large helper libraries (e.g. Imaris’ HDF-based format). However, these additional libraries are optional; Bio-Formats has been coded using reflection so that it can both compile and run without them.

When deploying a JNLP-based application, using bioformats_package.jar directly is not the best approach, since every time Bio-Formats is updated, the server would need to feed another 15+ MB JAR file to the client. Rather, Web Start is a case where you should keep the JARs separate, since JNLP was designed to make management of JAR dependencies trivial for the end user. By keeping formats-gpl.jar and the optional dependencies separate, only a <1 MB JAR needs to be updated when formats-gpl.jar changes.

As a developer, you have the option of packaging formats-gpl.jar with as many or as few optional libraries as you wish, to cut down on file size as needed. You are free to make whatever kind of “stripped down” version you require. You could even build a custom formats-gpl.jar that excludes certain classes, if you like.

For an explicit enumeration of all the optional libraries included in bioformats_package.jar, see the package.libraries variable of the ant/toplevel.properties\(^{23}\) file of the distribution. You can also read our notes about each in the source distribution’s Ant build.xml\(^{24}\) script.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{25}\) or the previous versions\(^{26}\) page to find documentation for the version you are using.

### 13.2 Exporting files using Bio-Formats

This guide pertains to version 4.2 and later.

#### 13.2.1 Basic conversion

The first thing we need to do is set up a reader:

---


\(^{19}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/utils/PrintTimestamps.java

\(^{20}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/Simple_Read.java

\(^{21}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/Read_Image.java

\(^{22}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/bio-formats-plugins/utils/Mass_Importer.java

\(^{23}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/ant/toplevel.properties

\(^{24}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/build.xml#L240

\(^{25}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{26}\)http://www.openmicroscopy.org/site/support/legacy/
// create a reader that will automatically handle any supported format
IFormatReader reader = new ImageReader();
// tell the reader where to store the metadata from the dataset
MetadataStore metadata;

try {
    ServiceFactory factory = new ServiceFactory();
    OMEXMLService service = factory.getInstance(OMEXMLService.class);
    metadata = service.createOMEXMLMetadata();
} catch (DependencyException exc) {
    throw new FormatException("Could not create OME-XML store.", exc);
} catch (ServiceException exc) {
    throw new FormatException("Could not create OME-XML store.", exc);
}

reader.setMetadataStore(metadata);
// initialize the dataset
reader.setId("/path/to/file");

Now, we set up our writer:

// create a writer that will automatically handle any supported output format
IFormatWriter writer = new ImageWriter();
// give the writer a MetadataRetrieve object, which encapsulates all of the
// dimension information for the dataset (among many other things)
writer.setMetadataRetrieve(MetadataTools.asRetrieve(reader.getMetadataStore()));
// initialize the writer
writer.setId("/path/to/output/file");

Note that the extension of the file name passed to ‘writer.setId(...)’ determines the file format of the exported file.

Now that everything is set up, we can start writing planes:

for (int series=0; series<reader.getSeriesCount(); series++) {
    reader.setSeries(series);
    writer.setSeries(series);
    for (int image=0; image<reader.getImageCount(); image++) {
        writer.saveBytes(image, reader.openBytes(image));
    }
}

Finally, make sure to close both the reader and the writer. Failure to do so can cause:

- file handle leaks
- memory leaks
- truncated output files

Fortunately, closing the files is very easy:

reader.close();
writer.close();
13.2.2 Converting large images

The flaw in the previous example is that it requires an image plane to be fully read into memory before it can be saved. In many cases this is fine, but if you are working with very large images (especially > 4 GB) this is problematic. The solution is to break each image plane into a set of reasonably-sized tiles and save each tile separately - thus substantially reducing the amount of memory required for conversion.

For now, we’ll assume that your tile size is 1024 x 1024, though in practice you will likely want to adjust this. Assuming you have an IFormatReader and IFormatWriter set up as in the previous example, let’s start writing planes:

```java
int tileWidth = 1024;
int tileHeight = 1024;
for (int series=0; series<reader.getSeriesCount(); series++) {
    reader.setSeries(series);
    writer.setSeries(series);

    // determine how many tiles are in each image plane
    // for simplicity, we’ll assume that the image width and height are
    // multiples of 1024
    int tileRows = reader.getSizeY() / tileHeight;
    int tileColumns = reader.getSizeX() / tileWidth;

    for (int image=0; image<reader.getImageCount(); image++) {
        for (int row=0; row<tileRows; row++) {
            for (int col=0; col<tileColumns; col++) {
                // open a tile - in addition to the image index, we need to specify
                // the (x, y) coordinate of the upper left corner of the tile,
                // along with the width and height of the tile
                int xCoordinate = col * tileWidth;
                int yCoordinate = row * tileHeight;
                byte[] tile =
                    reader.openBytes(image, xCoordinate, yCoordinate, tileWidth, tileHeight);
                writer.saveBytes(
                    image, tile, xCoordinate, yCoordinate, tileWidth, tileHeight);
            }
        }
    }
}
```

As noted, the example assumes that the width and height of the image are multiples of the tile dimensions. Be careful, as this is not always the case; the last column and/or row may be smaller than preceding columns/rows. An exception will be thrown if you attempt to read or write a tile that is not completely contained by the original image plane. Most writers perform best if the tile width is equal to the image width, although specifying any valid width should work.

As before, you need to close the reader and writer.

13.2.3 Converting to multiple files

The recommended method of converting to multiple files is to use a single IFormatWriter, like so:

```java
// you should have set up a reader as in the first example
ImageWriter writer = new ImageWriter();
writer.setMetadataRetrieve(MetadataTools.asRetrieve(reader.getMetadataStore()));
// replace this with your own filename definitions
// in this example, we’re going to write half of the planes to one file
// and half of the planes to another file
String[] outputFiles =
    new String[] {"/path/to/file/1.tiff", "/path/to/file/2.tiff"};
writer.setId(outputFiles[0]);
```
int planesPerFile = reader.getImageCount() / outputFiles.length;
for (int file=0; file<outputFiles.length; file++) {
    writer.changeOutputFile(outputFiles[file]);
    for (int image=0; image<planesPerFile; image++) {
        int index = file * planesPerFile + image;
        writer.saveBytes(image, reader.openBytes(index));
    }
}
}

reader.close();
writer.close();

The advantage here is that the relationship between the files is preserved when converting to formats that support multi-file datasets internally (namely OME-TIFF). If you are only converting to graphics formats (e.g. JPEG, AVI, MOV), then you could also use a separate IFormatWriter for each file, like this:

```java
// again, you should have set up a reader already
String[] outputFiles = new String[] {"/path/to/file/1.avi", "/path/to/file/2.avi"};
int planesPerFile = reader.getImageCount() / outputFiles.length;
for (int file=0; file<outputFiles.length; file++) {
    ImageWriter writer = new ImageWriter();
    writer.setMetadataRetrieve(MetadataTools.asRetrieve(reader.getMetadataStore()));
    writer.setId(outputFiles[file]);
    for (int image=0; image<planesPerFile; image++) {
        int index = file * planesPerFile + image;
        writer.saveBytes(image, reader.openBytes(index));
    }
    writer.close();
}
```

13.2.4 Known issues

List of Trac tickets

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

13.3 Further details on exporting raw pixel data to OME-TIFF files

This document explains how to export pixel data to OME-TIFF using Bio-Formats version 4.2 and later.

The first thing that must happen is we must create the object that stores OME-XML metadata. This is done as follows:

```java
ServiceFactory factory = new ServiceFactory();
OMEXMLService service = factory.getInstance(OMEXMLService.class);
IMetadata omexml = service.createOMEXMLMetadata();
```

The ‘omexml’ object can now be used in our code to store OME-XML metadata, and by the file format writer to retrieve OME-XML metadata.

Now that we have somewhere to put metadata, we need to populate as much metadata as we can. The minimum amount of metadata required is:

```java
27http://trac.openmicroscopy.org.uk/ome/query?status=accepted&status=new&status=reopened&keywords= export&component=Bio-
28http://www.openmicroscopy.org/site/support/bio-formats5.0/
29http://www.openmicroscopy.org/site/support/legacy/
```
• endianness of the pixel data
• the order in which dimensions are stored
• the bit depth of the pixel data
• the number of channels
• the number of timepoints
• the number of Z sections
• the width (in pixels) of an image
• the height (in pixels) of an image
• the number of samples per channel (3 for RGB images, 1 otherwise)

We populate that metadata as follows:

```java
omexml.setImageID("Image:0", 0);
omexml.setPixelsID("Pixels:0", 0);

// specify that the pixel data is stored in big-endian order
// replace 'TRUE' with 'FALSE' to specify little-endian order
omexml.setPixelsBinDataBigEndian(Boolean.TRUE, 0, 0);

omexml.setPixelsDimensionOrder(DimensionOrder.XYCZT, 0);
omexml.setPixelsType(PixelType.UINT16, 0);
omexml.setPixelsSizeX(new PositiveInteger(width), 0);
omexml.setPixelsSizeY(new PositiveInteger(height), 0);
omexml.setPixelsSizeZ(new PositiveInteger(zSectionCount), 0);
omexml.setPixelsSizeC(new PositiveInteger(channelCount * samplesPerChannel), 0);
omexml.setPixelsSizeT(new PositiveInteger(timepointCount), 0);

for (int channel=0; channel<channelCount; channel++) {
    omexml.setChannelID("Channel:0:" + channel, 0, channel);
    omexml.setChannelSamplesPerPixel(new PositiveInteger(samplesPerChannel), 0, channel);
}
```

There is much more metadata that can be stored; please see the Javadoc for loci.formats.meta.MetadataStore for a complete list.

Now that we have defined all of the metadata, we need to create a file writer:

```java
ImageWriter writer = new ImageWriter();
```

Now we must associate the ‘omexml’ object with the file writer:

```java
writer.setMetadataRetrieve(omexml);
```

The writer now knows to retrieve any metadata that it needs from ‘omexml’.

We now tell the writer which file it should write to:

```java
writer.setId("output-file.ome.tiff");
```

It is critical that the file name given to the writer ends with ‘.ome.tiff’ or ‘.ome.tif’, as it is the file name extension that determines which format will be written.

Now that everything is set up, we can save the image data. This is done plane by plane, and we assume that the pixel data is stored in a 2D byte array ‘pixelData’:

13.3. Further details on exporting raw pixel data to OME-TIFF files
Finally, we must tell the writer that we are finished, so that the output file can be properly closed:

```java
writer.close();
```

There should now be a complete OME-TIFF file at whichever path was specified above.

---

### Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^30] or the previous versions[^31] page to find documentation for the version you are using.

## 13.4 Converting files from FV1000 OIB/OIF to OME-TIFF

This document explains how to convert a file from FV1000 OIB/OIF to OME-TIFF using Bio-Formats version 4.2 and later.

The first thing that must happen is we must create the object that stores OME-XML metadata. This is done as follows:

```java
ServiceFactory factory = new ServiceFactory();
OMEXMLService service = factory.getInstance(OMEXMLService.class); IMetadata omexml = service.createOMEXMLMetadata();
```

The ‘omexml’ object can now be used by both a file format reader and a file format writer for storing and retrieving OME-XML metadata.

Now that have somewhere to put metadata, we need to create a file reader and writer:

```java
ImageReader reader = new ImageReader();
ImageWriter writer = new ImageWriter();
```

Now we must associate the ‘omexml’ object with the file reader and writer:

```java
reader.setMetadataStore(omexml);
writer.setMetadataRetrieve(omexml);
```

The reader now knows to store all of the metadata that it parses into ‘omexml’, and the writer knows to retrieve any metadata that it needs from ‘omexml’.

We now tell the reader and writer which files will be read from and written to, respectively:

```java
reader.setId("input-file.oib");
writer.setId("output-file.ome.tiff");
```
It is critical that the file name given to the writer ends with "".ome.tiff"" or "".ome.tif"", as it is the file name extension that determines which format will be written.

Now that everything is set up, we can convert the image data. This is done plane by plane:

```java
for (int series=0; series<reader.getSeriesCount(); series++) {
    reader.setSeries(series);
    writer.setSeries(series);
    byte[] plane = new byte[FormatTools.getPlaneSize(reader)];
    for (int image=0; image<reader.getImageCount(); image++) {
        reader.openBytes(image, plane);
        writer.saveBytes(image, plane);
    }
}
```

The body of the outer ‘for’ loop may also be replaced with the following:

```java
reader.setSeries(series);
writer.setSeries(series);
for (int image=0; image<reader.getImageCount(); image++) {
    byte[] plane = reader.openBytes(image);
    writer.saveBytes(image, plane);
}
```

But note that this will be a little slower.

Finally, we must tell the reader and writer that we are finished, so that the input and output files can be properly closed:

```java
reader.close();
writer.close();
```

There should now be a complete OME-TIFF file at whichever path was specified above.

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{32}\) or the previous versions\(^{33}\) page to find documentation for the version you are using.

---

### 13.5 Using Bio-Formats in MATLAB

This section assumes that you have installed the MATLAB toolbox as instructed in the **MATLAB user information page**. Note the minimum supported MATLAB version is R2007b (7.5).

As described in **Using Java Libraries**\(^{34}\), every installation of MATLAB includes a JVM allowing use of the Java API and third-party Java libraries. All the helper functions included in the MATLAB toolbox make use of the Bio-Formats Java API. Please refer to the **Javadocs**\(^{35}\) for more information.

#### 13.5.1 Increasing JVM memory settings

The default JVM settings in MATLAB can result in `java.lang.OutOfMemoryError: Java heap space` exceptions when opening large image files using Bio-Formats. Information about the Java heap space usage in MATLAB can be retrieved using:

\(^{32}\)[http://www.openmicroscopy.org/site/support/bio-formats5.0/]

\(^{33}\)[http://www.openmicroscopy.org/site/support/legacy/]

\(^{34}\)[http://uk.mathworks.com/help/matlab/matlab_external/product-overview.html]

\(^{35}\)[http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/]

---

13.5. Using Bio-Formats in MATLAB
Default JVM settings can be increased by creating a `java.opts` file in the startup directory and overriding the default memory settings. We recommend using `-Xmx512m` in your `java.opts` file. Calling:

```
bfCheckJavaMemory()
```

will also throw a warning if the runtime memory is lower than the recommended value.

If errors of type `java.lang.OutOfMemoryError: PermGen space` are thrown while using Bio-Formats with the Java bundled with MATLAB (Java 6 or 7), you may try to increase the default values of `-XX:MaxPermSize` and `-XX:PermSize` via the `java.opts` file.

See also:

http://www.mathworks.com/matlabcentral/answers/92813 How do I increase the heap space for the Java VM in MATLAB 6.0 (R12) and later versions?

[ome-users] Release of OMERO & Bio-Formats 5.1.1

### 13.5.2 Opening an image file

The first thing to do is initialize a file with the `bfopen` function:

```
data = bfopen('/path/to/data/file');
```

This function returns an \( n \)-by-4 cell array, where \( n \) is the number of series in the dataset. If \( s \) is the series index between 1 and \( n \):

- The `data{s, 1}` element is an \( m \)-by-2 cell array, where \( m \) is the number of planes in the \( s \)-th series. If \( t \) is the plane index between 1 and \( m \):
  - The `data{s, 1}{t, 1}` element contains the pixel data for the \( t \)-th plane in the \( s \)-th series.
  - The `data{s, 1}{t, 2}` element contains the label for the \( t \)-th plane in the \( s \)-th series.
- The `data{s, 2}` element contains original metadata key/value pairs that apply to the \( s \)-th series.
- The `data{s, 3}` element contains color lookup tables for each plane in the \( s \)-th series.
- The `data{s, 4}` element contains a standardized OME metadata structure, which is the same regardless of the input file format, and contains common metadata values such as physical pixel sizes - see OME metadata below for examples.

### Accessing planes

Here is an example of how to unwrap specific image planes for easy access:

```
seriesCount = size(data, 1);
series1 = data{1, 1};
series2 = data{2, 1};
series3 = data{3, 1};
metadataList = data{1, 2};
% etc
series1_planeCount = size(series1, 1);
series1_plane1 = series1{1, 1};
series1_label1 = series1{1, 2};
series1_plane2 = series1{2, 1};
series1_label2 = series1{2, 2};
```

---

37https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/bfopen.m
series1_plane3 = series1(3, 1);
series1_label3 = series1(3, 2);

Displaying images

If you want to display one of the images, you can do so as follows:

```matlab
series1_colorMaps = data{1, 3};
figure('Name', 'series1_label1');
if (isempty(series1_colorMaps{1}))
    colormap(gray);
else
    colormap(series1_colorMaps{1}{1,:});
end
imagesc(series1_plane1);
```

This will display the first image of the first series with its associated color map (if present). If you would prefer not to apply the color maps associated with each image, simply comment out the calls to `colormap`.

If you have the image processing toolbox, you could instead use:

```matlab
imshow(series1_plane1, []);
```

You can also create an animated movie (assumes 8-bit unsigned data):

```matlab
v = linspace(0, 1, 256)';
cmap = [v v v];
for p = 1 : size(series1, 1)
    M(p) = im2frame(uint8(series1{p, 1}), cmap);
end
if feature('ShowFigureWindows')
    movie(M);
end
```

Retrieving metadata

There are two kinds of metadata:

- **Original metadata** is a set of key/value pairs specific to the input format of the data. It is stored in the `data{s, 2}` element of the data structure returned by `bfopen`.

- **OME metadata** is a standardized metadata structure, which is the same regardless of input file format. It is stored in the `data{s, 4}` element of the data structure returned by `bfopen`, and contains common metadata values such as physical pixel sizes, instrument settings, and much more. See the OME Model and Formats documentation for full details.

### Original metadata

To retrieve the metadata value for specific keys:

```matlab
% Query some metadata fields (keys are format-dependent)
metadata = data{1, 2};
subject = metadata.get('Subject');
title = metadata.get('Title');
```

---

38http://www.openmicroscopy.org/site/support/ome-model/

13.5. Using Bio-Formats in MATLAB
To print out all of the metadata key/value pairs for the first series:

```java
metadataKeys = metadata.keySet().iterator();
for (i = 1; i <= metadata.size(); i++)
    key = metadataKeys.nextElement();
    value = metadata.get(key);
    fprintf('%s = %s
', key, value)
end
```

**OME metadata**

Conversion of metadata to the OME standard is one of Bio-Formats’ primary features. The OME metadata is always stored the same way, regardless of input file format.

To access physical voxel and stack sizes of the data:

```java
omeMeta = data{1, 4};
stackSizeX = omeMeta.getPixelsSizeX(0).getValue(); % image width, pixels
stackSizeY = omeMeta.getPixelsSizeY(0).getValue(); % image height, pixels
stackSizeZ = omeMeta.getPixelsSizeZ(0).getValue(); % number of Z slices
voxelSizeXdefaultValue = omeMeta.getPixelsPhysicalSizeX(0).value(); % returns value in default unit
voxelSizeXdefaultUnit = omeMeta.getPixelsPhysicalSizeX(0).unit().getSymbol(); % returns the default unit type
voxelSizeXdouble = voxelSizeX.getDoubleValue(); % The numeric value represented by this object after conversion to type double
voxelSizeY = omeMeta.getPixelsPhysicalSizeY(0).value(ome.units.UNITS.MICROM); % in µm
voxelSizeYdouble = voxelSizeY.getDoubleValue(); % The numeric value represented by this object after conversion to type double
voxelSizeZ = omeMeta.getPixelsPhysicalSizeZ(0).value(ome.units.UNITS.MICROM); % in µm
voxelSizeZdouble = voxelSizeZ.getDoubleValue(); % The numeric value represented by this object after conversion to type double
```

For more information about the methods to retrieve the metadata, see the MetadataRetrieve\(^{39}\) Javadoc page.

To convert the OME metadata into a string, use the `dumpXML()` method:

```java
omeXML = char(omeMeta.dumpXML());
```

### 13.5.3 Reading from an image file

The main inconvenience of the `bfopen.m`\(^{40}\) function is that it loads all the content of an image regardless of its size.

To access the file reader without loading all the data, use the low-level `bfGetReader.m`\(^{41}\) function:

```java
reader = bfGetReader('path/to/data/file');
```

You can then access the OME metadata using the `getMetadataStore()` method:

```java
omeMeta = reader.getMetadataStore();
```

Individual planes can be queried using the `bfGetPlane.m`\(^{42}\) function:

\(^{39}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/meta/MetadataRetrieve.html

\(^{40}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/bfopen.m

\(^{41}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/bfGetReader.m

\(^{42}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/bfGetPlane.m
To switch between series in a multi-image file, use the `setSeries(int)` method. To retrieve a plane given a set of \((z, c, t)\) coordinates, these coordinates must be linearized first using `getIndex(int, int, int)`.

```plaintext
% Read plane from series iSeries at Z, C, T coordinates (iZ, iC, iT)
% All indices are expected to be 1-based
reader.setSeries(iSeries - 1);  
iPlane = reader.getIndex(iZ - 1, iC - 1, iT - 1) + 1;  
I = bfGetPlane(reader, iPlane);
```

### 13.5.4 Saving files

The basic code for saving a 5D array into an OME-TIFF file is located in the `bfsave.m` function.

For instance, the following code will save a single image of 64 pixels by 64 pixels with 8 unsigned bits per pixels:

```plaintext
plane = zeros(64, 64, 'uint8');  
bfsave(plane, 'single-plane.ome.tiff');
```

And the following code snippet will produce an image of 64 pixels by 64 pixels with 2 channels and 2 timepoints:

```plaintext
plane = zeros(64, 64, 1, 2, 2, 'uint8');  
bfsave(plane, 'multiple-planes.ome.tiff');
```

By default, `bfsave` will create a minimal OME-XML metadata object containing basic information such as the pixel dimensions, the dimension order and the pixel type. To customize the OME metadata, it is possible to create a metadata object from the input array using `createMinimalOMEXMLMetadata.m`, add custom metadata and pass this object directly to `bfsave`:

```plaintext
plane = zeros(64, 64, 1, 2, 2, 'uint8');  
metadata = createMinimalOMEXMLMetadata(plane);  
pixelSize = ome.units.quantity.Length(java.lang.Double(.05), ome.units.UNITS.MICROM);  
metadata.setPixelsPhysicalSizeX(pixelSize, 0);  
metadata.setPixelsPhysicalSizeY(pixelSize, 0);  
pixelSizeZ = ome.units.quantity.Length(java.lang.Double(.2), ome.units.UNITS.MICROM);  
metadata.setPixelsPhysicalSizeZ(pixelSizeZ, 0);  
bfsave(plane, 'metadata.ome.tiff', 'metadata', metadata);
```

For more information about the methods to store the metadata, see the `MetadataStore` Javadoc page.

### 13.5.5 Improving reading performance

Initializing a Bio-Formats reader can consume substantial time and memory. Most of the initialization time is spend in the `setId(java.lang.String)` call. Various factors can impact the performance of this step including the file size, the amount of metadata in the image and also the file format itself.

One solution to improve reading performance is to use Bio-Formats memoization functionalities with the `loci.formats.Memoizer` reader wrapper. By essence, the speedup gained from memoization will only happen after the first initialization of the reader for a particular file.

---

43. [http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#setSeries(int)]
44. [http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#getIndex(int, int, int)]
45. [https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/bfsave.m]
46. [https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/matlab/createMinimalOMEXMLMetadata.m]
47. [http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/meta/MetadataStore.html]
49. [http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/Memoizer.html]
The simplest way to make use the Memoizer functionalities in MATLAB is illustrated by the following example:

```matlab
% Construct an empty Bio-Formats reader
r = bfGetReader();
% Decorate the reader with the Memoizer wrapper
r = loci.formats.Memoizer(r);
% Initialize the reader with an input file
% If the call is longer than a minimal time, the initialized reader will
% be cached in a file under the same directory as the initial file
% name .large_file.bfmemo
r.setId(pathToFile);

% Perform work using the reader

% Close the reader
r.close()

% If the reader has been cached in the call above, re-initializing the
% reader will use the memo file and complete much faster especially for
% large data
r.setId(pathToFile);

% Perform additional work

% Close the reader
r.close()
```

If the time required to call `setId(java.lang.String)` method is larger than `DEFAULT_MINIMUM_ELAPSED` or the minimum value passed in the constructor, the initialized reader will be cached in a memo file under the same folder as the input file. Any subsequent call to `setId()` with a reader decorated by the Memoizer on the same input file will load the reader from the memo file instead of performing a full reader initialization.

More constructors are described in the Memoizer javadocs allowing to control the minimal initialization time required before caching the reader and/or to define a root directory under which the reader should be cached.

As Bio-Formats is not thread-safe, reader memoization offers a new solution to increase reading performance when doing parallel work. For instance, the following example shows how to combine memoization and MATLAB parfor to do work on a single file in a parallel loop:

```matlab
% Construct a Bio-Formats reader decorated with the Memoizer wrapper
r = loci.formats.Memoizer(bfGetReader(), 0);
% Initialize the reader with an input file to cache the reader
r.setId(pathToFile);
% Close reader
r.close()

nWorkers = 4;

% Enter parallel loop
parfor i = 1 : nWorkers
    % Initialize a new reader per worker as Bio-Formats is not thread safe
    r2 = javaObject('loci.formats.Memoizer', bfGetReader(), 0);
    % Initialization should use the memo file cached before entering the
    % parallel loop
    r2.setId(pathToFile);

    % Perform work

    % Close the reader
```

---

50 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/Memoizer.html#setId(java.lang.String)
51 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/Memoizer.html#DEFAULT_MINIMUM_ELAPSED
52 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/Memoizer.html
13.6 Using Bio-Formats in Python

OME does not currently provide a Python implementation for Bio-Formats.

The CellProfiler project has implemented a Python wrapper around Bio-Formats used by the CellProfiler software which can be installed using `pip`:

```
pip install python-bioformats
```

See also:

- [https://pypi.python.org/pypi/python-bioformats](https://pypi.python.org/pypi/python-bioformats)  
  Source code of the CellProfiler Python wrapper for Bio-Formats

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

13.7 Interfacing with Bio-Formats from non-Java code

Bio-Formats is written in Java, and is easiest to use with other Java code. However, it is possible to call Bio-Formats from a program written in another language. But how to do so depends on your program’s needs.

Technologically, there are two broad categories of solutions: in-process approaches, and inter-process communication.

For details, see LOCI’s article Interfacing from non-Java code.

Recommended in-process solution: JACE C++ bindings for the Java API

Recommended inter-process solution: Subimager

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

13.7.1 JACE C++ bindings for the Java API

To make Bio-Formats accessible to software written in C++, we have created a Bio-Formats C++ interface (BF-CPP for short). It uses LOCI’s jar2lib program to generate a C++ proxy class for each equivalent Bio-Formats Java class. The resulting proxies are then compiled into a library, which represents the actual interface from C++ to Bio-Formats. Using this library in your projects gives you access to the image support of Bio-Formats.

BF-CPP comes with some standalone examples which you can use as a starting point in your own project:

- showinf

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
• minimum_writer

Other projects using BF-CPP include:

• WiscScan which uses BF-CPP to write OME-TIFF files.
• XuvTools which uses an adapted version of BF-CPP called BlitzBioFormats.

See the build instructions (Windows, Mac OS X, Linux) for details on compiling BF-CPP from source. Once this is done, simply include it in your project as you would any other external library.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

13.7.2 Build instructions for C++ bindings

This package provides language bindings for calling into the Bio-Formats Java library from C++ in a cross-platform manner. As of this writing the bindings are functional with GCC on Linux and Mac OS X systems, as well as with Visual C++ 2005 and Visual C++ 2008 on Windows.

Compile-time dependencies

To build the Bio-Formats C++ bindings from source, the following modules are required:

• Apache Maven Maven is a software project management and comprehension tool. Along with Ant, it is one of the supported build systems for the Bio-Formats Java library, and is used to generate the Bio-Formats C++ bindings.
• CMake CMake is a cross-platform, open source build system generator, commonly used to build C++ projects in a platform-independent manner. CMake supports GNU make as well as Microsoft Visual Studio, allowing the Bio-Formats C++ bindings to be compiled on Windows, Mac OS X, Linux and potentially other platforms.
• Boost Thread Boost is a project providing open source portable C++ source libraries. It has become a suite of de facto standard libraries for C++. The Bio-Formats C++ bindings require the Boost Thread module in order to handle C++ threads in a platform independent way.
• Java Development Kit At runtime, only the Java Runtime Environment (JRE) is necessary to execute the Bio-Formats code. However, the full J2SE development kit is required at compile time on some platforms (Windows in particular), since it comes bundled with the JVM shared library (jvm.lib) necessary to link with Java.

For information on installing these dependencies, refer to the page for your specific platform: Windows, Mac OS X, Linux.

How to build

The process of building the Bio-Formats C++ bindings is divided into two steps:

1. Generate a C++ project consisting of “proxies” which wrap the Java code. This step utilizes the Maven project management tool, specifically a Maven plugin called cppwrap.
2. Compile this generated C++ project. This step utilizes the cross-platform CMake build system.

For details on executing these build steps, refer to the page for your specific platform: Windows, Mac OS X, Linux.

Build results

If all goes well, the build system will:

1. Generate the Bio-Formats C++ proxy classes;

63http://loci.wisc.edu/software/wiscscan
64http://www.openmicroscopy.org/site/support/ome-model/ome-tiff
65http://www.xuvtools.org/devel/libblitzbioformats
66http://www.openmicroscopy.org/site/support/bio-formats5.0/
67http://www.openmicroscopy.org/site/support/legacy/
2. Build the Jace C++ library;
3. Build the Java Tools C++ library;
4. Build the Bio-Formats C++ shared library;
5. Build the showinf and minimum_writer command line tools, for testing the functionality.

Please be patient, as the build may require several minutes to complete.

Afterwards, the dist/formats-bsd subdirectory will contain the following files:

1. libjace.so / libjace.jnilib / jace.dll : Jace shared library
2. libformats-bsd.so / libformats-bsd.dylib / formats-bsd.dll : C++ shared library for BSD-licensed readers and writers
3. jace-runtime.jar : Jace Java classes needed at runtime
4. bioformats_package.jar : Bio-Formats Java library needed at runtime
5. libjtools.so / libjtools.jnilib / jtools.dll : Java Tools shared library
6. showinf / showinf.exe : Example command line application
7. minimum_writer / minimum_writer.exe : Example command line application

Items 1-4 are necessary and required to deploy Bio-Formats with your C++ application. Item 5 (jtools) is a useful helper library for managing the Java virtual machine from C++, but is not strictly necessary to use Bio-Formats. All other files, including the example programs and various build files generated by CMake, are not needed.

If you prefer, instead of using the bioformats_package.jar bundle, you can provide individual JAR files as appropriate for your application. For details, see using Bio-Formats as a Java library.

Please direct any questions to the OME team on the forums or mailing lists.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

13.7.3 Building C++ bindings in Windows

Compile-time dependencies – Windows

Windows users will need to visit the appropriate web sites and download and install the relevant binaries for all the dependencies. To configure the tools, you will need to edit or create several environment variables on your system. Access them by clicking the “Environment Variables” button from Control Panel, System, Advanced tab. Use semicolons to separate multiple directories in the PATH variable.

Compile-time dependencies – Windows – Maven

Download Maven.

Unpack the Maven archive into your Program Files, then add the folder’s bin subdirectory to your PATH environment variable; e.g.:

C:\Program Files\apache-maven-3.0.4\bin

Once set, new Command Prompts will recognize “mvn” as a valid command.

---

72http://www.openmicroscopy.org/community/
73http://lists.openmicroscopy.org.uk/mailman/listinfo/
74http://www.openmicroscopy.org/site/support/bio-formats5.0/
75http://www.openmicroscopy.org/site/support/legacy/
76http://maven.apache.org/
Compile-time dependencies – Windows – CMake

Download and run the CMake installer\(^77\).
During installation, select the “Add CMake to the system PATH for all users” option to ensure that Bio-Formats build system can find your CMake executable.
Once installed, new Command Prompts will recognize “cmake” and “cmake-gui” as valid commands.

Compile-time dependencies – Windows – Boost

Download Boost\(^78\).
You can either build and install from source using the instructions in the Boost documentation, or follow the link under ‘Other downloads’ to the prebuilt binaries for several Visual Studio versions.

Compile-time dependencies – Windows – Java Development Kit

Download and install the JDK\(^79\).
After the installation is complete, create a new environment variable called JAVA_HOME pointing to your Java installation; e.g.:
\[
C:\Program Files\Java\jdk1.6.0_25
\]
Setting JAVA_HOME is the easiest way to ensure that Maven can locate Java.
You will also need to append your JDK’s client or server VM folder to the PATH; e.g.:
\[
%JAVA_HOME%\jre\bin\client
\]
This step ensures that a directory containing jvm.dll is present in the PATH. If you do not perform this step, you will receive a runtime error when attempting to initialize a JVM from native code.
Optionally, you can add the bin subdirectory to the PATH; e.g.:
\[
%JAVA_HOME%\bin
\]
Once set, new Command Prompts will recognize (e.g.) “javac” as a valid command.

Compile-time dependencies – Windows – Visual C++

In addition to the other prerequisites, you will also need a working copy of Visual C++. We have tested compilation with Visual C++ 2005 Professional and Visual C++ 2008 Express; other versions may or may not work.

You can download Visual C++ Express for free\(^80\).
You must launch the environment at least once before you will be able to compile the Bio-Formats C++ bindings.

How to build - Windows

Run Command Prompt and change to your Bio-Formats working copy. Then run:

```
# generate the Bio-Formats C++ bindings
dir components\formats-bsd
mvn -DskipTests package dependency:copy-dependencies cppwrap:wrap

# build the Bio-Formats C++ bindings
dir target\cppwrap
mkdir build
```

\(^77\) [http://cmake.org/](http://cmake.org/)
\(^78\) [http://www.boost.org/users/download/](http://www.boost.org/users/download/)
\(^80\) [http://www.microsoft.com/express/](http://www.microsoft.com/express/)
cd build
cmake-gui ..

The CMake GUI will open. Click the Configure button, and a dialog will appear. Select your installed version of Visual Studio, and click Finish.

When configuring, you can use the J2L_WIN_BUILD_DEBUG flag to indicate if this will be a Debug or Release build. If the flag is checked it will build as Debug, unchecked will build as Release.

Once configuration is complete, click Configure again, repeating as necessary until the Generate button becomes available. Then click Generate. Once generation is complete, close the CMake window.

Back at the Command Prompt, type:

start jace.sln

The solution will then open in Visual Studio. Select Release or Debug as appropriate from the drop-down menu. Press F7 to compile (or select Build Solution from the Build menu).

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{81}\) or the previous versions\(^{82}\) page to find documentation for the version you are using.

### 13.7.4 Building C++ bindings in Mac OS X

#### Compile-time dependencies – Mac OS X

To install dependencies on Mac OS X, we advise using Homebrew\(^{83}\):

```
brew install maven cmake boost
```

Unless otherwise configured, this will install binaries into `/usr/local/`.

#### How to build – Mac OS X

The following commands will generate and build the Bio-Formats C++ bindings:

```
# generate the C++ bindings
cd components/formats-bsd
mvn -DskipTests package dependency:copy-dependencies cppwrap:wrap

# compile the C++ bindings
cd target/cppwrap
mkdir build
cd build
cmake ..
make
```

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{84}\) or the previous versions\(^{85}\) page to find documentation for the version you are using.
13.7.5 Building C++ bindings in Linux

Compile-time dependencies – Linux

The following directions are specific to Ubuntu Linux. Other Linux distributions may have similar packages available; check your package manager.

To install dependencies on Ubuntu Linux, execute:

```bash
# install code generation prerequisites
sudo aptitude install maven2

# install build prerequisites
sudo aptitude install build-essential cmake libboost-thread-dev

# install Java Development Kit
sudo aptitude install sun-java6-jdk
sudo update-alternatives --config java
```

Then select Sun’s Java implementation as the system default.

It may be possible to use a different Java compiler (i.e., omit the sun-java6-jdk package and update-alternatives step), but we have only tested the compilation process with Sun’s Java compiler.

How to build – Linux

The following commands will generate and build the Bio-Formats C++ bindings:

```bash
# generate the Bio-Formats C++ bindings
cd components/formats-bsd
mvn -DskipTests package dependency:copy-dependencies cppwrap:wrap

# build the Bio-Formats C++ bindings
cd target/cppwrap
mkdir build
cd build
cmake ..
make
```
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FOURTEEN

USING BIO-FORMATS AS A NATIVE C++ LIBRARY

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^1\) or the previous versions\(^2\) page to find documentation for the version you are using.

14.1 C++ overview

A completely native Bio-Formats C++ interface is now available. Unlike the JACE bindings, this does not wrap the Java implementation. With this release, TIFF reading and writing, and OME-TIFF reading are available. OME-TIFF writing will be available soon. All other readers and writers from the Java implementation are currently unavailable; the intention is that support for these will be added over time.

Note: The C++ implementation is functional in Bio-Formats version 5.1. However, API stability will not be guaranteed until version 5.2 since it may be necessary to refactor certain parts of the API for optimal usability, robustness and performance. Applications built against version 5.1 of the API may require updating to work with version 5.2, if they make use of any part of the API which is changed incompatibly.

14.1.1 Prebuilt packages

MacOS X Homebrew

Run:

```bash
brew tap homebrew/science
brew install bioformats-cpp [--without-docs] [--with-qt5]
```

--without-docs

Do not build the HTML version of this manual (built by default).

--with-qt5

Build the Qt5 OpenGL viewer widget library ome-qtwidgets and bf-test view image viewer (not built by default).

14.1.2 Prerequisites

In order to build the C++ library and its documentation, a number of packages are required to be installed. Note that the minimum version is the minimum version we regularly test with; older versions may work but are not supported. Some packages are required only for building Bio-Formats (BF build). A subset of these are required for building client applications making use of Bio-Formats (Client build) For end-user deployment (Deploy), the library packages rather than the development packages should be preferred; in some cases such as for Boost and Qt5, these are split up into a separate package for each library.

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^2\)http://www.openmicroscopy.org/site/support/legacy/
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<tr>
<td>GLM*</td>
<td>0.9.6</td>
<td>0.9.5</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Qt5*</td>
<td>5.2</td>
<td>5.0</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CMake</td>
<td>3.0</td>
<td>2.8.12</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Python</td>
<td>2.7</td>
<td>2.6</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Python Genshi</td>
<td>0.7</td>
<td>0.6</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Git</td>
<td>2.1.x</td>
<td>1.7.x</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GTest</td>
<td>1.7</td>
<td>1.5</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Doxygen†</td>
<td>1.8</td>
<td>1.6</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Graphviz†</td>
<td>2.x</td>
<td>1.8.10</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Python Sphinx‡§</td>
<td>1.2.x</td>
<td>1.1.x</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TeX (XeLaTeX)‡§</td>
<td>TeXLive 2014</td>
<td>TeXLive 2012</td>
<td></td>
<td>*</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Required for Bio-Formats build; headers may be needed for client build; libraries and any data files required for deployment
- Optional for Bio-Formats build; if used for the Bio-Formats build, headers may be required for client build and libraries and any data files required for deployment
- Optional, needed to build the OpenGL image viewer and client applications
- † Optional, needed to build the API reference
- ‡ Optional, needed to build the manual pages
- § Optional, needed to build the manual (HTML and PDF)

Due to lacking a package manager, if building on Windows most of the above packages will require downloading and installing by hand. Links for these are provided below.

**Quick start**

Install the following packages to build Bio-Formats C++. A subset of these packages (or their dependencies) may be used for deployment, where the development package headers and tools for building documentation etc. are not required. Run the appropriate command below for your platform to install the build dependencies:

**BSD Ports**
```
pkg install devel/boost-all devel/cmake science/hdf5 graphics/png lang/python
textproc/py-genshi graphics/tiff textproc/xerces-c3 devel/git
devel/googletest math/glm devel/qt5 graphics/graphviz
devel/apache-ant java/openjdk7 textproc/py-sphinx print/texlive-full
```

**Debian/Ubuntu**
```
apt-get install build-essential libboost-all-dev cmake libhdf5-dev
dep/12-dev python python-genshi libtiff5-dev libxerces-c-dev
dev/git libgtest-dev libglm-dev qt5-default libqt5-opengui5-dev
dev/qt5-svg5-dev graphviz ant ant-contrib
ant-optimal openjdk-7-jdk openjdk-7-jre python-sphinx
texlive-full
```

**Homebrew**
```
brew install boost cmake hdf5 libpng python libtiff xerces-c
dev/gl slm qt5 graphviz ant
```

**RedHat/CentOS**
```
yum install libhdf5-devel libpng-devel python python-genshi
dev/libtiff xerces-c-devel
dev/git gtest-devel graphviz java-1.7.0-openjdk
```

Note that Homebrew and RedHat/CentOS do not provide packages for everything you need; see below for details.

**Basic toolchain**

A functional compiler, assembler and linker are required to build C++ code.

If possible, install the following packages:
<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>N/A*</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>build-essential</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A†</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>N/A‡</td>
</tr>
<tr>
<td>Windows</td>
<td>N/A§</td>
</tr>
</tbody>
</table>

* Available by default
† Install Xcode
‡ Run `yum groupinstall "Development Tools"`
§ Install Visual Studio or Visual Studio Express

**Boost**

If possible, install one of the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/boost-all</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libboost-all-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>boost</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>boost-devel</td>
</tr>
</tbody>
</table>

1.48 or later needed for Boost.Geometry; 1.54 or later needed for Boost.Geometry spatial indexes. RHEL/CentOS 6 users might want to look at the [Boost 1.48 SCL](https://www.softwarecollections.org/en/scis/denisarnaud/boost148/) or build a more recent Boost release.

**CMake**

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/cmake</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>cmake</td>
</tr>
<tr>
<td>Homebrew</td>
<td>cmake</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>cmake</td>
</tr>
</tbody>
</table>

- Website
- Download

**HDF5**

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>science/hdf5</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libhdf5-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>hdf5</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>libhdf5-devel</td>
</tr>
</tbody>
</table>

**PNG**

If possible, install the following packages:

---

### System Packages

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>graphics/png</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libpng12-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>libpng</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>libpng-devel</td>
</tr>
</tbody>
</table>

### Python

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>lang/python</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>python</td>
</tr>
<tr>
<td>Homebrew</td>
<td>python</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>python</td>
</tr>
</tbody>
</table>

- Website
- Download
- Extra packages for Windows

For Python on Windows, either download separate installers for each package, or install `setuptools` and `pip` for Python, then `pip install` needed packages; ensure downloaded packages are 64-bit if using 64-bit Python.

### Python Genshi

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>textproc/py-genshi</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>python-genshi</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>python-genshi</td>
</tr>
</tbody>
</table>

Use `pip install genshi` if a packaged version is not available.

### TIFF

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>graphics/tiff</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libtiff5-dev*</td>
</tr>
<tr>
<td>Homebrew</td>
<td>libtiff</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>libtiff-devel</td>
</tr>
</tbody>
</table>

* libtiff4-dev with older releases

4.0.2 and earlier do not have TIFFField accessor functions.

### Xerces-C

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>textproc/xerces-c3</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libxerces-c-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>xerces-c</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>xerces-c-devel</td>
</tr>
</tbody>
</table>

---

7. [https://www.python.org/](https://www.python.org/)
8. [https://www.python.org/download/releases/2.7.8/](https://www.python.org/download/releases/2.7.8/)
Git

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/git</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>git</td>
</tr>
<tr>
<td>Homebrew</td>
<td>git</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>git</td>
</tr>
</tbody>
</table>

- Website\(^{10}\)
- Download\(^{11}\)

Google Test (gtest)

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/googletest</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libgtest-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A*</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>gtest-devel</td>
</tr>
</tbody>
</table>

\* gtest is not available in homebrew\(^{12}\)

An embedded copy of GTest is provided; it is only necessary to use a system-provided or self-built copy of GTest if the embedded copy is not functional on a specific system.

If using an external GTest, make sure that `GTEST_ROOT` is set in the environment, or that `~DGTEST_ROOT=/path/to/gtest` is passed to `make` and that this points to the location where you installed the `gtest` library. If the library is located on the default library search path, this is not necessary.

- Website\(^{13}\)
- Zip download\(^{14}\)
- SVN tag\(^{15}\)

GLM

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>math/glm</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>libglm-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>glm</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>N/A</td>
</tr>
</tbody>
</table>

**Note:** Older versions will allow compilation but use degrees rather than radians, which will lead to unexpected results.

- Website\(^{16}\)
- Download\(^{17}\)

\(^{10}\)http://www.git-scm.com/
\(^{11}\)http://www.git-scm.com/downloads
\(^{12}\)http://answers.ros.org/question/42335/mac-os-x-install-error-no-available-formula-for-gtest/
\(^{13}\)https://code.google.com/p/googletest/
\(^{14}\)https://code.google.com/p/googletest/downloads/detail\?name=gtest-1.7.0.zip
\(^{15}\)http://googletest.googlecode.com/svn/tags/release-1.7.0
\(^{16}\)http://glm.g-truc.net/0.9.6/index.html
\(^{17}\)http://sourceforge.net/projects/ogl-math/files/
Qt5

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/qt5</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>qt5-default libqt5-opengl5-dev libqt5-svg5-dev</td>
</tr>
<tr>
<td>Homebrew</td>
<td>qt5*</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>N/A</td>
</tr>
</tbody>
</table>

* Add /usr/local/opt/qt5/bin to PATH
  • Website\(^\text{18}\)
  • Download\(^\text{19}\)

Doxygen

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/doxygen</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>doxygen</td>
</tr>
<tr>
<td>Homebrew</td>
<td>doxygen</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>doxygen</td>
</tr>
</tbody>
</table>

  • Website\(^\text{20}\)
  • Download\(^\text{21}\)

Graphviz

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>graphics/graphviz</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>graphviz</td>
</tr>
<tr>
<td>Homebrew</td>
<td>graphviz</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>graphviz</td>
</tr>
</tbody>
</table>

  • Website\(^\text{22}\)
  • Download (for Windows)\(^\text{23}\)

Apache Ant

If possible, install one of the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>devel/apache-ant</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>ant ant-contrib ant-optional ant</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A</td>
</tr>
</tbody>
</table>

  • Website\(^\text{24}\)
  • Download\(^\text{25}\)

\(^\text{18}\)http://www.qt.io/
\(^\text{19}\)http://www.qt.io/download/
\(^\text{20}\)http://www.stack.nl/dimitri/doxygen/
\(^\text{21}\)http://www.stack.nl/dimitri/doxygen/download.html
\(^\text{22}\)http://graphviz.org/
\(^\text{23}\)http://graphviz.org/Download_windows.php
\(^\text{24}\)http://ant.apache.org/
\(^\text{25}\)http://ant.apache.org/bindownload.cgi
Java

If possible, install one of the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>java/openjdk7</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>openjdk-7-jdk openjdk-7-jre</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>java-1.7.0-openjdk</td>
</tr>
</tbody>
</table>

- Download

Python Sphinx

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>textproc/py-sphinx</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>python-sphinx</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A (use pip)</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>N/A (use pip)</td>
</tr>
</tbody>
</table>

Use `pip install sphinx` if a packaged version is not available.

TeX

If possible, install the following packages:

<table>
<thead>
<tr>
<th>System</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSD Ports</td>
<td>print/texlive-full</td>
</tr>
<tr>
<td>Debian/Ubuntu</td>
<td>texlive-full</td>
</tr>
<tr>
<td>Homebrew</td>
<td>N/A*</td>
</tr>
<tr>
<td>RedHat/CentOS</td>
<td>N/A†</td>
</tr>
</tbody>
</table>

* Install TeXLive or MacTeX
† Provides an obsolete version; install TeXLive
  - TeXLive website (for Unix)
  - TeXLive quick install (for Unix)
  - MacTeX website (for MacOS X)
  - MacTeX download (for MacOS X)
  - MikTeX website (for Windows)
  - MikTeX download (for Windows)

Local font configuration may be required to make the TeX Gyre fonts available:

- Linux and FreeBSD: Use the provided `fontconfig` template or create your own
- macOS X: Add to system using `FontBook`
- Windows: May need adding to the system fonts if not found automatically

---

27: https://www.tug.org/texlive/
28: https://www.tug.org/texlive/quickinstall.html
29: https://tug.org/mactex/
30: http://mirror.ctan.org/systems/mac/mactex/MacTeX.pkg
31: http://www.miktex.org/
32: http://www.miktex.org/download

14.1. C++ overview

108
14.1.3 Build environment

General

Custom configuration is needed primarily on Windows, where the needed tools may not be on the search path by default. There are several possible approaches here:

- Add to the system environment (globally)
- Add to the user environment (affects a single user)
- Set in a batch file and run this to set up the environment on demand (local to the command shell)

The first will affect all programs running on the system and so may cause problems, particularly if multiple configurations or tool versions are to be used. The last offers the greatest flexibility and safety, and can be sourced automatically when starting a shell if a console replacement such as ConsoleZ is used.

- Activate a python virtualenv if needed
- Ensure that needed tools are on the user PATH (e.g. ant, cmake, doxygen, dot, git, python, java, sphinx, xelatex)
- Set CMAKE_PREFIX_PATH if some libraries and tools are not on the default search path. Not all tools need to be on the default path; some will be discovered automatically by cmake

Homebrew

If qt5 and glm are installed, for building the Qt image viewer, ensure that /usr/local/opt/qt5/bin is on the PATH to allow Qt to be autodetected by cmake.

14.1.4 Source tree layout

Source tree layout:

```bash
cpp
   -- cmake
   -- ext
   -- lib
       |   -- ome
       |       -- bioformats
       |       |   -- detail
       |       |   -- in
       |       |   -- out
       |       |   -- tiff
       |       |   -- common
       |       |       |   -- endian
       |       |       |   -- xml
       |       |       |   |   -- dom
       |       |       |   -- compat
       |       |       |   -- internal
       |       |       |   -- qtwidgets
       |       |       |   -- test
       |       |       |   -- xml
       -- libexec
       |   -- info
       |   -- view
   -- share
   -- test
```

Top-level directories inside cpp:

- cmake CMake build infrastructure
- ext External third-party code
- lib Bio-Formats library headers and sources
libexec  Bio-Formats internal binaries (not direct public API)

share  Bio-Formats architecture-independent data files

test  Bio-Formats unit tests

Components in lib and test:

bioformats  Bio-Formats reader and writer interfaces and implementations

common  Common functionality used by all other components

compat  Compatibility workarounds

internal  Private implementation details

qtwidgets  Qt5 widgets for image rendering with OpenGL

test  Unit test common functions

xml  OME XML model and metadata

14.1.5 Configuring

Bio-Formats uses **cmake**, a generic cross-platform build system which generates build files for a large number of common build systems and IDEs. For example, on BSD, Linux and MacOS X, **Unix make** Makefile files may be created. On Windows, Visual Studio **msbuild** .sln solution files and .vcxproj project may be created. However, Eclipse, Sublime Text or several other IDEs or alternative build systems may be used instead, if desired.

Start by creating a temporary build directory. This directory may be in any location inside or outside the Bio-Formats source tree. However, you may not use the source directory as the build directory. (This fills the source tree full of autogenerated files.)

Run **cmake** from the temporary build directory:

```bash
% mkdir build
% cd build
% cmake /path/to/bioformats
```

Run **cmake** `-LH` to see the configurable project options; use `-LAH` to see advanced options. The following basic options are supported:

**bioformats-superbuild=(ON|OFF)**  Build Bio-Formats as part of a “super-build” project. This will download and build all needed library dependencies (Boost, libtiff etc.) prior to building Bio-Formats. This option is disabled by default since most platforms provide all the libraries by default. However, it is enabled by default when using Microsoft Visual C++, since this platform does not provide libraries unless you have built your own.

**cxxstd-autodetect=(ON|OFF)**  Enable or disable (default) C++ compiler standard autodetection. If enabled, the compiler will be put into C++11 mode if available, otherwise falling back to C++03 or C++98. If disabled, the default compiler standard mode is used, and it is the responsibility of the user to add the appropriate compiler options to build using the required standard. This is useful if autodetection fails or a compiler is buggy in certain modes (e.g. GCC 4.4 or 4.6 require `-std=gnu++98` or elsestdarg support is broken).

**doxygen=(ON|OFF)**  Enable doxygen documentation. These will be enabled by default if doxygen is found.

**embedded-gtest=(ON|OFF)**  Enable the use of an embedded copy of the Google Test (gtest) library. This is off by default but will be enabled automatically if a system copy is not found. This may be enabled explicitly to override the autodetection.

**extended-tests=(ON|OFF)**  Some of the unit tests are comprehensive and run many thousands of tests. These are enabled by default, but by setting to OFF a representative subset of the tests will be run instead to save time.

**extra-warnings=(ON|OFF)**  Enable or disable additional compiler warnings in addition to the default set. These are disabled by default since they trigger a large number of false positives, particularly in third-party libraries outside our control.

**fatal-warnings=(ON|OFF)**  Make compiler warnings into fatal errors. This is disabled by default.

**sphinx=(ON|OFF)**  Build manual pages and HTML documentation with Sphinx. Enabled by default if Sphinx is autodetected.

**sphinx-pdf=(ON|OFF)**  Build PDF documentation with Sphinx. Enabled by default if Sphinx and XeLaTeX are autodetected.

**test=(ON|OFF)**  Enable unit tests. Tests are enabled by default.
For example, to disable tests, run `cmake -Dtest=OFF`. Options will typically be enabled by default if the prerequisites are available.

The installation prefix may be set at this point using `-DCMAKE_INSTALL_PREFIX=prefix`. The build system and compiler to use may also be specified. Please see the `cmake` documentation for further details of all configurable options, and run `cmake --help` to list the available generators for your platform.

### C++11

C++11 features such as `std::shared_ptr` are used when using a C++11 or C++14 compiler, or when `-Dcxxstd-autodetect=ON` is used and the compiler can be put into a C++11 or C++14 compatibility mode. When using an older compatibility mode such as C++98, the Boost equivalents of C++11 library features will be used as fallbacks to provide the same functionality. In both cases these types are imported into the `ome::compat` namespace, for example as `ome::compat::shared_ptr`, and the types in this namespace should be used for portability when using any part of the API which use types from this namespace.

### Linux and MacOS X

The default generator is `Unix Makefiles`, and the standard `CXX`, `CXXFLAGS` and `LDFLAGS` environment variables may be set to explicitly specify the compiler, compiler flags and linker flags, respectively. These may be useful for adding additional `-I` and `-L` include and library search paths, for example.

If you wish to use an IDE such as Eclipse or KDevelop, an alternative generator may be used.

### Windows

On Windows, the generator will require specifying by hand, and this will configure the version of Visual Studio (or other compiler) to use. For example, `-G "Visual Studio 11 Win64"` will configure for generating Visual Studio 2012 64-bit build files for use with the Visual C++ compiler.

**Note:** There is no need to use the Visual Studio command shell when running `cmake`.

### 14.1.6 Building

For all platforms and generators, it should usually be possible to build using:

```
% cmake --build
```

which will invoke the platform- and generator-specific build as appropriate.

To build the API reference documentation, run:

```
% cmake --build . --target doc
```

### Linux and MacOS X

If using `Unix Makefiles`, simply run:

```
% make
```

with any additional options required, for example `-j` to enable parallel building, or `VERBOSE=1` to show the details of every command being executed.

To build the API reference documentation, run:
% make doc

If using an IDE, open the generated project file and proceed using the IDE to build the project.

**Windows**

If using Visual Studio, the generated project files may be opened using the IDE and then built within the IDE. Alternatively, the project files may be built directly using the `msbuild` command-line tool inside a Visual Studio command prompt (or an appropriately configured command prompt which has run `VCVARSALL.BAT` or equivalent to configure the environment).

### 14.1.7 Testing

For all platforms and generators, it should usually be possible to run all tests using `ctest`. Run:

```
% ctest
```

or to run verbosely:

```
% ctest -V
```

Additional flags allow specification of the build configuration to use, logging, parallel building and other options. Please see the `ctest` documentation for further details.

Individual test programs may be run by hand if required.

**Linux and MacOS X**

To run all tests, run:

```
% cmake --build . --target test
```

or verbosely:

```
% cmake --build . --target test -- ARGS=-V
```

If using Unix Makefiles, simply run:

```
% make test
```

or verbosely:

```
% make test ARGS=-V
```

**Windows**

To run all tests, run:

```
> msbuild RUN_TESTS.vcproj
```
14.1.8 Installation

Linux and MacOS X

To install the headers and libraries directly on the system into the configured prefix:

% cmake --build . --target install

Alternatively, to install into a staging directory:

% cmake --build . --target install -- DESTDIR=/path/to/staging/directory install

If using Unix Makefiles, simply run:

% make install

Alternatively, to install into a staging directory:

% make DESTDIR=/path/to/staging/directory install

Windows

When using Visual Studio, there should be an INSTALL.vcxproj project which may be run using msbuild, for example:

> msbuild INSTALL.vcxproj /p:platform=x64

Installation layout

A typical installation layout:

$CMAKE_INSTALL_PREFIX
    -- bin
    -- include
    | -- ome
    |    -- bioformats
    |    -- common
    |    -- compat
    |    -- xml
    -- lib
    -- libexec
    -- share
    | -- icons
    | -- man
    | -- xml

14.1.9 Using the library

The Doxygen API reference is used to document all aspects of the Bio-Formats API.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version.

http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/annotated.html
14.2 C++ conversion details

The C++ codebase has been primarily a conversion of the original Java codebase, with some additional helper functions and classes added where needed. The intention is that the basic interfaces and classes should be identical between the two languages unless this is prevented by fundamental differences between the languages.

This section is intended to be useful for

- Users of the existing Java interface, who wish to understand the differences between the two implementations
- Developers who wish to work on the C++ interface

In addition to documenting the specific language and class compatibility issues, this section also documents the idioms in use in the C++ code which might not be immediately clear by looking at the API reference, and which may not be familiar to Java developers.

14.2.1 C++ and Java type incompatibility

While C++ and Java have some basic syntactical similarities, there are several basic differences in their type systems.

Java types

Java has primitive types and classes.

```java
int i;
double d;
```

- No unsigned primitive integer types

```java
Pixels pixels = new Pixels();
```

- All classes are derived from root `Object`
- Objects are by reference only
- Objects and arrays are always allocated with `new`
- Destruction is non-deterministic
- All passing is by value (primitives and object references)

```java
Pixels[] array = new Pixels[5];
```

- Arrays have an intrinsic size.
- Arrays are safe to index out of bounds (an exception is thrown).

C++ types

C++ has primitive types, structures and classes.
int16_t i1;
uint32_t i2;
double d;

- Primitive integer types may be signed or unsigned.
- Integer types are of defined size.

// Allocate on the stack, or as a struct or class member:
Pixels pixels;

// Allocate on the heap
Pixels *pixelsptr1 = new Pixels();

// Pointer to existing instance
const Pixels *pixelsptr2 = &pixels;

// Reference to existing instance
Pixels& pixelsref(pixels);

- Classes have no common root
- All types may be instances, pointers or references
- Object construction may be on the stack, on the heap using new or in place using placement new.
- Pointers and references may refer to const type
- Pointers may be const
- References are implicitly const (similar to final)
- Destruction is deterministic
- new should never be used in modern C++ code (see below)

Pixels array[5];

- Arrays "decay" to bare pointers
- Arrays are not safe to index out of bounds
- Size information lost at runtime
- Never use arrays outside static initializers

Simplified type names

typedef is used to create an alias for an existing type.

typedef std::vector<std::string> string_list;
string_list l;
string_list::const_iterator i = l.begin();
// NOT std::vector<std::string>::const_iterator

typedef std::vector<Pixels> plist;
plist pl(6);
plist::size_type idx = 2;
// size_type NOT unsigned int or uint32_t
pl.at(idx) = ...;

Used in standard container types e.g. size_type, value_type and in classes and class templates in Bio-Formats. Consistency is needed for generic programming—use the standard type names to enable interoperability with standard algorithms.
14.2.2 Exception handling

Java

Throws details which exceptions are thrown by a method. Java exceptions are also “checked”, requiring the caller to catch and handle all exceptions which might be thrown, aside from RuntimeException and its subclasses.

C++

C++ has exception specifications like Java, however they are useless aside from nothrow. This is because if an exception is thrown which does not match the specification, it will abort the program with a bad_exception which makes them unusable in practice.

Exceptions can be thrown at any point with the exception that they should never be thrown in a destructor. It is not necessary or typical to check exceptions except where needed. All code must be exception-safe given that an exception could be thrown at any point; the design considerations for exception safety are covered below.

14.2.3 Interfaces

Java supports single-inheritance, plus interfaces. C++ supports true multiple-inheritance, which is rather more flexible, at the expense of being rather more complicated and dangerous. However, the Java single-inheritance-plus-interfaces model can be implemented in C++ using a subset of the facilities provided by multiple inheritance. Rather than being enforced by the language, it is a set of idioms. These must be rigorously followed or else things will fail horribly!

C++ interfaces are classes with:
- No instance variables
- Pure virtual methods
- protected default constructor
- public virtual destructor
- Deleted copy constructor and assignment operator

C++ classes implementing interfaces:
- Use public inheritance for parent class
- Use virtual public inheritance for implemented interfaces
- Have a virtual destructor

When compiled with optimization enabled, the interface classes should have zero storage overhead. If implementing classes do not use virtual public inheritance, compilation will fail as soon as a second class in the inheritance hierarchy also implements the interface.

14.2.4 Reference handling and memory management

Pointer problems

Plain (or “dumb”) C++ pointers can be dangerous if used incorrectly. The Bio-Formats API make a point of never using them unless absolutely necessary. For automatic objects allocated on the stack, allocation and deallocation is automatic and safe:

```cpp
{  
    Image i(filename);  
    i.read_plane();  

    // Object destroyed when i goes out of scope  
}
```
In this case, the object’s destructor was run and the memory freed automatically.

Looking at the case where a pointer is used to reference manually-allocated memory on the heap:

```cpp
{  
    Image *i = new Image(filename);  
    i->read_plane();  
    // Memory not freed when pointer i goes out of scope
}  
```

In this case `new` was not paired with the corresponding `delete`, resulting in a **memory leak**. This is the code with the “leak” fixed:

```cpp
{  
    Image *i = new Image(filename);  
    i->read_plane(); // throws exception; memory leaked  
    delete i; // never called
}  
```

`new` and `delete` are now paired, but the code is not exception-safe. If an exception is thrown, memory will still be leaked. Manual memory management requires correct clean up for every exit point in the function, including both all return statements and thrown exceptions. Here, we handle this correctly:

```cpp
{  
    Image *i = new Image(filename);  
    try {  
        i->read_plane(); // throws exception  
    } catch (const std::runtime_error& e) {  
        delete i; // clean up
        throw; // rethrow
    }  
    delete i; // never called for exceptions
}  
```

However, this does not scale. This is painful and error prone when scaled to an entire codebase. Even within this simple function, there is only a single variable with a single exception and single return to deal with. Imagine the combinatorial explosion when there are several variables with different lifetimes and scopes, multiple return points and several exceptions to handle–this is easy to get wrong, so a more robust approach is needed.

Use of `new` is not in the general case safe or sensible. The Bio-Formats API never passes pointers allocated with `new`, nor requires any manual memory management. Instead, “smart” pointers are used throughout to manage memory safely and automatically.

**ome::compat::shared_ptr as a “smart” pointer**

The unsafe example above, has been rewritten to use `ome::compat::shared_ptr`:

```cpp
// Start of block
{  
    ome::compat::shared_ptr<Image> i(ome::compat::make_shared<Image>(filename));  
    i->read_plane(); // throws exception  
    // Memory freed when i's destructor is
```
Rather than managing the memory by hand, responsibility for this is delegated to a “smart” pointer, `ome::compat::shared_ptr`. The memory is freed by the `ome::compat::shared_ptr` destructor which is run at the end of the block scope, on explicit `return`, or when cleaned up by exception stack unwinding.

**Note:** `ome::compat::shared_ptr` is either a `std::shared_ptr` or a `boost::shared_ptr`, depending upon whether C++11 features are available or not, respectively.

- `shared_ptr` object lifetime manages the resource
- `new` replaced with `ome::compat::make_shared`
- May be used as class members; lifetime is tied to class instance
- Clean up for all exit points is automatic and safe
- Allows ownership transfer and sharing
- Allows reference without ownership using `weak_ptr`
- `weak_ptr` references the object but does not prevent it being freed when the last `shared_ptr` reference is lost; this is useful for cycle breaking and is used by the OME XML model objects for references

### Resource Acquisition Is Initialization

Resource Acquisition Is Initialization (RAII) is a programming idiom used throughout modern C++ libraries and applications, including the Standard Library,

- A class is a proxy for a resource
- The resource is acquired when object is initialised
- The resource is released when object is destroyed
- Any resource may be managed (e.g. memory, files, locks, mutexes)
- The C++ language and runtime guarantees make resource management deterministic and reliable
- Safe for use in any scope
- Exception safe
- Used throughout modern C++ libraries and applications

Because this relies implicitly upon the deterministic object destruction guarantees made by the C++ language, this is not used widely in Java APIs which often require manual management of resources such as open files. Used carefully, RAII will prevent resource leaks and result in robust, safe code.

The `FormatReader` API is currently not using RAII due to the use of the `FormatHandler::setId()` interface.

### C++ reference variants

```
// Non-constant Constant
// ------------------------------------- ----------------------------------------------
// Pointer
Image * i; const Image * i;
Image * const i;
const Image * const i;
// Reference
Image& i; const Image& i;
// Shared pointer
ome::compat::shared_ptr<Image> i; ome::compat::shared_ptr<const Image> i;
```
Java has one reference type. Here, we have 22. Clearly, not all of these will typically be used. Below, a subset of these are shown for use for particular purposes.

Class member types:

```cpp
Image i; // Concrete instance
ome::compat::shared_ptr<Image> i; // Reference
ome::compat::weak_ptr<Image> i; // Weak reference
```

Wherever possible, a concrete instance should be preferred. This is not possible for polymorphic types, where a reference is required. In this situation, an `ome::compat::shared_ptr` is preferred if the class owns the member and/or needs control over its lifetime. If the class does not have ownership then an `ome::compat::weak_ptr` will allow safe access to the object if it still exists. In circumstances where manual lifetime management is required, e.g. for performance, and the member is guaranteed to exist for the duration of the object’s lifetime, a plain pointer or reference may be used. A pointer will be used if it is possible for it to be null, or it may be reassigned more than once, or if it is assigned after initial construction. If properly using RAII, using references should be possible and preferred over bare pointers in all cases.

Argument types:

```cpp
// Ownership retained
void read_plane(const Images& image);
```

```
// Ownership shared or transferred
void read_plane(const ome::compat::shared_ptr<Image>& image);
```

Passing primitive types by value is acceptable. However, passing a struct or class by value will implicitly copy the object into the callee’s stack frame, which may be expensive (and requires a copy constructor which will not be guaranteed or even possible for polymorphic types). Passing by reference avoids the need for any copying, and passing by `const` reference will prevent the callee from modifying the object, also making it clear that there is no transfer of ownership. Passing using an `ome::compat::shared_ptr` is possible but not recommended—the copy will involve reference counting overhead which can kill multi-threaded performance since it requires synchronization between all threads; use a `const` reference to an `ome::compat::shared_ptr` to avoid the overhead. If ownership should be transferred or shared with the callee, use a non-`const` reference.

To be absolutely clear, plain pointers are never used and are not acceptable for ownership transfer. A plain reference also makes it clear there is no ownership transfer.

Return types:

```cpp
Image get_image(); // Ownership transferred
Images get_image(); // Ownership retained
ome::compat::shared_ptr<Image> get_image(); // Ownership shared/trans
ome::compat::shared_ptr<Image>& get_image(); // Ownership shared
```

If the callee does not retain a copy of the original object, it can’t pass by reference since it can’t guarantee the object remaining in scope after it returns, hence it must create a temporary value and pass by value. If the callee does retain a copy, it has the option of passing by reference. Passing by reference is preferred when possible. Passing by value implies ownership transfer. Passing
by reference implies ownership retention. Passing an `ome::compat::shared_ptr` by value or reference implies sharing ownership since the caller can retain a reference; if passing by value ownership may be transferred since this implies the callee is not retaining a reference to it (but this is not guaranteed).

Again, to be absolutely clear, plain pointers are never used and are not acceptable for ownership transfer. A plain reference also makes it clear there is no ownership transfer.

- Safety: References cannot be null
- Storing polymorphic types requires use of a `shared_ptr`
- Referencing polymorphic types may require use of a `shared_ptr`
- Safety: To avoid cyclic dependencies, use `weak_ptr`
- Safety: To allow object destruction while maintaining a safe reference, use `weak_ptr`
- `weak_ptr` is not directly usable
- `weak_ptr` is convertible back to `shared_ptr` for use if the object is still in existence
- C++11 move semantics (`&&`) improve the performance of ownership transfer

### 14.2.5 Containers

#### Safe array passing

C++ arrays are not safe to pass in or out of functions since the size is not known unless passed separately.

```cpp
class Image
{
    // Unsafe; size unknown
    uint8_t[] getLUT();
    void setLUT(uint8_t[]& lut);
};
```

C++ arrays “decay” to “bare” pointers, and pointers have no associated size information.

`ome::compat::array` is a safe alternative. This is either a C++11 `std::array` or `boost::array` with older compilers.

```cpp
class Image
{
    typedef ome::compat::array<uint8_t, 256> LUT;

    // Safe; size defined
    const LUT& getLUT() const;
    void setLUT(const LUT&);
};
```

`ome::compat::array` is an array-like object (a class which behaves like an array). Its type and size are defined in the template, and it may be passed around like any other object. Its `array::at()` method provides strict bounds checking, while its index `array::operator[]()` provides unchecked access.

### 14.2.6 Storing and passing unrelated types

#### Types with a common base

```cpp
std::vector<ome::compat::shared_ptr<Base> > v;
v.push_back(ome::compat::make_shared<Derived>());
```
This can store any type derived from Base. An ome::compat::shared_ptr is essential. Without it, bare pointers to the base would be stored, and memory would be leaked when elements are removed from the container (unless externally managed [generally unsafe]). The same applies to passing polymorphic types.

Java containers can be problematic:

- Java can store root Object in containers
- Java can pass and return root Object in methods.
- This is not possible in C++: there is no root object.
- An alternative approach is needed.

**Arbitrary types**

boost::any may be used to store any type:

```cpp
std::vector<boost::any> v;
v.push_back(Anything);
```

- Assign and store any type
- Type erasure (similar to Java generics)
- Use for containers of arbitrary types
- Flexible, but need to cast to each type used to extract
- Code will not be able to handle all possible types meaningfully

This is the most flexible solution, but in order to get a value back out, requires casting it to its specific type. This can mean a situation could arise where values are stored of types which cannot be handled since it is not possible to write the code to handle every single possibility ahead of time. However, if the open-ended flexibility is needed, this is available.

**A fixed set of types**

boost::variant may be used to store a limited set of different types: This avoids the boost::any problem of not being able to handle all possible types, since the scope is limited to a set of allowed types, and a static_visitor can ensure that all types are supported by the code at compile time.

```cpp
typedef boost::variant<int, std::string> variants;
std::vector<variants> v;
v.push_back(43);
v.push_back("ATTO 647N");
```

- Store a set of discriminated types
- “External polymorphism” via static_visitor
- Used to store original metadata
- Used to store nD pixel data of different pixel types

This is not an alternative to a common root object. Instead, this is a discriminated union, which can store one of a defined set of “variant” types. A static visitor pattern may be used to generate code to operate on all of the supported types. The variant type may be used as a class member, passed by value, passed by reference or stored in a container like any other type. Due to the way it is implemented to store values, it does not necessarily need wrapping in an ome::compat::shared_ptr since it can behave as a value type (depending upon the context).

Java uses polymorphism to store and pass the root Object around. The boost::variant and boost::any approaches use templates to (internally) create a common base and manage the stored objects. However, the end user does not need to deal with this complexity directly—the use of the types is quite transparent.
Variant example: MetadataMap

This example demonstrates the use of variants with a simple expansion for two different categories of type (scalars and vectors of scalars).

The MetadataMap class stores key-value pairs, where the value can be either a string, Boolean, or several integer and floating point types, or vectors of any of these types. When converting the data to other forms, it is necessary to flatten the vector types to a set of separate key-value pairs with the key having a numbered suffix, one for each element in the vector.

```cpp
{
    MetadataMap map;
    MetadataMap flat_map (map.flatten());
}
```

A flattened map is created using the following method:

```cpp
MetadataMap MetadataMap::flatten() const {
    MetadataMap newmap;
    for (MetadataMap::const_iterator i = oldmap.begin();
         i != oldmap.end(); ++i) {
        MetadataMapFlattenVisitor v(newmap, i->first);
        boost::apply_visitor(v, i->second);
    }
    return newmap;
}
```

The MetadataMapFlattenVisitor is implemented thusly:

```cpp
// Flatten MetadataMap vector values
struct MetadataMapFlattenVisitor : public boost::static_visitor<>
{
    MetadataMap& map; // Map of flattened elements
    const MetadataMap::key_type& key; // Current key

    MetadataMapFlattenVisitor (MetadataMap& map, const MetadataMap::key_type& key) :
        map(map), key(key) {}

    // Output a scalar value of arbitrary type.
    template<typename T>
    void operator() (const T& v) const {
        map.set(key, v);
    }

    // Output a vector value of arbitrary type.
    template<typename T>
    void operator() (const std::vector<T>& c) const {
        typename std::vector<T>::size_type idx = 1;
        for (typename std::vector<T>::const_iterator i = c.begin();
             i != c.end(); ++i, ++idx) {
            std::ostringstream os;
            os << key << "#" << idx;
            map.set(os.str(), *i);
        }
    }
};
```

The MetadataMapFlattenVisitor is derived from boost::static_visitor, and its templated operator method is specialized and expanded once for each type supported by the variant type used by the map. In the above example, two separate overloaded operators are provided, one for scalar values which is a simple copy, and one for vector values which splits the elements.
into separate keys in the new map. The important part is the call to \texttt{apply\_visitor()}, which takes as arguments the visitor object and the variant to apply it to.

This could be done with a large set of conditionals using \texttt{boost::get\textless T\textgreater (value)} for each supported type. The benefit of the \texttt{boost::static\_visitor} approach is that it ensures that all the types are supported \textit{at compile time}, and in effect results in the same code. If any types are not supported, the code will fail to compile.

\textbf{Variant example: VariantPixelBuffer equality comparison}

This example demonstrates the use of variants with a combinatorial expansion of types.

The \texttt{VariantPixelBuffer} class can contain \texttt{PixelBuffer} classes of various pixel types. Comparing for equality is only performed if the pixel types of the two objects are the same:

\begin{verbatim}
{    VariantPixelBuffer a, b;
    if (a == b) {
        // Buffers are the same.
    }
}
\end{verbatim}

This is implemented using an overloaded equality operator:

\begin{verbatim}
bool VariantPixelBuffer::operator ==
    (const VariantPixelBuffer& rhs) const
{
    return boost::apply\_visitor(PBCompareVisitor(),
                                buffer, rhs.buffer);
}
\end{verbatim}

As before, this is implemented in terms of a \texttt{boost::static\_visitor}, but note that this time it is specialized for \texttt{bool}, meaning that the return type of \texttt{apply\_visitor()} will also be \texttt{bool}, and the operator methods must also return this type.

\begin{verbatim}
struct PBCompareVisitor : public boost::static\_visitor\textless bool\textgreater {
    template <typename T, typename U>
    bool operator() (const T& /* lhs */,
                    const U& /* rhs */) const {
        return false;
    }

    template <typename T>
    bool operator() (const T& lhs,
                    const T& rhs) const {
        return lhs && rhs && (*lhs == *rhs);
    }
};
\end{verbatim}

Unlike the last example, the operator methods now have two arguments, both of which are variant types, and the \texttt{apply\_visitor()} call is passed two variant objects in addition to the visitor object. This causes the templates to be expanded for all pairwise combinations of the possible types. When the types are not equal, the first templated operator is called, which always returns false. When the types are equal the second operator is called; this checks both operands are not null and then performs an equality comparison using the buffer contents. Given that all the operators are inline, we would hope that a good compiler would cause all the false cases to be optimized out after expansion.

\textbf{Variant example: VariantPixelBuffer SFINAE}

This example demonstrates the use of variants with SFINAE.

C++ has a concept known as Substitution Failure Is Not An Error (SFINAE), which refers to it not being an error for a candidate template to fail argument substitution during overload resolution. While this is in and of itself a fairly obscure language detail,
it enables overloading of a method not just on type, but different categories of type, for example integer and floating point types, signed and unsigned integer types, simple and complex types, or combinations of all of these. This is particularly useful when writing algorithms to process pixel data.

Use of SFINAE has been made accessible through the creation of `boost::enable_if (std::enable_if in C++11), and type traits` (type category checking classes such as `is_integer`). The following code is an example of how one might write a visitor for adapting an algorithm to separate integer, floating point, complex floating point and bitmask cases.

```cpp
struct TypeCategoryVisitor : public boost::static_visitor<>
{
    typedef ome::bioformats::PixelProperties<ome::xml::model::enums::PixelType::BIT>::std_type bit_type;

    TypeCategoryVisitor()
    {}

    // Integer pixel types
    template <typename T>
    typename boost::enable_if_c<
        boost::is_integral<T>::value,
        void
    >::type
    operator() (ome::compat::shared_ptr<ome::bioformats::PixelBuffer<T>> & buf)
    {
        // Integer algorithm.
    }

    // Floating point pixel types
    template <typename T>
    typename boost::enable_if_c<
        boost::is_floating_point<T>::value,
        void
    >::type
    operator() (ome::compat::shared_ptr<ome::bioformats::PixelBuffer<T>> & buf)
    {
        // Floating point algorithm.
    }

    // Complex floating point pixel types
    template <typename T>
    typename boost::enable_if_c<
        boost::is_complex<T>::value,
        void
    >::type
    operator() (ome::compat::shared_ptr<ome::bioformats::PixelBuffer<T>> & buf)
    {
        // Complex floating point algorithm.
    }

    // BIT/bool pixel type. Note this is a simple overload since it is
    // a simple type, not a category of different types.
    void
    operator() (ome::compat::shared_ptr<ome::bioformats::PixelBuffer<bit_type>> & buf)
    {
        // Boolean algorithm.
    }
};
```

This visitor may be used with `apply_visitor()` in a similar manner to the previously demonstrated visitors.

`enable_if` has two parameters, the first being a conditional, the second being the return type (in this example, all the methods return `void`). If the conditional is true, then the type expands to the return type and the template is successfully substituted. If the conditional is false (types do not match), then the substitution fails and the template will not be used. Note that the conditional is itself a type, which can be confusing, since all this logic is driven by conditional template expansion.

Normal templates are specialized for a type. This approach allows specialization for different `categories` of type. Without this approach it would be necessary to write separate overloads for each individual type (each integer type, each floating point type, each complex type, etc.), even when the logic would be identical for e.g. the different integer types. This approach therefore removes the need for unnecessary code duplication, and the type traits checks make each type category explicit to the reader.

14.2. C++ conversion details
14.3 Tutorial

14.3.1 Metadata

Bio-Formats supports several different classes of metadata, from very basic information about the image dimensions and pixel type to detailed information about the acquisition hardware and experimental parameters. From simplest to most complex, these are:

**Core metadata**  Basic information describing an individual 5D image (series), including dimension sizes, dimension order and pixel type

**Original metadata**  Key-value pairs describing metadata from the original file format for the image. Two forms exist: global metadata for an entire dataset (image collection) and series metadata for an individual 5D image.

**Metadata store**  A container for all image metadata providing interfaces to get and set individual metadata values. This is a superset of the core and original metadata content (it can represent all values contained within the core and original metadata). It is an alternative representation of the OME-XML data model objects, and is used by the Bio-Formats reader and writer interfaces.

**OME-XML data model objects**  The abstract OME-XML data model is realized as a collection of *model objects*. Classes are generated from the elements of the OME-XML data model schema, and a tree of the model objects acts as a representation of the OME data model which may be modified and manipulated. The model objects may be created from an OME-XML text document, and vice versa.

For the simplest cases of reading and writing image data, the core metadata interface will likely be sufficient. If specific individual parameters from the original file format are needed, then original metadata may also be useful. For more advanced processing and rendering, the metadata store should be the next source of information, for example to get information about the image scale, stage position, instrument setup including light sources, light paths, detectors etc., and access to plate/well information, regions of interest etc. Direct access to the OME-XMl data model objects is an alternative to the metadata store, but is more difficult to use; certain modifications to the data model may only be made via direct access to the model objects, otherwise the higher-level metadata store interface should be preferred.

The header file `ome/bioformats/MetadataTools.h` provides several convenience functions to work with and manipulate the various forms of metadata, including conversion of Core metadata to and from a metadata store.

### Core metadata

Core metadata is accessible through the getter methods in the `FormatReader` interface. These operate on the *current* series, set using the `setSeries()` method. The `CoreMetadata` objects are also accessible directly using the `getCoreMetadataList` method. The `FormatReader` interface should be preferred; the objects themselves are more of an implementation detail at present.

```cpp
void readMetadata(const FormatReader& reader,
                  std::ostream& stream)
{
    // Get total number of images (series)
    dimension_size_type ic = reader.getSeriesCount();
    stream << "Image count: " << ic << '\n';

    // Loop over images
    for (dimension_size_type i = 0; i < ic; ++i)
    {
```

---

36`http://www.openmicroscopy.org/site/support/bio-formats5.0/`
37`http://www.openmicroscopy.org/site/support/legacy/`
38`http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/MetadataTools_8h_source.html`
// Change the current series to this index
reader.setSeries(i);

// Print image dimensions (for this image index)
stream << "Dimensions for Image " << i << ':' << '
' << "\n\tX = " << reader.getSizeX() << '
' << "\n\tY = " << reader.getSizeY() << '
' << "\n\tZ = " << reader.getSizeZ() << '
' << "\n\tT = " << reader.getSizeT() << '
' << "\n\tC = " << reader.getSizeC() << '
' << "\n\tEffectiveC = " << reader.getEffectiveSizeC() << '
' << ' ';

for (dimension_size_type channel = 0; channel < reader.getEffectiveSizeC(); ++channel)
{
    stream << "\n\tChannel " << channel << ':' << '
' << "\n\tRGB = " << (reader.isRGB(channel) ? "true" : "false") << '
' << "\n\tRGBC = " << reader.getRGBChannelCount(channel) << '
' << ' ';
}
stream << '
';

// Get total number of planes (for this image index)
dimension_size_type pc = reader.getImageCount();
stream << "\tPlane count: " << pc << '
';

// Loop over planes (for this image index)
for (dimension_size_type p = 0; p < pc; ++p)
{
    // Print plane position (for this image index and plane
    // index)
    ome::compat::array<dimension_size_type, 3> coords = reader.getZCTCoords(p);
    stream << "\tPosition of Plane " << p << ':' << '
' << "\tTheZ = " << coords[0] << '
' << "\tTheT = " << coords[2] << '
' << "\tTheC = " << coords[1] << ' ';
}
}]

If implementing a reader, it is fairly typical to set the basic image metadata in CoreMetadata objects, and then use the fill-Metadata() function in ome/bioformats/MetadataTools.h39 to fill the reader’s metadata store with this information, before filling the metadata store with additional (non-core) metadata as required. When writing an image, a metadata store is required in order to provide the writer with all the metadata needed to write an image. If the metadata store was not already obtained from a reader, fillMetadata() may also be used in this situation to create a suitable metadata store:

shared_ptr< ome::xml::meta::OMEXMLMetadata>
createMetadata()
{
    // OME-XML metadata store.
    shared_ptr< ome::xml::meta::OMEXMLMetadata> meta(make_shared< ome::xml::meta::OMEXMLMetadata>());

    // Create simple CoreMetadata and use this to set up the OME-XML
    // metadata. This is purely for convenience in this example; a
    // real writer would typically set up the OME-XML metadata from an
    // existing MetadataRetrieve instance or by hand.
    std::vector<shared_ptr<CoreMetadata>> > seriesList;
    shared_ptr<CoreMetadata> core(make_shared<CoreMetadata>());
    core->sizeX = 512U;
    core->sizeY = 512U;

39http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/MetadataTools_8h_source.html
core->sizeC.clear(); // defaults to 1 channel with 1 subchannel; clear this
core->sizeC.push_back(3U); // replace with single RGB channel
core->pixelType = ome::xml::model::enums::PixelFormat::UINT16;
core->interleaved = false;
core->bitsPerPixel = 12U;
core->dimensionOrder = DimensionOrder::XYZTC;
seriesList.push_back(core);

fillMetadata(*meta, seriesList);

return meta;
}

Full example source: metadata-formatreader.cpp, metadata-formatreader.cpp

See also:
- CoreMetadata
- FormatReader

Original metadata

Original metadata is stored in two forms: in a MetadataMap which is accessible through the FormatReader interface, which offers access to individual keys and the whole map for both global and series metadata. It is also accessible using the metadata store; original metadata is stored as an XMLAnnotation. The following example demonstrates access to the global and series metadata using the FormatReader interface to get access to the maps:

```cpp
void readOriginalMetadata(const FormatReader& reader, std::ostream& stream)
{
    // Get total number of images (series)
    dimension_size_type ic = reader.getSeriesCount();
    stream << "Image count: " << ic << '\n';

    // Get global metadata
    const MetadataMap& global = reader.getGlobalMetadata();

    // Print global metadata
    stream << "Global metadata:\n" << global << '\n';

    // Loop over images
    for (dimension_size_type i = 0 ; i < ic; ++i)
    {
        // Change the current series to this index
        reader.setSeries(i);

        // Print series metadata
        const MetadataMap& series = reader.getSeriesMetadata();

        // Print image dimensions (for this image index)
        stream << "Metadata for Image " << i << ":\n" << series
                << '\n';
    }
}
```

40http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1CoreMetadata.html
41http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1FormatReader.html
It would also be possible to use `getMetadataValue()` and `getSeriesMetadataValue()` to obtain values for individual keys. Note that the `MetadataMap` values can be scalar values or lists of scalar values; call the `flatten()` method to split the lists into separate key-value pairs with a numbered suffix.

Full example source: `metadata-formatreader.cpp`

See also:
- `MetadataMap`[^42]
- `FormatReader`[^43]
- `OriginalMetadataAnnotation`[^44]

**Metadata store**

Access to metadata is provided via the `MetadataStore` and `MetadataRetrieve` interfaces. These provide setters and getters, respectively, to store and retrieve metadata to and from an underlying abstract metadata store. The primary store is the `OMEXMLMetadata` which stores the metadata in OME-XML data model objects (see below), and implements both interfaces. However, other storage classes are available, and may be used to filter the stored metadata, combine different stores, or do nothing at all. Additional storage backends could also be implemented, for example to allow metadata retrieval from a relational database, or JSON/YAML.

When using `OMEXMLMetadata` the convenience function `createOMEXMLMetadata()` is the recommended method for creating a new instance and then filling it with the content from an OME-XML document. This is overloaded to allow the OME-XML to be obtained from various sources. For example, from a file:

```
// Create metadata directly from file
shared_ptr<OMEXMLMetadata> filemeta(createOMEXMLMetadata(filename));
```

Alternatively from a DOM tree:

```
// XML platform (required by Xerces)
xmllib::Platform xmlplat;
// XML DOM tree containing parsed file content
xmllib::dom::Document inputdoc(xmllib::dom::createDocument(filename));
// Create metadata from DOM document
shared_ptr<OMEXMLMetadata> dommeta(createOMEXMLMetadata(inputdoc));
```

The convenience function `getOMEXML()` may be used to reverse the process, i.e. obtain an OME-XML document from the store. Note the use of `convert()`. Only the `OMEXMLMetadata` class can dump an OME-XML document, therefore if the source of the data is another class implementing the `MetadataRetrieve` interface, the stored data will need to be copied into an `OMEXMLMetadata` instance first.

```
meta::OMEXMLMetadata *omexmlmeta = dynamic_cast<meta::OMEXMLMetadata *>(meta);
if (!omexmlmeta)
    {
        convertmeta = make_shared<meta::OMEXMLMetadata>();
        meta::convert(meta, &convertmeta);
        omexmlmeta = &convertmeta;
    }
// Get OME-XML text from metadata store (and validate it)
std::string omexml(getOMEXML(omexmlmeta, true));
```

Conceptually, the metadata store contains lists of objects, accessed by index (insertion order). In the example below, `getImageCount()` method is used to find the number of images. This is then used to safely loop through each of the available images. Each of the `getPixelsSizeA()` methods takes the image index as its only argument. Internally, this is used to find the Image

[^42]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1MetadataMap.html
[^43]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1FormatReader.html
[^44]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1xml_1_1model_1_1OriginalMetadataAnnotation.html
model object for the specified index, and then call the `getSizeA()` method on that object and return the result. Since objects can contain other objects, some accessor methods require the use of more than one index. For example, an `Image` object can contain multiple `Plane` objects. Similar to the above example, there is a `getPlaneCount()` method, however since it is contained by an `Image` it has an additional image index argument to get the plane count for the specified image. Likewise its accessors such as `getPlaneTheZ()` take two arguments, the image index and the plane index. Internally, these indices will be used to find the Image, then the Plane, and then call `getTheZ()`. When using the `MetadataRetrieve` interface with an OMEXMLMetadata store, the methods are simply a shorthand for navigating through the tree of model objects.

```cpp
void queryMetadata(const MetaDataRetrieve& meta, const std::string& state, std::ostream& stream)
{
    // Get total number of images (series)
    index_type ic = meta.getImageCount();
    stream << "Image count: " << ic << '\n';

    // Loop over images
    for (index_type i = 0 ; i < ic; ++i)
    {
        // Print image dimensions (for this image index)
        stream << "Dimensions for Image " << i << ' ' << state << ':'
                << "\n\tX = " << meta.getPixelsSizeX(i)
                << "\n\tY = " << meta.getPixelsSizeY(i)
                << "\n\tZ = " << meta.getPixelsSizeZ(i)
                << "\n\tT = " << meta.getPixelsSizeT(i)
                << "\n\tC = " << meta.getPixelsSizeC(i)
                << '\n';

        // Get total number of planes (for this image index)
        index_type pc = meta.getPlaneCount(i);
        stream << "\tPlane count: " << pc << '\n';

        // Loop over planes (for this image index)
        for (index_type p = 0 ; p < pc; ++p)
        {
            // Print plane position (for this image index and plane
            // index)
            stream << "\tPosition of Plane " << p << ' ';
            << "\n\tTheZ = " << meta.getPlaneTheZ(i, p)
            << "\n\tTheT = " << meta.getPlaneTheT(i, p)
            << "\n\tTheC = " << meta.getPlaneTheC(i, p)
            << '\n';
        }
    }
}
```

The methods for storing data using the `MetadataStore` interface are similar. The set methods use the same indices as the get methods, with the value to set as an additional initial argument. The following example demonstrates how to update dimension sizes for images in the store:

```cpp
void updateMetadata(MetaDataRetrieve& meta)
{
    // Get total number of images (series)
    index_type ic = meta.getImageCount();

    // Loop over images
    for (index_type i = 0 ; i < ic; ++i)
    {
        // Change image dimensions (for this image index)
        meta.setPixelsSizeX(12, i);
        meta.setPixelsSizeY(24, i);
    }
}
```
When adding new objects to the store, as opposed to updating existing ones, some additional considerations apply. An new object is added to the store if the object corresponding to an index does not exist and the index is the current object count (i.e. one past the end of the last valid index). Note that for data model objects with a setID() method, this method alone will trigger insertion and must be called first, before any other methods which modify the object. The following example demonstrates the addition of a new Image to the store, plus contained Plane objects.

```cpp
void addMetadata (meta::Metadata& meta) {
  // Get total number of images (series)
  index_type i = meta.getImageCount();

  // Size of Z, T and C dimensions
  index_type nz = 3;
  index_type nt = 1;
  index_type nc = 4;

  // Create new image; the image index is the same as the image count, i.e. one past the end of the current limit; createID
  // creates a unique identifier for the image
  meta.setImageID (createID("Image", i), i);
  // Set Pixels identifier using createID and the same image index
  meta.setPixelsID (createID("Pixels", i), i);
  // Now set the dimension order, pixel type and dimension sizes for this image, using the same image index
  meta.setPixelsDimensionOrder (model::enums::DimensionOrder::XYZTC, i);
  meta.setPixelsType (model::enums::PixelType::UINT8, i);
  meta.setPixelsSizeX (256, i);
  meta.setPixelsSizeY (256, i);
  meta.setPixelsSizeZ (nz, i);
  meta.setPixelsSizeT (nt, i);
  meta.setPixelsSizeC (nc, i);

  // Plane count
  index_type pc = nz * nc * nt;

  // Loop over planes
  for (index_type p = 0; p < pc; ++p) {
    // Get the Z, T and C coordinate for this plane index
    array<dimension_size_type, 3> coord =
      getZCTCoords("XYZTC", nz, nc, nt, pc, p);
    // Set the plane position using the image index and plane index to reference the correct plane
    meta.setPlaneTheZ (coord[0], i, p);
    meta.setPlaneTheT (coord[2], i, p);
    meta.setPlaneTheC (coord[1], i, p);
  }

  // Add MetadataOnly to Pixels since this is an example without TiffData or BinData
  meta::OMEXMLMetadata *omexmlmeta = dynamic_cast<meta::OMEXMLMetadata*>(meta);
  if (omexmlmeta)
    addMetadataOnly(*omexmlmeta, i);
}
```
The data model objects are not typically used directly, but are created, modified and queried using the Metadata interfaces (above), so in practice these examples should not be needed.

To create a tree of OME-XML data model objects from OME-XML text:

```cpp
// XML DOM tree containing parsed file content
xml::dom::Document inputdoc(xml::dom::createDocument(filename));
// OME Model (needed only during parsing to track model object references)
model::detail::OMEModel model;
// OME Model root object
shared_ptr<model::OME> modelroot(make_shared<model::OME>());
// Fill OME model object tree from XML DOM tree
modelroot->update(inputdoc.getDocumentElement(), model);
```

In this example, the OME-XML text is read from a file into a DOM tree. This could have been read directly from a string or stream if the source was not a file. The DOM tree is then processed using the OME root object’s `update()` method, which uses the data from the DOM tree elements to create a tree of corresponding model objects contained by the root object.

To reverse the process, taking a tree of OME-XML model objects and converting them back of OME-XML text:

```cpp
// Schema version to use
const std::string schema("http://www.openmicroscopy.org/Schemas/OME/2013-06");
// XML DOM tree (initially containing an empty OME root element)
xml::dom::Document outputdoc(xml::dom::createEmptyDocument(schema, "OME");
// Fill output DOM document from OME-XML model
modelroot->asXMLElement(outputdoc);
// Dump DOM tree as text to stream
xml::dom::writeDocument(outputdoc, stream);
```

Here, the OME root object’s `asXMLElement()` method is used to copy the data from the OME root object and its children into an XML DOM tree. The DOM tree is then converted to text for output.

Full example source: `model-io.cpp`

See also:
- OME model classes
- OME

### 14.3.2 Pixel data

The Bio-Formats Java implementation stores and passes pixel values in a raw byte array. Due to limitations with C++ array passing, this was not possible for the C++ implementation. While a vector or other container could have been used, several problems...
remain. The type and endianness of the data in the raw bytes is not known, and the dimension ordering and dimension extents are also unknown, which imposes a significant burden on the programmer to correctly process the data. The C++ implementation provides two types to solve these problems.

The `PixelBuffer` class is a container of pixel data. It is a template class, templated on the pixel type in use. The class contains the order of the dimensions, and the size of each dimension, making it possible to process pixel data without need for externally-provided metadata to describe its structure. This class may be used to contain and process pixel data of a specific pixel type. Internally, the pixel data is contained within a `boost::multi_array` as a 9D hyper-volume, though its usage in this release of Bio-Formats is limited to 5D. The class can either contain its own memory allocation for pixel data, or it can reference memory allocated or mapped externally, allowing use with memory-mapped data, for example.

In many situations, it is desirable to work with arbitrary pixel types, or at least the set of pixel types defined in the OME data model in its `PixelType` enumeration. The `VariantPixelBuffer` fulfills this need, using `boost::variant` to allow it to create a `PixelBuffer` specialized for any of the pixel types in the OME data model. This is used to allow transfer and processing of any supported pixel type, for example by the `FormatReader` class' `getLookupTable()` and `openBytes()` methods, and the corresponding `.getWriter` class' `setLookupTable()` and `saveBytes()` methods.

An additional problem with supporting many different pixel types is that each operation upon the pixel data, for example for display or analysis, may require implementing separately for each pixel type. This imposes a significant testing and maintenance burden. `VariantPixelBuffer` solves this problem through use of `boost::apply_visitor()` and `boost::static_visitor`, which allow algorithms to be defined in a template and compiled for each pixel type. They also allow algorithms to be specialized for different classes of pixel type, for example signed vs. unsigned, integer vs. floating point, or simple vs. complex, or special-cased per type e.g. for bitmasks. When `boost::apply_visitor()` is called with a specified algorithm and `VariantPixelBuffer` object, it will select the matching algorithm for the pixel type contained within the buffer, and then invoke it on the buffer. This permits the programmer to support arbitrary pixel types without creating a maintenance nightmare, and without unnecessary code duplication.

The 9D pixel buffer makes a distinction between the logical dimension order (used by the API) and the storage order (the layout of the pixel data in memory). The logical order is defined by the values in the `Dimensions` enum. The storage order is specified by the programmer when creating a pixel buffer.

The following example shows creation of a pixel buffer with a defined size, and default storage order\(^1\):

```c++

// Language type for FLOAT pixel data
typedef PixelProperties<PixelType::FLOAT>::std_type float_pixel_type;

// Create PixelBuffer for floating point data
// X=512 Y=512 Z=16 T=1 C=3 S/z/t/c=1
PixelBuffer<float_pixel_type> buffer
  (boost::extents[512][512][16][1][3][1][1][1], PixelType::FLOAT);
```

The storage order may be set explicitly. The order may be created by hand, or with a helper function\(^2\). While the helper function is limited to supporting the ordering defined by the data model, specifying the order by hand allows additional flexibility. Manual ordering may be used to allow the indexing for individual dimensions to run backward rather than forward, which is useful if the Y-axis requires inverting, for example. The following example shows creation of two pixel buffers with defined storage order using the helper function:

```c++

// Language type for UINT16 pixel data
typedef PixelProperties<PixelType::UINT16>::std_type uint16_pixel_type;

// Storage order is XYCTZ2tzc; subchannels are not interleaved
// dimensions
PixelBufferBase::storage_order_type order1
  (PixelBufferBase::make_storage_order(DimensionOrder::XYCTZ, false));

// Create PixelBuffer for unsigned 16-bit data with specified storage order
// X=512 Y=512 Z=16 T=1 C=3 S/z/t/c=1
PixelBuffer<UINT16_pixel_type> buffer1
  (boost::extents[512][512][16][1][3][1][1][1], PixelType::UINT16);
```

\(^1\)http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/namespaceme_1_1bioformats.html#a0e9bb405a4815c189fd78325f68a91a
\(^2\)http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1PixelBufferBase.html#a419ad49f2e90937a57b8b174b56380b
\(^3\)http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1PixelBufferBase.html#ac7e922610bf561f311d13c3d7fcaeb69
// Language type for INT8 pixel data
typedef PixelProperties<PixelType::INT8>::std_type int8_pixel_type;

// Storage order is SXYZCTtc; subchannels are interleaved
// ("chunky") before XY; lowercase letters are unused Modulo dimensions
PixelBufferBase::storage_order_type order2 =
    (PixelBufferBase::make_storage_order(DimensionOrder::XYZCT, true));

// Create PixelBuffer for signed 8-bit RGB data with specified storage order
// X=1024 Y=1024 Z=1 T=1 C=1 S=3 z/t/c=1
PixelBuffer<int8_pixel_type> buffer2 =
    boost::extents[1024][1024][1][1][1][3][1][1][1],
    PixelType::INT8,
    ome::bioformats::ENDIAN_NATIVE,
    order2);

Note that the logical order of the dimension extents is unchanged.

In practice, it is unlikely that you will need to create any PixelBuffer objects directly. The FormatReader and FormatWriter interfaces use VariantPixelBuffer objects, and in the case of the reader interface the getLookupTable() and openBytes() methods can be passed a default-constructed VariantPixelBuffer and it will be set up automatically, changing the image dimensions, dimension order and pixel type to match the data being fetched, if the size, order and type do not match. For example, to read all pixel data in an image using openBytes():

```cpp
void readPixelData(const FormatReader& reader, 
                   std::ostream& stream) 
{
    // Get total number of images (series)
    dimension_size_type ic = reader.getSeriesCount();
    stream << "Image count: " << ic << 'n';

    // Loop over images
    for (dimension_size_type i = 0; i < ic; ++i) 
    {
        // Change the current series to this index
        reader.setSeries(i);

        // Get total number of planes (for this image index)
        dimension_size_type pc = reader.getImageCount();
        stream << "Plane count: " << pc << 'n';

        // Pixel buffer
        VariantPixelBuffer buf;

        // Loop over planes (for this image index)
        for (dimension_size_type p = 0; p < pc; ++p) 
        {
            // Read the entire plane into the pixel buffer.
            reader.openBytes(p, buff);

            // If this wasn't an example, we would do something
            // exciting with the pixel data here.
            stream << "Pixel data for Image " << i
                 << " Plane " << p << " contains "
                 << buff.num_elements() << " pixels\n";
        }
    }
}
```
To perform the reverse process, writing pixel data with `saveBytes()`:

```cpp
void writePixelData(FormatWriter& writer,
                    std::ostream& stream)
{
    // Total number of images (series)
    dimension_size_type ic = 1;
    stream << "Image count: " << ic << '\n';

    // Loop over images
    for (dimension_size_type i = 0 ; i < ic; ++i)
    {
        // Change the current series to this index
        writer.setSeries(i);

        // Total number of planes.
        dimension_size_type pc = 1;
        stream << "Plane count: " << pc << '\n';

        // Loop over planes (for this image index)
        for (dimension_size_type p = 0 ; p < pc; ++p)
        {
            // Pixel buffer; size 512 × 512 with 3 subchannels of type
            // uint16_t. It uses the native endianness and has a
            // storage order of XYZTC without interleaving
            // (subchannels are planar).
            shared_ptr<PixelBuffer<PixelProperties<PixelType::UINT16>::std_type> >
                buffer(make_shared<PixelBuffer<PixelProperties<PixelType::UINT16>::std_type> >
                        (boost::extents[512][512][1][1][1][1][1][1][1],
                         PixelType::UINT16, ome::bioformats::ENDIAN_NATIVE,
                         PixelBufferBase::make_storage_order(DimensionOrder::XYZTC, false)));

            // Fill each subchannel with a different intensity ramp in
            // the 12-bit range. In a real program, the pixel data
            // would typically be obtained from data acquisition or
            // another image.
            for (dimension_size_type x = 0; x < 512; ++x)
                for (dimension_size_type y = 0; y < 512; ++y)
                    {
                        PixelBufferBase::indices_type idx;
                        std::fill(idx.begin(), idx.end(), 0);
                        idx[DIM_SPATIAL_X] = x;
                        idx[DIM_SPATIAL_Y] = y;

                        idx[DIM_SUBCHANNEL] = 0;
                        buffer->at(idx) = (static_cast<float>(x) / 512.0f) * 4096.0f;
                        idx[DIM_SUBCHANNEL] = 1;
                        buffer->at(idx) = (static_cast<float>(y) / 512.0f) * 4096.0f;
                        idx[DIM_SUBCHANNEL] = 2;
                        buffer->at(idx) = (static_cast<float>((x+y) / 1024.0f) * 4096.0f;
                    }

            VariantPixelBuffer vbuffer(buffer);
            stream << "PixelBuffer PixelType is " << buffer->pixelType() << '\n';
            stream << "VariantPixelBuffer PixelType is " << vbuffer.pixelType() << '\n';
            stream << std::flush;

            // Write the the entire pixel buffer to the plane.
            writer.saveBytes(p, vbuffer);

            stream << "Wrote " << buffer->num_elements() << ' ' << buffer->pixelType() << " pixels\n;";
        }
    }
}
```
Both buffer classes provide access to the pixel data so that it may be accessed, manipulated and passed elsewhere. The PixelBuffer class provides an at method. This allows access to individual pixel values using a 9D coordinate:

```cpp
// Set all pixel values for Z=2 and C=1 to 0.5
// 9D index, default values to zero if unused
PixelBuffer<float_pixel_type>::indices_type idx;
// Set Z and C indices
idx[ome::bioformats::DIM_SPATIAL_Z] = 2;
idx[ome::bioformats::DIM_CHANNEL] = 1;
idx[ome::bioformats::DIM_TEMPORAL_T] =
idx[ome::bioformats::DIM_SUBCHANNEL] =
idx[ome::bioformats::DIM_MODULO_Z] =
idx[ome::bioformats::DIM_MODULO_T] =
idx[ome::bioformats::DIM_MODULO_C] = 0;
for (uint16_t x = 0; x < 512; ++x)
{  
    idx[ome::bioformats::DIM_SPATIAL_X] = x;
    for (uint16_t y = 0; y < 512; ++y)
    {  
        idx[ome::bioformats::DIM_SPATIAL_Y] = y;
        buffer.at(idx) = 0.5f;
    }
}
```

Conceptually, this is the same as using an index for a normal 1D array, but extended to use an array of nine indices for each of the nine dimensions, in the logical storage order. The VariantPixelBuffer does not provide an at method for efficiency reasons. Instead, visitors should be used for the processing of bulk pixel data. For example, this is one way the minimum and maximum pixel values could be obtained:

```cpp
// Visitor to compute min and max pixel value for pixel buffer of any pixel type
// The static_visitor specialization is the required return type of the operator() methods and boost::apply_visitor()
struct MinMaxVisitor : public boost::static_visitor<std::pair<double, double>>
{
    // The min and max values will be returned in a pair. double is used since it can contain the value for any pixel type
    typedef std::pair<double, double> result_type;

    // Get min and max for any non-complex pixel type
    template<typename T>
    result_type operator() (const T& v) {
        typedef typename T::element_type::value_type value_type;
        value_type *min = std::min_element(v->data(), v->data() + v->num_elements());
        value_type *max = std::max_element(v->data(), v->data() + v->num_elements());

        return result_type(static_cast<double>(*min),
                            static_cast<double>(*max));
    }

    // Less than comparison for real part of complex numbers
    template<typename T>
    static bool
```
complex_real_less(const T & lhs, const T & rhs)
{
    return std::real(lhs) < std::real(rhs);
}

// Greater than comparison for real part of complex numbers
template<typename T>
static bool complex_real_greater(const T & lhs, const T & rhs)
{
    return std::real(lhs) > std::real(rhs);
}

// Get min and max for complex pixel types (COMPLEX and
// DOUBLECOMPLEX)
// This is the same as for simple pixel types, except for the
// addition of custom comparison functions and conversion of the
// result to the real part.

void applyVariant()
{
    // Make variant buffer (int32, 16x16 single plane)
    VariantPixelBuffer variant(boost::extents[16][16][1][1][1][1][1][1],
                                PixelType::INT32);
    // Get buffer size
    VariantPixelBuffer::size_type size = variant.num_elements();
    // Create sample random-ish data
    std::vector<int32_t> vec;
    for (VariantPixelBuffer::size_type i = 0; i < size; ++i)
    {
        int32_t val = static_cast<int32_t>(i + 42);
        vec.push_back(val);
    }
    std::random_shuffle(vec.begin(), vec.end());
    // Assign sample data to buffer.
    variant.assign(vec.begin(), vec.end());
    // Create and apply visitor
    MinMaxVisitor visitor;
    MinMaxVisitor::result_type result = boost::apply_visitor(visitor, variant.vbuffer());
    std::cout << "Min is " << result.first << ", max is " << result.second << '\n';
}
This example demonstrates several features:

- The visitor operators can return values to the caller (for more complex algorithms, the visitor class could use member variables and additional methods)
- The operator is expanded once for each pixel type
- The operators can be special-cased for individual pixel types; here we use the SFINAE rule to implement a specialization for an entire category of pixel types (complex numbers), but standard function overloading and templates will also work for more common cases
- Pixel data can be assigned to the buffer with a single `assign()` call.

The Bio-Formats source uses pixel buffer visitors for several purposes, for example to load pixel data into OpenGL textures, which automatically handles pixel format conversion and repacking of pixel data as needed.

While the pixel buffers may appear complex, they do permit the Bio-Formats library to support all pixel types with relative ease, and it will allow your applications to also handle multiple pixel types by writing your own visitors. Assignment of one buffer to another will also repack the pixel data if they use different storage ordering (i.e. the logical ordering is used for the copy), which can be useful if you need the pixel data in a defined ordering.

If all you want is access to the raw data, as in the Java API, you are not required to use the above features. Simply use the `data()` method on the buffer to get a pointer to the raw data. Note that you will need to multiply the buffer size obtained with `num_elements()` by the size of the pixel type (`bytesPerPixel()` or `sizeof()` on the buffer value_type).

Alternatively, it is also possible to access the underlying `boost::multi_array` using the `array()` method, if you need access to functionality not wrapped by `PixelBuffer`.

Full example source: `pixeldata.cpp`

See also:

- `PixelFormat`
- `PixelBuffer`
- `VariantPixelBuffer`
- `FormatReader::getLookupTable`
- `FormatReader::openBytes`
- `FormatWriter::setLookupTable`
- `FormatWriter::saveBytes`

### 14.3.3 Reading images

Image reading is performed using the `FormatReader` interface. This is an abstract reader interface implemented by file-format-specific reader classes. Examples of readers include `TIFFReader`, which implements reading of Baseline TIFF (optionally with additional ImageJ metadata), and `OMETIFFReader` which implements reading of OME-TIFF (TIFF with OME-XML metadata).

Using a reader involves these steps:

1. Create a reader instance.
2. Set options to control reader behavior.
3. Call `setId()` to specify the image file to read.
4. Retrieve desired metadata and pixel data.
5. Close the reader.
These steps are illustrated in this example:

```cpp
// Create TIFF reader
shared_ptr<FormatReader> reader(make_shared<TIFFReader>());

// Set reader options before opening a file
reader->setMetadataFiltered(false);
reader->setGroupFiles(true);

// Open the file
reader->setId(filename);

// Display series core metadata
readMetadata("reader, std::cout");

// Display global and series original metadata
readOriginalMetadata("reader, std::cout");

// Read pixel data
readPixelData("reader, std::cout");

// Explicitly close reader
reader->close();
```

Here we create a reader to read TIFF files, set two options (metadata filtering and file grouping), and then call `setId()`. At this point the reader has been set up and initialized, and we can then read metadata and pixel data, which we covered in the preceding sections. You might like to combine this example with the `MinMaxVisitor` example to make it display the minimum and maximum values for each plane in an image; if you try running the example with TIFF images of different pixel types, it will transparently adapt to any supported pixel type.

**Note:** Reader option-setting methods may only be called before `setId()`. Reader state changing and querying methods such as `setSeries()` and `getSeries()`, metadata retrieval and pixel data retrieval methods may only be called after `setId()`. If these constraints are violated, a `FormatException` will be thrown.

Full example source: `metadata-formatreader.cpp`

See also:
- `FormatReader`[^62]
- `TIFFReader`[^63]
- `OMETIFFReader`[^64]

### 14.3.4 Writing images

Image writing is performed using the `FormatWriter` interface. This is an abstract writer interface implemented by file-format-specific writer classes. Examples of writers include `MinimalTIFFWriter`, which implements writing of Baseline TIFF and `OMETIFFWriter` which implements writing of OME-TIFF (TIFF with OME-XML metadata).

Using a writer involves these steps:

1. Create a writer instance.
2. Set metadata store to use.
3. Set options to control writer behavior.
4. Call `setId()` to specify the image file to write.
5. Store pixel data for each plane of each image in the specified dimension order.
6. Close the writer.

[^62]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1FormatReader.html
[^63]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1in_1_1TIFFReader.html
[^64]: http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1in_1_1OMETIFFReader.html
These steps are illustrated in this example:

```cpp
// Create metadata for the file to be written.
shared_ptr<ome::xml::metadata::MetadataRetrieve> meta(createMetadata());

// Create TIFF writer
shared_ptr<FormatWriter> writer(make_shared<OMETIFFWriter>());

// Set writer options before opening a file
writer->setMetadataRetrieve(meta);
writer->setInterleaved(false);

// Open the file
writer->setId(filename);

// Write pixel data
writePixelData("writer, std::cout);

// Explicitly close writer
writer->close();
```

Here we create a writer to write OME-TIFF files, set the metadata store using metadata we create, then set a writer option (sample interleaving), and then call `setId()`. At this point the writer has been set up and initialized, and we can then write the pixel data, which we covered in the preceding sections. Finally we call `close()` to flush all data.

**Note:** Metadata store setting and writer option-setting methods may only be called before `setId()`. Writer state changing and querying methods such as `setSeries()` and `getSeries()`, and pixel data storage methods may only be called after `setId()`. If these constraints are violated, a `FormatException` will be thrown.

**Note:** `close()` should be called explicitly to catch any errors. While this will be called by the destructor, the destructor can’t throw exceptions and any errors will be silently ignored.

Full example source: `metadata-formatwriter.cpp`

See also:

- `FormatWriter`
- `TIFFWriter`
- `OMETIFFWriter`

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 14.4 Environment

The Bio-Formats libraries and programs are configured and built to use a set of search paths for different components. It should not be necessary to override these defaults. The `bf` command will be able to autodetect the installation directory configure paths on most platforms, and the Bio-Formats libraries are also able to determine the paths on most platforms so long as the library search path is configured correctly. However, the following environment variables may be used to override the defaults if this proves necessary:

65 http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1FormatWriter.html
66 http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1out_1_1MinimalTIFFWriter.html
67 http://downloads.openmicroscopy.org/latest/bio-formats-cpp5.1/api/classome_1_1bioformats_1_1out_1_1OMETIFFWriter.html
68 http://www.openmicroscopy.org/site/support/bio-formats5.0/
69 http://www.openmicroscopy.org/site/support/legacy/
14.4.1 Installation root

BIOFORMATS_HOME

The root of the installation (if applicable). Setting this will allow the installation to be used in a location other than the one configured. It will also default all the following variables unless they are explicitly overridden individually. This is not useful if an absolute installation path has been configured (e.g. if using /usr/local).

14.4.2 Basic paths

These may be shared with other packages if configured to do so (e.g. if using /usr/local). See GNUInstallDirs\(^70\) for more details. Not all of these paths are currently used, but may be used in the future.

BIOFORMATS_BINDIR Programs invocable directly by an end user (on the default PATH)

BIOFORMATS_SBINDIR Programs invocable directly by an end user or admin (not on the default PATH)

BIOFORMATS_SYSLIBEXECDIR Programs not typically invoked directly (called internally by the Bio-Formats tools and libraries as needed)

BIOFORMATS_SYSCONFDIR Configuration files

BIOFORMATS_SHAREDSTATEDIR Shared state

BIOFORMATS_LOCALSTATEDIR Local state

BIOFORMATS_LIBDIR Libraries

BIOFORMATS_INCLUDEDIR C and C++ include files

BIOFORMATS_OLDINCLUDEDIR C and C++ include files (system)

BIOFORMATS_DATAROOTDIR Read-only architecture-independent data (root)

BIOFORMATS_SYSDATADIR Read-only architecture-independent data

BIOFORMATS_INFODIR GNU Info documentation files

BIOFORMATS_LOCALEDIR Locale data

BIOFORMATS_MANDIR Manual pages

BIOFORMATS_DOCDIR Documentation files

14.4.3 Bio-Formats package-specific paths

These are used only by Bio-Formats and are not shared with other packages. They are all subdirectories under the basic paths, above.

BIOFORMATS_DATADIR Bio-Formats data files

BIOFORMATS_ICONDIR Bio-Formats icons

BIOFORMATS_LIBEXECDIR Bio-Formats program executables

BIOFORMATS_SCHEMADIR Bio-Formats OME-XML model schemas

BIOFORMATS_TRANSFORMDIR Bio-Formats OME-XML model transforms

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^71\) or the previous versions\(^72\) page to find documentation for the version you are using.

\(^{70}\)http://www.cmake.org/cmake/help/v3.0/module/GNUInstallDirs.html

\(^{71}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{72}\)http://www.openmicroscopy.org/site/support/legacy/
14.5 bf-test

14.5.1 Synopsis

bf-test command [options]

14.5.2 Description

bf-test is a front end for running the Bio-Formats (C++) command-line tools.
This takes care of setting up the environment to ensure that all needed libraries, programs and data files are made available. It is of course possible to run the tools directly if desired.

14.5.3 Options

-h, --help
  Show this manual page.

-u, --usage
  Show usage information.

-V, --version
  Print version information.

14.5.4 Commands

Commonly-used commands are:

info (or showinf)  Display and validate image metadata
view (or glview)   View image pixel data

14.5.5 See also

Environment, bf-test info, bf-test view.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{73}\) or the previous versions\(^{74}\) page to find documentation for the version you are using.

14.6 bf-test info

14.6.1 Synopsis

bf-test info [options] file

14.6.2 Description

bf-test info displays the metadata for an image file, including the core and original metadata, and can optionally display and validate the OME-XML metadata.

Note: Viewing is currently restricted to the first series of an OME-TIFF file using the 2013-06 schema. Future releases will extend this to multiple series, all schema versions and additional file formats.

\(^{73}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{74}\)http://www.openmicroscopy.org/site/support/legacy/
14.6.3 Options

-h, --help
    Show this manual page.

-u, --usage
    Show usage summary.

-V, --version
    Print version information.

--debug
    Show debug output.

-q, --quiet
    Show less output.

-v, --verbose
    Show more output.

--format=reader
    Use the specified format reader (UNIMPLEMENTED).

--flat
    Flatten subresolutions.

--no-flat (default)
    Do not flatten subresolutions.

--merge
    Combine separate channels into an RGB image (UNIMPLEMENTED).

--no-merge
    Do not combine separate channels into an RGB image (UNIMPLEMENTED) (default).

--group
    Group files in multi-file datasets into a single dataset.

--no-group
    Files in multi-file datasets are not into a single dataset (default).

--stitch
    Group files with similar names (UNIMPLEMENTED).

--no-stitch
    Do not group files with similar names (UNIMPLEMENTED) (default).

--separate
    Separate an RGB image into separate channels (UNIMPLEMENTED).

--no-separate
    Do not separate an RGB image into separate channels (UNIMPLEMENTED) (default).

series=n
    Use the specified series (UNIMPLEMENTED).

resolution=n
    Use the specified sub-resolution (only if not flattened with –flat) (UNIMPLEMENTED).

--input-order=XY[ ZTC]
    Override the dimension input order (UNIMPLEMENTED).

--output-order=XY[ ZTC]
    Override the dimension output order (UNIMPLEMENTED).

--core
    Display core metadata (default).

--no-core
    Do not display core metadata.
--orig
   Display original format-specific global and series metadata (default).

--no-orig
   Do not display original format-specific global and series metadata.

--filter
   Filter original format-specific global and series metadata.

--no-filter
   Do not filter original format-specific global and series metadata (default).

--omexml
   Display OME-XML metadata.

--no-omexml
   Do not display OME-XML metadata (default).

--validate
   Validate OME-XML metadata (default). Note this will only have an effect if --omexml is used.

--no-validate
   Do not validate OME-XML metadata.

--sa
   Display structured annotations (default) (UNIMPLEMENTED).

--no-sa
   Do not display structured annotations.

--used
   Display used files (default).

--no-used
   Do not display used files.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{75}\) or the previous versions\(^{76}\) page to find documentation for the version you are using.

14.7 bf-test view

14.7.1 Synopsis

bf-test view [options] file

14.7.2 Description

bf-test view renders the pixel data of an image file using OpenGL.

Open an image using File → Open.

Note: Viewing is currently restricted to the first series of an OME-TIFF file using the 2013-06 schema. Future releases will extend this to multiple series, all schema versions and additional file formats.

Note: The viewer currently supports viewing of multi-dimensional greyscale planes; RGB images are not yet supported. This will be rectified in a future update.

\(^{75}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{76}\)http://www.openmicroscopy.org/site/support/legacy/
14.7.3 Navigation

The Navigation dock allows navigation between the constituent planes of an image. The Plane slider allows the absolute plane number to be changed, while individual Z, T, C sliders permit the Z slice, timepoint or channel to be changed, respectively. These sliders will only be available for images using these dimensions. Additional ModuloZ, ModuloT and ModuloC sliders may be present for images with Modulo annotations, for example with certain FLIM datasets.

14.7.4 Rendering

The Rendering dock allows the rendering settings to be adjusted. This is currently limited to Min and Max sliders to specify the lower and upper bounds of the display range for linear contrast adjustment. This range is used to render with a HiLo lookup table.

Note: The rendering settings will be improved in a future update to allow alternate lookup tables and per-channel rendering settings.

14.7.5 2D Camera

The view may be zoomed, panned and rotated. Select the desired operation using View → Zoom, View → Pan or View → Rotate, or use the corresponding toolbar icon.

- **zoom** Press and hold the first mouse button anywhere in the image view, then drag up or down to zoom out or zoom in, respectively.
- **pan** Press and hold the first mouse button anywhere in the image view, then drag to move the image.
- **rotate** Press and hold the first mouse button anywhere in the image view, then drag up or down to rotate the image counterclockwise or clockwise, respectively.

14.7.6 Environment

**BIOFORMATS_OPENGL_DEBUG** If set (to any value), create an OpenGL debugging context and verbosely log all OpenGL activity
15.1 Testing code changes

15.1.1 Automated tests

At the bottom of many commit messages in https://github.com/openmicroscopy/bioformats, you will find a few lines similar to this:

To test, please run:

ant -Dtestng.directory=$DATA/metamorph test-automated

This shows the command(s) necessary to run automated tests against the files likely to be affected by that commit. If you want to run these tests, you will need to do the following:

Clone bioformats.git and checkout the appropriate branch (by following the directions on the Git usage\(^3\) page). Run this command to build all of the JAR files:

$ ant clean jars

Switch to the test-suite component:

$ cd components/test-suite

Run the tests, where $DATA is the path to the full data repository:

$ ant -Dtestng.directory=$DATA/metamorph test-automated

On Windows, the arguments to the test command must be quoted:

> ant "-Dtestng.directory=$DATA\metamorph" test-automated

By default, 512 MB of memory are allocated to the JVM. You can increase this by adding the ‘-Dtestng.memory=XXXm’ option. You should now see output similar to this:

1\(^{http://www.openmicroscopy.org/site/support/bio-formats5.0/}\)
2\(^{http://www.openmicroscopy.org/site/support/legacy/}\)
3\(^{http://www.openmicroscopy.org/site/support/contributing/using-git.html}\)
15.1. MATLAB tests

Tests for the Bio-Formats MATLAB toolbox are written using the xunit framework and are located under components/formats-gpl/test/matlab.

To run these tests, you will need to download or clone matlab-xunit⁴, a xUnit framework with JUnit-compatible XML output. Then add this package together with the Bio-Formats MATLAB to your MATLAB path:

```matlab
$ Add the matlab-xunit toolbox to the MATLAB path
addpath('path/to/matlab-xunit');
$ Add the Bio-Formats MATLAB source to the MATLAB path
$ For developers working against the source code
addpath('path/to/bioformats/components/formats-gpl/matlab');
```

⁴https://github.com/openmicroscopy/bioformats/tree/v5.1.3/components/formats-gpl/test/matlab
⁵https://github.com/psexton/matlab-xunit

15.1.2 TESTING code changes

If Ant reports that the build was successful, then there is nothing that you need to do. Otherwise, it is helpful if you can provide the command, branch name, number of failures at the bottom of the Ant output, and the bio-formats-software-test-*.log file.

Each of the dots represents a single passed test; a ‘-‘ is a skipped test, and an ‘F’ is a failed test. This is mostly just for your amusement if you happen to be staring at the console while the tests run, as a more detailed report is logged to bio-formats-software-test-$DATE.log (where “$DATE” is the date on which the tests started in “yyyy-MM-dd_hh-mm-ss” format).

Bio-Formats Documentation, Release 5.1.3
addpath('/path/to/bioformats/artifacts');
% For developers working against a built artifact, e.g. a release
% addpath('/path/to/bfmatlab');

You can run all the MATLAB tests using `runxunit`:

```plaintext
cd /path/to/bioformats/components/formats-gpl/test/matlab
runxunit
```

Individual test classes can be run by passing the name of the class:

```plaintext
cd /path/to/bioformats/components/formats-gpl/test/matlab
runxunit TestBfsave
```

Individual test methods can be run by passing the name of the class and the name of the method:

```plaintext
cd /path/to/bioformats/components/formats-gpl/test/matlab
runxunit TestBfsave:testLZW
```

Finally to output the test results under XML format, you can use the `-xmlfile` option:

```plaintext
cd /path/to/bioformats/components/formats-gpl/test/matlab
runxunit -xmlfile test-output.xml
```

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^6\) or the previous versions\(^7\) page to find documentation for the version you are using.

---

### 15.2 Public test data

Most of the data-driven tests would benefit from having a comprehensive set of public sample data (see also #4086\(^8\)).

Formats for which we already have public sample data:

A `(*)` indicates that we could generate more public data in this format.

- ICS (*)
- Leica LEI
- IPLab
- BMP (*)
- Image-Pro SEQ
- QuickTime (*)
- Bio-Rad PIC
- Image-Pro Workspace
- Fluoview/ABD TIFF (*)
- Perkin Elmer Ultraview
- Gatan DM3

\(^6\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^7\)http://www.openmicroscopy.org/site/support/legacy/
\(^8\)http://trac.openmicroscopy.org.uk/ome/ticket/4086
• Zeiss LSM
• Openlab LIFF (*)
• Leica LIF (*)
• TIFF (*)
• Khoros (http://netghost.narod.ru/gff/sample/images/viff/index.htm)
• MNG (Download®) (*)

Formats for which we can definitely generate public sample data:
• PNG/APNG
• JPEG
• PGM
• FITS
• PCX
• GIF
• Openlab Raw
• OME-XML
• OME-TIFF
• AVI
• PICT
• LIM
• PSD
• Targa
• Bio-Rad Gel
• Fake
• ECAT-7 (minctocat)
• NRRD
• JPEG-2000
• Micromanager
• Text
• DICOM
• MINC (rawtoninc)
• NIFTI (dicomnifti)
• Analyze 7.5 (medcon)
• SDT
• FV1000 .oib/.oif
• Zeiss ZVI
• Leica TCS
• Aperio SVS
• Imaris (raw)

Formats for which I need to check whether or not we can generate public sample data:
• IPLab Mac (Ivision)

• Deltavision
• MRC
• Gatan DM2
• Imaris (HDF)
• EPS
• Alicona AL3D
• Visitech
• InCell
• L2D
• FEI
• NAF
• MRW
• ARF
• LI-FLIM
• Oxford Instruments
• VG-SAM
• Hamamatsu HIS
• WA-TOP
• Seiko
• TopoMetrix
• UBM
• Quesant
• RHK
• Molecular Imaging
• JEOL
• Amira
• Unisoku
• Perkin Elmer Densitometer
• Nikon ND2
• SimplePCI .cxd
• Imaris (TIFF)
• Molecular Devices Gel
• Imacon .iff
• LEO
• JPK
• Nikon NEF
• Nikon TIFF
• Prairie
• Metamorph TIFF/STK/ND
• Improvision TIFF
• Photoshop TIFF
15.3 Generating test images

Sometimes it is nice to have a file of a specific size or pixel type for testing. To generate a file (that contains gradient images):

```
touch "my-special-test-file&pixelType=uint8&sizeX=8192&sizeY=8192.fake"
```

Whatever is before the `&` is the image name; remaining key value pairs should be pretty self-explanatory. Just replace the values with whatever you need for testing.

Additionally, you can put such values in a separate .ini file:

```
touch my-special-test-file.fake
echo "pixelType=uint8" >> my-special-test-file.fake.ini
echo "sizeX=8192" >> my-special-test-file.fake.ini
echo "sizeY=8192" >> my-special-test-file.fake.ini
```

In fact, just the .fake.ini file alone suffices:

```
echo "pixelType=uint8" >> my-special-test-file.fake
echo "sizeX=8192" >> my-special-test-file.fake
echo "sizeY=8192" >> my-special-test-file.fake
```

If you include a “[GlobalMetadata]” section to the ini file, then all the included values will be accessible from the global metadata map:

```
echo "[GlobalMetadata]" >> my-special-test-file.fake.ini
echo "my.key=some.value" >> my-special-test-file.fake.ini
```
There are a few other keys that can be added as well:

<table>
<thead>
<tr>
<th>Key</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>thumbSizeX</td>
<td>number of pixels wide, for the thumbnail</td>
</tr>
<tr>
<td>thumbSizeY</td>
<td>number of pixels tall, for the thumbnail</td>
</tr>
<tr>
<td>physicalSizeX</td>
<td>real width of the pixels, supports units defaulting to microns</td>
</tr>
<tr>
<td>physicalSizeY</td>
<td>real height of the pixels, supports units defaulting to microns</td>
</tr>
<tr>
<td>physicalSizeZ</td>
<td>real depth of the pixels, supports units defaulting to microns</td>
</tr>
<tr>
<td>sizeZ</td>
<td>number of Z sections</td>
</tr>
<tr>
<td>sizeC</td>
<td>number of channels</td>
</tr>
<tr>
<td>sizeT</td>
<td>number of timepoints</td>
</tr>
<tr>
<td>bitsPerPixel</td>
<td>number of valid bits (&lt;= number of bits implied by pixel type)</td>
</tr>
<tr>
<td>acquisitionDate</td>
<td>timestamp formatted as &quot;yyyy-MM-dd_HH-mm-ss&quot;</td>
</tr>
<tr>
<td>rgb</td>
<td>number of channels that are merged together</td>
</tr>
<tr>
<td>dimOrder</td>
<td>dimension order (e.g. XYZCT)</td>
</tr>
<tr>
<td>little</td>
<td>whether or not the pixel data should be little-endian</td>
</tr>
<tr>
<td>interleaved</td>
<td>whether or not merged channels are interleaved</td>
</tr>
<tr>
<td>indexed</td>
<td>whether or not a color lookup table is present</td>
</tr>
<tr>
<td>falseColor</td>
<td>whether or not the color lookup table is just for making the image look pretty</td>
</tr>
<tr>
<td>series</td>
<td>number of series (Images)</td>
</tr>
<tr>
<td>lutLength</td>
<td>number of entries in the color lookup table</td>
</tr>
<tr>
<td>exposureTime</td>
<td>time of exposure, supports units defaulting to seconds</td>
</tr>
<tr>
<td>plates</td>
<td>number of plates to generate</td>
</tr>
<tr>
<td>plateAcqs</td>
<td>number of plate runs</td>
</tr>
<tr>
<td>plateRows</td>
<td>number of rows per plate</td>
</tr>
<tr>
<td>plateCols</td>
<td>number of rows per plate</td>
</tr>
<tr>
<td>fields</td>
<td>number of fields per well</td>
</tr>
<tr>
<td>annLong, annDou-ble, annMap, annComment, annBool, annTime, annTag, annTerm, annXml</td>
<td>number of annotations of the given type to generate</td>
</tr>
</tbody>
</table>

You can often work with the .fake file directly, but in some cases support for those files is disabled and so you will need to convert the file to something else. Make sure that you have Bio-Formats built and the JARs in your CLASSPATH (individual JARs or just bioformats_package.jar):

```
bfconvert test&pixelType=uint8&sizeX=8192&sizeY=8192.fake test.tiff
```

If you do not have the command line tools installed, substitute `loci.formats.tools.ImageConverter` for `bfconvert`.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 15.4 Writing a new file format reader

This document is a brief guide to writing new Bio-Formats file format readers.

All format readers should extend either `loci.formats.FormatReader` or an existing reader.

### 15.4.1 Methods to override

- `isSingleFile(java.lang.String)` Whether or not the named file is expected to be the only file in the dataset. This only needs

  [13](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
  [14](http://www.openmicroscopy.org/site/support/legacy/)
  [15](http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isSingleFile(java.lang.String))
  [16](http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatReader.html)
to be overridden for formats whose datasets can contain more than one file.

- `isThisType(loci.common.RandomAccessInputStream)` Check the first few bytes of a file to determine if the file can be read by this reader. You can assume that index 0 in the stream corresponds to the index 0 in the file. Return true if the file can be read; false if not (or if there is no way of checking).

- `fileGroupOption(java.lang.String)` Returns an indication of whether or not the files in a multi-file dataset can be handled individually. The return value should be one of the following:
  - `FormatTools.MUST_GROUP`: the files cannot be handled separately
  - `FormatTools.CAN_GROUP`: the files may be handled separately or as a single unit
  - `FormatTools.CANNOT_GROUP`: the files must be handled separately

This method only needs to be overridden for formats whose datasets can contain more than one file.

- `getSeriesUsedFiles(boolean)` You only need to override this if your format uses multiple files in a single dataset. This method should return a list of all files associated with the given file name and the current series (i.e. every file needed to display the current series). If the `noPixels` flag is set, then none of the files returned should contain pixel data. For an example of how this works, see `lociformats.in.PerkinElmerReader`. It is recommended that the first line of this method be `FormatTools.assertId(currentId, true, 1) - this ensures that the file name is non-null.

- `openBytes(int, byte[], int, int, int, int)` Returns a byte array containing the pixel data for a subimage specified image from the given file. The dimensions of the subimage (upper left X coordinate, upper left Y coordinate, width, and height) are specified in the final four int parameters. This should throw a `FormatException` if the image number is invalid (less than 0 or == the number of images). The ordering of the array returned by openBytes should correspond to the values returned by `isLittleEndian` and `isInterleaved`. Also, the length of the byte array should be [image width * image height * bytes per pixel]. Extra bytes will generally be truncated. It is recommended that the first line of this method be `FormatTools.checkPlaneParameters(this, no, buf.length, x, y, w, h) - this ensures that all of the parameters are valid.

- `initFile(java.lang.String)` The majority of the file parsing logic should be placed in this method. The idea is to call this method once (and only once) when the file is first opened. Generally, you will want to start by calling `super.initFile(String)`. You will also need to set up the stream for reading the file, as well as initializing any dimension information and metadata. Most of this logic is up to you; however, you should populate the `core` variable (see `loci.formats.CoreMetadata`).

Note that each variable is initialized to 0 or null when `super.initFile(String)` is called. Also, `super.initFile(String)` constructs a Hashtable called `metadata` where you should store any relevant metadata.

The most common way to set up the OME-XML metadata for the reader is to initialize the MetadataStore using the `makeFilterMetadata()` method and populate the Pixels elements of the metadata store from the `core` variable using the `MetadataTools.populatePixels(MetadataStore, FormatReader)` method:

```java
# Initialize the OME-XML metadata from the core variable
MetadataStore store = makeFilterMetadata();
MetadataTools.populatePixels(store, this);
```

---

18 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isThisType(loci.common.RandomAccessInputStream)
20 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isLittleEndian()
21 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#isInterleaved()
22 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
23 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#core
24 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/PerkinElmerReader.java
25 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
26 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
27 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
28 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
29 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#openBytes(int,byte[],int,int,int,int)
30 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#core
31 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/CoreMetadata.html
32 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#makeFilterMetadata()
33 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#metadata
If the reader includes metadata at the plane level, you can initialize the Plane elements under the Pixels using `MetadataTools.populatePixels(MetadataStore, FormatReader, doPlane)`:

```java
MetadataTools.populatePixels(store, this, true);
```

Once the metadata store has been initialized with the core properties, additional metadata can be added to it using the setter methods. Note that for each of the model components, the `setObjectID()` method should be called before any of the `setObjectProperty()` methods, e.g.:

```java
// Add an oil immersion objective with achromat
String objectiveID = MetadataTools.createLSID("Objective", 0, 0);
store.setObjectiveID(objectiveID, 0, 0);
store.setObjectiveImmersion(getImmersion("Oil"), 0, 0);
```

- `close(boolean)` Cleans up any resources used by the reader. Global variables should be reset to their initial state, and any open files or delegate readers should be closed.

Note that if the new format is a variant of a format currently supported by Bio-Formats, it is more efficient to make the new reader a subclass of the existing reader (rather than subclassing `loci.formats.FormatReader`). In this case, it is usually sufficient to override `initFile(java.lang.String)` and `isThisType(byte[])`.

Every reader also has an instance of `loci.formats.CoreMetadata`. All readers should populate the fields in CoreMetadata, which are essential to reading image planes.

If you read from a file using something other than `loci.common.RandomAccessInputStream` or `loci.common.Location`, you must use the file name returned by `Location.getMappedId(String)`, not the file name passed to the reader. Thus, a stub for `initFile(String)` might look like this:

```java
protected void initFile(String id) throws FormatException, IOException {
    super.initFile(id);

    RandomAccessInputStream in = new RandomAccessInputStream(id);
    // Alternatively,
    // FileInputStream in = new FileInputStream(Location.getMappedId(id));

    // read basic file structure and metadata from stream
}
```

For more details, see `loci.common.Location.mapId(java.lang.String, java.lang.String)` and `loci.common.Location.getMappedId(java.lang.String)`.

### 15.4.2 Variables to populate

There are a number of global variables defined in `loci.formats.FormatReader` that should be populated in the constructor of any implemented reader.

These variables are:

- `suffixNecessary` Indicates whether or not a file name suffix is required; true by default

---

36 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/IFormatReader.html#close(boolean)
37 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormatReader.html
38 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormReader.html
39 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormReader.html#isThisType(byte[])
40 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/CoreMetadata.html
42 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/Location.html
43 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/Location.html#mapId(java.lang.String, java.lang.String)
44 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/Location.html#getMappedId(java.lang.String)
45 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormReader.html
46 http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/formats/FormReader.html#suffixNecessary
• **suffixSufficient** indicates whether or not a specific file name suffix guarantees that this reader can open a particular file; true by default.

• **hasCompanionFiles** indicates whether or not there is at least one file in a dataset of this format that contains only metadata (no images); false by default.

• **datasetDescription** A brief description of the layout of files in datasets of this format; only necessary for multi-file datasets.

• **domains** An array of imaging domains for which this format is used. Domains are defined in the `loci.formats.FormatTools` package.

### 15.4.3 Other useful things

- **loci.common.RandomAccessInputStream** is a hybrid RandomAccessFile/InputStream class that is generally more efficient than either RandomAccessFile or InputStream, and implements the DataInput interface. It is recommended that you use this for reading files.

- **loci.common.Location** provides an API similar to java.io.File, and supports File-like operations on URLs. It is highly recommended that you use this instead of File. See the Javadocs for additional information.

- **loci.common.DataTools** provides a number of methods for converting bytes to shorts, ints, longs, etc. It also supports reading most primitive types directly from a RandomAccessInputStream (or other DataInput implementation).

- **loci.formats.ImageTools** provides several methods for manipulating primitive type arrays that represent images. Consult the source or Javadocs for more information.

- If your reader relies on third-party code which may not be available to all users, it is strongly suggested that you make a corresponding service class that interfaces with the third-party code. Please see **Bio-Formats service and dependency infrastructure** for a description of the service infrastructure, as well as the `loci.formats.services` package.

- Several common image compression types are supported through subclasses of `loci.formats.codec.BaseCodec`. These include JPEG, LZW, LZO, Base64, ZIP and RLE (PackBits).

- If you wish to convert a file’s metadata to OME-XML (strongly encouraged), please see **Bio-Formats metadata processing** for further information.

- Once you have written your file format reader, add a line to the `readers.txt` file with the fully qualified name of the reader, followed by a ‘#’ and the file extensions associated with the file format. Note that `loci.formats.ImageReader`, the master file format reader, tries to identify which format reader to use according to the order given in `readers.txt`, so be sure to place your reader in an appropriate position within the list.

- The easiest way to test your new reader is by calling “java loci.formats.tools.ImageInfo <file name>”. If all goes well, you should see all of the metadata and dimension information, along with a window showing the images in the file. `loci.formats.ImageReader` can take additional parameters; a brief listing is provided below for reference, but it is recommended that you take a look at the contents of `loci.formats.tools.ImageInfo` to see exactly what each one does.
## Argument and Action

<table>
<thead>
<tr>
<th>Argument</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>-version</td>
<td>print the library version and exit</td>
</tr>
<tr>
<td>file</td>
<td>the image file to read</td>
</tr>
<tr>
<td>-nopix</td>
<td>read metadata only, not pixels</td>
</tr>
<tr>
<td>-nocore</td>
<td>do not output core metadata</td>
</tr>
<tr>
<td>-nometa</td>
<td>do not parse format-specific metadata table</td>
</tr>
<tr>
<td>-nofilter</td>
<td>do not filter metadata fields</td>
</tr>
<tr>
<td>-thumbs</td>
<td>read thumbnails instead of normal pixels</td>
</tr>
<tr>
<td>-minmax</td>
<td>compute min/max statistics</td>
</tr>
<tr>
<td>-merge</td>
<td>combine separate channels into RGB image</td>
</tr>
<tr>
<td>-nogroup</td>
<td>force multi-file datasets to be read as individual files</td>
</tr>
<tr>
<td>-stitch</td>
<td>stitch files with similar names</td>
</tr>
<tr>
<td>-separate</td>
<td>split RGB image into separate channels</td>
</tr>
<tr>
<td>-expand</td>
<td>expand indexed color to RGB</td>
</tr>
<tr>
<td>-omexml</td>
<td>populate OME-XML metadata</td>
</tr>
<tr>
<td>-normalize</td>
<td>normalize floating point images*</td>
</tr>
<tr>
<td>-fast</td>
<td>paint RGB images as quickly as possible*</td>
</tr>
<tr>
<td>-debug</td>
<td>turn on debugging output</td>
</tr>
<tr>
<td>-range</td>
<td>specify range of planes to read (inclusive)</td>
</tr>
<tr>
<td>-series</td>
<td>specify which image series to read</td>
</tr>
<tr>
<td>-swap</td>
<td>override the default input dimension order</td>
</tr>
<tr>
<td>-shuffle</td>
<td>override the default output dimension order</td>
</tr>
<tr>
<td>-map</td>
<td>specify file on disk to which name should be mapped</td>
</tr>
<tr>
<td>-preload</td>
<td>pre-read entire file into a buffer; significantly reduces the time required to read the images, but requires more memory</td>
</tr>
<tr>
<td>-crop</td>
<td>crop images before displaying; argument is ‘x,y,w,h’</td>
</tr>
<tr>
<td>-autoscale</td>
<td>used in combination with ‘-fast’ to automatically adjust brightness and contrast</td>
</tr>
<tr>
<td>-novalid</td>
<td>do not perform validation of OME-XML</td>
</tr>
<tr>
<td>-omexml-only</td>
<td>only output the generated OME-XML</td>
</tr>
<tr>
<td>-format</td>
<td>read file with a particular reader (e.g., ZeissZVI)</td>
</tr>
</tbody>
</table>

* May result in loss of precision

- If you wish to test using TestNG, loci.tests.testng.FormatReaderTest provides several basic tests that work with all Bio-Formats readers. See the FormatReaderTest source code for additional information.
- For more details, please look at the source code and Javadocs. Studying existing readers is probably the best way to get a feel for the API; we would recommend first looking at loci.formats.in.ImarisReader (this is the most straightforward one). loci.formats.in.LIFReader and InCellReader are also good references that show off some of the nicer features of Bio- Formats.

If you have questions about Bio-Formats, please contact the OME team.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 15.5 Bio-Formats service and dependency infrastructure

#### 15.5.1 Description

The Bio-Formats service infrastructure is an interface driven pattern for dealing with external and internal dependencies. The design goal was mainly to avoid the cumbersome usage of ReflectedUniverse where possible and to clearly define both...
service dependency and interface between components. This is generally referred to as dependency injection\(^\text{72}\), dependency inversion\(^\text{73}\) or component based design\(^\text{74}\).

It was decided, at this point, to forgo the usage of potentially more powerful but also more complicated solutions such as:

- Spring (http://spring.io)
- Guice (http://code.google.com/p/google-guice/)
- ...

The Wikipedia page for dependency injection\(^\text{75}\) contains many other implementations in many languages.

An added benefit is the potential code reuse possibilities as a result of decoupling of dependency and usage in Bio-Formats readers. Implementations of the initial Bio-Formats services were completed as part of BioFormatsCleanup and tickets #463\(^\text{76}\) and #464\(^\text{77}\).

### 15.5.2 Writing a service

- **Interface** – The basic form of a service is an interface which inherits from loci.common.services.Service\(^\text{78}\). Here is a very basic example using the (now removed) OMENotesService:

```java
public interface OMENotesService extends Service {
    /**
     * Creates a new OME Notes instance.
     * @param filename Path to the file to create a Notes instance for.
     */
    public void newNotes(String filename);
}
```

- **Implementation** – This service then has an implementation, which is usually located in the Bio-Formats component or package which imports classes from an external, dynamic or other dependency. Again looking at the OMENotesService:

```java
public class OMENotesServiceImpl extends AbstractService
    implements OMENotesService {
    /**
     * Default constructor.
     */
    public OMENotesServiceImpl() {
        checkClassDependency(Notes.class);
    }

    /* (non-Javadoc)
     * @see loci.formats.dependency.OMENotesService#newNotes()
     */
    public void newNotes(String filename) {
        new Notes(null, filename);
    }
}
```

- **Style**
  - Extension of AbstractService to enable uniform runtime dependency checking is recommended. Java does not check class dependencies until classes are first instantiated so if you do not do this, you may end up with Class-

\(^{72}\)http://en.wikipedia.org/wiki/Dependency_injection
\(^{74}\)http://en.wikipedia.org/wiki/Component-based_software_engineering
\(^{75}\)http://en.wikipedia.org/wiki/Dependency_injection
\(^{76}\)http://trac.openmicroscopy.org.uk/ome/ticket/463
\(^{77}\)http://trac.openmicroscopy.org.uk/ome/ticket/464
\(^{78}\)http://downloads.openmicroscopy.org/latest/bio-formats5.1/api/loci/common/services/Service.html
Bio-Formats Documentation, Release 5.1.3

NotFound or the like exceptions being emitted from your service methods. This is to be strongly discouraged. If a service has unresolvable classes on its CLASSPATH instantiation should fail, not service method invocation.

- Service methods should not burden the implementer with numerous checked exceptions. Also external dependency exception instances should not be allowed to directly leak from a service interface. Please wrap these using a ServiceException.

- By convention both the interface and implementation are expected to be in a package named loci.*.services. This is not a hard requirement but should be followed where possible.

**Registration** – A service’s interface and implementation must finally be registered with the loci.common.services.ServiceFactory via the services.properties file. Following the OMENotesService again, here is an example registration:

```java
...
# OME notes service (implementation in legacy ome-notes component)
loci.common.services.OMENotesService=loci.ome.notes.services.OMENotesServiceImpl
...
```

See also:

- loci.common.services.Service. Source code for loci.common.services.Service interface
- loci.common.services.ServiceFactory. Source code for loci.common.services.Service interface

### 15.5.3 Using a service

OMENotesService service = null;
try {
    ServiceFactory factory = new ServiceFactory();
    service = factory.getInstance(OMENotesService.class);
} catch (DependencyException de) {
    LOGGER.info("", de);
}
...

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 15.6 Code generation with xsd-fu

xsd-fu is a Python application designed to digest OME XML schema and produce an object-oriented Java infrastructure to ease work with an XML DOM tree. It is usually run automatically when building from source (see Building from source) and so running it by hand should not be needed. xsd-fu is primarily used to generate the OME-XML model objects, enums and enum handlers, plus the MetadataStore and MetadataRetrieve interfaces and implementations.

#### 15.6.1 Available options

- **--dry-run**
  Run all source generation processing, but don’t write output files. In combination with --print-depends or --print-generated, this option may be used to dynamically introspect command dependencies and output to create build rules on the fly for e.g. `cmake`.

---

80. [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
81. [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
--debug
Enable xsd-fu debugging messages and template debugging. The code templates contain diagnostic messages to debug the template processing, which are normally suppressed in the code output; enabling debugging will add these diagnostic messages to the generated code.

-l language, --language=language
Generate code for the specified language. Currently supported options are C++ and Java.

--metadata-package=package
Package or namespace for the metadata store and retrieve classes.

--ome-xml-metadata-package=package
Package or namespace for the OME-XML metadata classes.

--ome-xml-model-package=package
Package or namespace for the OME-XML model classes.

--ome-xml-model-enums-package=package
Package or namespace for the OME-XML model enum classes.

--ome-xml-model-enum-handlers-package=package
Package or namespace for the OME-XML model enum handler classes.

-o dir, --output-directory=dir
Output generated code into the specified directory. The directory will be created if it does not already exist. Note that the directory is the root of the source tree; generated classes will be placed into the appropriate module-specific locations under this root.

--print-depends
Print a list of the files required during template processing, including schema files, templates and custom template fragments. Particularly useful with --dry-run to introspect command dependencies.

--print-generated
Print a list of the files generated during template processing. Particularly useful with --dry-run to determine what a given command would generate.

-q, --quiet
Do not print names of generated files.

-t path, --template-path=path
Path to search for Genshi template files. Defaults to the language-specific template directory in components/xsd-fu.

-n, --xsd-namespace
XML schema namespace to use. Defaults to xsd:.

-v, --verbose
Print names of generated files as they are processed.

15.6.2 Available commands

- doc_gen
- metadata
- omero_metadata
- omero_model
- omexml_metadata
- omexml_metadata_all
- omexml_model
- omexml_model_all
- omexml_model Enums
- omexml_model_enum_handlers
- omexml_model_enum_includeall
15.6.3 Running the code generator

Run xsd-fu script with no arguments to examine the syntax:

```
./components/xsd-fu/xsd-fu
Error: Missing subcommand
```

xsd-fu: Generate classes from an OME-XML schema definition

Usage: ./components/xsd-fu/xsd-fu command [options...] -o output_dir schema_files...

Options:
- d, --dry-run Do not create output files
- d, --debug Enable xsd-fu and template debugging
- l, --language=lang Generated language
- m, --metadata-package=pkg Metadata package
- o, --ome-xml-metadata-package=pkg OME-XML metadata class package
- o, --ome-xml-model-package=pkg OME-XML model package
- o, --ome-xml-model-enum-package=pkg OME-XML model enum package
- o, --ome-xml-model-enum-handlers-package=pkg OME-XML model enum handler package
- o, --output-directory=dir Generated output directory
- q, --quiet Do not output file names
- t, --template-path=path Genshi template path
- v, --verbose Output generated file names
- n, --xsd-namespace XML schema namespace

Available subcommands:
  debug
doc_gen
omexml_model_enum_handlers
omexml_modelEnums
omexml_model
metadata
omero_metadata
omero_model
omexml_metadata
tab_gen

Default XSD namespace: "xsd:"

Default Java OME-XML package: "ome.xml.model"
Default Java OME-XML enum package: "ome.xml.model.enums"
Default Java OME-XML enum handler package: "ome.xml.model.enums.handlers"
Default Java metadata package: "loci.formats.meta"
Default Java OME-XML metadata package: "loci.formats.ome"

Default C++ OME-XML package: "ome::xml::model"
Default C++ OME-XML enum package: "ome::xml::model::enums"
Default C++ metadata package: "ome::xml::meta"
Default C++ OME-XML metadata package: "ome::xml::meta"

Examples:
  ./components/xsd-fu/xsd-fu -l Java -n 'xsd:' --ome-xml-model-package=ome.xml.model -o omexml /path/to/schemas/ome.xsd
  ./components/xsd-fu/xsd-fu -l C++ -n 'xsd:' --ome-xml-model-package=ome::xml::model -o omexml /path/to/schemas/ome.xsd

Report bugs to OME Devel <ome-devel@lists.openmicroscopy.org.uk>

Note: It should not be necessary to run it by hand for a normal Bio-Formats build. xsd-fu is run automatically as part of the main Bio-Formats build from version 5.0 when building the ome-xml and scifio components. It is still useful to run by hand when debugging, or using non-standard targets.
15.6.4 Generating the OME-XML Java model and metadata classes

The following sections outline how to generate parts of the OME-XML Java interfaces and implementations for the object model and metadata store, which are composed of:

- OME model objects
- enumerations for OME model properties
- enumeration handlers for regular expression matching of enumeration strings
- Metadata store and Metadata retrieve interfaces for all OME model properties
- various implementations of Metadata store and/or Metadata retrieve interfaces

All of the above can be generated by this Ant command:

$ cd components/ome-xml
$ ant generate-source

Run:

$ ant generate-source -v

to see the command-line options used.

15.6.5 Working with Enumerations and Enumeration Handlers

XsdFu code generates enumeration regular expressions using a flexible configuration file. Each enumeration has a key-value listing of regular expression to exact enumeration value matches. For example:

```
[Correction]
".*Pl.*Apo.*" = "PlanApo"
".*Pl.*Flu.*" = "PlanFluor"
"\s*Vio.*Corr.*" = "VioletCorrected"
".*S.*Flu.*" = "SuperFluor"
".*Neo.*flu.*" = "NeoFluar"
".*Flu.*tar.*" = "Fluotar"
".*Fluo.*" = "Fluor"
".*Flua.*" = "Fluar"
"\s*Apo.*" = "Apo"
```

15.6.6 Generate OMERO model specification files

Run xsd-fu with the omero_model subcommand.

15.6.7 Special thanks

A special thanks goes out to Dave Kuhlman for his fabulous work on generateDS which xsd-fu makes heavy use of internally.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

84 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/xsd-fu/cfg/enum_handler.cfg
85 http://www.davekuhlman.org/
86 http://www.davekuhlman.org/generateDS.html
87 http://www.openmicroscopy.org/site/support/bio-formats5.0/
88 http://www.openmicroscopy.org/site/support/legacy/
15.7 Scripts for performing development tasks

The tools directory contains several scripts which are useful for building and performing routine updates to the code base.

15.7.1 bump_maven_version.py

This updates the Maven POM version numbers for all pom.xml files that set groupId to ome. The script takes a single argument, which is the new version. For example, to update the POM versions prior to release:

./tools/bump_maven_version.py 5.1.0

and to switch back to snapshot versions immediately after release:

./tools/bump_maven_version.py 5.1.1-SNAPSHOT

15.7.2 test-build

This is the script used by Travis to test each commit. It compiles and runs tests on each of the components in the Bio-Formats repository according to the arguments specified. Valid arguments are:

- **clean**: cleans the Maven build directories
- **maven**: builds all Java components using Maven and runs unit tests
- **cpp**: builds the native C++ code alone
- **cppwrap**: builds the auto-generated C++ bindings for the Java API
- **sphinx**: builds the Sphinx documentation alone
- **ant**: builds all Java components using Ant and runs unit tests
- **all**: equivalent of clean maven cppwrap sphinx ant

15.7.3 update_copyright

This updates the end year in the copyright blocks of all source code files. The command takes no arguments, and sets the end year to be the current year. As update_copyright is a Bash script, it is not intended to be run on Windows.

See open Trac tickets for Bio-Formats[^44] for information on work currently planned or in progress.

For more general guidance about how to contribute to OME projects, see the Contributing developers documentation[^100].

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^91] or the previous versions[^92] page to find documentation for the version you are using.

[^44]: https://trac.openmicroscopy.org.uk/ome/report/44
[^100]: http://www.openmicroscopy.org/site/support/contributing/index.html
[^91]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^92]: http://www.openmicroscopy.org/site/support/legacy/
Part IV

Formats
Bio-Formats supports over 140 different file formats. The Dataset Structure Table explains the file extension you should choose to open/import a dataset in any of these formats, while the Supported Formats table lists all of the formats and gives an indication of how well they are supported and whether Bio-Formats can write, as well as read, each format. The Summary of supported metadata fields table shows an overview of the OME data model fields populated for each format.

We are always looking for examples of files to help us provide better support for different formats. If you would like to help, you can upload files using our QA system uploader\(^3\). If you have any questions, or would prefer not to use QA, please email the ome-users mailing list\(^4\). If your format is already supported, please refer to the ‘we would like to have’ section on the individual page for that format, to see if your dataset would be useful to us.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^5\) or the previous versions\(^6\) page to find documentation for the version you are using.
This table shows the extension of the file that you should choose if you want to open/import a dataset in a particular format.

<table>
<thead>
<tr>
<th>Format name</th>
<th>File to choose</th>
<th>Structure of files</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIM</td>
<td>.aim</td>
<td>Single file</td>
</tr>
<tr>
<td>ARF</td>
<td>.arf</td>
<td>Single file</td>
</tr>
<tr>
<td>Adobe Photoshop</td>
<td>.psd</td>
<td>Single file</td>
</tr>
<tr>
<td>Adobe Photoshop TIFF</td>
<td>.tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>Alicona AL3D</td>
<td>.al3d</td>
<td>Single file</td>
</tr>
<tr>
<td>Amersham Biosciences GEL</td>
<td>.gel</td>
<td>Single file</td>
</tr>
<tr>
<td>Amira</td>
<td>.am, .amiramesh, .grey, .hx, .labels</td>
<td>Single file</td>
</tr>
<tr>
<td>Analyze 7.5</td>
<td>.img, .hdr</td>
<td>One .img file and one similarly-named .hdr file</td>
</tr>
<tr>
<td>Andor SIF</td>
<td>.sif</td>
<td>Single file</td>
</tr>
<tr>
<td>Animated PNG</td>
<td>.png</td>
<td>Single file</td>
</tr>
<tr>
<td>Aperio SVS</td>
<td>.svs</td>
<td>Single file</td>
</tr>
<tr>
<td>Audio Video Interleave</td>
<td>.avi</td>
<td>Single file</td>
</tr>
<tr>
<td>BD Pathway</td>
<td>.exp, .tif</td>
<td>Multiple files (.exp, .dye, .ltp, …) plus one or more directories containing .tif and .bmp files</td>
</tr>
<tr>
<td>Bio-Rad GEL</td>
<td>.1sc</td>
<td>Single file</td>
</tr>
<tr>
<td>Bio-Rad PIC</td>
<td>.pic, .xml, .raw</td>
<td>One or more .pic files and an optional .lse.xml file</td>
</tr>
<tr>
<td>Bitplane Imaris</td>
<td>.ims</td>
<td>Single file</td>
</tr>
<tr>
<td>Bitplane Imaris 3 (TIFF)</td>
<td>.ims</td>
<td>Single file</td>
</tr>
<tr>
<td>Bitplane Imaris 5.5 (HDF)</td>
<td>.ims</td>
<td>Single file</td>
</tr>
<tr>
<td>Bruker</td>
<td>(no extension)</td>
<td>One ‘fid’ and one ‘acqp’ plus several other metadata files and a ‘pdata’ directory</td>
</tr>
<tr>
<td>Burleigh</td>
<td>.img</td>
<td>Single file</td>
</tr>
<tr>
<td>Canon RAW</td>
<td>.cr2, .crw, .jpg, .thm, .wav</td>
<td>Single file</td>
</tr>
<tr>
<td>CellSens VSI</td>
<td>.vsi, .ets</td>
<td>One .vsi file and an optional directory with a similar name that contains at least one subdirectory with .ets files</td>
</tr>
<tr>
<td>CellWorx</td>
<td>.pnl, .htd, .log</td>
<td>One .htd file plus one or more .pnl or .tif files and optionally one or more .log files</td>
</tr>
<tr>
<td>Cellomics C01</td>
<td>.c01, .dib</td>
<td>One or more .c01 files</td>
</tr>
<tr>
<td>Compix Simple-PCI</td>
<td>.cxd</td>
<td>Single file</td>
</tr>
<tr>
<td>DICOM</td>
<td>.dic, .dcm, .dicom, .jp2, .j2ki, .j2kr, .raw, .ima</td>
<td>One or more .dcm or .dicom files</td>
</tr>
<tr>
<td>DNG</td>
<td>.cr2, .crw, .jpg, .thm, .wav, .tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>Deltavision</td>
<td>.dv, .r3d, .r3d_d3d, .dv.log, .r3d.log</td>
<td>One .dv, .r3d, or .d3d file and up to two optional .log files</td>
</tr>
<tr>
<td>ECAT7</td>
<td>.v</td>
<td>Single file</td>
</tr>
<tr>
<td>Encapsulated PostScript</td>
<td>.eps, .epsi, .ps</td>
<td>Single file</td>
</tr>
<tr>
<td>Format name</td>
<td>File to choose</td>
<td>Structure of files</td>
</tr>
<tr>
<td>--------------------------</td>
<td>----------------</td>
<td>-----------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>EvotecFlex</td>
<td>.flex, .mea, .res</td>
<td>One directory containing one or more .flex files, and an optional directory containing an .mea and .res file. The .mea and .res files may also be in the same directory as the .flex file(s).</td>
</tr>
<tr>
<td>FEI TIFF</td>
<td>.tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>FEI/Philips</td>
<td>.img</td>
<td>Single file</td>
</tr>
<tr>
<td>Flexible Image Transport</td>
<td>.fits, .fts</td>
<td>Single file</td>
</tr>
<tr>
<td>Fujifilm Asis</td>
<td>.img, .inf</td>
<td>Single file</td>
</tr>
<tr>
<td>Gatan DM2</td>
<td>.dm2</td>
<td>Single file</td>
</tr>
<tr>
<td>Gatan Digital Micrograph</td>
<td>.dm3</td>
<td>Single file</td>
</tr>
<tr>
<td>Graphics Interchange Format</td>
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<td>Single file</td>
</tr>
<tr>
<td>Hamamatsu Aquacosmos</td>
<td>.naf</td>
<td>Single file</td>
</tr>
<tr>
<td>Hamamatsu HIS</td>
<td>.his</td>
<td>Single file</td>
</tr>
<tr>
<td>Hamamatsu NDPI</td>
<td>.ndpi</td>
<td>Single file</td>
</tr>
<tr>
<td>Hamamatsu NDPI3</td>
<td>.ndpis</td>
<td>One .ndpis file and at least one .ndpi file</td>
</tr>
<tr>
<td>Hamamatsu VMS</td>
<td>.vms</td>
<td>One .vms file plus several .jpg files</td>
</tr>
<tr>
<td>Hitachi</td>
<td>.txt</td>
<td>One .txt file plus one similarly-named .tif, .bmp, or .jpg file</td>
</tr>
<tr>
<td>IMAGIC</td>
<td>.hed, .img</td>
<td>One .hed file plus one similarly-named .img file</td>
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<tr>
<td>IMOD</td>
<td>.mod</td>
<td>Single file</td>
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<tr>
<td>INR</td>
<td>.ini</td>
<td>Single file</td>
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<tr>
<td>IPLab</td>
<td>.ipl</td>
<td>Single file</td>
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<tr>
<td>IVision</td>
<td>.ipm</td>
<td>Single file</td>
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<tr>
<td>Imacon</td>
<td>.iff</td>
<td>Single file</td>
</tr>
<tr>
<td>Image Cytometry Standard</td>
<td>.ics, .ids</td>
<td>One .ics and possibly one .ids with a similar name</td>
</tr>
<tr>
<td>Image-Pro Sequence</td>
<td>.seq</td>
<td>Single file</td>
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<tr>
<td>Image-Pro Workspace</td>
<td>.ipw</td>
<td>Single file</td>
</tr>
<tr>
<td>Improvision TIFF</td>
<td>.tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>InCell 1000/2000</td>
<td>.xdce, .xml, .tif, .tif, .xlog</td>
<td>One .xdce file with at least one .tif/.tif or .im file</td>
</tr>
<tr>
<td>InCell 3000</td>
<td>.frm</td>
<td>Single file</td>
</tr>
<tr>
<td>JEOL</td>
<td>.dat, .img, .par</td>
<td>A single .dat file or an .img file with a similarly-named .par file</td>
</tr>
<tr>
<td>JPEG</td>
<td>.jpeg, .jpeg, .jpe</td>
<td>Single file</td>
</tr>
<tr>
<td>JPEG-2000</td>
<td>.jp2, .j2k, .jpf</td>
<td>Single file</td>
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<td>JPK Instruments</td>
<td>.jpk</td>
<td>Single file</td>
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<tr>
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<td>.jpx</td>
<td>Single file</td>
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<tr>
<td>Khoros XV</td>
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<tr>
<td>Kodak Molecular Imaging</td>
<td>.bip</td>
<td>Single file</td>
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<td>LEO</td>
<td>.sxm, .tif, .tif</td>
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</tr>
<tr>
<td>Li-FLIM</td>
<td>.fli</td>
<td>Single file</td>
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<tr>
<td>Laboratory Imaging</td>
<td>.lim</td>
<td>Single file</td>
</tr>
<tr>
<td>Leica</td>
<td>.lei, .tif, .tif, .raw</td>
<td>One .lei file with at least one .tif/.tif file and an optional .txt file</td>
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<td>Leica Image File Format</td>
<td>.lif</td>
<td>Single file</td>
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<tr>
<td>Leica SCN</td>
<td>.scn</td>
<td>Single file</td>
</tr>
<tr>
<td>Leica TCS TIFF</td>
<td>.tif, .tiff, .xml</td>
<td>Single file</td>
</tr>
<tr>
<td>Li-Cor L2D</td>
<td>.l2d, .scn, .tif</td>
<td>One .l2d file with one or more directories containing .tif/.tif files</td>
</tr>
<tr>
<td>MIAS</td>
<td>.tif, .tiff, .txt</td>
<td>One directory per plate containing one directory per well, each with one or more .tif/.tif files</td>
</tr>
<tr>
<td>MINC MRI</td>
<td>.mnc</td>
<td>Single file</td>
</tr>
<tr>
<td>Medical Research Council</td>
<td>.mrc, .st, .ali, .map, .rec</td>
<td>Single file</td>
</tr>
<tr>
<td>Metamorph STK</td>
<td>.stk, .nd, .tif, .tif</td>
<td>One or more .stk or .tif/.tif files plus an optional .nd file</td>
</tr>
<tr>
<td>Metamorph TIFF</td>
<td>.tif, .tif</td>
<td>One or more .tif/.tif files</td>
</tr>
</tbody>
</table>

Continued on next page
<table>
<thead>
<tr>
<th>Format name</th>
<th>File to choose</th>
<th>Structure of files</th>
</tr>
</thead>
<tbody>
<tr>
<td>Micro-Manager</td>
<td>.tif, .tiff, .txt, .xml</td>
<td>A ‘metadata.txt’ file plus or more .tif files</td>
</tr>
<tr>
<td>Minolta MRW</td>
<td>.mrw</td>
<td>Single file</td>
</tr>
<tr>
<td>Molecular Imaging</td>
<td>.stp</td>
<td>Single file</td>
</tr>
<tr>
<td>Multiple Network Graphics</td>
<td>.mng</td>
<td>Single file</td>
</tr>
<tr>
<td>NIFTI</td>
<td>.nii, .img, .hdr</td>
<td>A single .nii file or one .img file and a similarly-named .hdr file</td>
</tr>
<tr>
<td>NOAA-HRD Gridded Data Format</td>
<td>(no extension)</td>
<td>Single file</td>
</tr>
<tr>
<td>NRRD</td>
<td>.nrrd, .nhdr</td>
<td>A single .nrrd file or one .nhdr file and one other file containing the pixels</td>
</tr>
<tr>
<td>Nikon Elements TIFF</td>
<td>.tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>Nikon ND2</td>
<td>.nd2</td>
<td>Single file</td>
</tr>
<tr>
<td>Nikon NEF</td>
<td>.nef, .tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>Nikon TIFF</td>
<td>.tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>OME-TIFF</td>
<td>.ome.tiff, .ome.tiff</td>
<td>One or more .ome.tiff files</td>
</tr>
<tr>
<td>OME-XML</td>
<td>.ome</td>
<td>Single file</td>
</tr>
<tr>
<td>Olympus APL</td>
<td>.apl, .tnb, .mtb, .tif</td>
<td>One .apl file, one .mtb file, one .tnb file, and a directory containing one or more .tif files</td>
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<tr>
<td>Olympus FV1000</td>
<td>.oib, .oif, .pty, .lut</td>
<td>Single .oib file or one .oif file and a similarly-named directory containing .tif/.tifff files</td>
</tr>
<tr>
<td>Olympus Fluoview/ABD TIFF</td>
<td>.tif, .tiff</td>
<td>One or more .tif/.tifff files, and an optional .txt file</td>
</tr>
<tr>
<td>Olympus SIS TIFF</td>
<td>.tif, .tiff</td>
<td>Single file</td>
</tr>
<tr>
<td>Olympus ScanR</td>
<td>.dat, .xml, .tif</td>
<td>One .xml file, one ‘data’ directory containing .tif/.tifff files, and optionally two .dat files</td>
</tr>
<tr>
<td>Olympus Slidebook</td>
<td>.sld, .spl</td>
<td>Single file</td>
</tr>
<tr>
<td>Openlab LIFF</td>
<td>.liff</td>
<td>Single file</td>
</tr>
<tr>
<td>Openlab RAW</td>
<td>.raw</td>
<td>Single file</td>
</tr>
<tr>
<td>Oxford Instruments</td>
<td>.top</td>
<td>Single file</td>
</tr>
<tr>
<td>PCX</td>
<td>.pcx</td>
<td>Single file</td>
</tr>
<tr>
<td>PICT</td>
<td>.pict, .pct</td>
<td>Single file</td>
</tr>
<tr>
<td>POV-Ray</td>
<td>.df3</td>
<td>Single file</td>
</tr>
<tr>
<td>Perkin Elmer Densitometer</td>
<td>.hdr, .img</td>
<td>One .hdr file and a similarly-named .img file</td>
</tr>
<tr>
<td>PerkinElmer</td>
<td>.ano, .cfg, .csv, .htm, .rec, .tim, .zpo, .tif</td>
<td>One .htm file, several other metadata files (.tim, .ano, .csv, ...) and either .tif files or .2, .3, .4, etc. files</td>
</tr>
<tr>
<td>PerkinElmer Operetta</td>
<td>.tif, .tiff, .xml</td>
<td>Directory with XML file and one .tif/.tifff file per plane</td>
</tr>
<tr>
<td>Portable Gray Map</td>
<td>.pgm</td>
<td>Single file</td>
</tr>
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16.1 Flex Support

OMERO.importer supports importing analyzed Flex files from an Opera system.

Basic configuration is done via the importer.ini. Once the user has run the Importer once, this file will be in the following location:

- C:\Documents and Settings\<username>\omero\importer.ini

The user will need to modify or add the [FlexReaderServerMaps] section of the INI file as follows:

```
...[FlexReaderServerMaps]
CIA-1 = \\hostname1\mount;\\archivehost1\mount
CIA-2 = \\hostname2\mount;\\archivehost2\mount
```

where the key of the INI file line is the value of the “Host” tag in the .mea measurement XML file (here: <Host name="CIA-1">) and the value is a semicolon-separated list of escaped UNC path names to the Opera workstations where the Flex files reside.

Once this resolution has been encoded in the configuration file and you have restarted the importer, you will be able to select the .mea measurement XML file from the Importer user interface as the import target.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^1\) or the previous versions\(^2\) page to find documentation for the version you are using.

---

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^2\)http://www.openmicroscopy.org/site/support/legacy/
### SUPPORTED FORMATS

*Ratings legend and definitions*

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\(^1\)http://www.openmicroscopy.org/site/support/ome-model/ome-tiff/index.html
\(^2\)http://www.openmicroscopy.org/site/support/ome-model/ome-xml/index.html
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Continued on next page

³http://www.zeiss.com/czi
Bio-Formats currently supports 143 formats

### Ratings legend and definitions

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**Pixels**  Our estimation of Bio-Formats’ ability to reliably extract complete and accurate pixel values from files in that format. The better this score, the more confident we are that Bio-Formats will successfully read your file without displaying an error message or displaying an erroneous image.

**Metadata**  Our certainty in the thoroughness and correctness of Bio-Formats’ metadata extraction and conversion from files of that format into standard OME-XML. The better this score, the more confident we are that all meaningful metadata will be parsed and populated as OME-XML.

**Openness**  This is not a direct expression of Bio-Formats’ performance, but rather indicates the level of cooperation the format’s controlling interest has demonstrated toward the scientific community with respect to the format. The better this score, the more tools (specification documents, source code, sample files, etc.) have been made available.

**Presence**  This is also not directly related to Bio-Formats, but instead represents our understanding of the format’s popularity, and is also as a measure of compatibility between applications. The better this score, the more common the format and the more software packages include support for it.

**Utility**  Our opinion of the format’s suitability for storing metadata-rich microscopy image data. The better this score, the wider the variety of information that can be effectively stored in the format.

**Export**  This indicates whether Bio-Formats is capable of writing the format (Bio-Formats can read every format on this list).

**BSD**  This indicates whether format is BSD-licensed. By default, format readers and writers are GPL-licensed.

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 17.1 3i SlideBook

Extensions: .sld

Developer: Intelligent Imaging Innovations

Owner: Intelligent Imaging Innovations

Support

BSD-licensed: 

---

4http://www.openmicroscopy.org/site/support/bio-formats5.0/

5http://www.openmicroscopy.org/site/support/legacy/

6http://www.intelligent-imaging.com/

7http://www.intelligent-imaging.com/
Export: ❌

Officially Supported Versions: 4.1, 4.2

Supported Metadata Fields: 3i SlideBook

We currently have:

- Numerous SlideBook datasets

We would like to have:

- A SlideBook specification document
- More SlideBook datasets (preferably acquired with the most recent SlideBook software)

Ratings

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▲
Utility: ▼

Additional Information

Source Code: SlidebookReader.java

Notes:

We strongly encourage users to export their .sld files to OME-TIFF using the SlideBook software. Bio-Formats is not likely to support the full range of metadata that is included in .sld files, and so exporting to OME-TIFF from SlideBook is the best way to ensure that all metadata is preserved. Free software from 3I can export the files to OME-TIFF post-acquisition, see https://www.slidebook.com/reader.php

See also:

Slidebook software overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 17.2 3i SlideBook6

Extensions: .sld

Developer: Intelligent Imaging Innovations

Owner: Intelligent Imaging Innovations

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions: 4.1, 4.2, 5.0, 5.5, 6.0

Supported Metadata Fields: 3i SlideBook6

We currently have:

---

9 https://www.slidebook.com
10 http://www.openmicroscopy.org/site/support/bio-formats5.0/
11 http://www.openmicroscopy.org/site/support/legacy/
12 http://www.intelligent-imaging.com/
13 http://www.intelligent-imaging.com/
• Numerous SlideBook datasets

We would like to have:
• A SlideBook specification document
• More SlideBook datasets (preferably acquired with the most recent SlideBook software)

Ratings

Pixels: 🔺
Metadata: ▼
Openness: ▼
Presence: 🔺
Utility: ▼

Additional Information

Source Code: SlideBook6Reader.java

Notes:

As of Bioformats 5.1.2 the native binary file SlideBook6Reader.dll of the proper architecture (x32 or x64) must be in the java binary path for this reader to work. This file is available from 3i Support and is currently only available for Windows systems.

See also:

Slidebook software overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.3 Andor Bio-Imaging Division (ABD) TIFF

Extensions: .tif

Developer: Andor Bioimaging Department

Owner: Andor Technology

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Andor Bio-Imaging Division (ABD) TIFF

We currently have:

• an ABD-TIFF specification document (from 2005 November, in PDF)
• a few ABD-TIFF datasets

We would like to have:

Ratings

Pixels: 🔺

15support@intelligent-imaging.com
16https://www.slidebook.com
17http://www.openmicroscopy.org/site/support/bio-formats5.0/
18http://www.openmicroscopy.org/site/support/legacy/
19http://www.andor.com/
Metadata:  
Openness:  
Presence:  
Utility:  

Additional Information

Source Code: FluoviewReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties. With a few minor exceptions, the ABD-TIFF format is identical to the Fluoview TIFF format.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.4 AIM

Extensions: .aim

Developer: SCANCO Medical AG

Support

BSD-licensed:  
Export:  

Officially Supported Versions:

Supported Metadata Fields: AIM

We currently have:

• one .aim file

We would like to have:

• an .aim specification document
• more .aim files

Ratings

Pixels:  
Metadata:  
Openness:  
Presence:  
Utility:  

Additional Information

Source Code: AIMReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
versions page to find documentation for the version you are using.

## 17.5 Alicona 3D

Extensions: .al3d

Owner: Alicona Imaging

**Support**

BSD-licensed: ✗

Export: ✗

**Officially Supported Versions:** 1.0

**Supported Metadata Fields:** *Alicona 3D*

We currently have:

- an *AL3D specification document* (v1.0, from 2003, in PDF)
- a few AL3D datasets

We would like to have:

- more AL3D datasets (Z series, T series, 16-bit)

**Ratings**

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: ▼

Utility: ▲

**Additional Information**

Source Code: [AliconaReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/AliconaReader.java)

Notes:

Known deficiencies:

- Support for 16-bit AL3D images is present, but has never been tested.
- Texture data is currently ignored.

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 17.6 Amersham Biosciences Gel

Extensions: .gel

Developer: Molecular Dynamics

---

26. [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
27. [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
30. [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
31. [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
Owner: GE Healthcare Life Sciences

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Amersham Biosciences Gel

We currently have:

- a GEL specification document (Revision 2, from 2001 Mar 15, in PDF)
- a few GEL datasets

We would like to have:

Ratings

Pixels: 

Metadata: 

Openness: 

Presence: 

Utility: 

Additional Information

Source Code: GelReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

See also:

GEL Technical Overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.7 Amira Mesh

Extensions: .am, .amiramesh, .grey, .hx, .labels

Developer: Visage Imaging

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Amira Mesh

We currently have:

- a few Amira Mesh datasets

32http://www.gelifesciences.com/
33https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/GelReader.java
34http://www.awaresystems.be/imaging/tiff/tifftags/docs/gel.html
35http://www.openmicroscopy.org/site/support/bio-formats5.0/
36http://www.openmicroscopy.org/site/support/legacy/
37http://www.amiravis.com/
We would like to have:

- more Amira Mesh datasets

### Ratings

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
<th>Openness</th>
<th>Presence</th>
<th>Utility</th>
</tr>
</thead>
</table>

### Additional Information

Source Code: `AmiraReader.java`

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

### 17.8 Amnis FlowSight

Extensions: `.cif`

Owner: Amnis

### Support

- BSD-licensed: ✔
- Export: ❌

Officially Supported Versions:

Supported Metadata Fields: `Amnis FlowSight`

We currently have:

- a few sample datasets

We would like to have:

### Ratings

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
<th>Openness</th>
<th>Presence</th>
<th>Utility</th>
</tr>
</thead>
</table>

### Additional Information

Source Code: `FlowSightReader.java`

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions.

---

38https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/AmiraReader.java

39http://www.openmicroscopy.org/site/support/bio-formats5.0/

40http://www.openmicroscopy.org/site/support/legacy/

41http://www.amnis.com/

17.9 Analyze 7.5

Extensions: .img, .hdr

Developer: Mayo Foundation Biomedical Imaging Resource

Support

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Analyze 7.5

We currently have:

- an Analyze 7.5 specification document
- several Analyze 7.5 datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▼

Openness: ▲

Presence: ◀

Utility: ◀

Additional Information

Source Code: AnalyzeReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.10 Animated PNG

Extensions: .png

Developer: The Animated PNG Project

Support

BSD-licensed: ✔

Export: ✔
Officially Supported Versions:

Supported Metadata Fields: *Animated PNG*

Freely Available Software:
- Firefox 3+\(^{51}\)
- Opera 9.5+\(^{52}\)
- KSquirrel\(^{53}\)

We currently have:
- a specification document\(^{54}\)
- several APNG files

We would like to have:

**Ratings**

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: □

Utility: ▼

**Additional Information**

Source Code: APNGReader.java\(^{55}\)

Notes:

---

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{56}\) or the previous versions\(^{57}\) page to find documentation for the version you are using.

---

17.11 Aperio AFI

Extensions: .afi, .svs

Owner: Aperio\(^{58}\)

**Support**

BSD-licensed: \(\times\)

Export: \(\times\)

Officially Supported Versions:

Supported Metadata Fields: *Aperio AFI*

We currently have:

- several AFI datasets

---

\(^{51}\)http://www.mozilla.com/firefox

\(^{52}\)http://www.opera.com/download

\(^{53}\)http://ksquirrel.sourceforge.net/download.php

\(^{54}\)http://wiki.mozilla.org/APNG_Specification

\(^{55}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/APNGReader.java

\(^{56}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{57}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{58}\)http://www.aperio.com/
We would like to have:

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ▲
- Presence:
- Utility: ▲

**Additional Information**

Source Code: [AFIReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/AFIReader.java)

Notes:

See also:

Aperio ImageScope

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 17.12 Aperio SVS TIFF

**Extensions:** .svs

**Owner:** Aperio

**Support**

- BSD-licensed: ✗
- Export: ✗

**Officially Supported Versions:** 8.0, 8.2, 9.0

**Supported Metadata Fields:** *Aperio SVS TIFF*

We currently have:

- many SVS datasets
- an SVS specification document
- the ability to generate additional SVS datasets

We would like to have:

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ▲
- Presence:
- Utility: ▲

**Additional Information**

---


61 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)

62 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)

Source Code: SVSReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

See also:

Aperio ImageScope

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.13 Applied Precision CellWorX

Extensions: .htd, .pnl

Developer: Applied Precision

Support

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Applied Precision CellWorX

We currently have:

• a few CellWorX datasets

We would like to have:

• a CellWorX specification document
  • more CellWorX datasets

Ratings

Pixels:

Metadata:

Openness:

Presence:

Utility:

Additional Information

Source Code: CellWorxReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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64 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SVSReader.java
66 http://www.openmicroscopy.org/site/support/bio-formats5.0/
67 http://www.openmicroscopy.org/site/support/legacy/
68 http://www.api.com
70 http://www.openmicroscopy.org/site/support/bio-formats5.0/
71 http://www.openmicroscopy.org/site/support/legacy/
17.14 AVI (Audio Video Interleave)

Extensions: .avi
Developer: Microsoft

Support

BSD-licensed: ✔
Export: ✔

Officially Supported Versions:

Supported Metadata Fields: AVI (Audio Video Interleave)

Freely Available Software:

- AVI Reader plugin for ImageJ
- AVI Writer plugin for ImageJ

We currently have:

- several AVI datasets

We would like to have:

- more AVI datasets, including:
  - files with audio tracks and/or multiple video tracks
  - files compressed with a common unsupported codec
  - 2+ GB files

Ratings

Pixels: ▼
Metadata: ▲
Openness: ▼
Presence: ▲
Utility: ▼

Additional Information

Source Code: AVIReader.java

Notes:

- Bio-Formats can save image stacks as AVI (uncompressed).
- The following codecs are supported for reading:
  - Microsoft Run-Length Encoding (MSRLE)
  - Microsoft Video (MSV1)
  - Raw (uncompressed)
  - JPEG

See also:

AVI RIFF File Reference AVI on Wikipedia

---

72http://www.microsoft.com/
74http://rsb.info.nih.gov/ij/plugins/avi.html
75https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/AVIReader.java
77http://en.wikipedia.org/wiki/Audio_Video_Interleave
17.15 Axon Raw Format

Extensions: .arf
Owner: INDECBioSystems

Support
BSD-licensed: 

Export:

Officially Supported Versions:

Supported Metadata Fields: Axon Raw Format
We currently have:
• one ARF dataset
  • a specification document
We would like to have:
• more ARF datasets

Ratings
Pixels: 
Metadata: 
Openness: 
Presence: 
Utility:

Additional Information
Source Code: ARFReader.java
Notes:

17.16 BD Pathway

Extensions: .exp, .tif
Owner: BD Biosciences

Support
BSD-licensed: 

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *BD Pathway*

We currently have:

- a few BD Pathway datasets

We would like to have:

- more BD Pathway datasets

**Ratings**

Pixels: ▲

Metadata: ▲

Openness: □

Presence: ▼

Utility: □

**Additional Information**

Source Code: [BDReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/BDReader.java)

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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17.17 **Becker & Hickl SPCImage**

Extensions: .sdt

Owner: Becker-Hickl

**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Becker & Hickl SPCImage*

We currently have:

- an SDT specification document (from 2008 April, in PDF)
- an SDT specification document (from 2006 June, in PDF)
- Becker & Hickl’s SPCImage software
- a large number of SDT datasets
- the ability to produce new datasets

---

[^87]: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
[^88]: [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
[^90]: [http://www.becker-hickl.de/software/tcspace/tcspecialsoftware.htm](http://www.becker-hickl.de/software/tcspace/tcspecialsoftware.htm)
We would like to have:

**Ratings**

Pixels: ▲

Metadata: ▲

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: SDTReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

---

**17.18 Bio-Rad Gel**

Extensions: .1sc

Owner: Bio-Rad

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Bio-Rad Gel

We currently have:

- software that can read Bio-Rad Gel files
- several Bio-Rad Gel files

We would like to have:

- a Bio-Rad Gel specification
- more Bio-Rad Gel files

**Ratings**

Pixels:

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

[^91]: https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SDTReader.java

[^92]: http://www.openmicroscopy.org/site/support/bio-formats5.0.x

[^93]: http://www.openmicroscopy.org/site/support/legacy/

[^94]: http://www.bio-rad.com
Source Code: BioRadGelReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.19 Bio-Rad PIC

Extensions: .pic, .raw, .xml
Developer: Bio-Rad
Owner: Carl Zeiss, Inc.

Support
BSD-licensed: 
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Bio-Rad PIC

Freely Available Software:
• Bio-Rad PIC reader plugin for ImageJ

We currently have:
• a PIC specification document (v4.5, in PDF)
• an older PIC specification document (v4.2, from 1996 December 16, in DOC)
• a large number of PIC datasets
• the ability to produce new datasets

We would like to have:

Ratings
Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information
Source Code: BioRadReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

• Commercial applications that support this format include:
  • Bitplane Imaris

95 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/BioRadGelReader.java
96 http://www.openmicroscopy.org/site/support/bio-formats5.0/
97 http://www.openmicroscopy.org/site/support/legacy/
98 http://www.zeiss.com/
100 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/BioRadReader.java
101 http://www.bitplane.com/
17.20 Bio-Rad SCN

Extensions: .scn
Developer: Bio-Rad
Owner: Bio-Rad

Support

BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: Bio-Rad SCN

We currently have:
• a few Bio-Rad .scn files

We would like to have:

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: BioRadSCNReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.21 Bitplane Imaris

Extensions: .ims
Owner: Bitplane

Support

http://svi.nl/
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/ 
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.bitplane.com/
We currently have:

- an Imaris (RAW) specification document (from no later than 1997 November 11, in HTML)
- an Imaris 5.5 (HDF) specification document
- Bitplane’s bfFileReaderImaris3N code (from no later than 2005, in C++)
- several older Imaris (RAW) datasets
- one Imaris 3 (TIFF) dataset
- several Imaris 5.5 (HDF) datasets

We would like to have:

- an Imaris 3 (TIFF) specification document
- more Imaris 3 (TIFF) datasets

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ❌
- Presence: ▼
- Utility: ▼

**Additional Information**


**Notes:**

- There are three distinct Imaris formats:
  1. the old binary format (introduced in Imaris version 2.7)
  2. Imaris 3, a TIFF variant (introduced in Imaris version 3.0)
  3. Imaris 5.5, an HDF variant (introduced in Imaris version 5.5)

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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**17.22 Bruker MRI**

**Developer:** Bruker

**Support**

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: **Bruker MRI**

Freely Available Software:

- Bruker plugin for ImageJ

We currently have:

- a few Bruker MRI datasets

We would like to have:

- an official specification document

**Ratings**

Pixels: ▲

Metadata: △

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: BrukerReader.java

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.23 **Burleigh**

Extensions: .img

Owner: Burleigh Instruments

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: **Burleigh**

We currently have:

- Pascal code that can read Burleigh files (from ImageSXM)
- a few Burleigh files

We would like to have:

- a Burleigh file format specification
- more Burleigh files

---

118 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/BrukerReader.java
119 http://www.openmicroscopy.org/site/support/bio-formats5.0/
120 http://www.openmicroscopy.org/site/support/legacy/
**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: BurleighReader.java

Notes:

*Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.*

### 17.24 Canon DNG

Extensions: .cr2, .crw

Developer: Canon

**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Canon DNG*

Freely Available Software:

- IrfanView

We currently have:

- a few example datasets

We would like to have:

- an official specification document

**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: DNGReader.java

---

121 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/BurleighReader.java

122 http://www.openmicroscopy.org/site/support/bio-formats5.0/

123 http://www.openmicroscopy.org/site/support/legacy/

124 http://canon.com

125 http://www.irfanview.com/

126 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/DNGReader.java
17.25 CellH5

Extensions: .ch5
Developer: CellH5

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: CellH5

Freely Available Software: CellH5

We currently have:
• a few CellH5 datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ★
Openness: ▲
Presence: ●
Utility: ●

Additional Information

Source Code: CellH5Reader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.26 Cellomics

Extensions: .c01
Developer: Thermo Fisher Scientific

Support

127http://www.openmicroscopy.org/site/support/bio-formats5.0/
128http://www.openmicroscopy.org/site/support/legacy/
129http://cellh5.org/
130http://cellh5.org/
132http://www.openmicroscopy.org/site/support/bio-formats5.0/
133http://www.openmicroscopy.org/site/support/legacy/
134http://www.thermofisher.com/
BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Cellomics

We currently have:

• a few Cellomics .c01 datasets

We would like to have:

• a Cellomics .c01 specification document
• more Cellomics .c01 datasets

Ratings

Pixels: 🔺
Metadata: 🔻
Openness: 🔻
Presence: 🔻
Utility: 🔻

Additional Information

Source Code: CellomicsReader.java\textsuperscript{135}

Notes:

\textbf{Note:} This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{136} or the previous versions\textsuperscript{137} page to find documentation for the version you are using.

\section*{17.27 cellSens VSI}

Extensions: .vsi

Developer: Olympus\textsuperscript{138}

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: cellSens VSI

We currently have:

• a few example datasets

We would like to have:

• an official specification document

Ratings

Pixels: 🔻
Metadata: [ ]
17.28 CellVoyager

Extensions: .xml, .tif
Owner: Yokogawa

Support
BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: CellVoyager
We currently have:
• a few example datasets
We would like to have:

Ratings
Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information
Source Code: CellVoyagerReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

140 http://www.openmicroscopy.org/site/support/bio-formats5.0/
141 http://www.openmicroscopy.org/site/support/legacy/
142 http://www.yokogawa.com/
144 http://www.openmicroscopy.org/site/support/bio-formats5.0/
145 http://www.openmicroscopy.org/site/support/legacy/
17.29 DeltaVision

Extensions: .dv, .r3d
Owner: GE Healthcare (formerly Applied Precision)
Support
BSD-licensed: ✗
Export: ✗

Officially Supported Versions:
Supported Metadata Fields: DeltaVision
Freely Available Software:
  • DeltaVision Opener plugin for ImageJ

We currently have:
  • a DV specification document (v2.10 or newer, in HTML)
  • numerous DV datasets

We would like to have:

Ratings
Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information
Source Code: DeltavisionReader.java
Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

• The DeltaVision format is based on the Medical Research Council (MRC) file format.
• Commercial applications that support DeltaVision include:
  – Bitplane Imaris
  – SVI Huygens
  – Image-Pro Plus

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.30 DICOM

Extensions: .dcm, .dicom

Developer: National Electrical Manufacturers Association¹⁵⁴

Support

BSD-licensed: ✓

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: DICOM

Freely Available Software:

- OsiriX Medical Imaging Software¹⁵⁵
- ezDICOM¹⁵⁶
- Wikipedia’s list of freeware health software¹⁵⁷

Sample Datasets:

- MRI Chest from FreeVol-3D web site¹⁵⁸
- Medical Image Samples from Sebastien Barre’s Medical Imaging page¹⁵⁹
- DICOM sample image sets from OsiriX web site¹⁶⁰

We currently have:

- DICOM specification documents¹⁶¹ (PS 3 - 2007, from 2006 December 28, in DOC and PDF)
- numerous DICOM datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: ▲

Utility: ▼

Additional Information

Source Code: DicomReader.java¹⁶²

Notes:

- DICOM stands for “Digital Imaging and Communication in Medicine”.
- Bio-Formats supports both compressed and uncompressed DICOM files.

If you have a problematic DICOM file which you cannot send us for privacy reasons, please send us the exact error message and be aware that it may take several attempts to fix the problem blind.

See also:

¹⁵⁴http://www.nema.org/
¹⁵⁵http://www.osirix-viewer.com/
¹⁵⁶http://www.sph.sc.edu/comd/rorden/ezdicom.html
¹⁵⁷http://en.wikipedia.org/wiki/List_of_freeware_health_software#Imaging.2FVisualization
¹⁵⁸http://members.tripod.com/%7Eeclinis_immensus/free3d/hk-40.zip
¹⁵⁹http://www.barre.nom.fr/medical/samples/
¹⁶⁰http://osirix-viewer.com/datasets/
17.31 ECAT7

Extensions: .v
Developer: Siemens

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:
Supported Metadata Fields: ECAT7

We currently have:
• a few ECAT7 files

We would like to have:
• an ECAT7 specification document
• more ECAT7 files

Ratings

Pixels:  ◦
Metadata:  ◦
Openness:  ◊
Presence:  ◊
Utility:  ◊

Additional Information

Source Code: Ecat7Reader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.32 EPS (Encapsulated PostScript)

Extensions: .eps, .epsi, .ps
Developer: Adobe

Support

163http://medical.nema.org/
164http://www.openmicroscopy.org/site/support/bio-formats5.0/
165http://www.openmicroscopy.org/site/support/legacy/
166http://www.siemens.com
168http://www.openmicroscopy.org/site/support/bio-formats5.0/
169http://www.openmicroscopy.org/site/support/legacy/
170http://www.adobe.com/
BSD-licensed: ✅
Export: ✅

Officially Supported Versions:

Supported Metadata Fields: *EPS (Encapsulated PostScript)*

Freely Available Software:
- EPS Writer plugin for ImageJ

We currently have:
- a few EPS datasets
- the ability to produce new datasets

We would like to have:

**Ratings**

Pixels: 
Metadata: 
Openness: 

Presence: 🟢
Utility: 🔴

**Additional Information**

Source Code: EPSReader.java Source Code: EPSWriter.java

Notes:
- Bio-Formats can save individual planes as EPS.
- Certain types of compressed EPS files are not supported.

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

### 17.33 Evotec/PerkinElmer Opera Flex

Extensions: .flex, .mea, .res

Developer: Evotec Technologies, now PerkinElmer

**Support**

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Evotec/PerkinElmer Opera Flex

We currently have:
- many Flex datasets

We would like to have:

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172 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/EPSReader.java
174 http://www.openmicroscopy.org/site/support/bio-formats5.0/
175 http://www.openmicroscopy.org/site/support/legacy/
176 http://www.perkinelmer.com/
- a freely redistributable LuraWave LWF decoder

### Ratings

- Pixels: ⬆
- Metadata: ⬆
- Openness: ⬇
- Presence: ⬇
- Utility: ⬇

### Additional Information

Source Code: [FlexReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/FlexReader.java)

Notes:
The LuraWave LWF decoder library (i.e. lwf_jsdk2.6.jar) with license code is required to decode wavelet-compressed Flex files.

See also:
LuraTech (developers of the proprietary LuraWave LWF compression used for Flex image planes)

Note: This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous versions page to find documentation for the version you are using.

### 17.34 FEI

Extensions: .img

Developer: [FEI](http://www.fei.com)

Support

- BSD-licensed: ❌
- Export: ❌

Officially Supported Versions:

Supported Metadata Fields: [FEI](http://www.fei.com)

We currently have:

- a few FEI files

We would like to have:

- a specification document
- more FEI files

### Ratings

- Pixels: ⬇
- Metadata: ⬇
- Openness: ⬇
- Presence: ⬇
- Utility: ⬇

---

177 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/FlexReader.java
178 http://www.luratech.com/
179 http://www.openmicroscopy.org/site/support/bio-formats5.0/
180 http://www.openmicroscopy.org/site/support/legacy/
181 http://www.fei.com/
17.35 FEI TIFF

Extensions: .tiff
Developer: FEI

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: FEI TIFF

We currently have:
• a few FEI TIFF datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

Source Code: FEITiffReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.36 FITS (Flexible Image Transport System)

Extensions: .fits
Developer: National Radio Astronomy Observatory

Support

https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/FEIReader.java
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.fei.com

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.nrao.edu/
BSD-licensed: ✔
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: **FITS (Flexible Image Transport System)**

We currently have:
- a FITS specification document\(^{190}\) (NOST 100-2.0, from 1999 March 29, in HTML)
- several FITS datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▲
Presence: ☐
Utility: ▼

**Additional Information**

Source Code: FitsReader.java\(^{191}\)

Notes:

See also:

MAST:FITS homepage\(^{192}\)  FITS Support Office\(^{193}\)

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{194}\) or the previous versions\(^{195}\) page to find documentation for the version you are using.

### 17.37 Gatan Digital Micrograph

**Extensions:** .dm3

**Owner:** Gatan\(^{196}\)

**Support**

BSD-licensed: ✗
Export: ✗

Officially Supported Versions: 3

**Supported Metadata Fields:** *Gatan Digital Micrograph*

Freely Available Software:
- **DM3 Reader plugin for ImageJ**\(^{197}\)
- **EMAN**\(^{198}\)

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\(^{194}\)[http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
\(^{195}\)[http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
\(^{196}\)[http://www.gatan.com/](http://www.gatan.com/)
\(^{198}\)[http://blake.bcm.edu/EMAN/](http://blake.bcm.edu/EMAN/)
We currently have:

- Gatan's ImageReader2003 code (from 2003, in C++)
- numerous DM3 datasets

We would like to have:

- a DM3 specification document

**Ratings**

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
<th>Openness</th>
<th>Presence</th>
<th>Utility</th>
</tr>
</thead>
</table>

**Additional Information**

Source Code: GatanReader.java

Notes:

Commercial applications that support .dm3 files include Datasqueeze.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 17.38 Gatan Digital Micrograph 2

Extensions: .dm2

Developer: Gatan

**Support**

BSD-licensed: ![✗](https://www.icons8.com/icons/line/512px/x-red.png)

Export: ![✗](https://www.icons8.com/icons/line/512px/x-red.png)

Officially Supported Versions: 2

Supported Metadata Fields: *Gatan Digital Micrograph 2*

We currently have:

- Pascal code that can read DM2 files (from ImageSXM)
- a few DM2 files

We would like to have:

- an official DM2 specification document
- more DM2 files

**Ratings**

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
</tr>
</thead>
</table>

200http://www.datasqueezesoftware.com/
201http://www.openmicroscopy.org/site/support/bio-formats5.0/
202http://www.openmicroscopy.org/site/support/legacy/
203http://www.gatan.com
17.39 GIF (Graphics Interchange Format)

Extensions: .gif
Developer: CompuServe
Owner: Unisys

Support
BSD-licensed: ✔
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: GIF (Graphics Interchange Format)

Freely Available Software:
- Animated GIF Reader plugin for ImageJ
- GIF Stack Writer plugin for ImageJ

We currently have:
- a GIF specification document (Version 89a, from 1990, in HTML)
- numerous GIF datasets
- the ability to produce new datasets

We would like to have:

Ratings
Pixels: ▲
Metadata: ▲
Openness: ▼
Presence: ▲
Utility: ▼

Additional Information

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

205. http://www.openmicroscopy.org/site/support/bio-formats5.0/
206. http://www.openmicroscopy.org/site/support/legacy/
Source Code: GIFReader.java\textsuperscript{212}

Notes:

\textbf{Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{213} or the previous versions\textsuperscript{214} page to find documentation for the version you are using.}

### 17.40 Hamamatsu Aquacosmos NAF

Extensions: .naf

Developer: Hamamatsu\textsuperscript{215}

\textbf{Support}

BSD-licensed: \xmark

Export: \xmark

Officially Supported Versions:

Supported Metadata Fields: \textit{Hamamatsu Aquacosmos NAF}

We currently have:

- a few NAF files

We would like to have:

- a specification document
- more NAF files

\textbf{Ratings}

Pixels: 🔽

Metadata: 🔽

Openness: 🔽

Presence: 🔽

Utility: 🔽

\textbf{Additional Information}

Source Code: NAFReader.java\textsuperscript{216}

Notes:

\textbf{Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{217} or the previous versions\textsuperscript{218} page to find documentation for the version you are using.}

### 17.41 Hamamatsu HIS

Extensions: .his

Owner: Hamamatsu\textsuperscript{219}

\textsuperscript{212}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/GIFReader.java

\textsuperscript{213}http://www.openmicroscopy.org/site/support/bio-formats5.0/

\textsuperscript{214}http://www.openmicroscopy.org/site/support/legacy/

\textsuperscript{215}http://www.hamamatsu.com/

\textsuperscript{216}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/NAFReader.java

\textsuperscript{217}http://www.openmicroscopy.org/site/support/bio-formats5.0/

\textsuperscript{218}http://www.openmicroscopy.org/site/support/legacy/

\textsuperscript{219}http://www.hamamatsu.com
Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Hamamatsu HIS

We currently have:

• Pascal code that can read HIS files (from ImageSXM)
• several HIS files

We would like to have:

• an HIS specification
• more HIS files

Ratings

Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information

Source Code: HISReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.42 Hamamatsu ndpi

Extensions: .ndpi
Developer: Hamamatsu

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Hamamatsu ndpi

Freely Available Software:

• NDP.view

Sample Datasets:

• OpenSlide

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221 http://www.openmicroscopy.org/site/support/bio-formats5.0/
222 http://www.openmicroscopy.org/site/support/legacy/
223 http://www.hamamatsu.com
225 http://openslide.cs.cmu.edu/download/openslide-testdata/Hamamatsu/
We currently have:

- many example datasets

We would like to have:

- an official specification document

**Ratings**

Pixels: 🟠

Metadata: 🟠

Openness: 🟠

Presence: 🟠

Utility: 🟠

**Additional Information**

Source Code: NDPIReader.java

Notes:

*Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.*

## 17.43 Hamamatsu VMS

**Extensions:** .vms

**Developer:** Hamamatsu

**Support**

BSD-licensed: ✗

Export: ✗

**Officially Supported Versions:**

**Supported Metadata Fields:** *Hamamatsu VMS*

**Sample Datasets:**

- OpenSlide

We currently have:

- a few example datasets

We would like to have:

- an official specification document

**Ratings**

Pixels: 🟠

Metadata: 🟠

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227 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)

228 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)

229 [http://www.hamamatsu.com](http://www.hamamatsu.com)


231 [http://openslide.org/Hamamatsu%20format/](http://openslide.org/Hamamatsu%20format/)

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17.43. Hamamatsu VMS
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

Source Code: HamamatsuVMSReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 17.44 Hitachi S-4800

Extensions: .txt, .tif, .bmp, .jpg

Developer: Hitachi

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Hitachi S-4800

We currently have:

* several Hitachi S-4800 datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ▼
Utility: ▼

Additional Information

Source Code: HitachiReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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233 http://www.openmicroscopy.org/site/support/bio-formats5.0/
234 http://www.openmicroscopy.org/site/support/legacy/
236 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/HitachiReader.java
237 http://www.openmicroscopy.org/site/support/bio-formats5.0/
238 http://www.openmicroscopy.org/site/support/legacy/
17.45 I2I

Extensions: .i2i
Developer: Biomedical Imaging Group, UMass Medical School

Support
BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: I2I
We currently have:
• several example datasets
• a specification document
• an ImageJ plugin that can read I2I data

We would like to have:

Ratings
Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information
Source Code: I2IReader.java

Notes:
Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.46 ICS (Image Cytometry Standard)

Extensions: .ics, .ids
Developer: P. Dean et al.

Support
BSD-licensed: 
Export: 

Officially Supported Versions: 1.0, 2.0
Supported Metadata Fields: ICS (Image Cytometry Standard)
Freely Available Software:
• Libics (ICS reference library)
• ICS Opener plugin for ImageJ
• IrfanView

We currently have:
• numerous ICS datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ▲
Utility: ▲

Additional Information

Source Code: ICSReader.java
Source Code: ICSWriter.java

Notes:

• ICS version 1.0 datasets have two files - an .ics file that contains all of the metadata in plain-text format, and an .ids file that contains all of the pixel data.
• ICS version 2.0 datasets are a single .ics file that contains both pixels and metadata.

Commercial applications that can support ICS include:

• Bitplane Imaris
• SVI Huygens

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.47 Imacon

Extensions: .fff
Owner: Hasselblad

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Imacon

We currently have:
• one Imacon file

We would like to have:
• more Imacon files

Ratings

Pixels: 
Metadata: ◻
Openness: ◻
Presence: ◻
Utility: ◻

Additional Information

Source Code: ImaconReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.48 ImagePro Sequence

Extensions: .seq
Owner: Media Cybernetics

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: ImagePro Sequence

We currently have:

• the Image-Pro Plus software
• a few SEQ datasets
• the ability to produce more datasets

We would like to have:

• an official SEQ specification document

Ratings

Pixels: ▲
Metadata: ▲
Openness: ◻
Presence: ◻
Utility: ◻

Additional Information

https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/ImaconReader.java
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.mediacy.com/
17.49 ImagePro Workspace

Extensions: .ipw

Owner: Media Cybernetics

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: ImagePro Workspace

We currently have:

- the Image-Pro Plus software
- a few IPW datasets
- the ability to produce more datasets

We would like to have:

- an official IPW specification document
- more IPW datasets:
  - multiple datasets in one file
  - 2+ GB files

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▼

Presence: ▼

Utility: ▼

Additional Information

Source Code: IPWReader.java

Notes:

Bio-Formats uses a modified version of the Apache Jakarta POI library to read IPW files.

Note: This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://jakarta.apache.org/poi/) or the previous [version](http://www.mediacy.com/) page to find documentation for the version you are using.
17.50 IMAGIC

Extensions: .hed, .img

Developer: Image Science

Support

BSD-licensed: ☒

Export: ☒

Officially Supported Versions:

Supported Metadata Fields: IMAGIC

Freely Available Software:

• em2em

We currently have:

• one example dataset
  • official file format documentation

We would like to have:

• more example datasets

Ratings

Pixels: 🟠

Metadata: 🟠

Openness: 🟠

Presence: ☒

Utility: ☐

Additional Information

Source Code: ImagicReader.java

Notes:

See also:

IMAGIC specification

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.51 IMOD

Extensions: .mod
Developer: Boulder Laboratory for 3-Dimensional Electron Microscopy of Cells
Owner: Boulder Laboratory for 3-Dimensional Electron Microscopy of Cells

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: IMOD

Freely Available Software:
• IMOD

We currently have:
• a few sample datasets
• official documentation

We would like to have:

Ratings
Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information
Source Code: IMODReader.java

Notes:
Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.52 Improvision Openlab LIFF

Extensions: .liff
Developer: Improvision
Owner: PerkinElmer

Support

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
BSD-licensed: ✗
Export: ✗

Officially Supported Versions: 2.0, 5.0

Supported Metadata Fields: *Improvision Openlab LIFF*

We currently have:

- an Openlab specification document (from 2000 February 8, in DOC)
- Improvision’s XLIFFFileImporter code for reading Openlab LIFF v5 files (from 2006, in C++)
- several Openlab datasets

We would like to have:

- more Openlab datasets (preferably with 32-bit integer data)

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ▲
- Presence: ▲
- Utility: ▼

**Additional Information**

Source Code: [OpenlabReader.java]282

Notes:

*Please note that while we have specification documents for this format, we are not able to distribute them to third parties.*

See also:

[Openlab software review]283

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version284 or the previous versions285 page to find documentation for the version you are using.

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### 17.53 Improvision Openlab Raw

Extensions: .raw

Developer: Improvision286

Owner: PerkinElmer287

**Support**

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Improvision Openlab Raw*

We currently have:


284[http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)

285[http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)


• an Openlab Raw specification document\(^{288}\) (from 2004 November 09, in HTML)
• a few Openlab Raw datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: OpenlabRawReader.java\(^{289}\)

Notes:

**See also:**

Openlab software review\(^{290}\)

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{291}\) or the previous versions\(^{292}\) page to find documentation for the version you are using.

### 17.54 Improvision TIFF

Extensions: .tif

Developer: Improvision\(^{293}\)
Owner: PerkinElmer\(^{294}\)

**Support**

BSD-licensed: ✗
Export: ✗

**Officially Supported Versions:**

Supported Metadata Fields: *Improvision TIFF*

We currently have:

• an Improvision TIFF specification document
• a few Improvision TIFF datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▲
Openness: ▲

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\(^{288}\)http://cellularimaging.perkinelmer.com/support/technical_notes/detail.php?id=344
\(^{290}\)http://www.improvision.com/products/openlab/
\(^{291}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{292}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{293}\)http://www.improvision.com/
\(^{294}\)http://www.perkinelmer.com/
17.55 Imspector OBF

Extensions: .obf, .msr

Developer: Department of NanoBiophotonics, MPI-BPC

Owner: MPI-BPC

Support

BSD-licensed: ✔

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Imspector OBF

We currently have:

- a few .msr datasets
- a specification document

We would like to have:

Ratings

Pixels: ★

Metadata: ★

Openness: ★

Presence: ❌

Utility: ❌

Additional Information

Source Code: OBFReader.java

Notes:

296 http://www.improvision.com/products/openlab/
297 http://www.openmicroscopy.org/site/support/bio-formats5.0/
299 http://www.openmicroscopy.org/site/support/legacy/
300 http://www.mpibpc.mpg.de/
301 https://imspector.mpibpc.mpg.de/index.html
302 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/OBFReader.java

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.56 InCell 1000

Extensions: .xdce, .tif
Developer: GE

Support
BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: InCell 1000

We currently have:
  • a few InCell 1000 datasets

We would like to have:
  • an InCell 1000 specification document
  • more InCell 1000 datasets

Ratings
Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information
Source Code: InCellReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.57 InCell 3000

Extensions: .frm
Developer: GE

Support
BSD-licensed: 

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *InCell 3000*

Sample Datasets:
- Broad Bioimage Benchmark Collection

We currently have:
- a few example datasets

We would like to have:
- an official specification document

**Ratings**

Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: [InCell3000Reader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/InCell3000Reader.java)

Notes:

*Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.*

### 17.58 INR

Extensions: .inr

**Support**

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *INR*

We currently have:
- several sample .inr datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▼

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312 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
313 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)

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17.58. INR
17.59 Inveon

Extensions: .hdr

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Inveon

We currently have:

a few Inveon datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▼

Presence: ▼

Utility: ▼

Additional Information

Source Code: INRReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.60 IPLab

Extensions: .ipl

Developer: Scanalytics

Additional Information

Source Code: InveonReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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315 http://www.openmicroscopy.org/site/support/bio-formats5.0/
316 http://www.openmicroscopy.org/site/support/legacy/
318 http://www.openmicroscopy.org/site/support/bio-formats5.0/
319 http://www.openmicroscopy.org/site/support/legacy/
Owner: was BD Biosystems\textsuperscript{320}, now BioVision Technologies\textsuperscript{321} 

Support

BSD-licensed: ×

Export: ×

Officially Supported Versions:

Supported Metadata Fields: \textit{IPLab}

Freely Available Software:

• IPLab Reader plugin for ImageJ\textsuperscript{322}

We currently have:

• an IPLab specification document (v3.6.5, from 2004 December 1, in PDF)
• several IPLab datasets

We would like to have:

• more IPLab datasets (preferably with 32-bit integer or floating point data)

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: ▼

Utility: ▼

Additional Information

Source Code: IPLabReader.java\textsuperscript{323}

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Commercial applications that support IPLab include:

• Bitplane Imaris\textsuperscript{324}
• SVI Huygens\textsuperscript{325}

See also:

IPLab software review\textsuperscript{326}

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{327} or the previous versions\textsuperscript{328} page to find documentation for the version you are using.
17.61 IPLab-Mac

Extensions: .ipm
Owner: BioVision Technologies

Support

BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: IPLab-Mac

We currently have:
• a few IPLab-Mac datasets
• a specification document

We would like to have:
• more IPLab-Mac datasets

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: IvisionReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.62 JEOL

Extensions: .dat, .img, .par
Owner: JEOL

Support

BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: JEOL

We currently have:

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329http://biovis.com/
331http://www.openmicroscopy.org/site/support/bio-formats5.0/
332http://www.openmicroscopy.org/site/support/legacy/
333http://www.jeol.com
• Pascal code that reads JEOL files (from ImageSXM)
• a few JEOL files
We would like to have:
• an official specification document
• more JEOL files

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: JEOLReader.java

Notes:

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.63 JPEG

Extensions: .jpg

Developer: Independent JPEG Group

Support

BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: JPEG

We currently have:
• a JPEG specification document (v1.04, from 1992 September 1, in PDF)
• numerous JPEG datasets
• the ability to produce more datasets

We would like to have:

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 

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334[https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/JEOLReader.java]
335[http://www.openmicroscopy.org/site/support/bio-formats5.0/]
336[http://www.openmicroscopy.org/site/support/legacy/]
337[http://www.ijg.org/]
338[http://www.w3.org/Graphics/JPEG/jfif3.pdf]
Utility:

Additional Information

Source Code: JPEGReader.java\(^{339}\) Source Code: JPEGWriter.java\(^{340}\)

Notes:

Bio-Formats can save individual planes as JPEG. Bio-Formats uses the Java Image I/O\(^{341}\) API to read and write JPEG files. JPEG stands for “Joint Photographic Experts Group”.

See also:

JPEG homepage\(^{342}\)

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{343}\) or the previous versions\(^{344}\) page to find documentation for the version you are using.

17.64 JPEG 2000

Extensions: .jp2

Developer: Independent JPEG Group\(^{345}\)

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: JPEG 2000

Freely Available Software:

- JJ2000 (JPEG 2000 library for Java)\(^{346}\)

We currently have:

- a JPEG 2000 specification document (free draft from 2000, no longer available online)
- a few .jp2 files

We would like to have:

Ratings

Pixels: 

Metadata: 

Openness: 

Presence: 

Utility: 

Additional Information

Source Code: JPEG2000Reader.java\(^{347}\) Source Code: JPEG2000Writer.java\(^{348}\)

\(^{339}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/JPEGReader.java

\(^{340}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/out/JPEGWriter.java

\(^{341}\)http://docs.oracle.com/javase/6/docs/technotes/guides/imageio/

\(^{342}\)http://www.jpeg.org/jpeg/index.html

\(^{343}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{344}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{345}\)http://www.ijg.org/

\(^{346}\)http://code.google.com/p/jj2000/


Bio-Formats uses the JAI Image I/O Tools\textsuperscript{349} library to read JP2 files. JPEG stands for “Joint Photographic Experts Group”.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{350} or the previous versions\textsuperscript{351} page to find documentation for the version you are using.

17.65 JPK

Extensions: .jpk
Developer: JPK Instruments\textsuperscript{352}

Support

BSD-licensed: \xmark
Export: \xmark

Officially Supported Versions:

Supported Metadata Fields: JPK

We currently have:

- Pascal code that can read JPK files (from ImageSXM)
- a few JPK files

We would like to have:

- an official specification document
- more JPK files

Ratings

Pixels: \\
Metadata: \\
Openness: \\
Presence: \\
Utility: \\

Additional Information

Source Code: JPKReader.java\textsuperscript{353}

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{354} or the previous versions\textsuperscript{355} page to find documentation for the version you are using.

\textsuperscript{349}\url{https://java.net/projects/jai-imageio}
\textsuperscript{350}\url{http://www.openmicroscopy.org/site/support/bio-formats5.0/}
\textsuperscript{351}\url{http://www.openmicroscopy.org/site/support/legacy/}
\textsuperscript{352}\url{http://www.jpk.com}
\textsuperscript{353}\url{https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/JPKReader.java}
\textsuperscript{354}\url{http://www.openmicroscopy.org/site/support/bio-formats5.0/}
\textsuperscript{355}\url{http://www.openmicroscopy.org/site/support/legacy/}
17.66 JPX

Extensions: .jpx
Developer: JPEG Committee

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: JPX

We currently have:
• a few .jpx files

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ▼
Utility: ▼

Additional Information

Source Code: JPXReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.67 Khoros VIFF (Visualization Image File Format) Bitmap

Extensions: .xv
Developer: Khoral
Owner: AccuSoft

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Khoros VIFF (Visualization Image File Format) Bitmap

Sample Datasets:

http://www.jpeg.org/jpeg2000/
https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/JPXReader.java
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.khoral.com/company/
http://www.accusoft.com/company/

17.66. JPX
• VIFF Images

We currently have:

• several VIFF datasets

We would like to have:

**Ratings**

Pixels: ▼

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: KhorosReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 17.68 Kodak BIP

Extensions: .bip

Developer: Kodak/Carestream

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Kodak BIP

We currently have:

• a few .bip datasets

We would like to have:

• an official specification document

**Ratings**

Pixels: ▲

Metadata: ▲

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**


364 http://www.openmicroscopy.org/site/support/bio-formats5.0/

365 http://www.openmicroscopy.org/site/support/legacy/

366 http://carestream.com
Source Code: KodakReader.java

Notes:

See also:
Information on Image Station systems

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.69 Lambert Instruments FLIM

Extensions: .fli

Developer: Lambert Instruments

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Lambert Instruments FLIM

We currently have:

- an LI-FLIM specification document
- several example LI-FLIM datasets

We would like to have:

Ratings

Pixels: 

Metadata: 

Openness: 

Presence: 

Utility: 

Additional Information

Source Code: LiFlimReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.70 LaVision Imspector

Extensions: .msr
Developer: LaVision BioTec

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: LaVision Imspector

We currently have:
- a few .msr files

We would like to have:

Ratings
Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information
Source Code: InspectorReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

17.71 Leica LCS LEI

Extensions: .lei, .tif
Developer: Leica Microsystems CMS GmbH
Owner: Leica

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Leica LCS LEI

Freely Available Software:

http://www.lavisionbiotec.com/
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.leica-microsystems.com/
http://www.leica.com/
We currently have:

• an LEI specification document (beta 2.000, from no later than 2004 February 17, in PDF)
• many LEI datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ▲
Utility: ▲

Additional Information

Source Code: LeicaReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties. LCS stands for “Leica Confocal Software”. LEI presumably stands for “Leica Experimental Information”.

Commercial applications that support LEI include:

• Bitplane Imaris
• SVI Huygens
• Image-Pro Plus

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.72 Leica LAS AF LIF (Leica Image File Format)

Extensions: .lif

Developer: Leica Microsystems CMS GmbH

Owner: Leica

Support

BSD-licensed:

Export:

Officially Supported Versions: 1.0, 2.0

Supported Metadata Fields: Leica LAS AF LIF (Leica Image File Format)

Freely Available Software:

ftp://ftp.llt.de/softlib/LCSLite/LCSLite2611537.exe
https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/LeicaReader.java
http://www.bitplane.com/
http://svi.nl/
http://www.mediacy.com/
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.leica-microsystems.com/
http://www.leica.com/
• Leica LAS AF Lite\(^\text{390}\) (links at bottom of page)

We currently have:

• a LIF specification document (version 2, from no later than 2007 July 26, in PDF)
• a LIF specification document (version 1, from no later than 206 April 3, in PDF)
• numerous LIF datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: ☐
Utility: ▲

**Additional Information**

Source Code: LIFReader.java\(^\text{391}\)

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

LAS stands for “Leica Application Suite”. AF stands for “Advanced Fluorescence”.

Commercial applications that support LIF include:

• Bitplane Imaris\(^\text{392}\)
• SVI Huygens\(^\text{393}\)
• Amira\(^\text{394}\)

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^\text{395}\) or the previous versions\(^\text{396}\) page to find documentation for the version you are using.

### 17.73 Leica SCN

**Extensions:** .scn

**Developer:** Leica Microsystems\(^\text{397}\)

**Support**

BSD-licensed: ☒

Export: ☒

Officially Supported Versions: 2012-03-10

**Supported Metadata Fields:** Leica SCN

We currently have:

• a few sample datasets

\(^{390}\)http://www.leica-microsystems.com/products/microscope-software/software-for-life-science-research/las-x/
\(^{391}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/LIFReader.java
\(^{392}\)http://www.bitplane.com/
\(^{393}\)http://svi.nl/
\(^{394}\)http://www.amira.com/
\(^{395}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{396}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{397}\)http://www.leica-microsystems.com/
We would like to have:

- an official specification document
- sample datasets that cannot be opened

**Ratings**

Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: [LeicaSCNReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/LeicaSCNReader.java)

**Notes:**

*Note: This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous versions page to find documentation for the version you are using.*

### 17.74 LEO

Extensions: .sxm

Owner: Zeiss

**Support**

BSD-licensed: X

Export: X

**Officially Supported Versions:**

Supported Metadata Fields: *LEO*

We currently have:

- Pascal code that can read LEO files (from ImageSXM)
- a few LEO files

We would like to have:

- an official specification document
- more LEO files

**Ratings**

Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

[399]http://www.openmicroscopy.org/site/support/bio-formats5.0/
[400]http://www.openmicroscopy.org/site/support/legacy/
Additional Information

Source Code: LEOReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.75 Li-Cor L2D

Extensions: .l2d, .tif, .scn

Owner: LiCor Biosciences

Support

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Li-Cor L2D

We currently have:

• a few L2D datasets

We would like to have:

• an official specification document

• more L2D datasets

Ratings

Pixels: ▲

Metadata: ▼

Openness: □

Presence: □

Utility: □

Additional Information

Source Code: L2DReader.java

Notes:

L2D datasets cannot be imported into OME using server-side import. They can, however, be imported from ImageJ, or using the omeml utility.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

403 http://www.openmicroscopy.org/site/support/bio-formats5.0/
404 http://www.openmicroscopy.org/site/support/legacy/
405 http://www.licor.com/
406 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/L2DReader.java
407 http://www.openmicroscopy.org/site/support/bio-formats5.0/
408 http://www.openmicroscopy.org/site/support/legacy/
17.76 LIM (Laboratory Imaging/Nikon)

Extensions: .lim
Owner: Laboratory Imaging

Support

BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: LIM (Laboratory Imaging/Nikon)

We currently have:
  • several LIM files
  • the ability to produce more LIM files

We would like to have:
  • an official specification document

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: LIMReader.java

Notes:

Bio-Formats only supports uncompressed LIM files.

Commercial applications that support LIM include:
  • NIS Elements

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Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.77 MetaMorph 7.5 TIFF

Extensions: .tiff
Owner: Molecular Devices

Support

BSD-licensed: 
Export: 

Notes:

Commercial applications that support TIFF include:
  • MetaMorph 7.5

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409 http://www.lim.cz/
410 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/LIMReader.java
411 http://www.nis-elements.com/
412 http://www.openmicroscopy.org/site/support/bio-formats5.0/
413 http://www.openmicroscopy.org/site/support/legacy/
414 http://www.moleculardevices.com/
Officially Supported Versions:

Supported Metadata Fields: *MetaMorph 7.5 TIFF*

We currently have:

- a few Metamorph 7.5 TIFF datasets

We would like to have:

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ▲
- Presence: ▼
- Utility: ▼

**Additional Information**

Source Code: [MetamorphTiffReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/MetamorphTiffReader.java)

Notes:

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^16] or the previous versions[^17] page to find documentation for the version you are using.

### 17.78 MetaMorph Stack (STK)

Extensions: .stk, .nd

Owner: Molecular Devices[^18]

**Support**

- BSD-licensed: ✗
- Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *MetaMorph Stack (STK)*

We currently have:

- an STK specification document (from 2006 November 21, in DOC)
- an older STK specification document (from 2005 March 25, in DOC)
- an ND specification document (from 2002 January 24, in PDF)
- a large number of datasets

We would like to have:

**Ratings**

- Pixels: ▲
- Metadata: ▲
- Openness: ▲

[^15]: https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/MetamorphTiffReader.java
[^16]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^17]: http://www.openmicroscopy.org/site/support/legacy/
[^18]: http://www.moleculardevices.com/
17.79 MIAS (Maia Scientific)

Extensions: .tif
Developer: Maia Scientific

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: MIAS (Maia Scientific)
We currently have:
• several MIAS datasets
We would like to have:

Ratings
Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/MetamorphReader.java
http://www.bitplane.com/
http://svi.nl/
http://dimin.net/
http://www.metamorph.com/
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.selectscience.net/supplier/maia-scientific/?compID=6088

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.80 Micro-Manager

Extensions: .tif, .txt, .xml
Developer: Vale Lab

Support

BSD-licensed: ✔

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Micro-Manager

Freely Available Software:

- Micro-Manager

We currently have:

- many Micro-manager datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence:▼
Utility: ▼

Additional Information

Source Code: MicromanagerReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.81 MINC MRI

Extensions: .mnc

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
Developer: McGill University

Support

BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: MINC MRI

Freely Available Software:

- MINC

We currently have:

- a few MINC files

We would like to have:

Ratings

Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information

Source Code: MINCReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions' page to find documentation for the version you are using.

17.82 Minolta MRW

Extensions: .mrw
Developer: Minolta

Support

BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: Minolta MRW

Freely Available Software:

- dcraw

We currently have:

http://www.bic.mni.mcgill.ca/ServicesSoftware/MINC
http://www.bic.mni.mcgill.ca/ServicesSoftware/MINC
https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/MINCReader.java
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.konicaminolta.com/
http://www.cybercom.net/%7Edcoffin/dcraw/
• several .mrw files

We would like to have:

Ratings

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

Source Code: MRWReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.83 MNG (Multiple-image Network Graphics)

Extensions: .mng

Developer: MNG Development Group

Support

BSD-licensed: ✔
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: MNG (Multiple-image Network Graphics)

Freely Available Software:

• libmng (MNG reference library)

Sample Datasets:

• MNG sample files

We currently have:

• the libmng-testsuites package (from 2003 March 05, in C)
• a large number of MNG datasets

We would like to have:

Ratings

Pixels: ▼
Metadata: ▼
Openness: ▲

[443] http://www.openmicroscopy.org/site/support/bio-formats5.0/
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: MNGReader.java

Notes:

**See also:**
MNG homepage, MNG specification

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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17.84 Molecular Imaging

Extensions: .stp

Owner: Molecular Imaging Corp, San Diego CA (closed)

**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Molecular Imaging*

We currently have:

- Pascal code that reads Molecular Imaging files (from ImageSXM)
- a few Molecular Imaging files

We would like to have:

- an official specification document
- more Molecular Imaging files

**Ratings**

Pixels: ▼

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: MolecularImagingReader.java

Notes:

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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449 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/MNGReader.java
450 http://www.libpng.org/pub/mng/
451 http://www.libpng.org/pub/mng/spec
452 http://www.openmicroscopy.org/site/support/bio-formats5.0/
453 http://www.openmicroscopy.org/site/support/legacy/
454 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/MolecularImagingReader.java
17.85 MRC (Medical Research Council)

Extensions: .mrc

Developer: MRC Laboratory of Molecular Biology

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: MRC (Medical Research Council)

Sample Datasets:

- golgi.mrc

We currently have:

- an MRC specification document (in TXT)
- a few MRC datasets

We would like to have:

Ratings

Pixels: 🔺

Metadata: 🔺

Openness: 🔺

Presence: ❌

Utility: ❌

Additional Information

Source Code: MRCReader.java

Notes:

Commercial applications that support MRC include:

- Bitplane Imaris

See also:

MRC on Wikipedia

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.86 NEF (Nikon Electronic Format)

Extensions: .nef, .tiff

Developer: Nikon

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: NEF (Nikon Electronic Format)

Sample Datasets:

- neffile1.zip
- Sample NEF images

We currently have:

- a NEF specification document (v0.1, from 2003, in PDF)
- several NEF datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▼

Presence: ▼

Utility: ▼

Additional Information

Source Code: NikonReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

See also:

NEF Conversion

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.87 NIfTI

Extensions: .img, .hdr

Developer: National Institutes of Health

465 http://www.nikon.com/
466 http://www.outbackphoto.com/workshop/NEF_conversion/neffile1.zip
467 http://www.nikondigital.org/articles/library/nikon_d2x_first_impressions.htm
468 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/NikonReader.java
469 http://www.outbackphoto.com/workshop/NEF_conversion/nefconversion.html
470 http://www.openmicroscopy.org/site/support/bio-formats5.0/
471 http://www.openmicroscopy.org/site/support/legacy/
472 http://www.nih.gov/
Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *NIfTI*

Sample Datasets:

- *Official test data*[^473]

We currently have:

- *NIfTI specification documents*[^474]
  - several NIfTI datasets

We would like to have:

**Ratings**

Pixels: ★

Metadata: ★

Openness: ★

Presence: ★

Utility: ★

**Additional Information**

Source Code: *NiftiReader.java*[^475]

Notes:

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^476] or the previous versions[^477] page to find documentation for the version you are using.

### 17.88 Nikon Elements TIFF

Extensions: .tiff

Developer: *Nikon*[^478]

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *Nikon Elements TIFF*

We currently have:

- a few Nikon Elements TIFF files

We would like to have:

- more Nikon Elements TIFF files

[^474]: http://nifti.nimh.nih.gov/nifti-1/
[^475]: https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/NiftiReader.java
[^476]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^477]: http://www.openmicroscopy.org/site/support/legacy/
[^478]: http://www.nikon.com
17.89 Nikon EZ-C1 TIFF

Extensions: .tiff
Developer: Nikon

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: Nikon EZ-C1 TIFF

We currently have:
- a few Nikon EZ-C1 TIFF files

We would like to have:

Ratings
Pixels: ▲
Metadata: ▲
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information
Source Code: NikonTiffReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.90 Nikon NIS-Elements ND2

Extensions: .nd2
Developer: Nikon USA

Support
BSD-licensed: ☒
Export: ☒

Officially Supported Versions:
Supported Metadata Fields: Nikon NIS-Elements ND2

Freely Available Software:
• NIS-Elements Viewer from Nikon

We currently have:
• many ND2 datasets

We would like to have:
• an official specification document

Ratings
Pixels: ▲
Metadata: ▲
Openness: ▼
Presence: ▲
Utility: ▲

Additional Information
Source Code: NativeND2Reader.java

Notes:
There are two distinct versions of ND2: an old version, which uses JPEG-2000 compression, and a new version which is either uncompressed or Zip-compressed. We are not aware of the version number or release date for either format.

Bio-Formats uses the JAI Image I/O Tools library to read ND2 files compressed with JPEG-2000.

There is also an ND2 reader that uses Nikon’s native libraries. To use it, you must be using Windows and have Nikon’s ND2 reader plugin for ImageJ installed. Additionally, you will need to download LegacyND2Reader.dll and place it in your ImageJ plugin folder.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

486 http://www.nikonusa.com/
487 http://www.nikoninstruments.com/Products/Software/NIS-Elements-Advanced-Research/NIS-Elements-Viewer
488 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/NativeND2Reader.java
489 http://java.net/projects/jai-imageio
491 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/lib/LegacyND2Reader.dll?raw=true
492 http://www.openmicroscopy.org/site/support/bio-formats5.0/
493 http://www.openmicroscopy.org/site/support/legacy/
17.91 NRRD (Nearly Raw Raster Data)

Extensions: .nrrd, .nhdr, .raw, .txt

Developer: Teem developers

Support

BSD-licensed: ✓

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: NRRD (Nearly Raw Raster Data)

Freely Available Software:

• nrrd (NRRD reference library)

Sample Datasets:

• Diffusion tensor MRI datasets

We currently have:

• an nrrd specification document (v1.9, from 2005 December 24, in HTML)

We would like to have:

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: ▼

Utility: ▲

Additional Information

Source Code: NRRDReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.92 Olympus CellR/APL

Extensions: .apl, .mtb, .tnb, .tif, .obsep

Owner: Olympus

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *Olympus CellR/APL*

We currently have:
  • a few CellR datasets

We would like to have:
  • more Cellr datasets
  • an official specification document

**Ratings**

Pixels: 🔺

Metadata: 🔺

Openness: 🔺

Utility: 🔺

**Additional Information**

Source Code: [APLReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/APLReader.java)

Notes:

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^503] or the previous versions[^504] page to find documentation for the version you are using.

### 17.93 Olympus FluoView FV1000

Extensions: .oib, .oif

Owner: Olympus[^505]

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions: 1.0, 2.0

Supported Metadata Fields: *Olympus FluoView FV1000*

Freely Available Software:
  • FV-Viewer from Olympus[^506]

We currently have:
  • an OIF specification document (v2.0.0.0, from 2008, in PDF)
  • an FV1000 specification document (v1.0.0.0, from 2004 June 22, in PDF)
  • older FV1000 specification documents (draft, in DOC and XLS)
  • many FV1000 datasets

[^503]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^504]: http://www.openmicroscopy.org/site/support/legacy/
[^505]: http://www.olympus.com/
[^506]: http://www.olympus.co.uk/microscopy/22_FluoView_FV1000__Confocal_Microscope.htm
We would like to have:

- more OIB datasets (especially 2+ GB files)
- more FV1000 version 2 datasets

**Ratings**

- Pixels: [▲](#)
- Metadata: [▲](#)
- Openness: [ ]
- Presence: [ ]
- Utility: [▲](#)

**Additional Information**

Source Code: [FV1000Reader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/FV1000Reader.java)

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Bio-Formats uses a modified version of the [Apache Jakarta POI](http://jakarta.apache.org/poi/) library to read OIB files. OIF stands for “Original Imaging Format”. OIB stands for “Olympus Image Binary”. OIF is a multi-file format that includes an .oif file and a directory of .tif, .roi, .pty, .lut, and .bmp files. OIB is a single file format.

Commercial applications that support this format include:

- Bitplane Imaris
- SVI Huygens

See also:

[Olympus FluoView Resource Center](http://www.olympusfluoview.com)

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**Note**: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 17.94 Olympus FluoView TIFF

**Extensions**: .tif

**Owner**: Olympus

**Support**

- BSD-licensed: [X](#)
- Export: [X](#)

**Officially Supported Versions**

**Supported Metadata Fields**: *Olympus FluoView TIFF*

**Freely Available Software**:

- [DIMIX](http://www.dimin.net/)

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512. http://www.openmicroscopy.org/site/support/bio-formats5.0/
513. http://www.openmicroscopy.org/site/support/legacy/
515. http://www.dimin.net/
We currently have:

- a FluoView specification document (from 2002 November 14, in DOC)
- Olympus’ FluoView Image File Reference Suite (from 2002 March 1, in DOC)
- several FluoView datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▲
Openness: ▲
Presence: 
Utility: ▲

**Additional Information**

Source Code: FluoviewReader.java

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Commercial applications that support this format include:

- Bitplane Imaris
- SVI Huygens

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

### 17.95 Olympus ScanR

Extensions: .xml, .dat, .tif

Developer: Olympus

Owner: Olympus

**Support**

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *Olympus ScanR*

We currently have:

- several ScanR datasets

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516 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/FluoviewReader.java
517 http://www.bitplane.com/
518 http://svi.nl/
519 http://www.openmicroscopy.org/site/support/bio-formats5.0/
520 http://www.openmicroscopy.org/site/support/legacy/
521 http://www.olympus.com/
522 http://www.olympus.com/
We would like to have:

**Ratings**

Pixels: ▲
Metadata: □
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: `ScanrReader.java`\(^{523}\)

Notes:

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous [versions](http://www.openmicroscopy.org/site/support/legacy/) page to find documentation for the version you are using.

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### 17.96 Olympus SIS TIFF

Extensions: .tiff

Developer: Olympus\(^{526}\)

**Support**

BSD-licensed: ❌
Export: ❌

**Officially Supported Versions:**

**Supported Metadata Fields:** *Olympus SIS TIFF*

We currently have:

- a few example SIS TIFF files

We would like to have:

**Ratings**

Pixels: □
Metadata: □
Openness: □
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: `SISReader.java`\(^{527}\)

Notes:

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the [latest Bio-Formats 5.0.x version](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous [versions](http://www.openmicroscopy.org/site/support/legacy/) page to find documentation for the version you are using.

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\(^{523}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/ScanrReader.java

\(^{524}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{525}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{526}\)http://www.olympus-sis.com/

\(^{527}\)https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SISReader.java
17.97 OME-TIFF

Extensions: .ome.tiff

Developer: Open Microscopy Environment

Support

BSD-licensed: ✔

Export: ✔


Supported Metadata Fields: OME-TIFF

We currently have:

- an OME-TIFF specification document (from 2006 October 19, in HTML)
- many OME-TIFF datasets
- the ability to produce additional datasets

We would like to have:

Ratings

Pixels: 🔺

Metadata: 🔺

Openness: 🔺

Presence: 🔻

Utility: 🔺

Additional Information

Source Code: OMETiffReader.java Source Code: OMETiffWriter.java

Notes:

Bio-Formats can save image stacks as OME-TIFF.

Commercial applications that support OME-TIFF include:

- Bitplane Imaris
- SVI Huygens

See also:

OME-TIFF technical overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.98 OME-XML

Extensions: .ome

Developer: Open Microscopy Environment

Support

BSD-licensed: ✓

Export: ✓


Supported Metadata Fields: OME-XML

We currently have:

- OME-XML specification documents
- many OME-XML datasets
- the ability to produce more datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: ▼

Utility: ▲

Additional Information

Source Code: OMEXMLReader.java
Source Code: OMEXMLWriter.java

Notes:

Bio-Formats uses the OME-XML Java library to read OME-XML files.

Commercial applications that support OME-XML include:

- Bitplane Imaris
- SVI Huygens

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

541 http://www.openmicroscopy.org/
542 http://www.openmicroscopy.org/Schemas/
543 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/OMEXMLReader.java
545 http://www.openmicroscopy.org/site/support/ome-model/ome-xml/java-library.html
546 http://www.bitplane.com/
547 http://svi.nl/
548 http://www.openmicroscopy.org/site/support/bio-formats5.0/
549 http://www.openmicroscopy.org/site/support/legacy/
17.99 Oxford Instruments

Extensions: .top
Owner: Oxford Instruments

Support
BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: Oxford Instruments
We currently have:
• Pascal code that can read Oxford Instruments files (from ImageSXM)
• a few Oxford Instruments files
We would like to have:
• an official specification document
• more Oxford Instruments files

Ratings
Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information
Source Code: OxfordInstrumentsReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.100 PCORAW

Extensions: .pcoraw, .rec
Developer: PCO

Support
BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: PCORAW
We currently have:

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550 http://www.oxinst.com
552 http://www.openmicroscopy.org/site/support/bio-formats5.0/
553 http://www.openmicroscopy.org/site/support/legacy/
554 http://www.pco.de/
• a few example datasets

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▲
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: **PCORAWReader.java**

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

### 17.101 PCX (PC Paintbrush)

**Extensions:** .pcx

**Developer:** ZSoft Corporation

**Support**

BSD-licensed: ✔

Export: ✗

Officially Supported Versions:

**Supported Metadata Fields:** **PCX (PC Paintbrush)**

We currently have:

• several .pcx files
• the ability to generate additional .pcx files

We would like to have:

**Ratings**

Pixels: ▲
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: **PCXReader.java**

Notes:

---

555 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/PCORAWReader.java
556 http://www.openmicroscopy.org/site/support/bio-formats5.0/
557 http://www.openmicroscopy.org/site/support/legacy/
558 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/PCXReader.java

---

17.101. PCX (PC Paintbrush)
Commercial applications that support PCX include Zeiss LSM Image Browser. Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions' page to find documentation for the version you are using.

17.102 Perkin Elmer Densitometer

Extensions: .pds
Developer: PerkinElmer

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Perkin Elmer Densitometer

We currently have:

• a few PDS datasets

We would like to have:

• an official specification document
• more PDS datasets

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: PDSReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions' page to find documentation for the version you are using.

17.103 PerkinElmer Nuance

Extensions: .im3
Developer: PerkinElmer

Support

560 http://www.openmicroscopy.org/site/support/bio-formats5.0/
561 http://www.openmicroscopy.org/site/support/legacy/
562 http://www.perkinelmer.com
564 http://www.openmicroscopy.org/site/support/bio-formats5.0/
565 http://www.openmicroscopy.org/site/support/legacy/
566 http://www.perkinelmer.com/
17.104 PerkinElmer Operetta

Extensions: .tiff, .xml

Developer: PerkinElmer

Support

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: PerkinElmer Nuance

We currently have:

• a few sample datasets

We would like to have:

Ratings

Pixels: ▼

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

Additional Information

Source Code: IM3Reader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.104. PerkinElmer Operetta
Openness: 
Presence: ▼
Utility: 

Additional Information
Source Code: OperettaReader.java\textsuperscript{571}
Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{572} or the previous versions\textsuperscript{573} page to find documentation for the version you are using.

17.105 PerkinElmer UltraView

Extensions: .tif, .2, .3, .4, etc.
Owner: PerkinElmer\textsuperscript{574}

Support

BSD-licensed: 
Export: 

Officially Supported Versions:
Supported Metadata Fields: PerkinElmer UltraView

We currently have:

• several UltraView datasets

We would like to have:

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information
Source Code: PerkinElmerReader.java\textsuperscript{575}
Notes:

Other associated extensions include: .tim, .zpo, .csv, .htm, .cfg, .ano, .rec

Commercial applications that support this format include:

• Bitplane Imaris\textsuperscript{576}
• Image-Pro Plus\textsuperscript{577}

\textsuperscript{571}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/OperettaReader.java
\textsuperscript{572}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{573}http://www.openmicroscopy.org/site/support/legacy/
\textsuperscript{574}http://www.perkinelmer.com/
\textsuperscript{575}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/PerkinElmerReader.java
\textsuperscript{576}http://www.bitplane.com/
\textsuperscript{577}http://www.mediacy.com/
17.106 PGM (Portable Gray Map)

Extensions: .pgm
Developer: Netpbm developers

Support

BSD-licensed: ✓
Export: X

Officially Supported Versions:

Supported Metadata Fields: PGM (Portable Gray Map)

Freely Available Software:

• Netpbm graphics filter

We currently have:

• a PGM specification document (from 2003 October 3, in HTML)
• a few PGM files

We would like to have:

Ratings

Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information

Source Code: PGMReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.
17.107 Adobe Photoshop PSD

Extensions: .psd
Developer: Adobe

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions: 1.0
Supported Metadata Fields: Adobe Photoshop PSD

We currently have:
- a PSD specification document (v3.0.4, 16 July 1995)
- a few PSD files

We would like to have:
- more PSD files

Ratings

Pixels: ▼
Metadata: ▲
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

Source Code: PSDReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.108 Photoshop TIFF

Extensions: .tif, .tiff
Developer: Adobe

Support

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: Photoshop TIFF

We currently have:

---

586 http://www.adobe.com/
588 http://www.openmicroscopy.org/site/support/bio-formats5.0/
589 http://www.openmicroscopy.org/site/support/legacy/
590 http://www.adobe.com
Bio-Formats Documentation, Release 5.1.3

- a Photoshop TIFF specification document
- a few Photoshop TIFF files

We would like to have:

**Ratings**

**Pixels:**

**Metadata:**

**Openness:**

**Presence:**

**Utility:**

**Additional Information**

Source Code: PhotoshopTiffReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.109 PicoQuant Bin

Extensions: .bin

Developer: PicoQuant

**Support**

**BSD-licensed:**

**Export:**

Officially Supported Versions:

Supported Metadata Fields: PicoQuant Bin

Freely Available Software:

- SymphoTime64

We currently have:

- a few example datasets

We would like to have:

**Ratings**

**Pixels:**

**Metadata:**

**Openness:**

**Presence:**

**Utility:**

**Additional Information**

591 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/PhotoshopTiffReader.java

592 http://www.openmicroscopy.org/site/support/bio-formats5.0/

593 http://www.openmicroscopy.org/site/support/legacy/

594 http://www.picoquant.com/

17.110  PICT (Macintosh Picture)

Extensions: .pict

Developer: Apple Computer

Support

BSD-licensed: ✔

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: PICT (Macintosh Picture)

We currently have:

- many PICT datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▼

Openness: ▼

Presence: ▲

Utility: ◼

Additional Information

Source Code: PictReader.java

Notes:

QuickTime for Java is required for reading vector files and some compressed files.

See also:

PICT technical overview Another PICT technical overview
17.111 PNG (Portable Network Graphics)

Extensions: .png
Developer: PNG Development Group

Support
BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: PNG (Portable Network Graphics)

Freely Available Software:
- PNG Writer plugin for ImageJ

We currently have:
- a PNG specification document (W3C/ISO/IEC version, from 2003 November 10, in HTML)
- several PNG datasets

We would like to have:

Ratings
Pixels: ▲
Metadata: ▼
Openness: ▲
Presence: ▲
Utility: ▼

Additional Information
Source Code: APNGReader.java

Notes:
Bio-Formats uses the Java Image I/O API to read and write PNG files.

See also:
PNG technical overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.112 Prairie Technologies TIFF

Extensions: .tif, .xml, .cfg
Developer: Prairie Technologies

Note:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Prairie Technologies TIFF*

We currently have:

- many Prairie datasets

We would like to have:

**Ratings**

Pixels: ▲

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: PrairieReader.java

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

### 17.113 Quesant

Extensions: .afm

Developer: Quesant Instrument Corporation

Owner: KLA-Tencor Corporation

**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: *Quesant*

We currently have:

- Pascal code that can read Quesant files (from ImageSXM)
- several Quesant files

We would like to have:

- an official specification document
- more Quesant files

---


616.[http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)

617.[http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)

Ratings
Pixels: 🟢
Metadata: 🔴
Openness: 🔴
Presence: 🔴
Utility: 🔴

Additional Information
Source Code: QuesantReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.114 QuickTime Movie

Extensions: .mov
Owner: Apple Computer

Support
BSD-licensed: ✅
Export: ✅

Officially Supported Versions:

Supported Metadata Fields: QuickTime Movie

Freely Available Software:

• QuickTime Player

We currently have:

• a QuickTime specification document (from 2001 March 1, in HTML)
• several QuickTime datasets
• the ability to produce more datasets

We would like to have:

• more QuickTime datasets, including:
  – files compressed with a common, unsupported codec
  – files with audio tracks and/or multiple video tracks

Ratings
Pixels: 🟢
Metadata: 🔵
Openness: 🔴

---

620 http://www.openmicroscopy.org/site/support/bio-formats5.0/
621 http://www.openmicroscopy.org/site/support/legacy/
622 http://www.apple.com/
Bio-Formats has two modes of operation for QuickTime:

- QTJava mode requires QuickTime\(^{627}\) to be installed (32-bit JVM only, not supported with 64-bit).
- Native mode works on systems with no QuickTime (e.g. Linux).

Bio-Formats can save image stacks as QuickTime movies. The following table shows supported codecs:

<table>
<thead>
<tr>
<th>Codec</th>
<th>Description</th>
<th>Native</th>
<th>QTJava</th>
</tr>
</thead>
<tbody>
<tr>
<td>raw</td>
<td>Full Frames (Uncompressed)</td>
<td>read &amp; write</td>
<td>read &amp; write</td>
</tr>
<tr>
<td>iraw</td>
<td>Intel YUV Uncompressed</td>
<td>read only</td>
<td>read &amp; write</td>
</tr>
<tr>
<td>rle</td>
<td>Animation (run length encoded RGB)</td>
<td>read only</td>
<td>read &amp; write</td>
</tr>
<tr>
<td>jpeg</td>
<td>Still Image JPEG DIB</td>
<td>read only</td>
<td>read only</td>
</tr>
<tr>
<td>rpza</td>
<td>Apple Video 16 bit “road pizza”</td>
<td>read only (partial)</td>
<td>read only</td>
</tr>
<tr>
<td>mjpb</td>
<td>Motion JPEG codec</td>
<td>read only</td>
<td>read only</td>
</tr>
<tr>
<td>cvid</td>
<td>Cinepak</td>
<td></td>
<td>read &amp; write</td>
</tr>
<tr>
<td>svq1</td>
<td>Sorenson Video</td>
<td></td>
<td>read &amp; write</td>
</tr>
<tr>
<td>svq3</td>
<td>Sorenson Video 3</td>
<td></td>
<td>read &amp; write</td>
</tr>
<tr>
<td>mp4v</td>
<td>MPEG-4</td>
<td></td>
<td>read &amp; write</td>
</tr>
<tr>
<td>h263</td>
<td>H.263</td>
<td></td>
<td>read &amp; write</td>
</tr>
</tbody>
</table>

See also:

QuickTime software overview\(^{628}\)

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{629}\) or the previous versions\(^{630}\) page to find documentation for the version you are using.

### 17.115 RHK

Extensions: .sm2, .sm3

Owner: RHK Technologies\(^{631}\)

Support

BSD-licensed: 

Export:
Officially Supported Versions:
Supported Metadata Fields: *RHK*

We currently have:
- Pascal code that can read RHK files (from ImageXMX)
- a few RHK files

We would like to have:
- an official specification document
- more RHK files

**Ratings**

- **Pixels:** [ ]
- **Metadata:** [ ]
- **Openness:** [ ]
- **Presence:** [ ]
- **Utility:** [ ]

**Additional Information**

Source Code: RHKReader.java

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

### 17.116 SBIG

**Owner:** Santa Barbara Instrument Group (SBIG)

**Support**

- **BSD-licensed:** ✗
- **Export:** ✗

Officially Supported Versions:

Supported Metadata Fields: *SBIG*

We currently have:
- an official SBIG specification document
- a few SBIG files

We would like to have:
- more SBIG files

**Ratings**

- **Pixels:** [ ]
- **Metadata:** [ ]

---

633. http://www.openmicroscopy.org/site/support/bio-formats5.0/
634. http://www.openmicroscopy.org/site/support/legacy/
635. http://www.sbig.com
Openness:
Presence:
Utility:

Additional Information
Source Code: SBIGReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.117 Seiko

Extensions: .xqd, .xqf
Owner: Seiko

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Seiko

We currently have:
- Pascal code that can read Seiko files (from ImageSXM)
- a few Seiko files

We would like to have:
- an official specification document
- more Seiko files

Ratings
Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information
Source Code: SeikoReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
17.118 SimplePCI & HCImage

Extensions: .cxd
Developer: Compix

Support
BSD-licensed: ✗
Export: ✗

Officially Supported Versions:
Supported Metadata Fields: SimplePCI & HCImage

We currently have:
• several SimplePCI files

We would like to have:

Ratings
Pixels: ★
Metadata: ★
Openness: ★
Presence: ★
Utility: ★

Additional Information
Source Code: PCIReader.java
Notes:
Bio-Formats uses a modified version of the Apache Jakarta POI library to read CXD files.

See also:
SimplePCI software overview

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.119 SimplePCI & HCImage TIFF

Extensions: .tiff
Developer: Hamamatsu

Support
BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

644 http://hcimage.com
645 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/PCIReader.java
646 http://jakarta.apache.org/poi/
647 http://hcimage.com/simple-pci-legacy/
648 http://www.openmicroscopy.org/site/support/bio-formats5.0/
649 http://www.openmicroscopy.org/site/support/legacy/
650 http://hcimage.com/simple-pci-legacy/
Supported Metadata Fields: *SimplePCI & HCImage TIFF*

We currently have:

- a few SimplePCI TIFF datasets

We would like to have:

- more SimplePCI TIFF datasets

### Ratings

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
<th>Openness</th>
<th>Presence</th>
<th>Utility</th>
</tr>
</thead>
<tbody>
<tr>
<td>▲</td>
<td>▼</td>
<td>▲</td>
<td>▼</td>
<td>▼</td>
</tr>
</tbody>
</table>

### Additional Information

Source Code: [SimplePCITiffReader.java](https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SimplePCITiffReader.java)

Notes:  

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^652] or the previous versions[^653] page to find documentation for the version you are using.

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### 17.120 SM Camera

#### Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: *SM Camera*

We currently have:

- Pascal code that can read SM-Camera files (from ImageSXM)
- a few SM-Camera files

We would like to have:

- an official specification document
- more SM-Camera files

### Ratings

<table>
<thead>
<tr>
<th>Pixels</th>
<th>Metadata</th>
<th>Openness</th>
<th>Presence</th>
<th>Utility</th>
</tr>
</thead>
<tbody>
<tr>
<td>▼</td>
<td>▼</td>
<td>▼</td>
<td>▼</td>
<td>▼</td>
</tr>
</tbody>
</table>

### Additional Information


[^652]: http://www.openmicroscopy.org/site/support/bio-formats5.0/

[^653]: http://www.openmicroscopy.org/site/support/legacy/
Source Code: SMCameraReader.java\textsuperscript{654}

Notes:

\textbf{Note: This documentation is for the new Bio-Formats 5.1 version.} See the latest Bio-Formats 5.0.x version\textsuperscript{655} or the previous versions\textsuperscript{656} page to find documentation for the version you are using.

### 17.121 SPIDER

Extensions: .spi, .stk

Developer: Wadsworth Center\textsuperscript{657}

\textbf{Support}

BSD-licensed: 

Export: 

Officially Supported Versions: 

Supported Metadata Fields: \textit{SPIDER}

Freely Available Software:

- \textit{SPIDER}\textsuperscript{658}

We currently have:

- a few example datasets
- official file format documentation\textsuperscript{659}

We would like to have:

\textbf{Ratings}

Pixels: ▲

Metadata: ▲

Openness: ▲

Presence: □

Utility: □

\textbf{Additional Information}

Source Code: SpiderReader.java\textsuperscript{660}

Notes:

\textbf{Note: This documentation is for the new Bio-Formats 5.1 version.} See the latest Bio-Formats 5.0.x version\textsuperscript{661} or the previous versions\textsuperscript{662} page to find documentation for the version you are using.

\textsuperscript{654}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SMCameraReader.java

\textsuperscript{655}http://www.openmicroscopy.org/site/support/bio-formats5.0/

\textsuperscript{656}http://www.openmicroscopy.org/site/support/legacy/

\textsuperscript{657}http://www.wadsworth.org/spider_doc/spider/docs/spider.html

\textsuperscript{658}http://www.wadsworth.org/spider_doc/spider/docs/spider.html

\textsuperscript{659}http://www.wadsworth.org/spider_doc/spider/docs/image_doc.html

\textsuperscript{660}https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/SpiderReader.java

\textsuperscript{661}http://www.openmicroscopy.org/site/support/bio-formats5.0/

\textsuperscript{662}http://www.openmicroscopy.org/site/support/legacy/
17.122 Targa

Extensions: .tga
Developer: Truevision

Support
BSD-licensed: 🚧
Export: 🚧

Officially Supported Versions:
Supported Metadata Fields: Targa

We currently have:
• a Targa specification document
• a few Targa files

We would like to have:

Ratings
Pixels: 🟡
Metadata: 🟡
Openness: 🟡
Presence: 🟢
Utility: 🟢

Additional Information
Source Code: TargaReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.123 Text

Extensions: .txt

Support
BSD-licensed: ✅
Export: 🚧

Officially Supported Versions:
Supported Metadata Fields: Text

We currently have:

We would like to have:

Ratings
Pixels: 🟢
17.124 TIFF (Tagged Image File Format)

Extensions: .tif
Developer: Aldus and Microsoft
Owner: Adobe

Support
BSD-licensed: ✔
Export: ✔

Officially Supported Versions:
Supported Metadata Fields: TIFF (Tagged Image File Format)

Sample Datasets:
- LZW TIFF data gallery
- Big TIFF

We currently have:
- A TIFF specification document (v6.0, from 1992 June 3, in PDF)
- Many TIFF datasets
- A few BigTIFF datasets

We would like to have:

Ratings
Pixels:
Metadata:
Openness:
Presence:
Utility:

---

668 http://www.openmicroscopy.org/site/support/bio-formats5.0.x/
669 http://www.openmicroscopy.org/site/support/legacy/
670 http://www.adobe.com
671 http://marlin.life.utsa.edu/Data_Gallery.html
672 http://www.awaresystems.be/imaging/tiff/bigtiff.html#samples
Additional Information

Source Code: TiffReader.java[^674] Source Code: TiffWriter.java[^675]

Notes:

Bio-Formats can also read BigTIFF files (TIFF files larger than 4 GB). Bio-Formats can save image stacks as TIFF or BigTIFF.

See also:

TIFF technical overview[^676] BigTIFF technical overview[^677]

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^678] or the previous versions[^679] page to find documentation for the version you are using.

### 17.125 TillPhotonics TillVision

Extensions: .vws

Developer: TILL Photonics[^680]

**Support**

BSD-licensed: ✗

Export: ✗

Officially Supported Versions:

Supported Metadata Fields: TillPhotonics TillVision

We currently have:

- several TillVision datasets

We would like to have:

- an official specification document

**Ratings**

Pixels: ▼

Metadata: ▼

Openness: ▼

Presence: ▼

Utility: ▼

**Additional Information**

Source Code: TillVisionReader.java[^681]

Notes:

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version[^682] or the previous versions[^683] page to find documentation for the version you are using.

[^674]: https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/TiffReader.java
[^676]: http://www.awaresystems.be/imaging/tiff/faq.html#q3
[^677]: http://www.awaresystems.be/imaging/tiff/bigtiff.html
[^678]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^679]: http://www.openmicroscopy.org/site/support/legacy/
[^680]: http://www.till-photonics.com/
[^682]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^683]: http://www.openmicroscopy.org/site/support/legacy/
17.126 Topometrix

Extensions: .tfr, .ffr, .zfr, .zfp, .2fl

Owner: TopoMetrix (now Veeco) \(^684\)

Support

BSD-licensed: \(\times\)

Export: \(\times\)

Officially Supported Versions:

Supported Metadata Fields: Topometrix

We currently have:

- Pascal code that reads Topometrix files (from ImageSXM)
- a few Topometrix files

We would like to have:

- an official specification document
- more Topometrix files

Ratings

Pixels: [ ]

Metadata: [ ]

Openness: [ ]

Presence: [ ]

Utility: [ ]

Additional Information

Source Code: TopometrixReader.java \(^685\)

Notes:

\[Note:\ This\ documentation\ is\ for\ the\ new\ Bio-Formats\ 5.1\ version.\ See\ the\ latest\ Bio-Formats\ 5.0.x\ version\ \(^686\)\ or\ the\ previous\ versions\ \(^687\)\ page\ to\ find\ documentation\ for\ the\ version\ you\ are\ using.\]

17.127 Trestle

Extensions: .tif, .sld, .jpg

Support

BSD-licensed: \(\times\)

Export: \(\times\)

Officially Supported Versions:

Supported Metadata Fields: Trestle

Sample Datasets:

- OpenSlide \(^688\)

---

\(^684\) http://www.veeco.com/

\(^685\) https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/TopometrixReader.java

\(^686\) http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^687\) http://www.openmicroscopy.org/site/support/legacy/

\(^688\) http://openslide.cs.cmu.edu/download/openslide-testdata/Trestle/
We currently have:

- a few example datasets
- developer documentation from the OpenSlide project

We would like to have:

**Ratings**

Pixels: 
Metadata: 
Openness: 
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: [TrestleReader.java](http://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/TrestleReader.java)

Notes:

*Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version [here](http://www.openmicroscopy.org/site/support/bio-formats5.0/) or the previous versions [here](http://www.openmicroscopy.org/site/support/legacy/) page to find documentation for the version you are using.*

## 17.128 UBM

**Extensions:** .pr3

**Support**

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

- Supported Metadata Fields: **UBM**

We currently have:

- Pascal code that can read UBM files (from ImageSXM)
- one UBM file

We would like to have:

- an official specification document
- more UBM files

**Ratings**

Pixels: 
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼
Additional Information

Source Code: UBMReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.129 Unisoku

Extensions: .dat, .hdr

Owner: Unisoku

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Unisoku

We currently have:

- Pascal code that can read Unisoku files (from ImageSXM)
- a few Unisoku files

We would like to have:

- an official specification document
- more Unisoku files

Ratings

Pixels:

Metadata:

Openness:

Presence:

Utility:

Additional Information

Source Code: UnisokuReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

693 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/UBMReader.java
694 http://www.openmicroscopy.org/site/support/bio-formats5.0/
695 http://www.openmicroscopy.org/site/support/legacy/
696 http://www.unisoku.com
698 http://www.openmicroscopy.org/site/support/bio-formats5.0/
699 http://www.openmicroscopy.org/site/support/legacy/
17.130 Varian FDF

Extensions: .fdf
Developer: Varian, Inc.

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Varian FDF
We currently have:
• a few Varian FDF datasets
We would like to have:
• an official specification document
• more Varian FDF datasets

Ratings
Pixels:
Metadata:
Openness:
Presence:
Utility:

Additional Information
Source Code: VarianFDFReader.java

Notes: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.131 Veeco AFM

Extensions: .hdf
Developer: Veeco

Support
BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Veeco AFM
We currently have:

---

700 http://www.varianinc.com
702 http://www.openmicroscopy.org/site/support/bio-formats5.0/
703 http://www.openmicroscopy.org/site/support/legacy/
704 http://www.veeco.com
• a few sample datasets

We would like to have:

**Ratings**

Pixels: ▼
Metadata: ▼
Openness: ▲
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: VeecoReader.java

Notes:

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

---

### 17.132 VG SAM

Extensions: .dti

**Support**

BSD-licensed: ✗
Export: ✗

Officially Supported Versions:

Supported Metadata Fields: **VG SAM**

We currently have:

• a few VG-SAM files

We would like to have:

• an official specification document
• more VG-SAM files

**Ratings**

Pixels: ▼
Metadata: ▼
Openness: ▼
Presence: ▼
Utility: ▼

**Additional Information**

Source Code: VGSAMReader.java

Notes:

---

706 http://www.openmicroscopy.org/site/support/bio-formats5.0/
707 http://www.openmicroscopy.org/site/support/legacy/
17.133 VisiTech XYS

Extensions: .xys, .html
Developer: VisiTech International

Support

BSD-licensed: 
Export: 

Officially Supported Versions:

Supported Metadata Fields: VisiTech XYS

We currently have:

• several VisiTech datasets

We would like to have:

• an official specification document

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: VisitechReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

17.134 Volocity

Extensions: .mvd2
Developer: PerkinElmer

Support

BSD-licensed: 
Export: 

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.
Officially Supported Versions:
Supported Metadata Fields: Volocity

Sample Datasets:
  • PerkinElmer Downloads

We currently have:
  • many example Volocity datasets

We would like to have:
  • an official specification document
  • any Volocity datasets that do not open correctly

Ratings

Pixels: 
Metadata: 
Openness: 
Presence: 
Utility: 

Additional Information

Source Code: VolocityReader.java

Notes:

.mvd2 files are Metakit database files.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.135 Volocity Library Clipping

Extensions: .acff
Developer: PerkinElmer

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions:
Supported Metadata Fields: Volocity Library Clipping

We currently have:
  • several Volocity library clipping datasets

We would like to have:
  • any datasets that do not open correctly
  • an official specification document

716 http://cellularimaging.perkinelmer.com/downloads/
718 http://equi4.com/metakit/
719 http://www.openmicroscopy.org/site/support/bio-formats5.0/
720 http://www.openmicroscopy.org/site/support/legacy/
721 http://www.perkinelmer.com/pages/020/cellularimaging/products/volocity.xhtml
Ratings

Pixels: 🟠
Metadata: 🟠
Openness: 🟠
Presence: 🟠
Utility: 🟠

Additional Information

Source Code: VolocityClippingReader.java

Notes:

RGB .acif files are not yet supported. See #6413.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.136 WA-TOP

Extensions: .wat

Developer: WA Technology

Owner: Oxford Instruments

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

Supported Metadata Fields: WA-TOP

We currently have:

- Pascal code that can read WA-TOP files (from ImageSXM)
- a few WA-TOP files

We would like to have:

- an official specification document
- more WA-TOP files

Ratings

Pixels: 🟠
Metadata: 🟠
Openness: 🟠
Presence: 🟠
Utility: 🟠

Additional Information

723 http://trac.openmicroscopy.org.uk/ome/ticket/6413
724 http://www.openmicroscopy.org/site/support/bio-formats5.0/
725 http://www.openmicroscopy.org/site/support/legacy/
726 http://www.oxinst.com
Source Code: WATOPReader.java

Notes:

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

## 17.137 Windows Bitmap

Extensions: .bmp

Developer: Microsoft and IBM

### Support

BSD-licensed: ![checkmark]

Export: ![x]

Officially Supported Versions:

Supported Metadata Fields: *Windows Bitmap*

Freely Available Software:

- BMP Writer plugin for ImageJ

We currently have:

- many BMP datasets

We would like to have:

### Ratings

Pixels: ![green]

Metadata: ![green]

Openness: ![red]

Presence: ![green]

Utility: ![red]

### Additional Information

Source Code: BMPReader.java

Notes:

Compressed BMP files are currently not supported.

See also:

Technical Overview

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

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727 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/WATOPReader.java

728 http://www.openmicroscopy.org/site/support/bio-formats5.0/

729 http://www.openmicroscopy.org/site/support/legacy/


731 https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-bsd/src/loci/formats/in/BMPReader.java


733 http://www.openmicroscopy.org/site/support/bio-formats5.0/

734 http://www.openmicroscopy.org/site/support/legacy/
17.138 Woolz

Extensions: .wlz

Developer: MRC Human Genetics Unit

Support

BSD-licensed: ❌

Export: ✔

Officially Supported Versions:

Supported Metadata Fields: Woolz

Freely Available Software:

- Woolz

We currently have:

- a few Woolz datasets

We would like to have:

Ratings

Pixels: ▲

Metadata: ▼

Openness: ▲

Presence: ▼

Utility: ▼

Additional Information

Source Code: WlzReader.java

Source Code: WlzWriter.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.139 Zeiss Axio CSM

Extensions: .lms

Developer: Carl Zeiss Microscopy GmbH

Owner: Carl Zeiss Microscopy GmbH

Support

BSD-licensed: ❌

Export: ❌

Officially Supported Versions:

http://www.emouseatlas.org/emap/analysis_tools_resources/software/woolz.html

http://www.emouseatlas.org/emap/analysis_tools_resources/software/woolz.html

https://github.com/openmicroscopy/bioformats/blob/v5.1.3/components/formats-gpl/src/loci/formats/in/WlzReader.java


http://www.openmicroscopy.org/site/support/bio-formats5.0/

http://www.openmicroscopy.org/site/support/legacy/

http://www.zeiss.com/microscopy/

http://www.zeiss.com/microscopy/
Supported Metadata Fields: Zeiss Axio CSM

We currently have:

• one example dataset

We would like to have:

Ratings

Pixels: 

Metadata: 

Openness: 

Presence: 

Utility: 

Additional Information

Source Code: ZeissLMSReader.java

Notes:

This should not be confused with the more common Zeiss LSM format, which has a similar extension. As far as we know, the Axio CSM 700 system is the only one which saves files in the .lms format.

---

17.140 Zeiss AxioVision TIFF

Extensions: .xml, .tiff

Developer: Carl Zeiss Microscopy GmbH

Owner: Carl Zeiss Microscopy GmbH

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Zeiss AxioVision TIFF

Freely Available Software:

• Zeiss ZEN Lite

We currently have:

• many example datasets

We would like to have:

• an official specification document

---

744 http://www.openmicroscopy.org/site/support/bio-formats5.0.x
745 http://www.openmicroscopy.org/site/support/legacy/
746 http://www.zeiss.com/microscopy/
Ratings

Pixels: ▲
Metadata: ▲
Openness: ▼
Presence: ▼
Utility: ▼

Additional Information

Source Code: ZeissTIFFReader.java

Notes:

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

17.141 Zeiss AxioVision ZVI (Zeiss Vision Image)

Extensions: .zvi

Developer: Carl Zeiss Microscopy GmbH (AxioVision)

Owner: Carl Zeiss Microscopy GmbH

Support

BSD-licensed: ❌
Export: ❌

Officially Supported Versions: 1.0, 2.0

Supported Metadata Fields: Zeiss AxioVision ZVI (Zeiss Vision Image)

Freely Available Software:

• Zeiss Axiovision LE

We currently have:

• a ZVI specification document (v2.0.5, from 2010 August, in PDF)
• an older ZVI specification document (v2.0.2, from 2006 August 23, in PDF)
• an older ZVI specification document (v2.0.1, from 2005 April 21, in PDF)
• an older ZVI specification document (v1.0.26.01.01, from 2001 January 29, in DOC)
• Zeiss’ ZvImageReader code (v1.0, from 2001 January 25, in C++)
• many ZVI datasets

We would like to have:

Ratings

Pixels: ▲
Metadata: ▲
Openness: ▲

---

750) http://www.openmicroscopy.org/site/support/bio-formats5.0/
751) http://www.openmicroscopy.org/site/support/legacy/
753) http://www.zeiss.com/microscopy/

17.141. Zeiss AxioVision ZVI (Zeiss Vision Image)
Presence: 
Utility: 

**Additional Information**

**Source Code:** ZeissZVIReader.java

**Notes:**

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Bio-Formats uses a modified version of the Apache Jakarta POI library to read ZVI files. ImageJ/FIJI will use the ZVI reader plugin in preference to Bio-Formats if both are installed. If you have a problem which is solved by opening the file using the Bio-Formats Importer plugin, you can just remove the ZVIReader.class from the plugins folder.

Commercial applications that support ZVI include Bitplane Imaris.

**See also:**

Axiovision software overview

---

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

---

### 17.142 Zeiss CZI

**Extensions:** .czi

**Developer:** Carl Zeiss Microscopy GmbH

**Support**

BSD-licensed: ❌

Export: ❌

**Officially Supported Versions:**

**Supported Metadata Fields:** Zeiss CZI

**Freely Available Software:**

- Zeiss ZEN

We currently have:

- many example datasets
- official specification documents

We would like to have:

**Ratings**

**Pixels:** 

**Metadata:** 

**Openness:** 

**Presence:** 

---

756 http://jakarta.apache.org/poi/
757 http://www.bitplane.com/
759 http://www.openmicroscopy.org/site/support/bio-formats5.0/
760 http://www.openmicroscopy.org/site/support/legacy/
761 http://www.zeiss.com/czi
762 http://www.zeiss.com/czi
17.143 Zeiss LSM (Laser Scanning Microscope) 510/710

Extensions: .lsm, .mdb

Owner: Carl Zeiss Microscopy GmbH

Support

BSD-licensed: 

Export: 

Officially Supported Versions:

Supported Metadata Fields: Zeiss LSM (Laser Scanning Microscope) 510/710

Freely Available Software:

- Zeiss LSM Image Browser
- LSM Toolbox plugin for ImageJ
- LSM Reader plugin for ImageJ
- DIMIN

We currently have:

- LSM specification v3.2, from 2003 March 12, in PDF
- LSM specification v5.5, from 2009 November 23, in PDF
- LSM specification v6.0, from 2010 September 28, in PDF
- many LSM datasets

We would like to have:

Ratings

Pixels:

Metadata:

Openness:

Presence:

Utility:

Additional Information
Source Code: ZeissLSMReader.java

Notes:

Please note that while we have specification documents for this format, we are not able to distribute them to third parties.

Bio-Formats uses the MDB Tools Java port

Commercial applications that support this format include:

- SVI Huygens
- Bitplane Imaris
- Amira
- Image-Pro Plus

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.1 Format readers

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208 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheC
209 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
210 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
211 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform
212 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Visible
218 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_Description
220 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_NameSpace
221 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_NameSpace
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234http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeColor  
235http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeDashArray  
236http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth  
238http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheC  
239http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT  
240http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform  
244http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_Y  
247http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#MicrobeamManipulation_Type  
249http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_LotNumber  
252http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
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257 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Microscope_Type
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261 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
262 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Iris
264 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_LotNumber
266 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
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269 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_WorkingDistance
270 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_CorrectionCollar
273 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
275 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
278 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved

18.2. Metadata fields
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301 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits

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304 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ExternalIdentifier]
305 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID]
306 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Name]
308 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Rows]
313 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_Description]
315 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID]
317 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_Name]
320 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_FillColor]
324 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_FontStyle]

18.2. Metadata fields

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390 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Reagent_Description
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Continued on next page

430 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_Description
433 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#TagAnnotation_Value
434 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TiffData_FirstC
435 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TiffData_FirstT
440 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_Description
441 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_ID
442 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#Annotation_Namespace
443 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#TermAnnotation_Value
444 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#TermAnnotation_Description
446 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#TermAnnotation_Namespace
Table 18.2 – continued from previous page

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448 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SA_xsd.html#TimestampAnnotation_Value
449 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TransmittanceRange_CutIn
450 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TransmittanceRange_CutInTolerance
454 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TiffData_TiffData_UUID_FileName
458 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_ExternalDescription
463 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_Type
466 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_Index
### Table 18.2 – continued from previous page

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</table>

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

#### 18.2.1 SlidebookReader

This page lists supported metadata fields for the Bio-Formats Olympus Slidebook format reader. These fields are from the OME data model. Bio-Formats standardizes each format's original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 34 of them (7%).
- Of those, Bio-Formats fully or partially converts 34 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Olympus Slidebook format reader:

- Channel: ID
- Channel: NDFilter
- Channel: Name
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef

---

476 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
477 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
483 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate)
- Image: Name
- Instrument: ID
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: Model
- Objective: NominalMagnification
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: ExposureTime
- Plane: TheC
- Plane: TheT
- Plane: TheZ

18.2. Metadata fields
Total supported: 34
Total unknown or missing: 441

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

### 18.2.2 SlideBook6Reader

This page lists supported metadata fields for the Bio-Formats SlideBook 6 SLD (native) format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 37 of them (7%).
- Of those, Bio-Formats fully or partially converts 37 (100%).

### Supported fields

These fields are fully supported by the Bio-Formats SlideBook 6 SLD (native) format reader:

- Channel: ID
- Channel: Name
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef
- Image: Name
- Instrument: ID
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: NominalMagnification

---

513 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
514 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
519 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate)
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 37

Total unknown or missing: 438

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.3 AIMReader

This page lists supported metadata fields for the Bio-Formats AIM format reader.

These fields are from the OME data model\(^\text{555}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats AIM format reader:

- Channel : ID\(^\text{556}\)
- Channel : SamplesPerPixel\(^\text{557}\)
- Image : AcquisitionDate\(^\text{558}\)
- Image : ID\(^\text{559}\)
- Image : Name\(^\text{560}\)
- Pixels : BigEndian\(^\text{561}\)
- Pixels : DimensionOrder\(^\text{562}\)
- Pixels : ID\(^\text{563}\)
- Pixels : Interleaved\(^\text{564}\)
- Pixels : PhysicalSizeX\(^\text{565}\)
- Pixels : PhysicalSizeY\(^\text{566}\)
- Pixels : PhysicalSizeZ\(^\text{567}\)
- Pixels : SignificantBits\(^\text{568}\)
- Pixels : SizeC\(^\text{569}\)
- Pixels : SizeT\(^\text{570}\)
- Pixels : SizeX\(^\text{571}\)
- Pixels : SizeY\(^\text{572}\)

\(^\text{555}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^\text{556}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^\text{557}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^\text{558}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^\text{560}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^\text{561}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^\text{562}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^\text{564}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^\text{568}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^\text{569}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^\text{570}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^\text{571}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\(^\text{572}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
18.2.4 AliconaReader

This page lists supported metadata fields for the Bio-Formats Alicona AL3D format reader.

These fields are from the OME data model\(^580\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 33 of them (6%).
- Of those, Bio-Formats fully or partially converts 33 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Alicona AL3D format reader:

- Channel : ID\(^{581}\)
- Channel : SamplesPerPixel\(^{582}\)
- Detector : ID\(^{583}\)
- Detector : Type\(^{584}\)
- DetectorSettings : ID\(^{585}\)
- DetectorSettings : Voltage\(^{586}\)
- Image : AcquisitionDate\(^{587}\)
- Image : ID\(^{588}\)
- Image : InstrumentRef\(^{589}\)

\(^{573}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{574}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\(^{575}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\(^{576}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^{577}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^{578}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{579}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{580}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{581}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{582}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{583}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\(^{584}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\(^{585}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
\(^{587}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
• Image: Name
• Instrument: ID
• Objective: CalibratedMagnification
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: WorkingDistance
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 33
Total unknown or missing: 442

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous
18.2.5 GelReader

This page lists supported metadata fields for the Bio-Formats Amersham Biosciences GEL format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Amersham Biosciences GEL format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : Name
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : PhysicalSizeX
- Pixels : PhysicalSizeY
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

18.2.6 AmiraReader

This page lists supported metadata fields for the Bio-Formats Amira format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Amira format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved

634 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
638 http://www.openmicroscopy.org/site/support/bio-formats5.0/
639 http://www.openmicroscopy.org/site/support/legacy/
641 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
642 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
645 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

18.2. Metadata fields
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.7 FlowSightReader

This page lists supported metadata fields for the Bio-Formats FlowSight format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 20 of them (4%).
• Of those, Bio-Formats fully or partially converts 20 (100%).

Supported fields

These fields are fully supported by the Bio-Formats FlowSight format reader:

• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 20
Total unknown or missing: 455

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.8 AnalyzeReader

This page lists supported metadata fields for the Bio-Formats Analyze 7.5 format reader.
These fields are from the OME data model[688]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 24 of them (5%).
- Of those, Bio-Formats fully or partially converts 24 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Analyze 7.5 format reader:

- Channel : ID[689]
- Channel : SamplesPerPixel[690]
- Image : AcquisitionDate[691]
- Image : Description[692]
- Image : ID[693]
- Image : Name[694]
- Pixels : BigEndian[695]
- Pixels : DimensionOrder[696]
- Pixels : ID[697]
- Pixels : Interleaved[698]
- Pixels : PhysicalSizeX[699]
- Pixels : PhysicalSizeY[700]
- Pixels : PhysicalSizeZ[701]
- Pixels : SignificantBits[702]
- Pixels : SizeC[703]
- Pixels : SizeT[704]
- Pixels : SizeX[705]
- Pixels : SizeY[706]
- Pixels : SizeZ[707]
- Pixels : TimeIncrement[708]


18.2. Metadata fields
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 24
Total unknown or missing: 451

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.9 AFIReader

This page lists supported metadata fields for the Bio-Formats Aperio AFI format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 30 of them (6%).
• Of those, Bio-Formats fully or partially converts 30 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Aperio AFI format reader:

• Channel : EmissionWavelength
• Channel : ExcitationWavelength
• Channel : ID
• Channel : Name
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : InstrumentRef
• Image : Name
• Instrument : ID

713]http://www.openmicroscopy.org/site/support/bio-formats5.0/
714]http://www.openmicroscopy.org/site/support/legacy/
• Objective : ID
• Objective : NominalMagnification
• ObjectiveSettings : ID
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : PhysicalSizeX
• Pixels : PhysicalSizeY
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : ExposureTime
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 30
Total unknown or missing: 445

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions' page to find documentation for the version you are using.

18.2.10 SVSReader

This page lists supported metadata fields for the Bio-Formats Aperio SVS format reader.
These fields are from the OME data model\textsuperscript{748}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 29 of them (6%).
- Of those, Bio-Formats fully or partially converts 29 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Aperio SVS format reader:

- Channel: EmissionWavelength\textsuperscript{749}
- Channel: ExcitationWavelength\textsuperscript{750}
- Channel: ID\textsuperscript{751}
- Channel: SamplesPerPixel\textsuperscript{752}
- Image: AcquisitionDate\textsuperscript{753}
- Image: Description\textsuperscript{754}
- Image: ID\textsuperscript{755}
- Image: InstrumentRef\textsuperscript{756}
- Image: Name\textsuperscript{757}
- Instrument: ID\textsuperscript{758}
- Objective: ID\textsuperscript{759}
- Objective: NominalMagnification\textsuperscript{760}
- ObjectiveSettings: ID\textsuperscript{761}
- Pixels: BigEndian\textsuperscript{762}
- Pixels: DimensionOrder\textsuperscript{763}
- Pixels: ID\textsuperscript{764}
- Pixels: Interleaved\textsuperscript{765}
- Pixels: PhysicalSizeX\textsuperscript{766}
- Pixels: PhysicalSizeY\textsuperscript{767}
- Pixels: SignificantBits\textsuperscript{768}

\textsuperscript{748}http://www.openmicroscopy.org/site/support/ome-model/
\textsuperscript{749}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_EmissionWavelength
\textsuperscript{750}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ExcitationWavelength
\textsuperscript{751}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{752}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{753}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{754}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
\textsuperscript{755}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{756}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#InstrumentRef_ID
\textsuperscript{757}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\textsuperscript{758}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Instrument_ID
\textsuperscript{759}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
\textsuperscript{760}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
\textsuperscript{761}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_ID
\textsuperscript{762}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\textsuperscript{763}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\textsuperscript{764}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\textsuperscript{765}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\textsuperscript{766}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeX
\textsuperscript{767}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY
\textsuperscript{768}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
Bio-Formats Documentation, Release 5.1.3

- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 29
Total unknown or missing: 446

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.11 CellWorxReader

This page lists supported metadata fields for the Bio-Formats CellWorx format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 45 of them (9%).
- Of those, Bio-Formats fully or partially converts 45 (100%).

Supported fields

These fields are fully supported by the Bio-Formats CellWorx format reader:
- Channel: EmissionWavelength
- Channel: ExcitationWavelength
- Channel: ID
- Channel: Name
- Channel: SamplesPerPixel

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2. Metadata fields
• Detector: ID
• DetectorSettings: Gain
• DetectorSettings: ID
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Microscope: SerialNumber
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Plate: ID

789 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
792 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
794 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
795 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
802 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
807 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
810 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
811 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID
18.2.12 AVIReader

This page lists supported metadata fields for the Bio-Formats Audio Video Interleave format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Audio Video Interleave format reader:

- Plate: Name
- PlateAcquisition: EndTime
- PlateAcquisition: ID
- PlateAcquisition: MaximumFieldCount
- PlateAcquisition: StartTime
- PlateAcquisition: WellSampleRef
- Well: Column
- Well: ID
- Well: Row
- WellSample: ID
- WellSample: ImageRef
- WellSample: Index
- WellSample: PositionX
- WellSample: PositionY

Total supported: 45
Total unknown or missing: 430

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.
- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.13 ARFReader

This page lists supported metadata fields for the Bio-Formats ARF format reader.

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
These fields are from the OME data model\(^{850}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

### Supported fields

These fields are fully supported by the Bio-Formats ARF format reader:

- Channel: ID\(^{851}\)
- Channel: SamplesPerPixel\(^{852}\)
- Image: AcquisitionDate\(^{853}\)
- Image: ID\(^{854}\)
- Image: Name\(^{855}\)
- Pixels: BigEndian\(^{856}\)
- Pixels: DimensionOrder\(^{857}\)
- Pixels: ID\(^{858}\)
- Pixels: Interleaved\(^{859}\)
- Pixels: SignificantBits\(^{860}\)
- Pixels: SizeC\(^{861}\)
- Pixels: SizeT\(^{862}\)
- Pixels: SizeX\(^{863}\)
- Pixels: SizeY\(^{864}\)
- Pixels: SizeZ\(^{865}\)
- Pixels: Type\(^{866}\)
- Plane: TheC\(^{867}\)
- Plane: TheT\(^{868}\)
- Plane: TheZ\(^{869}\)

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\(^{850}\) http://www.openmicroscopy.org/site/support/ome-model/

\(^{851}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID

\(^{852}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel

\(^{853}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate


\(^{855}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

\(^{856}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

\(^{857}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder

\(^{858}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID

\(^{859}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved

\(^{860}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits

\(^{861}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC

\(^{862}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT

\(^{863}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX

\(^{864}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY

\(^{865}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ

\(^{866}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

\(^{867}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC

\(^{868}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT

\(^{869}\) http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
18.2.14 BDReader

This page lists supported metadata fields for the Bio-Formats BD Pathway format reader. These fields are from the OME data model\(^{872}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 57 of them (12%).
- Of those, Bio-Formats fully or partially converts 57 (100%).

Supported fields

These fields are fully supported by the Bio-Formats BD Pathway format reader:

- Channel: EmissionWavelength\(^{873}\)
- Channel: ExcitationWavelength\(^{874}\)
- Channel: ID\(^{875}\)
- Channel: Name\(^{876}\)
- Channel: SamplesPerPixel\(^{877}\)
- Detector: ID\(^{878}\)
- DetectorSettings: Binning\(^{879}\)
- DetectorSettings: Gain\(^{880}\)
- DetectorSettings: ID\(^{881}\)
- DetectorSettings: Offset\(^{882}\)
- Image: AcquisitionDate\(^{883}\)
- Image: ID\(^{884}\)
- Image: InstrumentRef\(^{885}\)
- Image: Name\(^{886}\)

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\(^{870}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{871}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{872}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_EmissionWavelength
\(^{873}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ExcitationWavelength
\(^{874}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{875}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
\(^{876}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\(^{877}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\(^{880}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{883}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
Bio-Formats Documentation, Release 5.1.3

- Image: ROIRef\(^{887}\)
- Instrument: ID\(^{888}\)
- Objective: ID\(^{889}\)
- Objective: LensNA\(^{890}\)
- Objective: Manufacturer\(^{891}\)
- Objective: NominalMagnification\(^{892}\)
- ObjectiveSettings: ID\(^{893}\)
- Pixels: BigEndian\(^{894}\)
- Pixels: DimensionOrder\(^{895}\)
- Pixels: ID\(^{896}\)
- Pixels: Interleaved\(^{897}\)
- Pixels: SignificantBits\(^{898}\)
- Pixels: SizeC\(^{899}\)
- Pixels: SizeT\(^{900}\)
- Pixels: SizeX\(^{901}\)
- Pixels: SizeY\(^{902}\)
- Pixels: SizeZ\(^{903}\)
- Pixels: Type\(^{904}\)
- Plane: DeltaT\(^{905}\)
- Plane: ExposureTime\(^{906}\)
- Plane: TheC\(^{907}\)
- Plane: TheT\(^{908}\)
- Plane: TheZ\(^{909}\)
- Plate: ColumnNamingConvention\(^{910}\)
- Plate: Description\(^{911}\)
- Plate: ID\(^{912}\)

\(^{887}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID
\(^{889}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
\(^{890}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_LensNA
\(^{891}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
\(^{892}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
\(^{893}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_ID
\(^{894}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{895}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^{896}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^{897}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{898}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^{899}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^{900}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^{901}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\(^{902}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\(^{903}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{904}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\(^{905}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_DeltaT
\(^{906}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_ExposureTime
\(^{908}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^{909}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^{910}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ColumnNamingConvention
\(^{911}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Description
\(^{912}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID
• Plate: Name
• Plate: RowNamingConvention
• PlateAcquisition: ID
• PlateAcquisition: MaximumFieldCount
• PlateAcquisition: WellSampleRef
• ROI: ID
• Rectangle: Height
• Rectangle: ID
• Rectangle: Width
• Rectangle: X
• Rectangle: Y
• Well: Column
• Well: ID
• Well: Row
• WellSample: ID
• WellSample: ImageRef
• WellSample: Index

Total supported: 57
Total unknown or missing: 418

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.15 SDTReader

This page lists supported metadata fields for the Bio-Formats SPCImage Data format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).

18.2. Metadata fields
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats SPCImage Data format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions' page to find documentation for the version you are using.

934 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
935 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
938 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
943 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
944 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
946 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
948 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
952 http://www.openmicroscopy.org/site/support/bio-formats5.0/
953 http://www.openmicroscopy.org/site/support/legacy/
18.2.16 BioRadGelReader

This page lists supported metadata fields for the Bio-Formats Bio-Rad GEL format reader.

These fields are from the OME data model\(^{954}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Bio-Rad GEL format reader:

- Channel : ID\(^{955}\)
- Channel : SamplesPerPixel\(^{956}\)
- Image : AcquisitionDate\(^{957}\)
- Image : ID\(^{958}\)
- Image : Name\(^{959}\)
- Pixels : BigEndian\(^{960}\)
- Pixels : DimensionOrder\(^{961}\)
- Pixels : ID\(^{962}\)
- Pixels : Interleaved\(^{963}\)
- Pixels : PhysicalSizeX\(^{964}\)
- Pixels : PhysicalSizeY\(^{965}\)
- Pixels : SignificantBits\(^{966}\)
- Pixels : SizeC\(^{967}\)
- Pixels : SizeT\(^{968}\)
- Pixels : SizeX\(^{969}\)
- Pixels : SizeY\(^{970}\)
- Pixels : SizeZ\(^{971}\)
- Pixels : Type\(^{972}\)

\(^{954}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{955}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{956}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{957}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{959}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{960}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{961}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^{962}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^{963}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{966}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^{967}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^{968}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^{969}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\(^{970}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\(^{971}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{972}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

18.2.17 BioRadReader

This page lists supported metadata fields for the Bio-Formats Bio-Rad PIC format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 40 of them (8%).
- Of those, Bio-Formats fully or partially converts 40 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Bio-Rad PIC format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Detector : Gain
- Detector : ID
- Detector : Offset
- Detector : Type
- DetectorSettings : Gain
- DetectorSettings : ID
- DetectorSettings : Offset
- Experiment : ID
- Experiment : Type

975 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
976 http://www.openmicroscopy.org/site/support/bio-formats5.0/
977 http://www.openmicroscopy.org/site/support/legacy/
979 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
983 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
988 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_Type
18.2. Metadata fields

- Image: AcquisitionDate
- Image: ID
- Image: InstrumentRef
- Image: Name
- Instrument: ID
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: LensNA
- Objective: Model
- Objective: NominalMagnification
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type

990 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
993 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
994 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
996 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Impression
1000 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
1002 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
1010 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
1011 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
1015 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 40
Total unknown or missing: 435

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.18 BioRadSCNReader

This page lists supported metadata fields for the Bio-Formats Bio-Rad SCN format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 29 of them (6%).
• Of those, Bio-Formats fully or partially converts 29 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Bio-Rad SCN format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Detector: ID
• DetectorSettings: Binning
• DetectorSettings: Gain
• DetectorSettings: ID
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Instrument: ID
• Microscope: Model
• Microscope: SerialNumber
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: ExposureTime
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 29
Total unknown or missing: 446

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

18.2.19 ImarisHDFReader

This page lists supported metadata fields for the Bio-Formats Bitplane Imaris 5.5 (HDF) format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

1033 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
1034 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
1037 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
1042 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
1044 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
1046 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
1050 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
1051 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1052 http://www.openmicroscopy.org/site/support/legacy/
1053 http://www.openmicroscopy.org/site/support/ome-model/
• The file format itself supports 23 of them (4%).
• Of those, Bio-Formats fully or partially converts 23 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Bitplane Imaris 5.5 (HDF) format reader:

- Channel: Color
- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ
Total supported: 23
Total unknown or missing: 452

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.20 BrukerReader

This page lists supported metadata fields for the Bio-Formats Bruker format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 23 of them (4%).
• Of those, Bio-Formats fully or partially converts 23 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Bruker format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Experimenter: ID
• Experimenter: Institution
• Experimenter: LastName
• Image: AcquisitionDate
• Image: ExperimenterRef
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits

[^1077]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^1078]: http://www.openmicroscopy.org/site/support/legacy/
[^1080]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
[^1083]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_LastName
[^1084]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
Bio-Formats Documentation, Release 5.1.3

- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 23
Total unknown or missing: 452

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.21 BurleighReader

This page lists supported metadata fields for the Bio-Formats Burleigh format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Burleigh format reader:
- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name

1095 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
1099 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
1102 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
1103 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1104 http://www.openmicroscopy.org/site/support/legacy/
1105 http://www.openmicroscopy.org/site/support/ome-model/
1107 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
1108 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
1110 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

18.2. Metadata fields
18.2.22 DNGReader

This page lists supported metadata fields for the Bio-Formats DNG format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats DNG format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19

Total unknown or missing: 456

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.23 CellH5Reader

This page lists supported metadata fields for the Bio-Formats CellH5 (HDF) format reader.

These fields are from the OME data model\(^{1152}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 31 of them (6%).
- Of those, Bio-Formats fully or partially converts 31 (100%).

Supported fields

These fields are fully supported by the Bio-Formats CellH5 (HDF) format reader:

- Channel : ID\(^{1153}\)
- Channel : SamplesPerPixel\(^{1154}\)
- Image : AcquisitionDate\(^{1155}\)
- Image : ID\(^{1156}\)
- Image : Name\(^{1157}\)
- Image : ROIRef\(^{1158}\)
- Pixels : BigEndian\(^{1159}\)
- Pixels : DimensionOrder\(^{1160}\)
- Pixels : ID\(^{1161}\)
- Pixels : Interleaved\(^{1162}\)
- Pixels : SignificantBits\(^{1163}\)
- Pixels : SizeC\(^{1164}\)
- Pixels : SizeT\(^{1165}\)
- Pixels : SizeX\(^{1166}\)
- Pixels : SizeY\(^{1167}\)
- Pixels : SizeZ\(^{1168}\)
- Pixels : Type\(^{1169}\)
- Plane : TheC\(^{1170}\)

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\(^{1152}\)http://www.openmicroscopy.org/site/support/ome-model/

\(^{1153}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID

\(^{1154}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel

\(^{1155}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate


\(^{1157}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

\(^{1158}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID

\(^{1159,1160}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

\(^{1161,1162}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder

\(^{1163,1164}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved

\(^{1165,1166}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits

\(^{1167,1168}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC

\(^{1169,1170}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT

\(^{1171}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX

\(^{1172}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY

\(^{1173}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ

\(^{1174}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

\(^{1175}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
• Plane: TheT
• Plane: TheZ
• ROI: ID
• ROI: Name
• Rectangle: Height
• Rectangle: ID
• Rectangle: StrokeColor
• Rectangle: TheC
• Rectangle: TheT
• Rectangle: TheZ
• Rectangle: Width
• Rectangle: X
• Rectangle: Y

Total supported: 31
Total unknown or missing: 444

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.24 CellomicsReader

This page lists supported metadata fields for the Bio-Formats Cellomics C01 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 31 of them (6%).
• Of those, Bio-Formats fully or partially converts 31 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Cellomics C01 format reader:

• Channel: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROI_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Rectangle_Height
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeColor
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• Channel: SamplesPerPixel\(^{1188}\)
• Image: AcquisitionDate\(^{1189}\)
• Image: ID\(^{1190}\)
• Image: Name\(^{1191}\)
• Pixels: BigEndian\(^{1192}\)
• Pixels: DimensionOrder\(^{1193}\)
• Pixels: ID\(^{1194}\)
• Pixels: Interleaved\(^{1195}\)
• Pixels: PhysicalSizeX\(^{1196}\)
• Pixels: PhysicalSizeY\(^{1197}\)
• Pixels: SignificantBits\(^{1198}\)
• Pixels: SizeC\(^{1199}\)
• Pixels: SizeT\(^{1200}\)
• Pixels: SizeX\(^{1201}\)
• Pixels: SizeY\(^{1202}\)
• Pixels: SizeZ\(^{1203}\)
• Pixels: Type\(^{1204}\)
• Plane: TheC\(^{1205}\)
• Plane: TheT\(^{1206}\)
• Plane: TheZ\(^{1207}\)
• Plate: ColumnNamingConvention\(^{1208}\)
• Plate: ID\(^{1209}\)
• Plate: Name\(^{1210}\)
• Plate: RowNamingConvention\(^{1211}\)
• Well: Column\(^{1212}\)
• Well: ID\(^{1213}\)

\(^{1188}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{1189}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{1191}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{1192}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{1193}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^{1194}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^{1195}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{1197}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY
\(^{1198}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^{1199}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^{1200}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^{1202}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\(^{1203}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{1204}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\(^{1205}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\(^{1206}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^{1207}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^{1208}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ColumnNamingConvention
\(^{1209}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID
\(^{1210}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Name
\(^{1211}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_RowNamingConvention
\(^{1212}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_Column
\(^{1213}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_ID
18.2.25 CellSensReader

This page lists supported metadata fields for the Bio-Formats CellSens VSI format reader.

These fields are from the OME data model\(^{1220}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 46 of them (9%).
- Of those, Bio-Formats fully or partially converts 46 (100%).

Supported fields

These fields are fully supported by the Bio-Formats CellSens VSI format reader:

- Channel: EmissionWavelength\(^{1221}\)
- Channel: ID\(^{1222}\)
- Channel: Name\(^{1223}\)
- Channel: SamplesPerPixel\(^{1224}\)
- Detector: Gain\(^{1225}\)
- Detector: ID\(^{1226}\)
- Detector: Manufacturer\(^{1227}\)
- Detector: Model\(^{1228}\)
- Detector: Offset\(^{1229}\)
- Detector: SerialNumber\(^{1230}\)

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{1218}\) or the previous versions\(^{1219}\) page to find documentation for the version you are using.
• Detector: Type
• DetectorSettings: Binning
• DetectorSettings: Gain
• DetectorSettings: ID
• DetectorSettings: Offset
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Objective: ID
• Objective: LensNA
• Objective: Model
• Objective: NominalMagnification
• Objective: WorkingDistance
• ObjectiveSettings: ID
• ObjectiveSettings: RefractiveIndex
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT

1231 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
1236 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
1243 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
1244 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_WorkingDistance
1246 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
18.2.26 CellVoyagerReader

This page lists supported metadata fields for the Bio-Formats CellVoyager format reader.

These fields are from the OME data model. Bio-Formats standardizes each format's original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 34 of them (7%).
- Of those, Bio-Formats fully or partially converts 34 (100%).

Supported fields

These fields are fully supported by the Bio-Formats CellVoyager format reader:

- Channel : ID
- Channel : Name
- Channel : PinholeSize
- Channel : SamplesPerPixel

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2. Metadata fields

- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ
- Plate: Columns
- Plate: Rows
- PlateAcquisition: EndTime
- PlateAcquisition: ID
- PlateAcquisition: MaximumFieldCount
- PlateAcquisition: StartTime
- Well: Column
- Well: ID
- Well: Row

• WellSample: ID
• WellSample: Index
• WellSample: PositionX
• WellSample: PositionY

Total supported: 34
Total unknown or missing: 441

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.27 DeltavisionReader

This page lists supported metadata fields for the Bio-Formats Deltavision format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 52 of them (10%).
• Of those, Bio-Formats fully or partially converts 52 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Deltavision format reader:

• Channel: EmissionWavelength
• Channel: ExcitationWavelength
• Channel: ID
• Channel: NDFilter
• Channel: Name
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Model
• Detector: Type
• DetectorSettings: Binning

1300 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_ID
1301 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_Index
1304 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1305 http://www.openmicroscopy.org/site/support/legacy/
1306 http://www.openmicroscopy.org/site/support/ome-model/
1311 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
1312 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
1315 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
• DetectorSettings: Gain
• DetectorSettings: ID
• DetectorSettings: ReadOutRate
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: InstrumentRef
• Image: Name
• ImagingEnvironment: Temperature
• Instrument: ID
• Objective: CalibratedMagnification
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: LensNA
• Objective: Manufacturer
• Objective: Model
• Objective: NominalMagnification
• Objective: WorkingDistance
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
Total supported: 52

Total unknown or missing: 423

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.28 DicomReader

This page lists supported metadata fields for the Bio-Formats DICOM format reader.

These fields are from the OME data model. Bio-Formats standardizes each format's original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 23 of them (4%).
- Of those, Bio-Formats fully or partially converts 23 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
18.2. Metadata fields
Supported fields

These fields are fully supported by the Bio-Formats DICOM format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 23

Total unknown or missing: 452
18.2.29 Ecat7Reader

This page lists supported metadata fields for the Bio-Formats ECAT7 format reader. These fields are from the OME data model\(^{1387}\). Bio-Formats standardizes each format's original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 23 of them (4%).
- Of those, Bio-Formats fully or partially converts 23 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats ECAT7 format reader:

- Channel: ID\(^{1388}\)
- Channel: SamplesPerPixel\(^{1389}\)
- Image: AcquisitionDate\(^{1390}\)
- Image: Description\(^{1391}\)
- Image: ID\(^{1392}\)
- Image: Name\(^{1393}\)
- Pixels: BigEndian\(^{1394}\)
- Pixels: DimensionOrder\(^{1395}\)
- Pixels: ID\(^{1396}\)
- Pixels: Interleaved\(^{1397}\)
- Pixels: PhysicalSizeX\(^{1398}\)
- Pixels: PhysicalSizeY\(^{1399}\)
- Pixels: PhysicalSizeZ\(^{1400}\)
- Pixels: SignificantBits\(^{1401}\)
- Pixels: SizeC\(^{1402}\)
- Pixels: SizeT\(^{1403}\)

\(^{1385}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{1386}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{1387}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{1388}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{1389}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{1390}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{1391}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
\(^{1393}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{1394}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{1395}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^{1396}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^{1397}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{1399}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY
\(^{1401}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^{1402}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^{1403}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 23
Total unknown or missing: 452

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.30 EPSReader

This page lists supported metadata fields for the Bio-Formats Encapsulated PostScript format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Encapsulated PostScript format reader:
• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder

1407 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
1411 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1412 http://www.openmicroscopy.org/site/support/legacy/
1414 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
1415 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
1417 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
1418 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
18.2.31 FlexReader

This page lists supported metadata fields for the Bio-Formats Evotec Flex format reader.

These fields are from the OME data model[^1436]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 69 of them (14%).
- Of those, Bio-Formats fully or partially converts 69 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Evotec Flex format reader:

- Channel : ID[^1437]
- Channel : LightSourceSettingsID[^1437]

[^1425]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
[^1427]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
[^1429]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
[^1433]: http://www.openmicroscopy.org/site/support/bio-formats5.0/
[^1434]: http://www.openmicroscopy.org/site/support/legacy/
[^1435]: http://www.openmicroscopy.org/site/support/ome-model/
• Channel : Name\textsuperscript{1438}
• Channel : SamplesPerPixel\textsuperscript{1439}
• Detector : ID\textsuperscript{1440}
• Detector : Type\textsuperscript{1441}
• DetectorSettings : Binning\textsuperscript{1442}
• DetectorSettings : ID\textsuperscript{1443}
• Dichroic : ID\textsuperscript{1444}
• Dichroic : Model\textsuperscript{1445}
• Filter : FilterWheel\textsuperscript{1446}
• Filter : ID\textsuperscript{1447}
• Filter : Model\textsuperscript{1448}
• Image : AcquisitionDate\textsuperscript{1449}
• Image : ID\textsuperscript{1450}
• Image : InstrumentRef\textsuperscript{1451}
• Image : Name\textsuperscript{1452}
• Instrument : ID\textsuperscript{1453}
• Laser : ID\textsuperscript{1454}
• Laser : LaserMedium\textsuperscript{1455}
• Laser : Type\textsuperscript{1456}
• Laser : Wavelength\textsuperscript{1457}
• LightPath : DichroicRef\textsuperscript{1458}
• LightPath : EmissionFilterRef\textsuperscript{1459}
• LightPath : ExcitationFilterRef\textsuperscript{1460}
• Objective : CalibratedMagnification\textsuperscript{1461}
• Objective : Correction\textsuperscript{1462}
• Objective : ID\textsuperscript{1463}

\textsuperscript{1438} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
\textsuperscript{1439} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{1440} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\textsuperscript{1441} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\textsuperscript{1442} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\textsuperscript{1443} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
\textsuperscript{1444} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Dichroic_ID
\textsuperscript{1445} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\textsuperscript{1446} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Filter_FilterWheel
\textsuperscript{1447} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Filter_ID
\textsuperscript{1448} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\textsuperscript{1449} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{1450} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{1451} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#InstrumentRef_ID
\textsuperscript{1452} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\textsuperscript{1453} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Instrument_ID
\textsuperscript{1454} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#LightSource_ID
\textsuperscript{1455} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#LightSource_LaserMedium
\textsuperscript{1456} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Laser_Type
\textsuperscript{1457} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Laser_Wavelength
\textsuperscript{1458} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DichroicRef_ID
\textsuperscript{1459} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#FilterRef_ID
\textsuperscript{1460} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
\textsuperscript{1461} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_CalibratedMagnification
\textsuperscript{1462} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
\textsuperscript{1463} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
• Objective: Immersion
• Objective: LensNA
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Plate: ColumnNamingConvention
• Plate: ExternalIdentifier

1464 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
1467 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
1474 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
1475 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
1479 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
1488 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ColumnNamingConvention
1489 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ExternalIdentifier
• Plate: ID
• Plate: Name
• Plate: RowNamingConvention
• PlateAcquisition: ID
• PlateAcquisition: MaximumFieldCount
• PlateAcquisition: StartTime
• PlateAcquisition: WellSampleRef
• Well: Column
• Well: ID
• Well: Row
• WellSample: ID
• WellSample: ImageRef
• WellSample: Index
• WellSample: PositionX
• WellSample: PositionY

Total supported: 69
Total unknown or missing: 406

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.32 FEIReader

This page lists supported metadata fields for the Bio-Formats FEI/Philips format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_RowNamingConvention
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_MaximumFieldCount
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_StartTime
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSampleRef_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_Index
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats FEI/Philips format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.33 FEITiffReader

This page lists supported metadata fields for the Bio-Formats FEI TIFF format reader. These fields are from the OME data model\(^\text{1529}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 39 of them (8%).
- Of those, Bio-Formats fully or partially converts 39 (100%).

Supported fields

These fields are fully supported by the Bio-Formats FEI TIFF format reader:

- Channel: ID\(^\text{1530}\)
- Channel: SamplesPerPixel\(^\text{1531}\)
- Detector: ID\(^\text{1532}\)
- Detector: Model\(^\text{1533}\)
- Detector: Type\(^\text{1534}\)
- Experimenter: ID\(^\text{1535}\)
- Experimenter: LastName\(^\text{1536}\)
- Image: AcquisitionDate\(^\text{1537}\)
- Image: Description\(^\text{1538}\)
- Image: ID\(^\text{1539}\)
- Image: InstrumentRef\(^\text{1540}\)
- Image: Name\(^\text{1541}\)
- Instrument: ID\(^\text{1542}\)
- Microscope: Model\(^\text{1543}\)
- Objective: Correction\(^\text{1544}\)
- Objective: ID\(^\text{1545}\)
- Objective: Immersion\(^\text{1546}\)
- Objective: NominalMagnification\(^\text{1547}\)
- Pixels: BigEndian\(^\text{1548}\)

\(^{1529}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{1530}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{1531}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{1532}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\(^{1533}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\(^{1534}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\(^{1535}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_ID
\(^{1536}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_LastName
\(^{1537}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{1538}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
\(^{1541}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{1543}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\(^{1544}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
\(^{1545}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
\(^{1546}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
\(^{1547}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
\(^{1548}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• StageLabel: Name
• StageLabel: X
• StageLabel: Y
• StageLabel: Z

Total supported: 39
Total unknown or missing: 436

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.34 FitsReader

This page lists supported metadata fields for the Bio-Formats Flexible Image Transport System format reader.
These fields are from the OME data model\(^{1571}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**
- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Flexible Image Transport System format reader:

- Channel: ID\(^{1572}\)
- Channel: SamplesPerPixel\(^{1573}\)
- Image: AcquisitionDate\(^{1574}\)
- Image: ID\(^{1575}\)
- Image: Name\(^{1576}\)
- Pixels: BigEndian\(^{1577}\)
- Pixels: DimensionOrder\(^{1578}\)
- Pixels: ID\(^{1579}\)
- Pixels: Interleaved\(^{1580}\)
- Pixels: SignificantBits\(^{1581}\)
- Pixels: SizeC\(^{1582}\)
- Pixels: SizeT\(^{1583}\)
- Pixels: SizeX\(^{1584}\)
- Pixels: SizeY\(^{1585}\)
- Pixels: SizeZ\(^{1586}\)
- Pixels: Type\(^{1587}\)
- Plane: TheC\(^{1588}\)
- Plane: TheT\(^{1589}\)
- Plane: TheZ\(^{1590}\)

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\(^{1571}\)http://www.openmicroscopy.org/site/support/ome-model/

\(^{1572}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Channel_ID

\(^{1573}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Channel_SamplesPerPixel

\(^{1574}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Image_AcquisitionDate


\(^{1576}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Image_Name

\(^{1577}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_BigEndian

\(^{1578}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_DimensionOrder

\(^{1579}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_ID

\(^{1580}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_Interleaved

\(^{1581}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SignificantBits

\(^{1582}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SizeC

\(^{1583}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SizeT

\(^{1584}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SizeX

\(^{1585}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SizeY

\(^{1586}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_SizeZ

\(^{1587}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Pixels_Type

\(^{1588}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Plane_TheC

\(^{1589}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Plane_TheT

\(^{1590}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OMEX-2015-01/ome_xsd.html#Plane_TheZ
18.2.35 GatanDM2Reader

This page lists supported metadata fields for the Bio-Formats Gatan DM2 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 30 of them (6%).
- Of those, Bio-Formats fully or partially converts 30 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Gatan DM2 format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Detector : ID
- DetectorSettings : Binning
- DetectorSettings : ID
- Experimenter : FirstName
- Experimenter : ID
- Experimenter : LastName
- Image : AcquisitionDate
- Image : ExperimenterRef
- Image : ID
- Image : InstrumentRef
- Image : Name
- Instrument : ID
18.2.36 GatanReader

This page lists supported metadata fields for the Bio-Formats Gatan Digital Micrograph format reader. These fields are from the OME data model\(^{1626}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 36 of them (7%).
- Of those, Bio-Formats fully or partially converts 36 (100%).

Total supported: **30**

Total unknown or missing: **445**

**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\(^{1624}\) or the previous versions\(^{1625}\) page to find documentation for the version you are using.

\(^{1608}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

\(^{1609}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder

\(^{1610}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID

\(^{1611}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved


\(^{1613}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY

\(^{1614}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits

\(^{1615}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC

\(^{1616}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT

\(^{1617}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX

\(^{1618}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY

\(^{1619}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ

\(^{1620}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type


\(^{1622}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT

\(^{1623}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ

\(^{1624}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{1625}\)http://www.openmicroscopy.org/site/support/legacy/

\(^{1626}\)http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats Gatan Digital Micrograph format reader:

- Channel: AcquisitionMode
- Channel: ID
- Channel: SamplesPerPixel
- Detector: ID
- DetectorSettings: ID
- DetectorSettings: Voltage
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Instrument: ID
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: NominalMagnification
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
18.2.37 GIFReader

This page lists supported metadata fields for the Bio-Formats Graphics Interchange Format format reader. These fields are from the OME data model\(^\text{1665}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Graphics Interchange Format format reader:

- **Channel**: ID\(^\text{1666}\)
- **Channel**: SamplesPerPixel\(^\text{1667}\)

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\(^{1651}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^{1653}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\(^{1654}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{1655}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\(^{1656}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_ExposureTime
\(^{1661}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^{1662}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^{1663}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{1664}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{1665}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{1666}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{1667}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.38 NAFReader

This page lists supported metadata fields for the Bio-Formats Hamamatsu Aquacosmos format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).

1668 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
1671 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
1674 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
1676 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
1677 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
1681 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
1685 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1686 http://www.openmicroscopy.org/site/support/legacy/
1687 http://www.openmicroscopy.org/site/support/ome-model/
• Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Hamamatsu Aquacosmos format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.39 HISReader

This page lists supported metadata fields for the Bio-Formats Hamamatsu HIS format reader. These fields are from the OME data model\(^\text{1709}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 27 of them (5%).
- Of those, Bio-Formats fully or partially converts 27 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Hamamatsu HIS format reader:

- Channel: ID\(^\text{1710}\)
- Channel: SamplesPerPixel\(^\text{1711}\)
- Detector: ID\(^\text{1712}\)
- Detector: Offset\(^\text{1713}\)
- Detector: Type\(^\text{1714}\)
- DetectorSettings: Binning\(^\text{1715}\)
- DetectorSettings: ID\(^\text{1716}\)
- Image: AcquisitionDate\(^\text{1717}\)
- Image: ID\(^\text{1718}\)
- Image: InstrumentRef\(^\text{1719}\)
- Image: Name\(^\text{1720}\)
- Instrument: ID\(^\text{1721}\)
- Pixels: BigEndian\(^\text{1722}\)
- Pixels: DimensionOrder\(^\text{1723}\)
- Pixels: ID\(^\text{1724}\)
- Pixels: Interleaved\(^\text{1725}\)
- Pixels: SignificantBits\(^\text{1726}\)
- Pixels: SizeC\(^\text{1727}\)

\(^\text{1709}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^\text{1710}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^\text{1711}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^\text{1712}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\(^\text{1713}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Offset
\(^\text{1714}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\(^\text{1715}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\(^\text{1717}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^\text{1720}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^\text{1722}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^\text{1723}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^\text{1724}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^\text{1725}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^\text{1726}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^\text{1727}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
Total supported: 27
Total unknown or missing: 448

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.40 NDPIReader

This page lists supported metadata fields for the Bio-Formats Hamamatsu NDPI format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 28 of them (5%).
• Of those, Bio-Formats fully or partially converts 28 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Hamamatsu NDPI format reader:

  * Channel : ID
  * Channel : SamplesPerPixel
  * Image : AcquisitionDate
  * Image : Description
  * Image : ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Microscope: Model
• Objective: ID
• Objective: NominalMagnification
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 28
Total unknown or missing: 447

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.41 HamamatsuVMSReader

This page lists supported metadata fields for the Bio-Formats Hamamatsu VMS format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 26 of them (5%).
- Of those, Bio-Formats fully or partially converts 26 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Hamamatsu VMS format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : InstrumentRef
- Image : Name
- Instrument : ID
- Objective : ID
- Objective : NominalMagnification
- ObjectiveSettings : ID
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : PhysicalSizeX
- Pixels : PhysicalSizeY
- Pixels : SignificantBits

18.2.42 HitachiReader

This page lists supported metadata fields for the Bio-Formats Hitachi format reader.

These fields are from the OME data model[1799]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 31 of them (6%).
- Of those, Bio-Formats fully or partially converts 31 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Hitachi format reader:

- Channel : ID
- Image : AcquisitionDate
- Image : ID
- Image : InstrumentRef
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Plane : TheC
- Plane : TheT
- Plane : TheZ

Total supported: 26
Total unknown or missing: 449

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2. Metadata fields

- Image: Name
- Instrument: ID
- Microscope: Model
- Microscope: SerialNumber
- Objective: ID
- Objective: WorkingDistance
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: PositionX
- Plane: PositionY
- Plane: PositionZ
- Plane: TheC
- Plane: TheT
- Plane: TheZ
18.2.43 I2IReader

This page lists supported metadata fields for the Bio-Formats I2I format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats I2I format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY

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18.3.1 [1831] http://www.openmicroscopy.org/site/support/bio-formats5.0/
18.3.2 [1832] http://www.openmicroscopy.org/site/support/legacy/
18.3.3 [1833] http://www.openmicroscopy.org/site/support/ome-model/
18.3.5 [1835] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
18.3.6 [1836] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
18.2.44 ICSReader

This page lists supported metadata fields for the Bio-Formats Image Cytometry Standard format reader. These fields are from the OME data model\textsuperscript{1855}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 72 of them (15%).
- Of those, Bio-Formats fully or partially converts 72 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Image Cytometry Standard format reader:

- Channel : EmissionWavelength\textsuperscript{1856}
- Channel : ExcitationWavelength\textsuperscript{1857}
- Channel : ID\textsuperscript{1858}
- Channel : Name\textsuperscript{1859}
- Channel : PinholeSize\textsuperscript{1860}
- Channel : SamplesPerPixel\textsuperscript{1861}
- Detector : ID\textsuperscript{1862}
- Detector : Manufacturer\textsuperscript{1863}
- Detector : Model\textsuperscript{1864}

\textsuperscript{1848}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\textsuperscript{1849}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\textsuperscript{1850}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\textsuperscript{1851}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\textsuperscript{1852}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\textsuperscript{1853}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{1854}http://www.openmicroscopy.org/site/support/legacy/
\textsuperscript{1855}http://www.openmicroscopy.org/site/support/ome-model/
18.2. Metadata fields

- Detector: Type
- DetectorSettings: Gain
- DetectorSettings: ID
- Dichroic: ID
- Dichroic: Model
- Experiment: ID
- Experiment: Type
- Experimenter: ID
- Experimenter: LastName
- Filter: ID
- Filter: Model
- FilterSet: DichroicRef
- FilterSet: EmissionFilterRef
- FilterSet: ExcitationFilterRef
- FilterSet: ID
- FilterSet: Model
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef
- Image: Name
- Instrument: ID
- Laser: ID
- Laser: LaserMedium
- Laser: Manufacturer
- Laser: Model
• Laser: Power
• Laser: RepetitionRate
• Laser: Type
• Laser: Wavelength
• Microscope: Manufacturer
• Microscope: Model
• Objective: CalibratedMagnification
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: LensNA
• Objective: Model
• Objective: WorkingDistance
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY

18.2. Metadata fields
Bio-Formats Documentation, Release 5.1.3

- Pixels: SizeZ
- Pixels: TimeIncrement
- Pixels: Type
- Plane: DeltaT
- Plane: ExposureTime
- Plane: PositionX
- Plane: PositionY
- Plane: PositionZ
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 72
Total unknown or missing: 403

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.45 ImaconReader

This page lists supported metadata fields for the Bio-Formats Imacon format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 23 of them (4%).
- Of those, Bio-Formats fully or partially converts 23 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Imacon format reader:
- Channel: ID
- Channel: SamplesPerPixel
- Experimenter: FirstName

12. http://www.openmicroscopy.org/site/support/bio-formats5.0/
• Experimenter : ID
• Experimenter : LastName
• Image : AcquisitionDate
• Image : ExperimenterRef
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 23
Total unknown or missing: 452

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.46 SEQReader

This page lists supported metadata fields for the Bio-Formats Image-Pro Sequence format reader.
These fields are from the OME data model\(^{1956}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Image-Pro Sequence format reader:

- Channel: ID\(^{1957}\)
- Channel: SamplesPerPixel\(^{1958}\)
- Image: AcquisitionDate\(^{1959}\)
- Image: ID\(^{1960}\)
- Image: Name\(^{1961}\)
- Pixels: BigEndian\(^{1962}\)
- Pixels: DimensionOrder\(^{1963}\)
- Pixels: ID\(^{1964}\)
- Pixels: Interleaved\(^{1965}\)
- Pixels: SignificantBits\(^{1966}\)
- Pixels: SizeC\(^{1967}\)
- Pixels: SizeT\(^{1968}\)
- Pixels: SizeX\(^{1969}\)
- Pixels: SizeY\(^{1970}\)
- Pixels: SizeZ\(^{1971}\)
- Pixels: Type\(^{1972}\)
- Plane: TheC\(^{1973}\)
- Plane: TheT\(^{1974}\)
- Plane: TheZ\(^{1975}\)

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\(^{1956}\)http://www.openmicroscopy.org/site/support/ome-model/
\(^{1958}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{1959}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{1965}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{1972}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.47 IPWReader

This page lists supported metadata fields for the Bio-Formats Image-Pro Workspace format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 20 of them (4%).
- Of those, Bio-Formats fully or partially converts 20 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Image-Pro Workspace format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX

1976 http://www.openmicroscopy.org/site/support/bio-formats5.0/
1977 http://www.openmicroscopy.org/site/support/legacy/
1978 http://www.openmicroscopy.org/site/support/ome-model/
1981 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
### 18.2.48 ImagicReader

This page lists supported metadata fields for the Bio-Formats IMAGIC format reader.

These fields are from the OME data model\(^1\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

#### Supported fields

These fields are fully supported by the Bio-Formats IMAGIC format reader:
- Channel : ID\(^2\)
- Channel : SamplesPerPixel\(^3\)
- Image : AcquisitionDate\(^4\)
- Image : ID\(^5\)
- Image : Name\(^6\)
- Pixels : BigEndian\(^7\)
- Pixels : DimensionOrder\(^8\)
- Pixels : ID\(^9\)

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\(^1\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY}  
\(^2\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID}  
\(^3\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel}  
\(^4\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate}  
\(^5\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID}  
\(^6\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name}  
\(^7\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian}  
\(^8\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder}  
\(^9\) \url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID}
18.2.49 IMODReader

This page lists supported metadata fields for the Bio-Formats IMOD format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 44 of them (9%).
- Of those, Bio-Formats fully or partially converts 44 (100%).

Supported fields

These fields are fully supported by the Bio-Formats IMOD format reader:

- Pixels : Interleaved
- Pixels : PhysicalSizeX
- Pixels : PhysicalSizeY
- Pixels : PhysicalSizeZ
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Pixels : Type
- Plane : TheC
- Plane : TheT
- Plane : TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Image: ROISetID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ
- Point: ID
- Point: StrokeColor
- Point: StrokeDashArray
- Plane: TheC
- Plane: TheT
- Plane: TheZ
- Point: StrokeColor
- Point: StrokeDashArray
• Point: StrokeWidth
• Point: TheZ
• Point: X
• Point: Y
• Polygon: ID
• Polygon: Points
• Polygon: StrokeColor
• Polygon: StrokeDashArray
• Polygon: StrokeWidth
• Polygon: TheZ
• Polyline: ID
• Polyline: Points
• Polyline: StrokeColor
• Polyline: StrokeDashArray
• Polyline: StrokeWidth
• Polyline: TheZ
• ROI: ID
• ROI: Name

Total supported: 44
Total unknown or missing: 431

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.50 OpenlabReader

This page lists supported metadata fields for the Bio-Formats Openlab LIFF format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- Point: StrokeWidth
- Point: TheZ
- Point: X
- Point: Y
- Polygon: ID
- Polygon: Points
- Polygon: StrokeColor
- Polygon: StrokeDashArray
- Polygon: StrokeWidth
- Polygon: TheZ
- Polyline: ID
- Polyline: Points
- Polyline: StrokeColor
- Polyline: StrokeDashArray
- Polyline: StrokeWidth
- Polyline: TheZ
- ROI: ID
- ROI: Name

18.2. Metadata fields
The file format itself supports 32 of them (6%).

Of those, Bio-Formats fully or partially converts 32 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Openlab LIFF format reader:

- Channel : ID
- Channel : Name
- Channel : SamplesPerPixel
- Detector : ID
- Detector : Type
- DetectorSettings : Gain
- DetectorSettings : ID
- DetectorSettings : Offset
- Image : AcquisitionDate
- Image : ID
- Image : InstrumentRef
- Image : Name
- Instrument : ID
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : PhysicalSizeX
- Pixels : PhysicalSizeY
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY

[http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate)
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : PositionX
• Plane : PositionY
• Plane : PositionZ
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 32
Total unknown or missing: 443

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.51 OpenlabRawReader

This page lists supported metadata fields for the Bio-Formats Openlab RAW format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Openlab RAW format reader:
• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : Name

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.52 ImprovisionTiffReader

This page lists supported metadata fields for the Bio-Formats Improvision TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 25 of them (5%).
• Of those, Bio-Formats fully or partially converts 25 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Improvision TIFF format reader:

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

18.2. Metadata fields 394
18.2.53 OBFReader

This page lists supported metadata fields for the Bio-Formats OBF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats OBF format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.54 InCellReader

This page lists supported metadata fields for the Bio-Formats InCell 1000/2000 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 67 of them (14%).
• Of those, Bio-Formats fully or partially converts 67 (100%).

Supported fields

These fields are fully supported by the Bio-Formats InCell 1000/2000 format reader:

• Channel: EmissionWavelength
• Channel: ExcitationWavelength
• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Model
• Detector: Type
• DetectorSettings: Binning

2174 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
2177 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
2178 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2179 http://www.openmicroscopy.org/site/support/legacy/
2180 http://www.openmicroscopy.org/site/support/ome-model/
2184 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
2185 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2188 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
• DetectorSettings : Gain
• DetectorSettings : ID
• Experiment : ID
• Experiment : Type
• Image : AcquisitionDate
• Image : Description
• Image : ExperimentRef
• Image : ID
• Image : InstrumentRef
• Image : Name
• ImagingEnvironment : Temperature
• Instrument : ID
• Objective : Correction
• Objective : ID
• Objective : Immersion
• Objective : LensNA
• Objective : Manufacturer
• Objective : NominalMagnification
• ObjectiveSettings : ID
• ObjectiveSettings : RefractiveIndex
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : PhysicalSizeX
• Pixels : PhysicalSizeY

**2191** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
**2192** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_ID
**2193** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_Type
**2194** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
**2195** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
**2196** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ExperimentRef_ID
**2199** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
**2202** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
**2203** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
**2204** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
**2205** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_LensNA
**2206** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
**2207** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
**2208** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_ID
**2209** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
**2210** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
**2211** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
**2212** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
**2213** http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : DeltaT
• Plane : ExposureTime
• Plane : PositionX
• Plane : PositionY
• Plane : PositionZ
• Plane : TheC
• Plane : TheT
• Plane : TheZ
• Plate : ColumnNamingConvention
• Plate : ID
• Plate : Name
• Plate : RowNamingConvention
• Plate : WellOriginX
• Plate : WellOriginY
• PlateAcquisition : ID
• PlateAcquisition : MaximumFieldCount
• PlateAcquisition : WellSampleRef
• Well : Column
• Well : ID
• Well : Row

• WellSample : ID

• WellSample : ImageRef

• WellSample : Index

• WellSample : PositionX

• WellSample : PositionY

Total supported: 67

Total unknown or missing: 408

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.55 InCell3000Reader

This page lists supported metadata fields for the Bio-Formats InCell 3000 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).

• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats InCell 3000 format reader:

• Channel : ID

• Channel : SamplesPerPixel

• Image : AcquisitionDate

• Image : ID

• Image : Name

• Pixels : BigEndian

• Pixels : DimensionOrder

• Pixels : ID

2242 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_Row

2243 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_ID


2245 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#WellSample_Index


2248 http://www.openmicroscopy.org/site/support/bio-formats5.0/

2249 http://www.openmicroscopy.org/site/support/legacy/

2250 http://www.openmicroscopy.org/site/support/ome-model/


2252 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel

2253 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate


2255 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

2256 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian


• Pixels: Interleaved\textsuperscript{2259}
• Pixels: SignificantBits\textsuperscript{2260}
• Pixels: SizeC\textsuperscript{2261}
• Pixels: SizeT\textsuperscript{2262}
• Pixels: SizeX\textsuperscript{2263}
• Pixels: SizeY\textsuperscript{2264}
• Pixels: SizeZ\textsuperscript{2265}
• Pixels: Type\textsuperscript{2266}
• Plane: TheC\textsuperscript{2267}
• Plane: TheT\textsuperscript{2268}
• Plane: TheZ\textsuperscript{2269}

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{2270} or the previous versions\textsuperscript{2271} page to find documentation for the version you are using.

18.2.56 INRReader

This page lists supported metadata fields for the Bio-Formats INR format reader.

These fields are from the OME data model\textsuperscript{2272}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats INR format reader:

• Channel: ID\textsuperscript{2273}
• Channel: SamplesPerPixel\textsuperscript{2274}
• Image: AcquisitionDate\textsuperscript{2275}

\textsuperscript{2259}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\textsuperscript{2260}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\textsuperscript{2261}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\textsuperscript{2262}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\textsuperscript{2263}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\textsuperscript{2264}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\textsuperscript{2265}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\textsuperscript{2266}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\textsuperscript{2267}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\textsuperscript{2268}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\textsuperscript{2269}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\textsuperscript{2270}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{2271}http://www.openmicroscopy.org/site/support/legacy/
\textsuperscript{2272}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{2273}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{2274}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.57 InveonReader

This page lists supported metadata fields for the Bio-Formats Inveon format reader.

18.2. Metadata fields
These fields are from the OME data model\textsuperscript{2297}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 30 of them (6%).
- Of those, Bio-Formats fully or partially converts 30 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Inveon format reader:

- Channel: ID\textsuperscript{2298}
- Channel: SamplesPerPixel\textsuperscript{2299}
- Experimenter: ID\textsuperscript{2300}
- Experimenter: Institution\textsuperscript{2301}
- Experimenter: UserName\textsuperscript{2302}
- Image: AcquisitionDate\textsuperscript{2303}
- Image: Description\textsuperscript{2304}
- Image: ExperimenterRef\textsuperscript{2305}
- Image: ID\textsuperscript{2306}
- Image: InstrumentRef\textsuperscript{2307}
- Image: Name\textsuperscript{2308}
- Instrument: ID\textsuperscript{2309}
- Microscope: Model\textsuperscript{2310}
- Pixels: BigEndian\textsuperscript{2311}
- Pixels: DimensionOrder\textsuperscript{2312}
- Pixels: ID\textsuperscript{2313}
- Pixels: Interleaved\textsuperscript{2314}
- Pixels: PhysicalSizeX\textsuperscript{2315}
- Pixels: PhysicalSizeY\textsuperscript{2316}
- Pixels: PhysicalSizeZ\textsuperscript{2317}

\textsuperscript{2297}http://www.openmicroscopy.org/site/support/ome-model/

\textsuperscript{2298}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID

\textsuperscript{2299}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel

\textsuperscript{2300}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_ID

\textsuperscript{2301}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_Institution

\textsuperscript{2302}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_UserName

\textsuperscript{2303}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate

\textsuperscript{2304}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description

\textsuperscript{2305}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ExperimenterRef_ID

\textsuperscript{2306}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID

\textsuperscript{2307}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#InstrumentRef_ID

\textsuperscript{2308}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

\textsuperscript{2309}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Instrument_ID

\textsuperscript{2310}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model

\textsuperscript{2311}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

\textsuperscript{2312}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder

\textsuperscript{2313}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID

\textsuperscript{2314}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved

\textsuperscript{2315}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeX

\textsuperscript{2316}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY

\textsuperscript{2317}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeZ
The file format itself supports 34 of them (7%).
Of those, Bio-Formats fully or partially converts 34 (100%).

Supported fields

These fields are fully supported by the Bio-Formats IVision format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Detector : ID
- Detector : Type

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
- DetectorSettings: Binning
- DetectorSettings: Gain
- DetectorSettings: ID
- Image: AcquisitionDate
- Image: ID
- Image: InstrumentRef
- Image: Name
- Instrument: ID
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: LensNA
- Objective: NominalMagnification
- ObjectiveSettings: ID
- ObjectiveSettings: RefractiveIndex
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: TimeIncrement
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 34
Total unknown or missing: 441

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.59 IPLabReader

This page lists supported metadata fields for the Bio-Formats IPLab format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 31 of them (6%).
• Of those, Bio-Formats fully or partially converts 31 (100%).

Supported fields

These fields are fully supported by the Bio-Formats IPLab format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Image: ROIRef
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID

Additional links:
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeX
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: DeltaT
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• ROI: ID
• Rectangle: Height
• Rectangle: ID
• Rectangle: Width
• Rectangle: X
• Rectangle: Y

Total supported: 31
Total unknown or missing: 444

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.60 JEOLReader

This page lists supported metadata fields for the Bio-Formats JEOL format reader.

These fields are from the OME data model[2401]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats JEOL format reader:

- Channel : ID[2402]
- Channel : SamplesPerPixel[2403]
- Image : AcquisitionDate[2404]
- Image : ID[2405]
- Image : Name[2406]
- Pixels : BigEndian[2407]
- Pixels : DimensionOrder[2408]
- Pixels : ID[2409]
- Pixels : Interleaved[2410]
- Pixels : SignificantBits[2411]
- Pixels : SizeC[2412]
- Pixels : SizeT[2413]
- Pixels : SizeX[2414]
- Pixels : SizeY[2415]
- Pixels : SizeZ[2416]
- Pixels : Type[2417]
- Plane : TheC[2418]
- Plane : TheT[2419]

• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.6 JPEG2000Reader

This page lists supported metadata fields for the Bio-Formats JPEG-2000 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats JPEG-2000 format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.62 JPEGReader

This page lists supported metadata fields for the Bio-Formats JPEG format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats JPEG format reader:

• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.63 JPKReader

This page lists supported metadata fields for the Bio-Formats JPK Instruments format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats JPK Instruments format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/oem-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.64 JPXReader

This page lists supported metadata fields for the Bio-Formats JPX format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
Supported fields

These fields are fully supported by the Bio-Formats JPX format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : Name
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Pixels : Type
- Plane : TheC
- Plane : TheT
- Plane : TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

2491 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2492 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
2495 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
2500 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
2501 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
2505 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
2509 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2510 http://www.openmicroscopy.org/site/support/legacy/
18.2.65 KhorosReader

This page lists supported metadata fields for the Bio-Formats Khoros XV format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Khoros XV format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : Name
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Pixels : Type
- Plane : TheC
- Plane : TheT

http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.66 KodakReader

This page lists supported metadata fields for the Bio-Formats Kodak Molecular Imaging format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 26 of them (5%).
• Of those, Bio-Formats fully or partially converts 26 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Kodak Molecular Imaging format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• ImagingEnvironment: Temperature
• Instrument: ID
• Microscope: Model
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved

2530 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
2531 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2532 http://www.openmicroscopy.org/site/support/legacy/
2534 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2535 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
2538 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
2542 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
2545 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: ExposureTime
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 26
Total unknown or missing: 449

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.67 LiFlimReader

This page lists supported metadata fields for the Bio-Formats LI-FLIM format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 25 of them (5%).
• Of those, Bio-Formats fully or partially converts 25 (100%).

Supported fields

These fields are fully supported by the Bio-Formats LI-FLIM format reader:

• Channel: ID

2550 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
2551 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
2555 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
2560 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2561 http://www.openmicroscopy.org/site/support/legacy/
2562 http://www.openmicroscopy.org/site/support/ome-model/
• Channel: `SamplesPerPixel`\textsuperscript{2564}
• Image: `AcquisitionDate`\textsuperscript{2565}
• Image: `ID`\textsuperscript{2566}
• Image: `Name`\textsuperscript{2567}
• Image: `ROIRef`\textsuperscript{2568}
• Pixels: `BigEndian`\textsuperscript{2569}
• Pixels: `DimensionOrder`\textsuperscript{2570}
• Pixels: `ID`\textsuperscript{2571}
• Pixels: `Interleaved`\textsuperscript{2572}
• Pixels: `SignificantBits`\textsuperscript{2573}
• Pixels: `SizeC`\textsuperscript{2574}
• Pixels: `SizeT`\textsuperscript{2575}
• Pixels: `SizeX`\textsuperscript{2576}
• Pixels: `SizeY`\textsuperscript{2577}
• Pixels: `SizeZ`\textsuperscript{2578}
• Pixels: `Type`\textsuperscript{2579}
• Plane: `DeltaT`\textsuperscript{2580}
• Plane: `ExposureTime`\textsuperscript{2581}
• Plane: `TheC`\textsuperscript{2582}
• Plane: `TheT`\textsuperscript{2583}
• Plane: `TheZ`\textsuperscript{2584}
• Polygon: `ID`\textsuperscript{2585}
• Polygon: `Points`\textsuperscript{2586}
• ROI: `ID`\textsuperscript{2587}

Total supported: 25

Total unknown or missing: 450

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version\textsuperscript{2588} or the previous

\begin{verbatim}
\textsuperscript{2564}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{2565}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{2566}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{2567}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\textsuperscript{2568}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID
\textsuperscript{2569}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\textsuperscript{2570}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\textsuperscript{2571}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\textsuperscript{2572}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\textsuperscript{2573}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\textsuperscript{2574}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\textsuperscript{2575}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\textsuperscript{2576}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\textsuperscript{2577}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\textsuperscript{2578}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\textsuperscript{2579}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\textsuperscript{2580}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_DeltaT
\textsuperscript{2581}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_ExposureTime
\textsuperscript{2582}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\textsuperscript{2583}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\textsuperscript{2584}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\textsuperscript{2585}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\textsuperscript{2586}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Polygon_Points
\textsuperscript{2587}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROI_ID

\end{verbatim}
18.2.68 ImspectorReader

This page lists supported metadata fields for the Bio-Formats Lavision Imspector format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Lavision Imspector format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.69 LeicaReader

This page lists supported metadata fields for the Bio-Formats Leica format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 56 of them (11%).
• Of those, Bio-Formats fully or partially converts 56 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Leica format reader:

• Channel: Color
• Channel: EmissionWavelength
• Channel: ExcitationWavelength
• Channel: ID
• Channel: Name
• Channel: PinholeSize
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Offset
• Detector: Type
• Detector: Voltage

References:

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
• DetectorSettings: ID
• Filter: ID
• Filter: Model
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• LightPath: EmissionFilterRef
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: LensNA
• Objective: Model
• Objective: NominalMagnification
• Objective: SerialNumber
• ObjectiveSettings: ID
• ObjectiveSettings: RefractiveIndex
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

18.2. Metadata fields
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: TimeIncrement
- Pixels: Type
- Plane: DeltaT
- Plane: ExposureTime
- Plane: PositionX
- Plane: PositionY
- Plane: TheC
- Plane: TheT
- Plane: TheZ
- StageLabel: Name
- StageLabel: Z
- TransmittanceRange: CutIn
- TransmittanceRange: CutOut

Total supported: 56
Total unknown or missing: 419

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.70 LIFReader

This page lists supported metadata fields for the Bio-Formats Leica Image File Format format reader.
These fields are from the OME data model[2671]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 85 of them (17%).
- Of those, Bio-Formats fully or partially converts 85 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Leica Image File Format format reader:

- Channel: Color[2672]
- Channel: ExcitationWavelength[2673]
- Channel: ID[2674]
- Channel: LightSourceSettingsAttenuation[2675]
- Channel: LightSourceSettingsID[2676]
- Channel: Name[2677]
- Channel: PinholeSize[2678]
- Channel: SamplesPerPixel[2679]
- Detector: ID[2680]
- Detector: Model[2681]
- Detector: Offset[2682]
- Detector: Type[2683]
- Detector: Zoom[2684]
- DetectorSettings : Gain[2685]
- DetectorSettings : ID[2686]
- DetectorSettings : Offset[2687]
- Filter : ID[2688]
- Filter : Model[2689]
- Image : AcquisitionDate[2690]
- Image : Description[2691]

2671 http://www.openmicroscopy.org/site/support/ome-model/
2675 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#LightSourceSettings_Attenuation
2677 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
2679 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2683 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
2684 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Zoom
2690 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
18.2. Metadata fields

- Image: ID
- Image: InstrumentRef
- Image: Name
- Image: ROIFRef
- Instrument: ID
- Label: FontSize
- Label: ID
- Label: StrokeWidth
- Label: Text
- Label: X
- Label: Y
- Laser: ID
- Laser: LaserMedium
- Laser: Type
- Laser: Wavelength
- LightPath: EmissionFilterRef
- Line: ID
- Line: X1
- Line: X2
- Line: Y1
- Line: Y2
- Microscope: Model
- Microscope: Type
- Objective: Correction
- Objective: ID
- Objective: Immersion
• Objective: LensNA
• Objective: Model
• Objective: NominalMagnification
• Objective: SerialNumber
• ObjectiveSettings: ID
• ObjectiveSettings: RefractiveIndex
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Polygon: ID
• Polygon: Points
• ROI: ID
• Rectangle: Height
• Rectangle: ID
• Rectangle: Width
• Rectangle: X
• Rectangle: Y
• TransmittanceRange: CutIn
• TransmittanceRange: CutOut

Total supported: 85
Total unknown or missing: 390

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.71 LeicaSCNReader

This page lists supported metadata fields for the Bio-Formats Leica SCN format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 33 of them (6%).
• Of those, Bio-Formats fully or partially converts 33 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Leica SCN format reader:

• Channel: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Polygon_Points
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Rectangle_Height
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TransmittanceRange_CutIn
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• Channel: IlluminationType
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Objective: CalibratedMagnification
• Objective: ID
• Objective: LensNA
• Objective: NominalMagnification
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_IlluminationType
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels: Type
• Plane: PositionX
• Plane: PositionY
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 33
Total unknown or missing: 442

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.72 LEOReader

This page lists supported metadata fields for the Bio-Formats LEO format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 27 of them (5%).
• Of those, Bio-Formats fully or partially converts 27 (100%).

Supported fields

These fields are fully supported by the Bio-Formats LEO format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Objective: Correction

2787 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
2793 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2794 http://www.openmicroscopy.org/site/support/legacy/
2795 http://www.openmicroscopy.org/site/support/ome-model/
2797 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2798 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
2803 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
- Objective: ID
- Objective: Immersion
- Objective: Working Distance
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 27
Total unknown or missing: 448

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.73 L2DReader

This page lists supported metadata fields for the Bio-Formats Li-Cor L2D format reader.
These fields are from the OME data model[^2825]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the [metadata summary table](http://www.openmicroscopy.org/site/support/ome-model/):

- The file format itself supports 29 of them (6%).
- Of those, Bio-Formats fully or partially converts 29 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Li-Cor L2D format reader:

- Channel: ID[^2826]
- Channel: LightSourceSettingsID[^2827]
- Channel: SamplesPerPixel[^2828]
- Image: AcquisitionDate[^2829]
- Image: Description[^2830]
- Image: ID[^2831]
- Image: InstrumentRef[^2832]
- Image: Name[^2833]
- Instrument: ID[^2834]
- Laser: ID[^2835]
- Laser: LaserMedium[^2836]
- Laser: Type[^2837]
- Laser: Wavelength[^2838]
- Microscope: Model[^2839]
- Microscope: Type[^2840]
- Pixels: BigEndian[^2841]
- Pixels: DimensionOrder[^2842]
- Pixels: ID[^2843]
- Pixels: Interleaved[^2844]
- Pixels: SignificantBits[^2845]

[^2825]: http://www.openmicroscopy.org/site/support/ome-model/
[^2828]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
[^2829]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
[^2840]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Microscope_Type

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[^2825]: http://www.openmicroscopy.org/site/support/ome-model/
[^2828]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
[^2829]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
[^2840]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Microscope_Type
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 29
Total unknown or missing: 446

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.74 LIMReader

This page lists supported metadata fields for the Bio-Formats Laboratory Imaging format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Laboratory Imaging format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name

2846 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
2847 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
2851 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
2855 http://www.openmicroscopy.org/site/support/bio-formats5.0/
2856 http://www.openmicroscopy.org/site/support/legacy/
2858 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
2859 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
2861 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.75 MetamorphTiffReader

This page lists supported metadata fields for the Bio-Formats Metamorph TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 38 of them (8%).
• Of those, Bio-Formats fully or partially converts 38 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Metamorph TIFF format reader:

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• ImagingEnvironment: Temperature
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Plate: ColumnNamingConvention
• Plate: ID
• Plate: RowNamingConvention
• Well: Column
• Well: ID
• Well: Row
• WellSample: ID
• WellSample: ImageRef
• WellSample: Index

Total supported: 38

Total unknown or missing: 437

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.76 MetamorphReader

This page lists supported metadata fields for the Bio-Formats Metamorph STK format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 46 of them (9%).
• Of those, Bio-Formats fully or partially converts 46 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Metamorph STK format reader:

• Channel: ID
• Channel: LightSourceSettingsID
Bio-Formats Documentation, Release 5.1.3

- Channel: LightSourceSettingsWavelength
- Channel: Name
- Channel: SamplesPerPixel
- Detector: ID
- Detector: Type
- DetectorSettings: Binning
- DetectorSettings: Gain
- DetectorSettings: ID
- DetectorSettings: ReadOutRate
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef
- Image: Name
- ImagingEnvironment: Temperature
- Instrument: ID
- Laser: ID
- Laser: LaserMedium
- Laser: Type
- Objective: ID
- Objective: LensNA
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved

18.2. Metadata fields
Total supported: 46
Total unknown or missing: 429

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.77 MIASReader

This page lists supported metadata fields for the Bio-Formats MIAS format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: Size
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: DeltaT
- Plane: ExposureTime
- Plane: PositionX
- Plane: PositionY
- Plane: PositionZ
- Plane: TheC
- Plane: TheT
- Plane: TheZ
• The file format itself supports 64 of them (13%).
• Of those, Bio-Formats fully or partially converts 64 (100%).

Supported fields

These fields are fully supported by the Bio-Formats MIAS format reader:

- Channel: Color
- Channel: ID
- Channel: Name
- Channel: SamplesPerPixel
- Ellipse: ID
- Ellipse: RadiusX
- Ellipse: RadiusY
- Ellipse: Text
- Ellipse: TheT
- Ellipse: TheZ
- Ellipse: X
- Ellipse: Y
- Experiment: Description
- Experiment: ID
- Experiment: Type
- Image: AcquisitionDate
- Image: ExperimentRef
- Image: ID
- Image: InstrumentRef
- Image: Name
- Image: ROIRef
- Instrument: ID
- Mask: FillColor

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Text
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_Description
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ExperimentRef_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/rome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/rome_xsd.html#ROIRef_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/rome_xsd.html#Shape_FillColor
• Mask: Height
• Mask: ID
• Mask: StrokeColor
• Mask: Width
• Mask: X
• Mask: Y
• Objective: ID
• Objective: Model
• Objective: NominalMagnification
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: ExposureTime
• Plane: TheC
• Plane: TheT
• Plane: TheZ

2993 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_Height
2994 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
2995 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeColor
3001 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
3004 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
3006 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
3009 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
3010 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

18.2. Metadata fields
• Plate: ColumnNamingConvention
• Plate: ExternalIdentifier
• Plate: ID
• Plate: Name
• Plate: RowNamingConvention
• PlateAcquisition: ID
• PlateAcquisition: MaximumFieldCount
• PlateAcquisition: WellSampleRef
• ROI: ID
• Well: Column
• Well: ID
• Well: Row
• WellSample: ID
• WellSample: ImageRef
• WellSample: Index

Total supported: 64
Total unknown or missing: 411

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.78 MicromanagerReader

This page lists supported metadata fields for the Bio-Formats Micro-Manager format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 38 of them (8%).
• Of those, Bio-Formats fully or partially converts 38 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ColumnNamingConvention
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ExternalIdentifier
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_RowNamingConvention
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_MaximumFieldCount
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSampleRef_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROI_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROI_ZOrder
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_Index
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_Contents
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats Micro-Manager format reader:

- Channel: ID
- Channel: Name
- Channel: SamplesPerPixel
- Detector: ID
- Detector: Manufacturer
- Detector: Model
- Detector: SerialNumber
- Detector: Type
- DetectorSettings: Binning
- DetectorSettings: Gain
- DetectorSettings: ID
- DetectorSettings: Voltage
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef
- Image: Name
- ImagingEnvironment: Temperature
- Instrument: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX

3038 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
3039 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
3041 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
3047 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
3052 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 38

Total unknown or missing: 437

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.79 MINCReader

This page lists supported metadata fields for the Bio-Formats MINC MRI format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 23 of them (4%).
• Of those, Bio-Formats fully or partially converts 23 (100%).

Supported fields

These fields are fully supported by the Bio-Formats MINC MRI format reader:

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 23
Total unknown or missing: 452

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.80 MRWReader

This page lists supported metadata fields for the Bio-Formats Minolta MRW format reader.

These fields are from the OME data model[103]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Minolta MRW format reader:

- Channel : ID[104]
- Channel : SamplesPerPixel[105]
- Image : AcquisitionDate[106]
- Image : ID[107]
- Image : Name[108]
- Pixels : BigEndian[109]
- Pixels : DimensionOrder[110]
- Pixels : ID[111]
- Pixels : Interleaved[112]
- Pixels : SignificantBits[113]
- Pixels : SizeC[114]
- Pixels : SizeT[115]
- Pixels : SizeX[116]
- Pixels : SizeY[117]
- Pixels : SizeZ[118]
- Pixels : Type[119]
- Plane : TheC[120]


18.2. Metadata fields
• Plane: TheT
• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.81 MNGReader

This page lists supported metadata fields for the Bio-Formats Multiple Network Graphics format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Multiple Network Graphics format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.82 MolecularImagingReader

This page lists supported metadata fields for the Bio-Formats Molecular Imaging format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 21 of them (4%).
• Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Molecular Imaging format reader:

• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.83 MRCReader

This page lists supported metadata fields for the Bio-Formats Medical Research Council format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Medical Research Council format reader:

18.2. Metadata fields
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.84 NikonReader

This page lists supported metadata fields for the Bio-Formats Nikon NEF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Nikon NEF format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
• Plane : TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.85 NiftiReader

This page lists supported metadata fields for the Bio-Formats NIfTI format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 24 of them (5%).
• Of those, Bio-Formats fully or partially converts 24 (100%).

Supported fields

These fields are fully supported by the Bio-Formats NIfTI format reader:

• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : Description
• Image : ID
• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : PhysicalSizeX
• Pixels : PhysicalSizeY
• Pixels : PhysicalSizeZ

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 24
Total unknown or missing: 451

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.86 NikonElementsTiffReader

This page lists supported metadata fields for the Bio-Formats Nikon Elements TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 50 of them (10%).
• Of those, Bio-Formats fully or partially converts 50 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Nikon Elements TIFF format reader:
• Channel: AcquisitionMode
• Channel: EmissionWavelength
• Channel: ExcitationWavelength

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_AcquisitionMode
• Channel : ID\textsuperscript{3249}
• Channel : Name\textsuperscript{3250}
• Channel : PinholeSize\textsuperscript{3251}
• Channel : SamplesPerPixel\textsuperscript{3252}
• Detector : ID\textsuperscript{3253}
• Detector : Model\textsuperscript{3254}
• Detector : Type\textsuperscript{3255}
• DetectorSettings : Binning\textsuperscript{3256}
• DetectorSettings : Gain\textsuperscript{3257}
• DetectorSettings : ID\textsuperscript{3258}
• DetectorSettings : ReadOutRate\textsuperscript{3259}
• DetectorSettings : Voltage\textsuperscript{3260}
• Image : AcquisitionDate\textsuperscript{3261}
• Image : ID\textsuperscript{3262}
• Image : InstrumentRef\textsuperscript{3263}
• Image : Name\textsuperscript{3264}
• ImagingEnvironment : Temperature\textsuperscript{3265}
• Instrument : ID\textsuperscript{3266}
• Objective : CalibratedMagnification\textsuperscript{3267}
• Objective : Correction\textsuperscript{3268}
• Objective : ID\textsuperscript{3269}
• Objective : Immersion\textsuperscript{3270}
• Objective : LensNA\textsuperscript{3271}
• Objective : Model\textsuperscript{3272}
• ObjectiveSettings : ID\textsuperscript{3273}
• ObjectiveSettings : RefractiveIndex\textsuperscript{3274}

\textsuperscript{3249} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{3250} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
\textsuperscript{3251} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_PinholeSize
\textsuperscript{3252} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{3253} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\textsuperscript{3254} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\textsuperscript{3255} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\textsuperscript{3256} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\textsuperscript{3257} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Gain
\textsuperscript{3258} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
\textsuperscript{3259} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ReadOutRate
\textsuperscript{3260} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Voltage
\textsuperscript{3261} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{3262} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{3263} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#InstrumentRef_ID
\textsuperscript{3264} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\textsuperscript{3265} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ImagingEnvironment_Temperature
\textsuperscript{3266} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Instrument_ID
\textsuperscript{3267} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_CalibratedMagnification
\textsuperscript{3268} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
\textsuperscript{3269} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_ID
\textsuperscript{3270} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
\textsuperscript{3271} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_LensNA
\textsuperscript{3272} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\textsuperscript{3273} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_ID
\textsuperscript{3274} http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 50
Total unknown or missing: 425

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.87 NikonTIFFReader

This page lists supported metadata fields for the Bio-Formats Nikon TIFF format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 47 of them (9%).
- Of those, Bio-Formats fully or partially converts 47 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Nikon TIFF format reader:

- Channel: EmissionWavelength
- Channel: ExcitationWavelength
- Channel: ID
- Channel: PinholeSize
- Channel: SamplesPerPixel
- Detector: Gain
- Detector: ID
- Detector: Type
- Dichroic: ID
- Dichroic: Model
- Filter: ID
- Filter: Model
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: InstrumentRef
- Image: Name
- Instrument: ID

http://www.openmicroscopy.org/site/support/ome-model/

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
• Laser: ID
• Laser: LaserMedium
• Laser: Model
• Laser: Type
• Laser: Wavelength
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: LensNA
• Objective: NominalMagnification
• Objective: WorkingDistance
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
18.2.88 NativeND2Reader

This page lists supported metadata fields for the Bio-Formats Nikon ND2 format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 52 of them (10%).
- Of those, Bio-Formats fully or partially converts 52 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Nikon ND2 format reader:

- Channel : AcquisitionMode
- Channel : Color
- Channel : EmissionWavelength
- Channel : ExcitationWavelength
- Channel : ID
- Channel : Name
- Channel : PinholeSize
- Channel : SamplesPerPixel
- Detector : ID
- Detector : Model
- Detector : Type

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.
• DetectorSettings : Binning
• DetectorSettings : Gain
• DetectorSettings : ID
• DetectorSettings : ReadOutRate
• DetectorSettings : Voltage
• Image : AcquisitionDate
• Image : ID
• Image : InstrumentRef
• Image : Name
• ImagingEnvironment : Temperature
• Instrument : ID
• Objective : CalibratedMagnification
• Objective : Correction
• Objective : ID
• Objective : Immersion
• Objective : LensNA
• Objective : Model
• ObjectiveSettings : ID
• ObjectiveSettings : RefractiveIndex
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : PhysicalSizeX
• Pixels : PhysicalSizeY
• Pixels : PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 52
Total unknown or missing: 423

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.89 NRRDReader

This page lists supported metadata fields for the Bio-Formats NRRD format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats NRRD format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous.
18.2.90 APLReader

This page lists supported metadata fields for the Bio-Formats Olympus APL format reader.

These fields are from the OME data model\(^3\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Olympus APL format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY

\(^1\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^2\)http://www.openmicroscopy.org/site/support/legacy/
\(^3\)http://www.openmicroscopy.org/site/support/ome-model/
\(^4\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^5\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^6\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^7\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\(^8\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^9\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^10\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^12\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^14\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY
\(^15\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^16\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^17\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\(^18\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\(^19\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.91 FV1000Reader

This page lists supported metadata fields for the Bio-Formats Olympus FV1000 format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 113 of them (23%).
• Of those, Bio-Formats fully or partially converts 113 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Olympus FV1000 format reader:

• Channel : EmissionWavelength
• Channel : ExcitationWavelength
• Channel : ID
• Channel : IlluminationType
• Channel : LightSourceSettingsID
• Channel : LightSourceSettingsWavelength
• Channel : Name
• Channel : SamplesPerPixel
• Detector : Gain
• Detector: ID
• Detector: Type
• Detector: Voltage
• DetectorSettings: ID
• Dichroic: ID
• Dichroic: Model
• Ellipse: FontSize
• Ellipse: ID
• Ellipse: RadiusX
• Ellipse: RadiusY
• Ellipse: StrokeWidth
• Ellipse: TheT
• Ellipse: TheZ
• Ellipse: Transform
• Ellipse: X
• Ellipse: Y
• Filter: ID
• Filter: Model
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• Image: ROIRef
• Instrument: ID
• Laser: ID
• Laser: LaserMedium

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_FontSize
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_RadiusY
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
18.2. Metadata fields

- Laser: Type
- Laser: Wavelength
- LightPath: DichroicRef
- LightPath: EmissionFilterRef
- Line: FontSize
- Line: ID
- Line: StrokeWidth
- Line: TheT
- Line: TheZ
- Line: Transform
- Line: X1
- Line: X2
- Line: Y1
- Line: Y2
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: LensNA
- Objective: Model
- Objective: NominalMagnification
- Objective: WorkingDistance
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved

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448 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Laser_Type
454 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
455 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
456 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
460 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Line_Y1
466 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
467 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_WorkingDistance
469 L http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: DeltaT
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Point: FontSize
• Point: ID
• Point: StrokeWidth
• Point: TheT
• Point: TheZ
• Point: X
• Point: Y
• Polygon: FontSize
• Polygon: ID
• Polygon: Points
• Polygon: StrokeWidth
• Polygon: TheT
• Polygon: TheZ
• Polygon: Transform
• Polyline: FontSize
• Polyline: ID
• Polyline: Points
• Polyline: StrokeWidth
• Polyline: TheT
• Polyline: TheZ
• Polyline: Transform
• ROI: ID
• Rectangle: FontSize
• Rectangle: Height
• Rectangle: ID
• Rectangle: StrokeWidth
• Rectangle: TheT
• Rectangle: TheZ
• Rectangle: Transform
• Rectangle: Width
• Rectangle: X
• Rectangle: Y
• TransmittanceRange: CutIn
• TransmittanceRange: CutOut

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Polygon_Points
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Polyline_Points
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Rectangle_Height
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_TheZ
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Transform
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TransmittanceRange_CutIn
18.2.92 FluoviewReader

This page lists supported metadata fields for the Bio-Formats Olympus Fluoview/ABD TIFF format reader. These fields are from the OME data model\textsuperscript{3568}. Bio-Formats standardizes each format's original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 49 of them (10%).
- Of those, Bio-Formats fully or partially converts 49 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Olympus Fluoview/ABD TIFF format reader:

- Channel : ID\textsuperscript{3569}
- Channel : Name\textsuperscript{3570}
- Channel : SamplesPerPixel\textsuperscript{3571}
- Detector : ID\textsuperscript{3572}
- Detector : Manufacturer\textsuperscript{3573}
- Detector : Model\textsuperscript{3574}
- Detector : Type\textsuperscript{3575}
- DetectorSettings : Gain\textsuperscript{3576}
- DetectorSettings : ID\textsuperscript{3577}
- DetectorSettings : Offset\textsuperscript{3578}
- DetectorSettings : ReadOutRate\textsuperscript{3579}
- DetectorSettings : Voltage\textsuperscript{3580}
- Image : AcquisitionDate\textsuperscript{3581}
- Image : Description\textsuperscript{3582}

\textsuperscript{3566}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{3567}http://www.openmicroscopy.org/site/support/legacy/
\textsuperscript{3568}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{3569}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
\textsuperscript{3570}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{3571}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\textsuperscript{3572}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
\textsuperscript{3573}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Model
\textsuperscript{3574}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\textsuperscript{3575}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Gain
\textsuperscript{3576}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
\textsuperscript{3577}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Offset
\textsuperscript{3578}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ReadOutRate
\textsuperscript{3581}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{3582}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
• Image: ID
• Image: InstrumentRef
• Image: Name
• ImagingEnvironment: Temperature
• Instrument: ID
• Objective: CalibratedMagnification
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: LensNA
• Objective: Model
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement

3585 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
3589 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
3591 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
3594 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
3602 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
3603 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 49
Total unknown or missing: 426

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.93 ScanRReader

This page lists supported metadata fields for the Bio-Formats Olympus ScanR format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 43 of them (9%).
• Of those, Bio-Formats fully or partially converts 43 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Olympus ScanR format reader:

• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Plate: ColumnNamingConvention
• Plate: Columns
• Plate: ID
• Plate: Name
• Plate: RowNamingConvention

18.2. Metadata fields
18.2.94 SISReader

This page lists supported metadata fields for the Bio-Formats Olympus SIS TIFF format reader.

These fields are from the OME data model\(^\text{3666}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 33 of them (6%).
- Of those, Bio-Formats fully or partially converts 33 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Olympus SIS TIFF format reader:

- **Channel**: ID\(^{3667}\)
- **Channel**: Name\(^{3668}\)

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3652\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Plate_Rows}
3653\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_ID}
3654\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#PlateAcquisition_MaximumFieldCount}
3655\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSampleRef_ID}
3656\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_Column}
3657\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_ID}
3658\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#Well_Row}
3659\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_ID}
3660\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ImageRef_ID}
3661\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#WellSample_Index}
3662\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_PositionX}
3663\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/SPW_xsd.html#WellSample_PositionY}
3664\url{http://www.openmicroscopy.org/site/support/bio-formats5.0/}
3665\url{http://www.openmicroscopy.org/site/support/legacy/}
3666\url{http://www.openmicroscopy.org/site/support/ome-model/}
3667\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID}
3668\url{http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name}
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Model
• Detector: Type
• DetectorSettings: ID
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: NominalMagnification
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY

18.2. Metadata fields
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 33
Total unknown or missing: 442

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.95 OMETiffReader

This page lists supported metadata fields for the Bio-Formats OME-TIFF format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats OME-TIFF format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved

3696 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
3700 http://www.openmicroscopy.org/site/support/bio-formats5.0/
3701 http://www.openmicroscopy.org/site/support/legacy/
3702 http://www.openmicroscopy.org/site/support/ome-model/
3704 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
3705 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
3708 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

18.2. Metadata fields
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

### 18.2.96 OMEXMLReader

This page lists supported metadata fields for the Bio-Formats OME-XML format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats OME-XML format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID

More details on the metadata fields can be found at the following links:

• Image : Name
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.97 OxfordInstrumentsReader

This page lists supported metadata fields for the Bio-Formats Oxford Instruments format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).
Supported fields

These fields are fully supported by the Bio-Formats Oxford Instruments format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version.
18.2.98 PCORAWReader

This page lists supported metadata fields for the Bio-Formats PCO-RAW format reader.

These fields are from the OME data model\(^\text{3771}\). Bio- Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 26 of them (5%).
- Of those, Bio-Formats fully or partially converts 26 (100%).

Supported fields

These fields are fully supported by the Bio-Formats PCO-RAW format reader:

- Channel : ID\(^{3772}\)
- Channel : SamplesPerPixel\(^{3773}\)
- Detector : ID\(^{3774}\)
- Detector : SerialNumber\(^{3775}\)
- DetectorSettings : Binning\(^{3776}\)
- DetectorSettings : ID\(^{3777}\)
- Image : AcquisitionDate\(^{3778}\)
- Image : Description\(^{3779}\)
- Image : ID\(^{3780}\)
- Image : Name\(^{3781}\)
- Instrument : ID\(^{3782}\)
- Pixels : BigEndian\(^{3783}\)
- Pixels : DimensionOrder\(^{3784}\)
- Pixels : ID\(^{3785}\)
- Pixels : Interleaved\(^{3786}\)
- Pixels : SignificantBits\(^{3787}\)

\(^{3769}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{3770}\)http://www.openmicroscopy.org/site/support/legacy/
\(^{3771}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{3772}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{3773}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\(^{3774}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
\(^{3775}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\(^{3776}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{3777}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Description
\(^{3779}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{3781}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{3782}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^{3783}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^{3784}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^{3785}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
This page lists supported metadata fields for the Bio-Formats PCX format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats PCX format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
Bio-Formats Documentation, Release 5.1.3

- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.100 PDSReader

This page lists supported metadata fields for the Bio-Formats Perkin Elmer Densitometer format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 23 of them (4%).
- Of those, Bio-Formats fully or partially converts 23 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats Perkin Elmer Densitometer format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: PositionX
- Plane: PositionY
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 23
Total unknown or missing: 452
Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.101 IM3Reader

This page lists supported metadata fields for the Bio-Formats Perkin-Elmer Nuance IM3 format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Perkin-Elmer Nuance IM3 format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

18.2.102 OperettaReader

This page lists supported metadata fields for the Bio-Formats PerkinElmer Operetta format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 43 of them (9%).
• Of those, Bio-Formats fully or partially converts 43 (100%).

Supported fields

These fields are fully supported by the Bio-Formats PerkinElmer Operetta format reader:

• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Experimenter: ID
• Experimenter: LastName
• Image: AcquisitionDate
• Image: ExperimenterRef
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_LastName
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Plate: Columns
• Plate: Description
• Plate: ExternalIdentifier
• Plate: ID
• Plate: Name
• Plate: Rows
• PlateAcquisition: ID
• PlateAcquisition: MaximumFieldCount
• PlateAcquisition: WellSampleRef

18.2. Metadata fields
• Well: Column
• Well: ID
• Well: Row
• WellSample: ID
• WellSample: ImageRef
• WellSample: Index

Total supported: 43
Total unknown or missing: 432

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.103 PerkinElmerReader

This page lists supported metadata fields for the Bio-Formats PerkinElmer format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 30 of them (6%).
• Of those, Bio-Formats fully or partially converts 30 (100%).

Supported fields

These fields are fully supported by the Bio-Formats PerkinElmer format reader:
• Channel: EmissionWavelength
• Channel: ExcitationWavelength
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef
• Image: Name
- Instrument: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: DeltaT
- Plane: ExposureTime
- Plane: PositionX
- Plane: PositionY
- Plane: PositionZ
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 30
Total unknown or missing: 445

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.104 PGMReader

This page lists supported metadata fields for the Bio-Formats Portable Any Map format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Portable Any Map format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : Name
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Pixels : Type
- Plane : TheC
- Plane : TheT

http://www.openmicroscopy.org/site/support/ome-model/

18.2. Metadata fields
18.2.105 PSDReader

This page lists supported metadata fields for the Bio-Formats Adobe Photoshop format reader. These fields are from the [OME data model](http://www.openmicroscopy.org/site/support/ome-model/). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the [metadata summary table](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ):

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Adobe Photoshop format reader:

- Channel : ID
- Channel : SamplesPerPixel
- Image : AcquisitionDate
- Image : ID
- Image : Name
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX

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3969 [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
3970 [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
3973 [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate)
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.106 PhotoshopTiffReader

This page lists supported metadata fields for the Bio-Formats Adobe Photoshop TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Adobe Photoshop TIFF format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
18.2.107 PQBinReader

This page lists supported metadata fields for the Bio-Formats PicoQuant Bin format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats PicoQuant Bin format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
This page lists supported metadata fields for the Bio-Formats PICT format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 21

Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.108 PictReader

This page lists supported metadata fields for the Bio-Formats PICT format reader.
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats PICT format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

**Total supported:** 19

**Total unknown or missing:** 456

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**Note:** This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
18.2.109 APNGReader

This page lists supported metadata fields for the Bio-Formats Animated PNG format reader.

These fields are from the OME data model\(^{4061}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Animated PNG format reader:

- Channel: ID\(^{4062}\)
- Channel: SamplesPerPixel\(^{4063}\)
- Image: AcquisitionDate\(^{4064}\)
- Image: ID\(^{4065}\)
- Image: Name\(^{4066}\)
- Pixels: BigEndian\(^{4067}\)
- Pixels: DimensionOrder\(^{4068}\)
- Pixels: ID\(^{4069}\)
- Pixels: Interleaved\(^{4070}\)
- Pixels: SignificantBits\(^{4071}\)
- Pixels: SizeC\(^{4072}\)
- Pixels: SizeT\(^{4073}\)
- Pixels: SizeX\(^{4074}\)
- Pixels: SizeY\(^{4075}\)
- Pixels: SizeZ\(^{4076}\)
- Pixels: Type\(^{4077}\)
- Plane: TheC\(^{4078}\)
- Plane: TheT\(^{4079}\)

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\(^{4061}\) [http://www.openmicroscopy.org/site/support/ome-model/](http://www.openmicroscopy.org/site/support/ome-model/)


\(^{4063}\) [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel)

\(^{4064}\) [http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate](http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate)


• Plane: TheZ

Total supported: 19

Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.110 PrairieReader

This page lists supported metadata fields for the Bio-Formats Prairie TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 46 of them (9%).
• Of those, Bio-Formats fully or partially converts 46 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Prairie TIFF format reader:

• Channel: EmissionWavelength
• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Type
• Detector: Zoom
• DetectorSettings: Gain
• DetectorSettings: ID
• DetectorSettings: Offset
• Image: AcquisitionDate
• Image: ID
• Image: InstrumentRef

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Zoom
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
18.2. Metadata fields

- Image: Name
- Instrument: ID
- Laser: ID
- Laser: Power
- Microscope: Model
- Objective: Correction
- Objective: ID
- Objective: Immersion
- Objective: LensNA
- Objective: Manufacturer
- Objective: NominalMagnification
- ObjectiveSettings: ID
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: TimeIncrement
- Pixels: Type
• Plane: DeltaT
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 46
Total unknown or missing: 429

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.111 QuesantReader

This page lists supported metadata fields for the Bio-Formats Quesant AFM format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Quesant AFM format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.112 NativeQTReader

This page lists supported metadata fields for the Bio-Formats QuickTime format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).
Supported fields

These fields are fully supported by the Bio-Formats QuickTime format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
This page lists supported metadata fields for the Bio-Formats RHK Technologies format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats RHK Technologies format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type

http://www.openmicroscopy.org/site/support/ome-model/

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.114 SBigReader

This page lists supported metadata fields for the Bio-Formats SBig format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats SBig format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/

18.2. Metadata fields
These fields are from the OME data model\textsuperscript{429}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Seiko format reader:

- Channel : ID\textsuperscript{4230}
- Channel : SamplesPerPixel\textsuperscript{4231}
- Image : AcquisitionDate\textsuperscript{4232}
This page lists supported metadata fields for the Bio-Formats Compix Simple-PCI format reader.

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
These fields are from the OME data model\textsuperscript{4254}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 29 of them (6%).
• Of those, Bio-Formats fully or partially converts 29 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Compix Simple-PCI format reader:

• Channel : ID\textsuperscript{4255}
• Channel : SamplesPerPixel\textsuperscript{4256}
• Detector : ID\textsuperscript{4257}
• Detector : Type\textsuperscript{4258}
• DetectorSettings : Binning\textsuperscript{4259}
• DetectorSettings : ID\textsuperscript{4260}
• Image : AcquisitionDate\textsuperscript{4261}
• Image : ID\textsuperscript{4262}
• Image : InstrumentRef\textsuperscript{4263}
• Image : Name\textsuperscript{4264}
• Instrument : ID\textsuperscript{4265}
• Pixels : BigEndian\textsuperscript{4266}
• Pixels : DimensionOrder\textsuperscript{4267}
• Pixels : ID\textsuperscript{4268}
• Pixels : Interleaved\textsuperscript{4269}
• Pixels : PhysicalSizeX\textsuperscript{4270}
• Pixels : PhysicalSizeY\textsuperscript{4271}
• Pixels : SignificantBits\textsuperscript{4272}
• Pixels : SizeC\textsuperscript{4273}
• Pixels : SizeT\textsuperscript{4274}

\textsuperscript{4254}http://www.openmicroscopy.org/site/support/ome-model/
\textsuperscript{4255}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{4256}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{4257}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_ID
\textsuperscript{4258}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Detector_Type
\textsuperscript{4259}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_Binning
\textsuperscript{4260}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#DetectorSettings_ID
\textsuperscript{4261}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{4262}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{4263}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#InstrumentRef_ID
\textsuperscript{4264}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\textsuperscript{4265}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Instrument_ID
\textsuperscript{4266}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\textsuperscript{4267}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\textsuperscript{4268}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeX
\textsuperscript{4269}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY
\textsuperscript{4270}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\textsuperscript{4271}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\textsuperscript{4272}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: DeltaT
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 29

Total unknown or missing: 446

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.

18.2.117 SimplePCITiffReader

This page lists supported metadata fields for the Bio-Formats SimplePCI TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 33 of them (6%).
• Of those, Bio-Formats fully or partially converts 33 (100%).

Supported fields

These fields are fully supported by the Bio-Formats SimplePCI TIFF format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Model
• Detector: Type
- DetectorSettings : Binning
- DetectorSettings : ID
- Image : AcquisitionDate
- Image : Description
- Image : ID
- Image : InstrumentRef
- Image : Name
- Instrument : ID
- Objective : ID
- Objective : Immersion
- Objective : NominalMagnification
- Pixels : BigEndian
- Pixels : DimensionOrder
- Pixels : ID
- Pixels : Interleaved
- Pixels : PhysicalSizeX
- Pixels : PhysicalSizeY
- Pixels : SignificantBits
- Pixels : SizeC
- Pixels : SizeT
- Pixels : SizeX
- Pixels : SizeY
- Pixels : SizeZ
- Pixels : Type
- Plane : ExposureTime
- Plane : TheC
18.2.118 SMCameraReader

This page lists supported metadata fields for the Bio-Formats SM Camera format reader. These fields are from the OME data model\(^4\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats SM Camera format reader:

- Channel : ID\(^5\)
- Channel : SamplesPerPixel\(^4\)
- Image : AcquisitionDate\(^5\)
- Image : ID\(^5\)
- Image : Name\(^5\)
- Pixels : BigEndian\(^5\)
- Pixels : DimensionOrder\(^5\)
- Pixels : ID\(^5\)
- Pixels : Interleaved\(^5\)
- Pixels : SignificantBits\(^5\)
- Pixels : SizeC\(^5\)
- Pixels : SizeT\(^5\)

---

\(^4\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^5\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^6\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^7\)http://www.openmicroscopy.org/site/support/legacy/
\(^8\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^9\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^10\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^12\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^13\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^14\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\(^15\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\(^16\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\(^17\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\(^18\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\(^19\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
18.2.119 SpiderReader

This page lists supported metadata fields for the Bio-Formats SPIDER format reader.

These fields are from the OME data model\(^4^{344}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

Supported fields

These fields are fully supported by the Bio-Formats SPIDER format reader:

- Channel: ID\(^4^{345}\)
- Channel: SamplesPerPixel\(^4^{346}\)
- Image: AcquisitionDate\(^4^{347}\)
- Image: ID\(^4^{348}\)
- Image: Name\(^4^{349}\)
- Pixels: BigEndian\(^4^{350}\)
- Pixels: DimensionOrder\(^4^{351}\)

\(^{4335}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
\(^{4336}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\(^{4337}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeZ
\(^{4338}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\(^{4339}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheC
\(^{4340}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT
\(^{4341}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheZ
\(^{4343}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/
\(^{4344}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/legacy/
\(^{4345}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\(^{4346}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\(^{4347}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\(^{4349}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
\(^{4350}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\(^{4351}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.120 TargaReader

This page lists supported metadata fields for the Bio-Formats Truevision Targa format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 20 of them (4%).
• Of those, Bio-Formats fully or partially converts 20 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Truevision Targa format reader:

4353 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
4356 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
4357 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
4358 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
4360 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
4362 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
4366 http://www.openmicroscopy.org/site/support/bio-formats5.0/
4367 http://www.openmicroscopy.org/site/support/legacy/
4368 http://www.openmicroscopy.org/site/support/ome-model/
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 20
Total unknown or missing: 455

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.121 TextReader

This page lists supported metadata fields for the Bio-Formats Text format reader.

18.2. Metadata fields
These fields are from the OME data model[^1]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

**Of the 475 fields documented in the metadata summary table:**

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Text format reader:

- Channel: ID[^2]
- Channel: SamplesPerPixel[^3]
- Image: AcquisitionDate[^4]
- Image: ID[^5]
- Image: Name[^6]
- Pixels: BigEndian[^7]
- Pixels: DimensionOrder[^8]
- Pixels: ID[^9]
- Pixels: Interleaved[^10]
- Pixels: SizeC[^12]
- Pixels: SizeT[^13]
- Pixels: SizeX[^14]
- Pixels: SizeY[^15]
- Pixels: SizeZ[^16]
- Pixels: Type[^17]
- Plane: TheC[^18]
- Plane: TheT[^19]
- Plane: TheZ[^20]

[^1]: http://www.openmicroscopy.org/site/support/ome-model/
[^3]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
[^4]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
[^7]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
[^17]: http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.122 TiffReader

This page lists supported metadata fields for the Bio-Formats Tagged Image File Format format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Tagged Image File Format format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT

4411 http://www.openmicroscopy.org/site/support/bio-formats5.0/
4412 http://www.openmicroscopy.org/site/support/legacy/
4413 http://www.openmicroscopy.org/site/support/ome-model/
4415 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
4416 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
4420 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
4426 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
4427 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.123 TillVisionReader

This page lists supported metadata fields for the Bio-Formats TillVision format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats TillVision format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Experiment: ID
• Experiment: Type
• Image: AcquisitionDate
• Image: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experiment_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.124 TopometrixReader

This page lists supported metadata fields for the Bio-Formats TopoMetrix format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
Supported fields

These fields are fully supported by the Bio-Formats TopoMetrix format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions for details.
18.2.125 TrestleReader

This page lists supported metadata fields for the Bio-Formats Trestle format reader. These fields are from the OME data model\textsuperscript{4488}. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 26 of them (5%).
- Of those, Bio-Formats fully or partially converts 26 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Trestle format reader:

- Channel : ID\textsuperscript{4489}
- Channel : SamplesPerPixel\textsuperscript{4490}
- Image : AcquisitionDate\textsuperscript{4491}
- Image : ID\textsuperscript{4492}
- Image : Name\textsuperscript{4493}
- Image : ROILref\textsuperscript{4494}
- Mask : Height\textsuperscript{4495}
- Mask : ID\textsuperscript{4496}
- Mask : Width\textsuperscript{4497}
- Mask : X\textsuperscript{4498}
- Mask : Y\textsuperscript{4499}
- Pixels : BigEndian\textsuperscript{4500}
- Pixels : DimensionOrder\textsuperscript{4501}
- Pixels : ID\textsuperscript{4502}
- Pixels : Interleaved\textsuperscript{4503}
- Pixels : SignificantBits\textsuperscript{4504}

\textsuperscript{4486}http://www.openmicroscopy.org/site/support/bio-formats5.0/
\textsuperscript{4487}http://www.openmicroscopy.org/site/support/legacy/
\textsuperscript{4488}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID
\textsuperscript{4489}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
\textsuperscript{4490}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
\textsuperscript{4491}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_ID
\textsuperscript{4492}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID
\textsuperscript{4493}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_Height
\textsuperscript{4494}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_Width
\textsuperscript{4495}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_X
\textsuperscript{4496}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Mask_Y
\textsuperscript{4498}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4499}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4500}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4501}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4502}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4503}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
\textsuperscript{4504}http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• ROI: ID

Total supported: 26
Total unknown or missing: 449

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.126 UBMReader

This page lists supported metadata fields for the Bio-Formats UBM format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats UBM format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
18.2.127 UnisokuReader

This page lists supported metadata fields for the Bio-Formats Unisoku STM format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 22 of them (4%).
- Of those, Bio-Formats fully or partially converts 22 (100%).

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2. Metadata fields
Supported fields

These fields are fully supported by the Bio-Formats Unisoku STM format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: Description
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

Total supported: 22

Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions.
18.2.128 VarianFDFReader

This page lists supported metadata fields for the Bio-Formats Varian FDF format reader.

These fields are from the OME data model\(^\text{4564}\). Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 25 of them (5%).
- Of those, Bio-Formats fully or partially converts 25 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Varian FDF format reader:

- Channel: ID\(^\text{4565}\)
- Channel: SamplesPerPixel\(^\text{4566}\)
- Image: AcquisitionDate\(^\text{4567}\)
- Image: ID\(^\text{4568}\)
- Image: Name\(^\text{4569}\)
- Pixels: BigEndian\(^\text{4570}\)
- Pixels: DimensionOrder\(^\text{4571}\)
- Pixels: ID\(^\text{4572}\)
- Pixels: Interleaved\(^\text{4573}\)
- Pixels: PhysicalSizeX\(^\text{4574}\)
- Pixels: PhysicalSizeY\(^\text{4575}\)
- Pixels: PhysicalSizeZ\(^\text{4576}\)
- Pixels: SignificantBits\(^\text{4577}\)
- Pixels: SizeC\(^\text{4578}\)
- Pixels: SizeT\(^\text{4579}\)
- Pixels: SizeX\(^\text{4580}\)

\(^{4562}\)http://www.openmicroscopy.org/site/support/bio-formats5.0/

\(^{4563}\)http://www.openmicroscopy.org/site/support/ome-model/

\(^{4564}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_ID

\(^{4565}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel

\(^{4566}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html(Image_AcquisitionDate


\(^{4568}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name

\(^{4569}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

\(^{4570}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder


\(^{4572}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved


\(^{4574}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_PhysicalSizeY


\(^{4576}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits

\(^{4577}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC

\(^{4578}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT

\(^{4579}\)http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 25

Total unknown or missing: 450

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.129 VeecoReader

This page lists supported metadata fields for the Bio-Formats Veeco format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:
• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Veeco format reader:
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : SignificantBits
• Pixels : SizeC
• Pixels : SizeT
• Pixels : SizeX
• Pixels : SizeY
• Pixels : SizeZ
• Pixels : Type
• Plane : TheC
• Plane : TheT
• Plane : TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.130 VGSAMReader

This page lists supported metadata fields for the Bio-Formats VG SAM format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats VG SAM format reader:

4598 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
4603 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
4604 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
4608 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
4612 http://www.openmicroscopy.org/site/support/bio-formats5.0/
4613 http://www.openmicroscopy.org/site/support/legacy/
4614 http://www.openmicroscopy.org/site/support/ome-model/
• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.131 VisitechReader

This page lists supported metadata fields for the Bio-Formats Visitech XYS format reader.

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

## Supported fields

These fields are fully supported by the Bio-Formats Visitech XYS format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ

---

4636 http://www.openmicroscopy.org/site/support/ome-model/
4638 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
4639 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
4642 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
4647 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
4648 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
4652 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.132 VolocityClippingReader

This page lists supported metadata fields for the Bio-Formats Volocity Library Clipping format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Volocity Library Clipping format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.133 VolocityReader

This page lists supported metadata fields for the Bio-Formats Volocity Library format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 38 of them (8%).
• Of those, Bio-Formats fully or partially converts 38 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Volocity Library format reader:

• Channel: ID
• Channel: Name
• Channel: SamplesPerPixel
• Detector: ID
• Detector: Model
• DetectorSettings: ID
• Image: AcquisitionDate
• Image: Description
• Image: ID

18.2. Metadata fields
• Image: InstrumentRef
• Image: Name
• Instrument: ID
• Objective: Correction
• Objective: ID
• Objective: Immersion
• Objective: NominalMagnification
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ

18.2. Metadata fields
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 38
Total unknown or missing: 437

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.134 WA TOPReader

This page lists supported metadata fields for the Bio-Formats WA Technology TOP format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 22 of them (4%).
• Of those, Bio-Formats fully or partially converts 22 (100%).

Supported fields

These fields are fully supported by the Bio-Formats WA Technology TOP format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: Description
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
•Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 22
Total unknown or missing: 453

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

### 18.2.135 BMPReader

This page lists supported metadata fields for the Bio-Formats Windows Bitmap format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 21 of them (4%).
- Of those, Bio-Formats fully or partially converts 21 (100%).

#### Supported fields

These fields are fully supported by the Bio-Formats Windows Bitmap format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate

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4743: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
4744: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
4745: [http://www.openmicroscopy.org/site/support/legacy/](http://www.openmicroscopy.org/site/support/legacy/)
4746: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
4747: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
4748: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
4749: [http://www.openmicroscopy.org/site/support/bio-formats5.0/](http://www.openmicroscopy.org/site/support/bio-formats5.0/)
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 21
Total unknown or missing: 454

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.136 WlzReader

This page lists supported metadata fields for the Bio-Formats Woolz format reader. These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
• The file format itself supports 26 of them (5%).
• Of those, Bio-Formats fully or partially converts 26 (100%).

**Supported fields**

These fields are fully supported by the Bio-Formats Woolz format reader:

- Channel: ID
- Channel: SamplesPerPixel
- Image: AcquisitionDate
- Image: ID
- Image: Name
- Pixels: BigEndian
- Pixels: DimensionOrder
- Pixels: ID
- Pixels: Interleaved
- Pixels: PhysicalSizeX
- Pixels: PhysicalSizeY
- Pixels: PhysicalSizeZ
- Pixels: SignificantBits
- Pixels: SizeC
- Pixels: SizeT
- Pixels: SizeX
- Pixels: SizeY
- Pixels: SizeZ
- Pixels: Type
- Plane: TheC
- Plane: TheT
- Plane: TheZ
- StageLabel: Name

---

4772 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
4773 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
4775 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
4776 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
4779 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
4784 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
4785 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
4789 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
4793 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#StageLabel_Name
• StageLabel : X
• StageLabel : Y
• StageLabel : Z

Total supported: 26
Total unknown or missing: 449

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.

18.2.137 ZeissLMSReader

This page lists supported metadata fields for the Bio-Formats Zeiss LMS format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 23 of them (4%).
- Of those, Bio-Formats fully or partially converts 23 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Zeiss LMS format reader:

• Channel : ID
• Channel : SamplesPerPixel
• Image : AcquisitionDate
• Image : ID
• Image : Name
• Instrument : ID
• Objective : ID
• Objective : NominalMagnification
• ObjectiveSettings : ID
• Pixels : BigEndian
• Pixels : DimensionOrder

http://www.openmicroscopy.org/site/support/bio-formats5.0/
http://www.openmicroscopy.org/site/support/legacy/
http://www.openmicroscopy.org/site/support/ome-model/
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_SamplesPerPixel
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

18.2. Metadata fields
18.2.138 ZeissTIFFReader

This page lists supported metadata fields for the Bio-Formats Zeiss AxioVision TIFF format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 19 of them (4%).
- Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Zeiss AxioVision TIFF format reader:

- Channel: ID
- Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.139 ZeissZVIReader

This page lists supported metadata fields for the Bio-Formats Zeiss Vision Image (ZVI) format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 19 of them (4%).
• Of those, Bio-Formats fully or partially converts 19 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Zeiss Vision Image (ZVI) format reader:

• Channel: ID
• Channel: SamplesPerPixel
• Image: AcquisitionDate
• Image: ID
• Image: Name
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: TheC
• Plane: TheT
• Plane: TheZ

Total supported: 19
Total unknown or missing: 456

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous version page to find documentation for the version you are using.
18.2.140 ZeissCZIReader

This page lists supported metadata fields for the Bio-Formats Zeiss CZI format reader. These fields are from the OME data model[4669]. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g., physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

- The file format itself supports 158 of them (33%).
- Of those, Bio-Formats fully or partially converts 158 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Zeiss CZI format reader:

- **Arc**: LotNumber
- **Arc**: Manufacturer
- **Arc**: Model
- **Arc**: Power
- **Arc**: SerialNumber
- **Channel**: AcquisitionMode
- **Channel**: Color
- **Channel**: EmissionWavelength
- **Channel**: ExcitationWavelength
- **Channel**: FilterSetRef
- **Channel**: Fluor
- **Channel**: ID
- **Channel**: IlluminationType
- **Channel**: Name
- **Channel**: PinholeSize
- **Channel**: SamplesPerPixel
- **Detector**: AmplificationGain
- **Detector**: Gain

• Detector: ID
• Detector: LotNumber
• Detector: Manufacturer
• Detector: Model
• Detector: Offset
• Detector: SerialNumber
• Detector: Type
• Detector: Zoom
• DetectorSettings: Binning
• DetectorSettings: Gain
• DetectorSettings: ID
• Dichroic: ID
• Dichroic: LotNumber
• Dichroic: Manufacturer
• Dichroic: Model
• Dichroic: SerialNumber
• Ellipse: ID
• Ellipse: RadiusX
• Ellipse: RadiusY
• Ellipse: Text
• Ellipse: X
• Ellipse: Y
• Experimenter: Email
• Experimenter: FirstName
• Experimenter: ID
• Experimenter: Institution

18.2. Metadata fields
• Experimenter: LastName
• Experimenter: MiddleName
• Experimenter: UserName
• Filament: LotNumber
• Filament: Manufacturer
• Filament: Model
• Filament: Power
• Filament: SerialNumber
• Filter: FilterWheel
• Filter: ID
• Filter: LotNumber
• Filter: Manufacturer
• Filter: Model
• Filter: SerialNumber
• Filter: Type
• FilterSet: DichroicRef
• FilterSet: EmissionFilterRef
• FilterSet: ExcitationFilterRef
• FilterSet: ID
• FilterSet: LotNumber
• FilterSet: Manufacturer
• FilterSet: Model
• FilterSet: SerialNumber
• Image: AcquisitionDate
• Image: Description
• Image: ExperimenterRef
• Image: ExperimentRef

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_LastName
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_MiddleName
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Experimenter_UserName
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_LotNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_LotNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Filter_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_AcquisitionDate

18.2. Metadata fields
• Image: ID
• Image: InstrumentRef
• Image: Name
• Image: ROIRef
• ImagingEnvironment: AirPressure
• ImagingEnvironment: CO2Percent
• ImagingEnvironment: Humidity
• ImagingEnvironment: Temperature
• Instrument: ID
• Laser: LotNumber
• Laser: Manufacturer
• Laser: Model
• Laser: Power
• Laser: SerialNumber
• LightEmittingDiode: LotNumber
• LightEmittingDiode: Manufacturer
• LightEmittingDiode: Model
• LightEmittingDiode: Power
• LightEmittingDiode: SerialNumber
• Line: ID
• Line: Text
• Line: X1
• Line: X2
• Line: Y1
• Line: Y2
• Microscope: LotNumber

18.2. Metadata fields
• Microscope : Manufacturer
• Microscope : Model
• Microscope : SerialNumber
• Microscope : Type
• Objective : CalibratedMagnification
• Objective : Correction
• Objective : ID
• Objective : Immersion
• Objective : Iris
• Objective : LensNA
• Objective : LotNumber
• Objective : Manufacturer
• Objective : Model
• Objective : NominalMagnification
• Objective : SerialNumber
• Objective : WorkingDistance
• ObjectiveSettings : CorrectionCollar
• ObjectiveSettings : ID
• ObjectiveSettings : Medium
• ObjectiveSettings : RefractiveIndex
• Pixels : BigEndian
• Pixels : DimensionOrder
• Pixels : ID
• Pixels : Interleaved
• Pixels : PhysicalSizeX
• Pixels : PhysicalSizeY

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_Manufacturer
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ManufacturerSpec_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Microscope_Type
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Manufacturer
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_SerialNumber
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_WorkingDistance
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_CorrectionCollar
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_RefractiveIndex
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian

18.2. Metadata fields
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: Type
• Plane: DeltaT
• Plane: ExposureTime
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT
• Plane: TheZ
• Polygon: ID
• Polygon: Points
• Polygon: Text
• Polyline: ID
• Polyline: Points
• Polyline: Text
• ROI: Description
• ROI: ID
• ROI: Name
• Rectangle: Height
• Rectangle : ID
• Rectangle : Text
• Rectangle : Width
• Rectangle : X
• Rectangle : Y
• TransmittanceRange : CutIn
• TransmittanceRange : CutInTolerance
• TransmittanceRange : CutOut
• TransmittanceRange : CutOutTolerance
• TransmittanceRange : Transmittance

Total supported: 158
Total unknown or missing: 317

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous page to find documentation for the version you are using.

18.2.141 ZeissLSMReader

This page lists supported metadata fields for the Bio-Formats Zeiss Laser-Scanning Microscopy format reader.

These fields are from the OME data model. Bio-Formats standardizes each format’s original metadata to and from the OME data model so that you can work with a particular piece of metadata (e.g. physical width of the image in microns) in a format-independent way.

Of the 475 fields documented in the metadata summary table:

• The file format itself supports 101 of them (21%).
• Of those, Bio-Formats fully or partially converts 101 (100%).

Supported fields

These fields are fully supported by the Bio-Formats Zeiss Laser-Scanning Microscopy format reader:

• Channel : Color
• Channel : ID
• Channel : Name
• Channel : PinholeSize

http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Text
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#TransmittanceRange_CutIn
http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Channel_Name
• Channel: SamplesPerPixel
• Detector: AmplificationGain
• Detector: Gain
• Detector: ID
• Detector: Type
• Detector: Zoom
• DetectorSettings: Binning
• DetectorSettings: ID
• Dichroic: ID
• Dichroic: Model
• Ellipse: FontSize
• Ellipse: ID
• Ellipse: RadiusX
• Ellipse: RadiusY
• Ellipse: StrokeWidth
• Ellipse: Transform
• Ellipse: X
• Ellipse: Y
• Experimenter: ID
• Experimenter: UserName
• Filter: ID
• Filter: Model
• Filter: Type
• Image: AcquisitionDate
• Image: Description
• Image: ID

18.2. Metadata fields
• Image: InstrumentRef
• Image: Name
• Image: ROIRef
• Instrument: ID
• Label: FontSize
• Label: ID
• Label: StrokeWidth
• Label: Text
• Label: X
• Label: Y
• Laser: ID
• Laser: LaserMedium
• Laser: Model
• Laser: Type
• Laser: Wavelength
• LightPath: DichroicRef
• LightPath: EmissionFilterRef
• Line: FontSize
• Line: ID
• Line: StrokeWidth
• Line: X1
• Line: X2
• Line: Y1
• Line: Y2
• Objective: Correction
• Objective: ID

5062 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Image_Name
5063 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#ROIRef_ID
5065 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_FontSize
5066 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
5067 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
5068 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_Text
5074 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Laser_Type
5078 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_FontSize
5079 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_ID
5080 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Shape_StrokeWidth
5081 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Line_X1
5083 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ROI_xsd.html#Line_Y1
5085 http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Correction

18.2. Metadata fields
• Objective: Immersion
• Objective: Iris
• Objective: LensNA
• Objective: NominalMagnification
• ObjectiveSettings: ID
• Pixels: BigEndian
• Pixels: DimensionOrder
• Pixels: ID
• Pixels: Interleaved
• Pixels: PhysicalSizeX
• Pixels: PhysicalSizeY
• Pixels: PhysicalSizeZ
• Pixels: SignificantBits
• Pixels: SizeC
• Pixels: SizeT
• Pixels: SizeX
• Pixels: SizeY
• Pixels: SizeZ
• Pixels: TimeIncrement
• Pixels: Type
• Plane: DeltaT
• Plane: PositionX
• Plane: PositionY
• Plane: PositionZ
• Plane: TheC
• Plane: TheT

\[5087\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Immersion
\[5088\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_Iris
\[5089\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_LensNA
\[5090\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Objective_NominalMagnification
\[5091\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#ObjectiveSettings_ID
\[5092\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_BigEndian
\[5093\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_DimensionOrder
\[5094\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_ID
\[5095\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Interleaved
\[5099\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SignificantBits
\[5100\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeC
\[5101\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeT
\[5103\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_SizeY
\[5105\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Pixels_Type
\[5106\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_DeltaT
\[5111\] http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#Plane_TheT

18.2. Metadata fields
- Plane: TheZ
- Polygon: FontSize
- Polygon: ID
- Polygon: Points
- Polygon: StrokeWidth
- Polyline: FontSize
- Polyline: ID
- Polyline: Points
- Polyline: StrokeWidth
- ROI: ID
- Rectangle: FontSize
- Rectangle: Height
- Rectangle: ID
- Rectangle: StrokeWidth
- Rectangle: Width
- Rectangle: X
- Rectangle: Y
- TransmittanceRange: CutIn
- TransmittanceRange: CutOut

Total supported: 101
Total unknown or missing: 374

Note: This documentation is for the new Bio-Formats 5.1 version. See the latest Bio-Formats 5.0.x version or the previous versions page to find documentation for the version you are using.
Individual files can be grouped together into a single fileset using a pattern file. This works for any single-file format that Bio-Formats supports, as long as all files are in the same format. It is most useful for sets of TIFF, JPEG, PNG, etc. files that do not have any associated metadata.

All files to be grouped together should be in the same folder. The pattern file should be in the same folder as the other files; it can have any name, but must have the .pattern extension. The pattern file is what must be opened or imported, so it may be helpful to give it a descriptive or easily-recognizable name.

The pattern file contains a single line of text that is specially formatted to describe how the files should be grouped. The file can be created in any text editor.

The text in the pattern file can take one of several forms. To illustrate, consider a folder with the following file names:

red.tiff
green.tiff
blue.tiff
test_Z0_C0.png
test_Z1_C0.png
test_Z0_C1.png
test_Z1_C1.png
test_Z0_C2.png
test_Z1_C2.png
test_Z00.tiff
test_Z01.tiff

A pattern file that groups red.tiff, green.tiff, and blue.tiff in that order would look like:

<red,green,blue>.tiff

A pattern that groups test_Z0_C0.png, test_Z1_C0.png, test_Z0_C2.png, and test_Z1_C2.png:

test_Z<0-1>_C<0-2:2>.png

The <> notation in general can accept a single literal value, a comma-separated list of literal values, a range of integer values, or a range of integer values with a step value greater than 1 (the range and step are separated by :). Note that inverting the values in a range (e.g. <2-0>) is not supported and will cause an exception to be thrown.

The characters immediately preceding the < can affect which dimension is assigned to the specified values. The values will be interpreted as:

- channels, if c, ch, w, or wavelength precede <
- timepoints, if t, tl, tp, or timepoint precede <
- Z sections, if z, zs, sec, fp, focal, or focalplane precede <
- series, if s, sp, or series precede <

Note that the listed dimension specifier characters are case insensitive. A separator character (underscore or space) must precede the dimension specifier if it is not at the beginning of the filename. In the above example, 2 Z sections and 2 out of 3 channels would be detected according to the dimension specifiers.
Leading zeros in the integer values must be specified. To group `test_Z00.tif` and `test_Z01.tif`:

```plaintext
test_Z<00-01>.tiff
```

or:

```plaintext
test_Z0<0-1>.tiff
```

Note that this pattern would not group the files correctly:

```plaintext
test_Z<0-1>.tiff
```

A pattern file that groups all PNG files beginning with `test_` would look like:

```plaintext
test_.*.png
```

This and most other Java-style regular expressions can be used in place of the `<>` notation above. See the `java.util.regex.Pattern Javadoc`\(^1\) for more information on constructing regular expressions.

---

\(^1\)http://docs.oracle.com/javase/6/docs/api/java/util/regex/Pattern.html
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