

The Open Microscopy Environment:

9th Annual User's Meeting

Institut Pasteur, Paris

Jason Swedlow

The OME Consortium



Centre for Gene Regulation & Expression
College of Life Sciences, University of Dundee
Dundee, Scotland, UK



Talk Outline

- Thank you!
- The Problem
- This Meeting...
- Our Progress
- Future Priorities...

Thank you!!!

- *Institut Pasteur*

- Christiane Pacaud
- Nathalie Aulner
- Anne Danckaert
- Sebastien Simard
- Sophie Gaudiard
- Spencer Shorte

- *University of Dundee*

- June Matthew
- Wilma Woudenberg

- *The OME Consortium*

Thank you!!!

wellcometrust

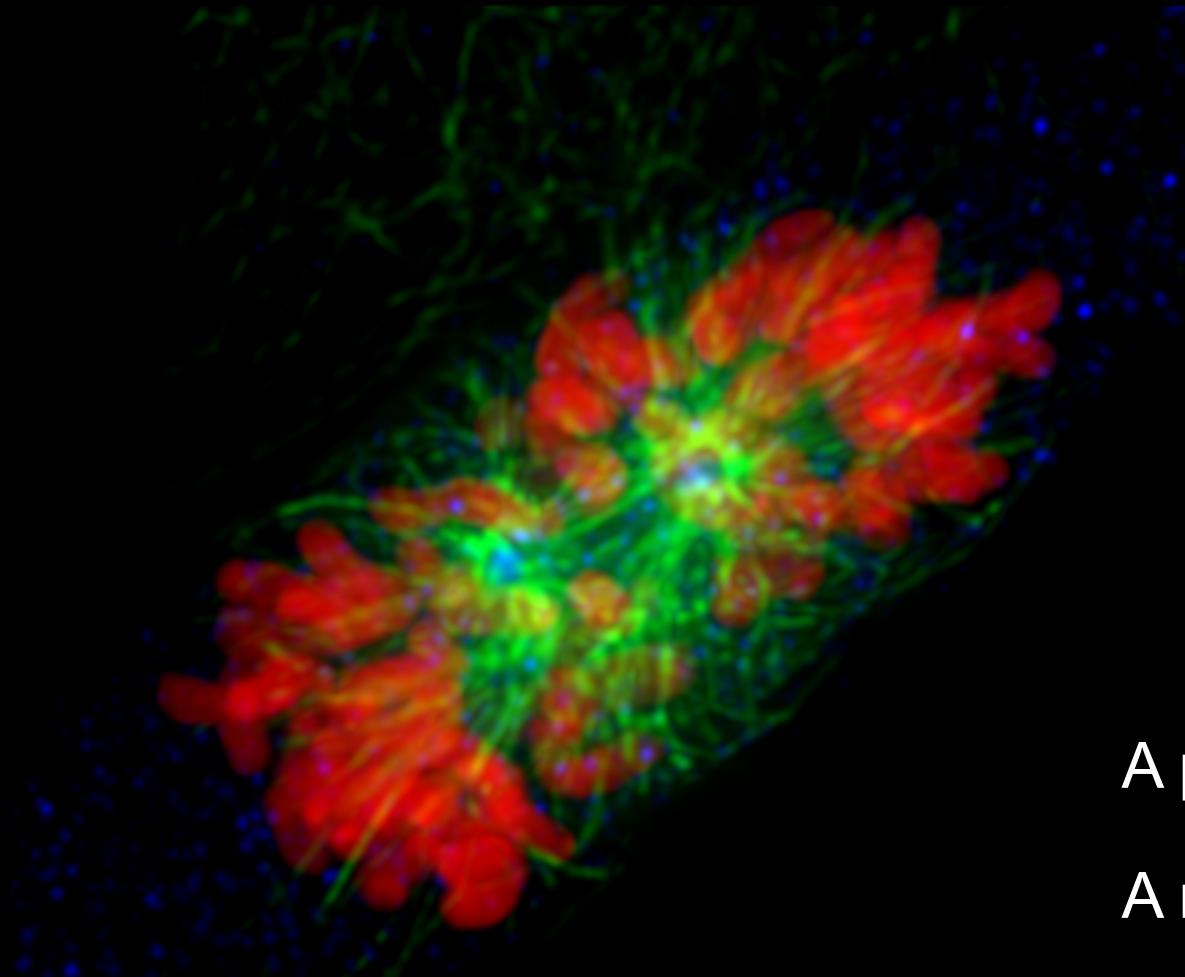


OME Consortium

- Dundee – Jason Swedlow, Colin Blackburn, Jean-Marie Burel, Mark Carroll, Gus Ferguson, Helen Flynn, Kenny Gillen, Roger Leigh, Simon Li, Dominik Lindner, June Matthew, Josh Moore, Will Moore, Andrew Patterson, Blazej Pindelski, Balaji Ramalingam, Aleksandra Tarkowska, Petr Walczysko, Wilma Woudenberg
- University of Wisconsin, Madison (LOCI) - Kevin Eliceiri, Curtis Rueden, Mark Hiner
- UT Southwestern – Gaudenz Danuser, Sebastien Besson
- Oxford – Ilan Davis, Douglas Russell
- CRS4 - Gianuigi Zanetti, Gianmauro Cucurru, Simone Leo, Luca Lianas
- Edinburgh – Richard Baldock, Bill Hill, Jianguo Rao
- Carnegie-Mellon – Robert Murphy, BK Cho, Ivan Cao-Berg
- Imperial – Paul French, Chris Dunsby, Ian Munro
- NIA, NIH – Ilya Goldberg, Chris Coletta
- Pasteur – Spencer Shorte, Sebastien Simard, Julien Jorde
- EBI – Gerard Kleywegt, Ardan Patwardhan, Ingvar Lagerstedt
- Glencoe Software – Chris Allan, Joshua Ballanco, Andreas Knab, Melissa Linkert, Chris MacLeod, Josh Moore, Carlos Neves, Liza Unson, Wilma Woudenberg

THE PROBLEM

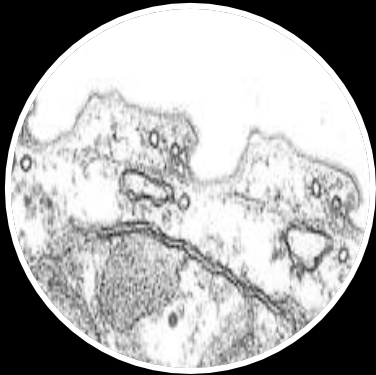
The Image Problem...



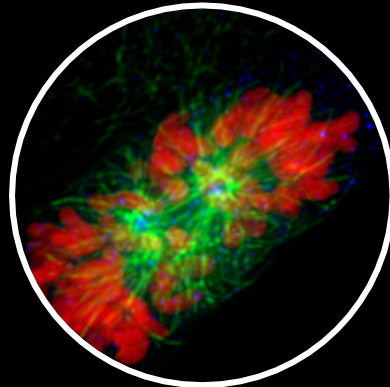
A pretty picture?

A measurement?

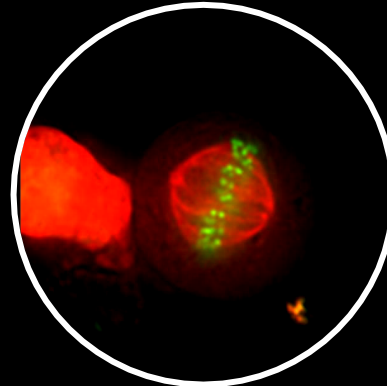
The Image Problem... is Ubiquitous



Organelles



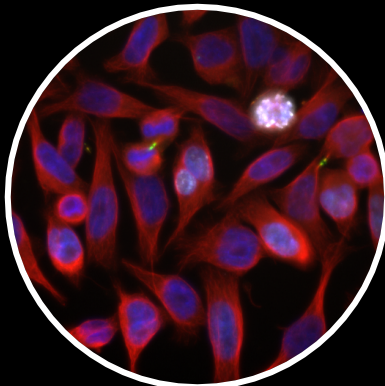
Cells



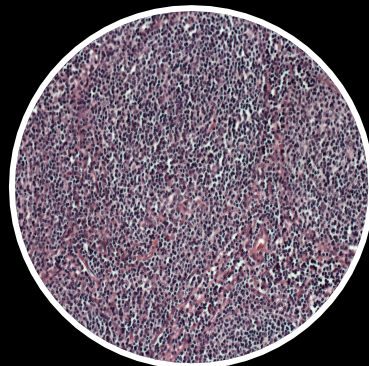
Dynamics



Physiology



Lead Discovery
Target Validation



Pathology



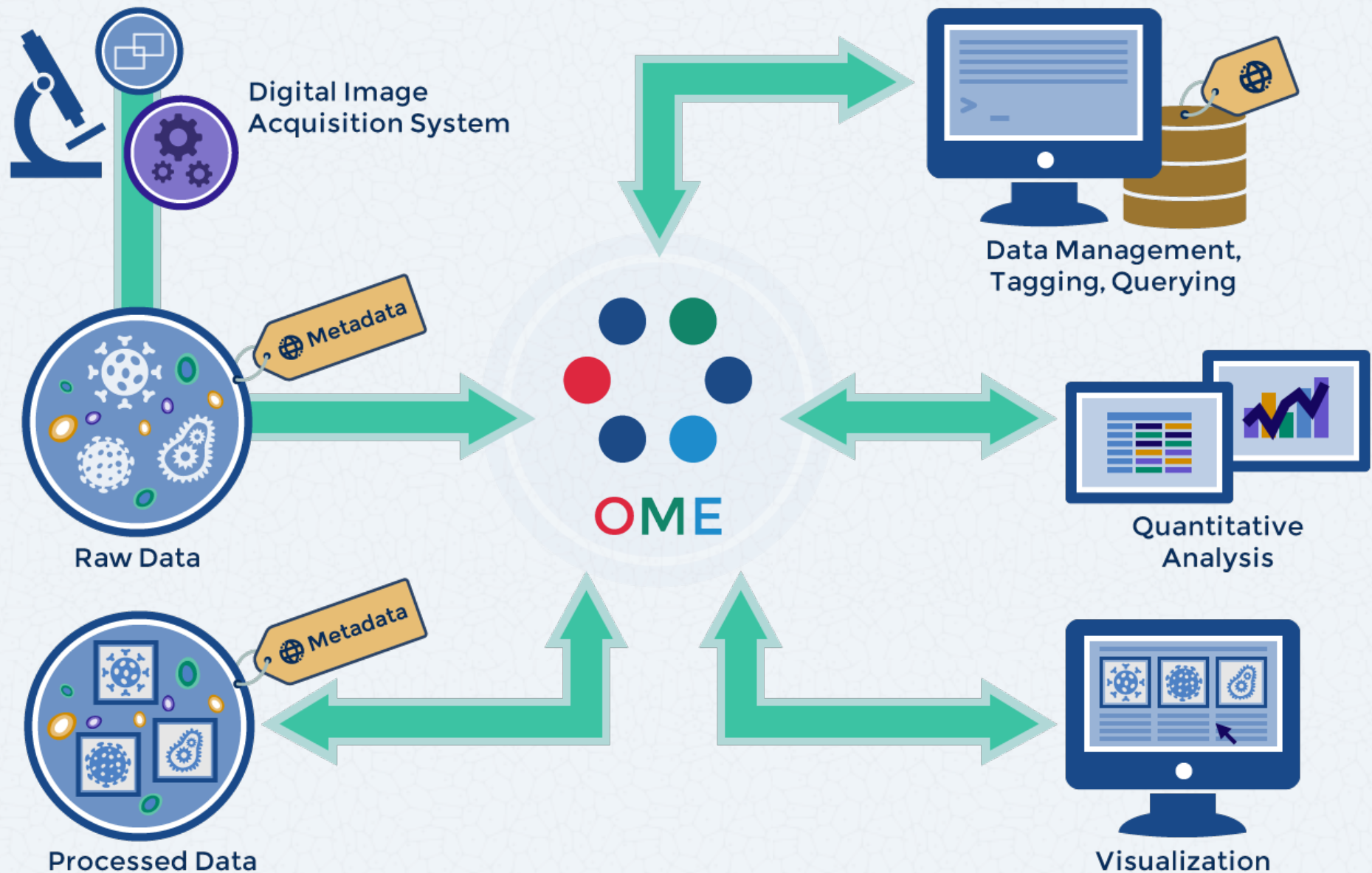
In Vivo

A pretty picture?

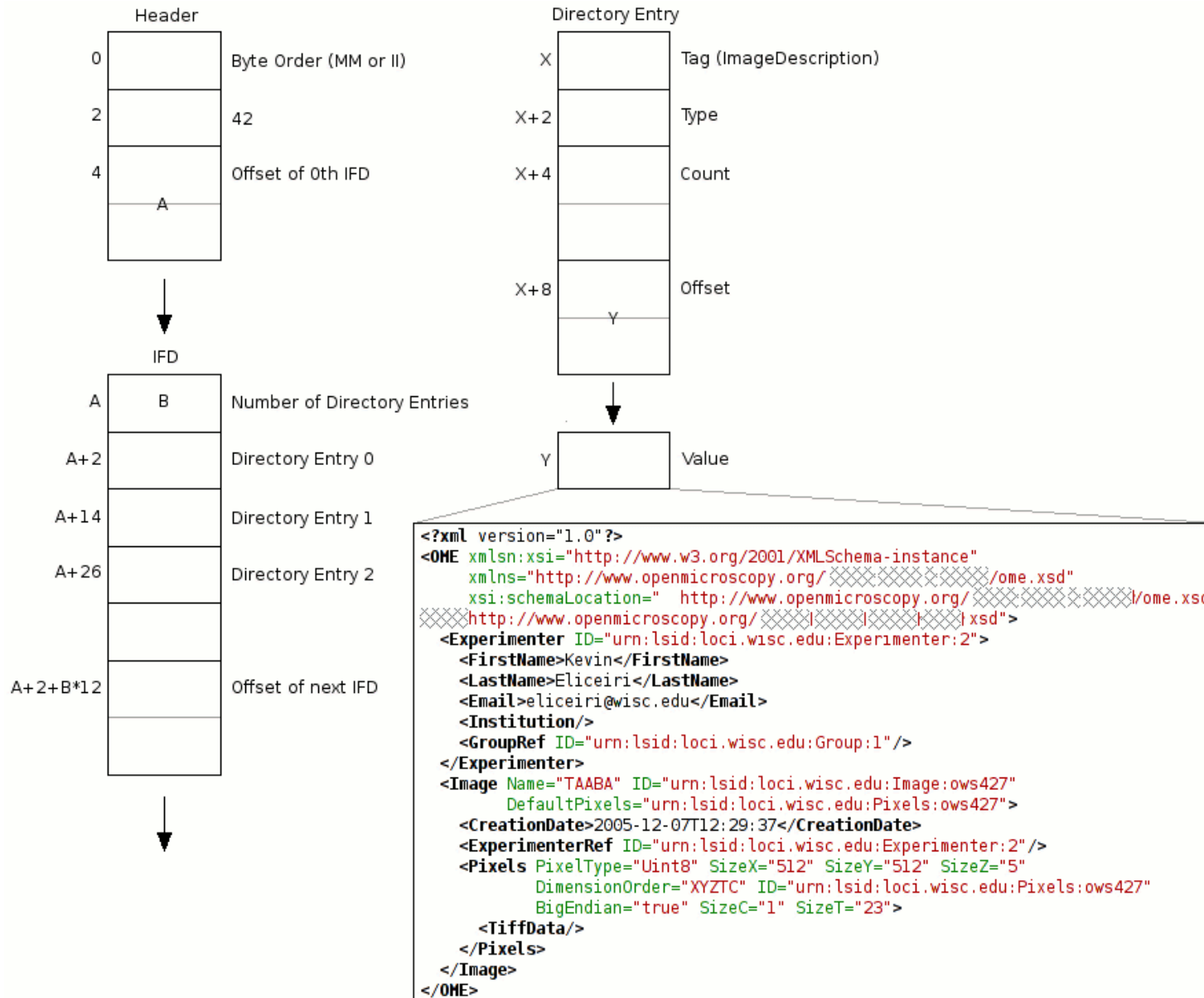
A measurement?

A resource?

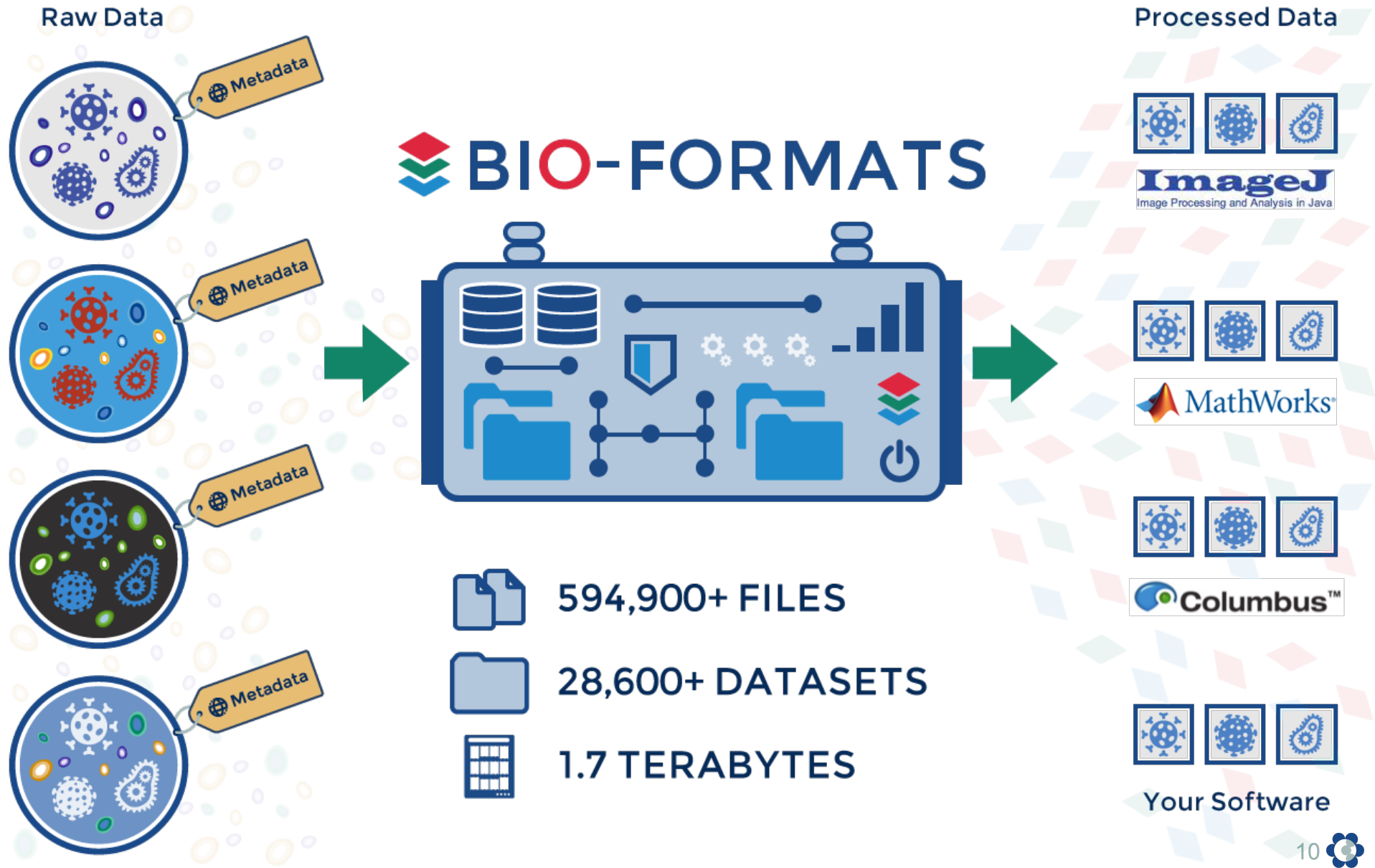
...Towards Image Informatics



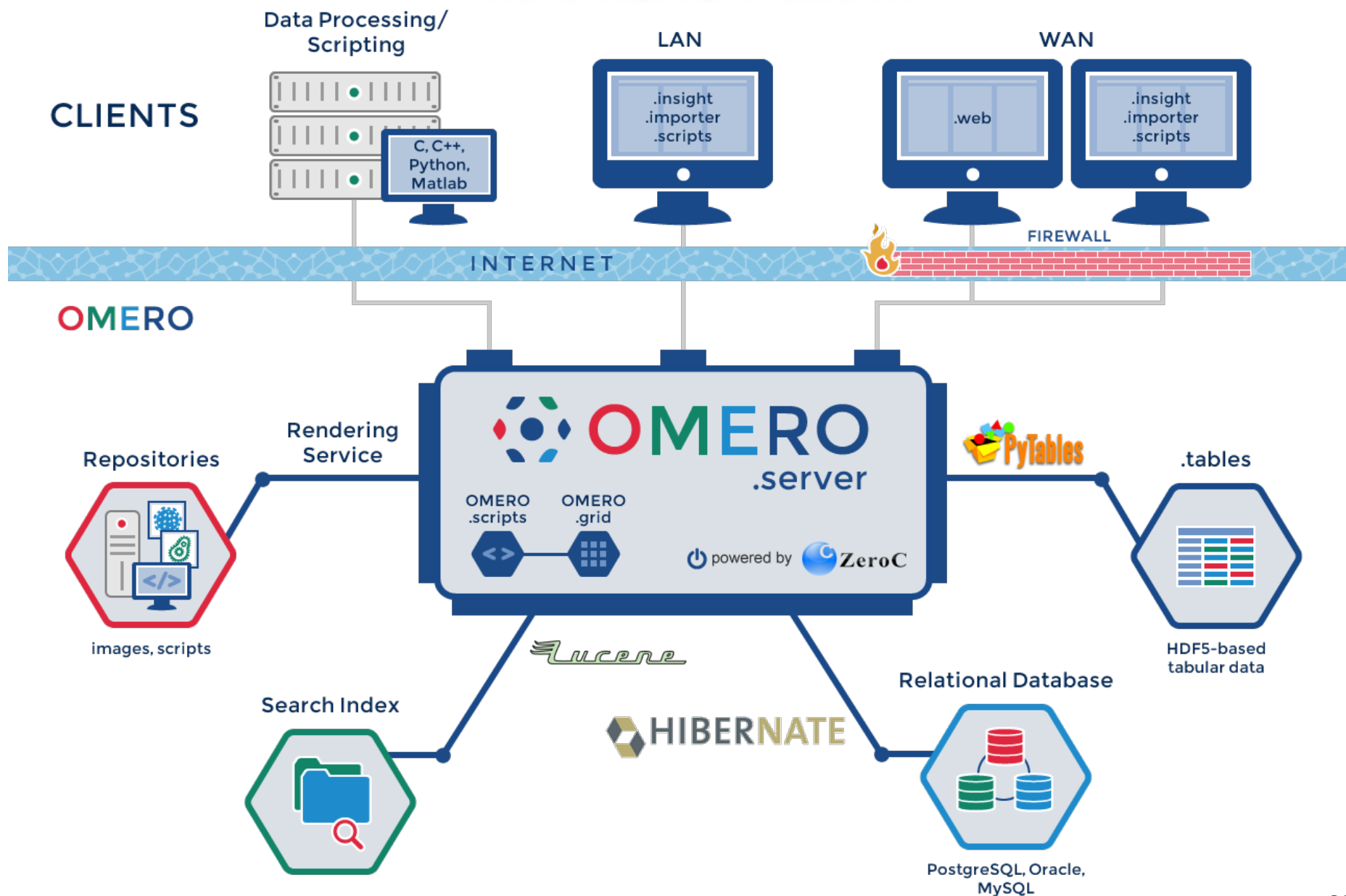
OME-TIFF: Common, Open Image File



BIO-FORMATS: Proprietary File Conversion



The OMERO Platform





OMERO & BIO-FORMATS: OMERO.insight Java Client

The screenshot displays the OMERO Java Client interface. On the left, a 'Projects' tree shows a hierarchy of folders and images. The main workspace contains a grid of 11 image thumbnails. The right panel shows the 'Image details' for image ID 3840635, including acquisition and import information. A 'Measurement Tool' window is open in the foreground, displaying a table of ROI data.

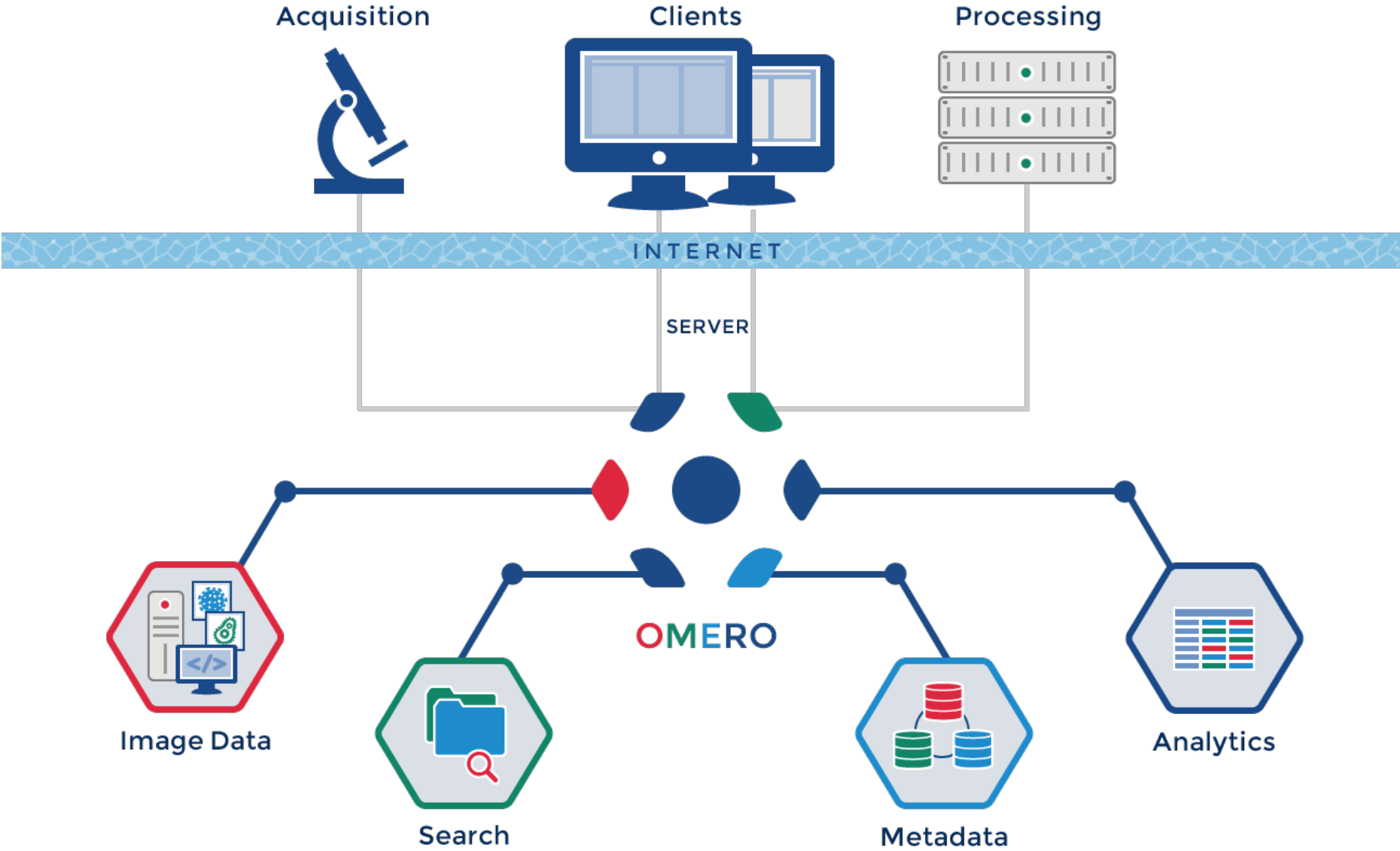
ROI	id	T	Z	Type	Text	Visible
▶	5662	[1,1]	[1,60]	<input type="checkbox"/>		<input checked="" type="checkbox"/>
▶	5663	[1,1]	[1,60]	<input type="checkbox"/>		<input checked="" type="checkbox"/>
▶	5664	[1,1]	[1,60]	<input type="checkbox"/>		<input checked="" type="checkbox"/>



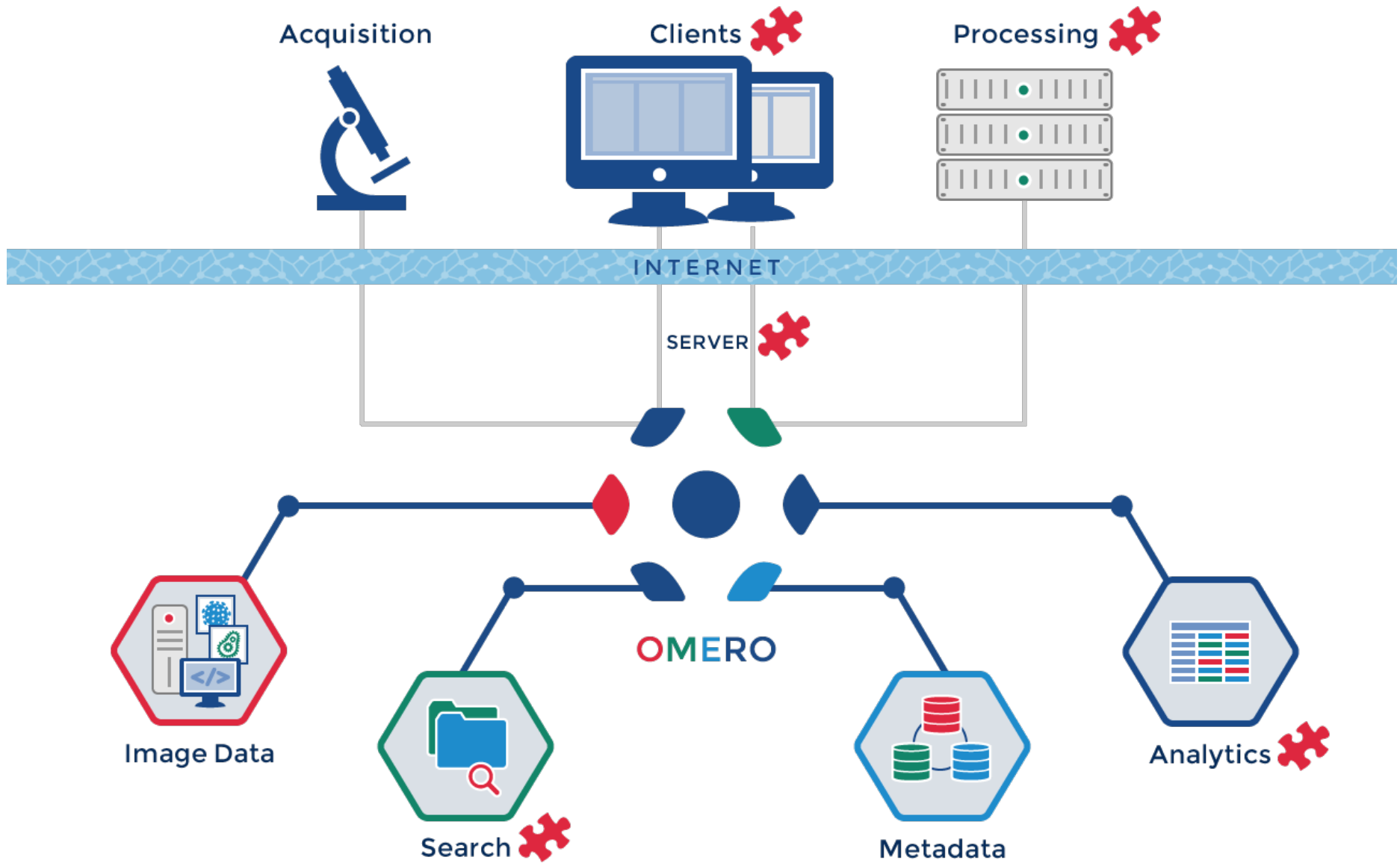
OMERO & BIO-FORMATS: OMERO.web Client

The screenshot displays the OMERO.web Client interface. The top navigation bar includes 'OMERO', 'Data', and 'History'. The user 'Jason Swedlow' is logged in. The main workspace shows a tree view of data under 'Alexia Ferrand', with the selected image being 'Z:/aferrand/HP1/101026-siRNA/101026-siCTL-GFPMCAK_SKIP_ACA_02_07_R3D_D3D.dv'. The central image viewer shows a microscopy image with a 'Viewing Options' panel on the left, including 'Normal' rendering, 'Max Intensity', 'Split Channel', 'Quality', 'Zoom (%)', and 'Line Plot'. The 'Rendering Details' panel shows channels for DAPI, FITC, RD-TR-PE, and CY-5. The 'Current Image' panel shows 'Z: 32/60 | T: 1/1' and 'ROI Count: 3'. The right sidebar contains metadata for the image, including 'IMAGE ID: 3840635', 'Owner: Alexia Ferrand', 'Acquisition Date: 2010-10-26 13:55:25', 'Imported Date: 2010-10-26 14:06:41', 'Dimensions (XY): 512 x 512', 'Pixels Type: uint16', 'Pixels Size (XYZ) (µm): 0.1001 x 0.1001 x 0.2000', 'Z-sections/Timepoints: 60 x 1', and 'Channels: DAPI, FITC, RD-TR-PE, CY-5'. A comment from Alexia Ferrand is also visible at the bottom right.

The OMERO Platform



The *Extensible* OMERO Platform



 Plugins Welcome

THIS MEETING.....

Meeting Purpose

9th Annual User's Mtg

- Attendees
 - OME Consortium
 - Invited Speakers
 - Broad cross-section of users
- *Day 1: Presentations*
 - Project Overview
 - Users & Guests
- *Day 2: Workshops & demos*
- Progress Report
- Future development priorities & planning

OUR PROGRESS

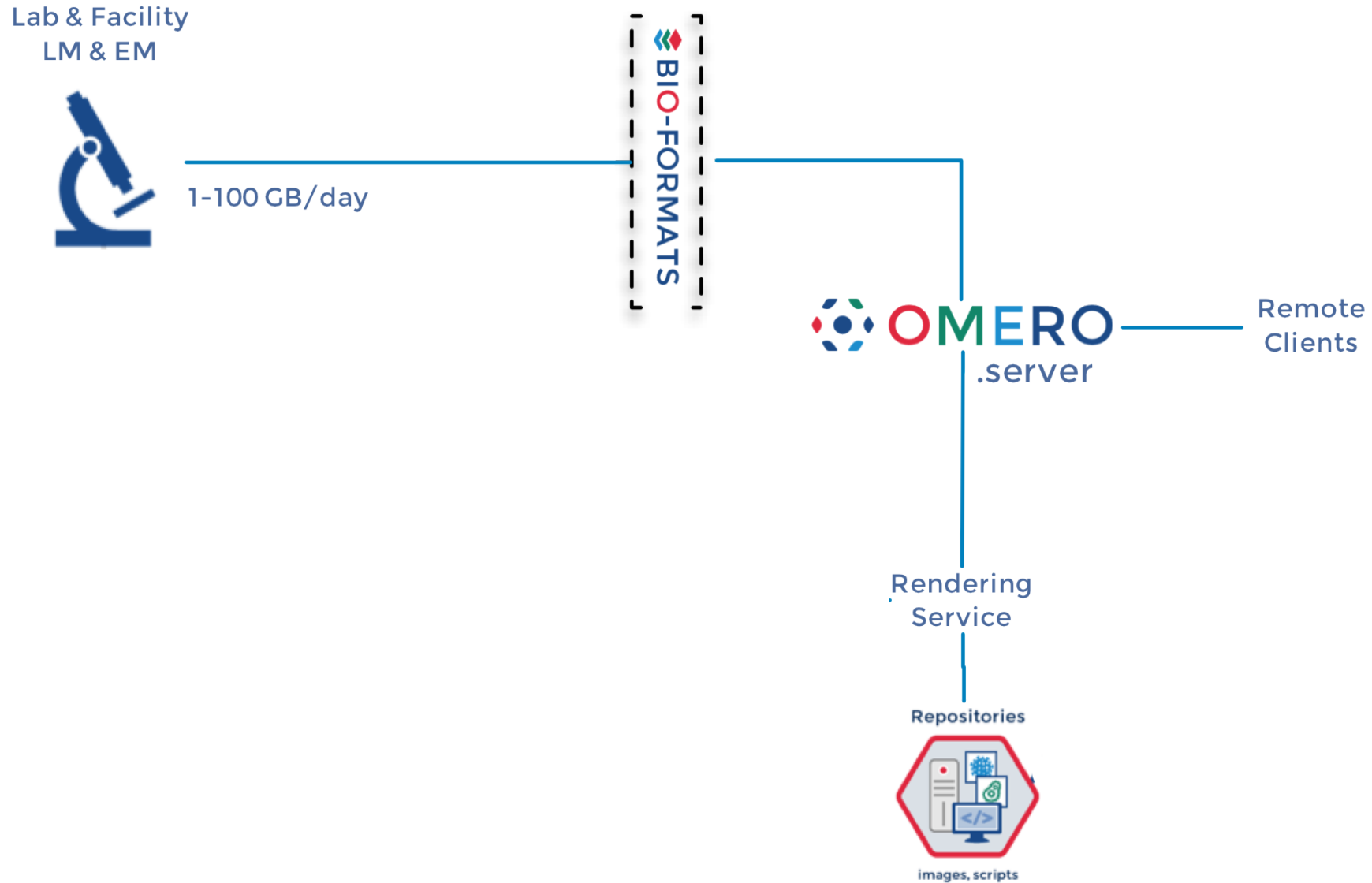
OME : 2011-2015

- More data types (FLIM, LSFM, 3DEM)
- Support complex, multi-dimensional, heterogeneous data
- Alternative image data storage methods (e.g., HDF5...)
- Validation of interfaces for analysis (esp. Matlab, Python, etc.)
- Integration of multi-parameter image-based search
- Analysis repositories
- Data sharing & publication

OME : 2013/2014 Progress

- *Software:*
 - OME Consortium: Ten teams
 - Bio-Formats & OMERO 4.4.x & 5.0.x releases
 - Good adoption
 - >60k Bio-Formats, ~2K server, ~4K client, ~1K web server
 - Consortium releases: FLIMfit, U-Track, Searcher, ImageJ2, Figure, mtools, csvtools, webtagging, biobank, WND-CHRM, ...
 - Search...
 - QA
 - Community & Documentation
- Several external examples of our work
 - Harvard LINCS
 - JCB DataViewer
 - Stowers ODR
 - SSBD, Riken
 - EMDatabank– 134 3D tomograms
 - Dundee Virtual Microscope
 -

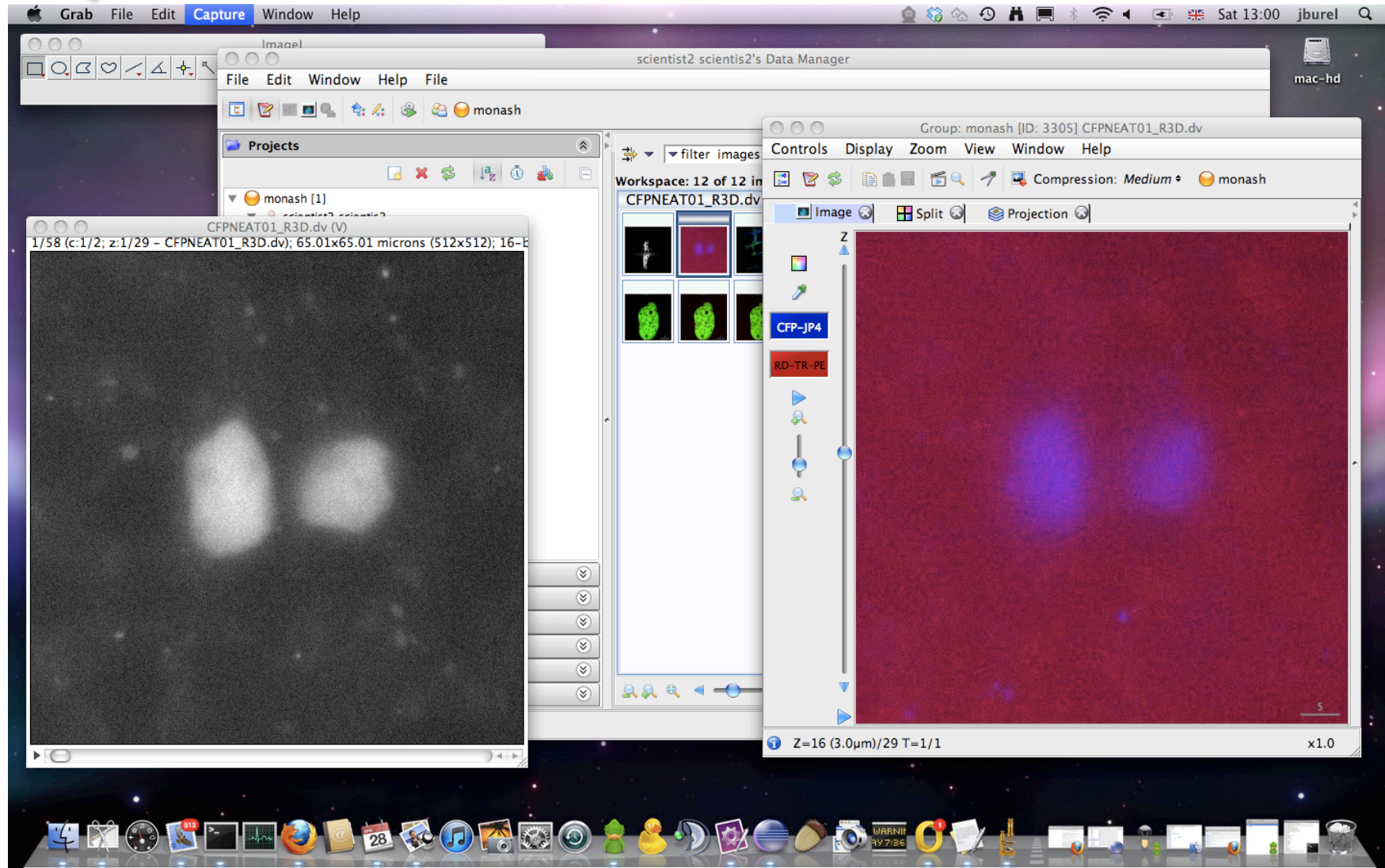
OMERO & BIO-FORMATS: Data Import & Access



OMERO-5.0 includes OMERO.fs, released Feb/2014 (Google: “OMERO 5.0”)



OMERO and ImageJ2





OMERO & mtools

The screenshot displays four windows from the OMERO mtools interface:

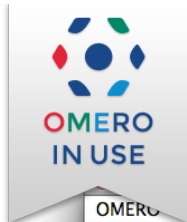
- Image Analysis:** Shows login fields for Username (jbloggs), Password (*****), and Server (nightshade.openmicroscopy.org.uk). It includes a list of experimental conditions (Control, Plk1 RNAi, Aurora B RNAi, SDS22 RNAi) and an "Analysis Type" section with radio buttons for 2D/3D Intensity Measure, Distance Measure, Line Measure, Event Timer, FLIP, and FRAP. A "Begin Analysis" button is at the bottom.
- Image Segmentation:** Features a "Select Image" dropdown (090829_HeLa_siCTL_coilin_ATUB01_02_...), a "Segment" dropdown (457), and radio buttons for "Group Objects" and "Separate Objects". It includes sliders for "Min Object Size" (1), "Expand mask" (0), and "Threshold" (838). A "Verify Z-sections" checkbox is checked. A "Save mask to server" checkbox is also checked. A "Reset default" button is next to the "Otsu thresholding" radio button. A "Slide for threshold" slider is visible at the bottom right. A "Begin Analysis" button is at the bottom.
- lineSelector:** Shows "Valid 'Ref' lines" (Ref1, Ref2, Ref3, Horizontal) and "Select a line" (Cell1, Body1). It includes a "Measurement queue" with entries like "Cell1 relative to Ref1" and "Body1 relative to Ref1". Buttons for "Add ->", "Add All ->", "Remove", and "Remove All" are present. A "Finish" button is at the bottom.
- objectSelector:** Displays a multi-channel image with a "617" dropdown and "Z: 2" and "Z: 6" sliders. It includes a "1. Choose channels to measure." step and a "2. Click on the object in the top window that you want to measure from." step. A "3. Click on the object in the bottom window that you want to measure to." step and a "4. Click the 'Accept' button." step are also present. An "Accept" button is at the bottom.



OMERO & u-track

The screenshot displays the OMERO Data Manager interface. The main window is titled "Sebastien Besson's Data Manager". On the left, a "Projects" sidebar shows a tree view with folders for "Sebastien Besson", "Biosensors [1]", "KMT [1]", "Tracking [3]", "Microtubules [1]", "QFSM [3]", "Single particle [2]", and "Orphaned Images". The "movie4CSUX488" folder is selected. The central workspace shows "Workspace: 1 of 1 image" with the image "movie4CSUX488 (Feb 5, 2013)". A toolbar above the workspace includes icons for filter images, zoom, and other image manipulation tools. On the right, a "General" tab is active, displaying "Image's details" and "Annotations". A yellow sticky note is overlaid on the annotations section, containing the following text: "Name: LCCB-analysis.zip", "Owner: Sebastien Besson", "File ID: 1786781", "Date Added: Thursday, July 18, 2013 11:16:50 AM BST", "Size: 2.8 Kb", and "Added by: Sebastien Besson".

In the foreground, a "Movie" window shows a large image with numerous red and white tracks overlaid on a dark background. Below this, a "Control Panel - U-Track" window is open. It features a menu bar with "File", "Debug", and "About". The main area displays "U-Track" and "Movie: /Users/sebastien/omero/3921662/movie.mat". There are navigation buttons for "Movie 1 of 1". Below this, there are three steps: "Step 1: Detection" (checked), "Step 2: Tracking" (checked), and "Step 3: Track analysis" (unchecked). Each step has "Setting" and "Result" buttons. A "Run" button is at the bottom, along with a "Force Run" checkbox. At the very bottom, there are "Movie Details...", "Save", and "Exit" buttons.



OMERO & FLIMfit

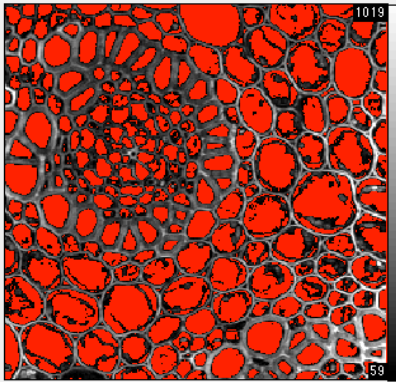
FLIMfit 4.3.2

OMERO File IRF Background Segmentation Tools Test Help

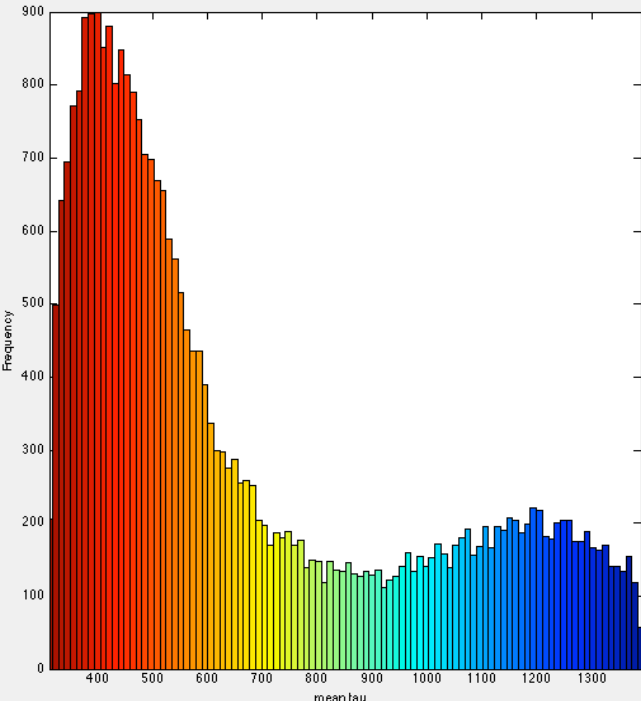
Dataset

	nm	File...
1	740	conv...

Mode: Integrated Intensity



Decay Parameter Images Gallery Histogram Correlation Plotter Plate



Plot	Di...	Me...	Min	Max	Auto
tau_1			1370	5930	<input checked="" type="checkbox"/>
tau_2			148	744	<input checked="" type="checkbox"/>
beta_1			0.0371	0.2930	<input checked="" type="checkbox"/>
beta_2			0.7070	0.9630	<input checked="" type="checkbox"/>
I0			5.4100	44.8000	<input checked="" type="checkbox"/>
I			67	638	<input checked="" type="checkbox"/>
mean_tau		<input checked="" type="checkbox"/>	312	1390	<input checked="" type="checkbox"/>
w_mean_...			867	3130	<input checked="" type="checkbox"/>
chl2			0.3900	1.2500	<input checked="" type="checkbox"/>

Reference Lifetime: 80
BG is Afterpulsing: Yes
Time Min.: 0
Time Max.: 1.245e+04
IRF Shift: 0
G Factor: 1

Parameter: mean...
Weighting: None
Classes: 100
Add False Colour: On
Source Data: Select...

Progress

Param	Type	Value
im_group		1
region		1
success %		99.9243
iterations		705421



OMERO.searcher

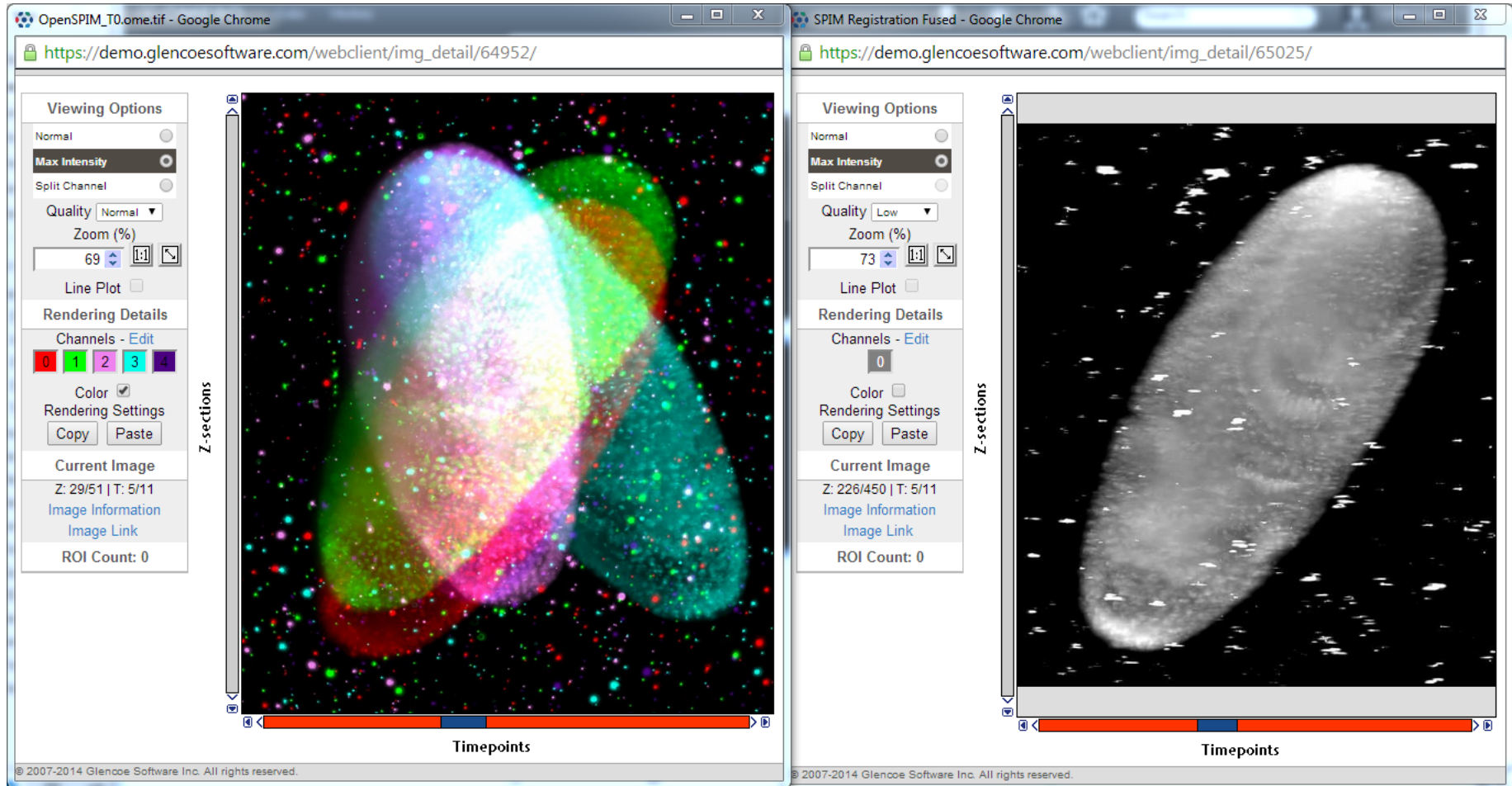
The screenshot displays the OMERO search interface. The top navigation bar includes 'OMERO', 'Data', 'History', and 'Gallery'. The user is logged in as 'Jason Demo'. The main area shows a grid of microscopy images with a 'Filter Images' search bar. On the left, a file tree shows a folder 'INCENP Staining 2' containing a subfolder 'PTRE 34' with various image files. On the right, the 'Image Content Search' panel is active, showing search parameters: Featureset Name: slf33, Retrieved images: 100, and Search Against: Dataset 091212-14_siCTL_LPM [3]. A 'Do Search' button is present. Below the search parameters is a table of search results.

Image	C.Z.T	Name	Negative	Positive
	0.27.0	jason_PTRE_P-TRE_19_R3D_D3D.dv.ome.tiff	<input type="radio"/>	<input checked="" type="radio"/>
	0.22.0	jason_PTRE_P-TRE_18_R3D_D3D.dv.ome.tiff	<input type="radio"/>	<input checked="" type="radio"/>
	0.42.0	jason_PTRE_P-TRE_11_R3D_D3D.dv.ome.tiff	<input type="radio"/>	<input checked="" type="radio"/>
	0.32.0	jason_PTRE_P-TRE_29_R3D_D3D.dv.ome.tiff	<input checked="" type="radio"/>	<input type="radio"/>
	0.32.0	jason_PTRE_P-TRE_17_R3D_D3D.dv.ome.tiff	<input checked="" type="radio"/>	<input type="radio"/>
	0.35.0	jason_PTRE_P-TRE_27_R3D_D3D.dv.ome.tiff	<input checked="" type="radio"/>	<input type="radio"/>
	0.40.0	jason_PTRE_P-TRE_5_R3D_D3D.dv.ome.tiff	<input checked="" type="radio"/>	<input type="radio"/>


BK Cho, Ivan Cao-Berg, Robert Murphy, CMU; Nature Meth, 9: 633-634
Simon Li, Univ Dundee



OMERO & Bio-Formats: LSFM MV Reconstruction



Emil Rozbicki & Chris Allan, Glencoe Software

Inspired by Preibisch et al. (2010) Nature Meth, 7: 418-419; http://fiji.sc/SPIM_Registration 



OMERO.biobank: Enabling Meta-Compute

The screenshot shows the Galaxy web interface. The browser address bar displays `seq.galaxy.crs4.it/#`. The main navigation bar includes **Galaxy**, **Analyze Data**, **Workflow**, **Shared Data**, **Visualization**, **Admin**, **Help**, and **User**. A status indicator shows **Using 8.2 TB**.

The **Tools** panel on the left lists categories: **Models**, **Phenotype Association**, **VCF Tools**, and **Seal**. Under **Seal**, several tools are listed with brief descriptions:

- Make Pathset**: Create a pathset for a set of files
- Cat paths**: Concatenate all components of a pathset into a single file.
- Split pathset**: Split a pathset according to a regular expression criteria
- Dist Bcl2Qseq**: Convert Illumina bcl files to qseq on Hadoop
- Demux**: Demultiplex Illumina runs on Hadoop

The **Saved Histories** panel features a search bar for history names and tags, an **Advanced Search** option, and a table of saved histories:

Name	Datasets
<input type="checkbox"/> sample_wf:130418_SN194_0302_AD1TWHACXX.Scarpa.LSa71.2013-05-09_04:18:08.784698	9
<input type="checkbox"/> sample_wf:130418_SN194_0302_AD1TWHACXX.Scarpa.LSa70.2013-05-08_22:44:42.392059	9
<input type="checkbox"/> sample_wf:130418_SN526_0229_AD1TYAACXX.Scarpa.LSa56.2013-05-08_17:31:33.041145	9
<input type="checkbox"/> sample_wf:130418_SN194_0302_AD1TWHACXX.Scarpa.LSa66.2013-05-08_15:46:59.411754	9
<input type="checkbox"/> sample_wf:130418_SN526_0229_AD1TYAACXX.Scarpa.LSa57.2013-05-08_12:51:26.984033	9
<input type="checkbox"/> sample_wf:130418_SN194_0302_AD1TWHACXX.Scarpa.LSa65.2013-05-08_12:21:27.215933	9
<input type="checkbox"/> sample_wf:130418_SN194_0302_AD1TWHACXX.Scarpa.LSa68.2013-05-08_11:04:34.384044	9

The **History** panel on the right displays a list of recent history items:

- 9: Demuxed (Scarpa.LSa70)
- 8: Demuxed (Scarpa.LSa69)
- 7: Demuxed (Scarpa.LSa67)
- 6: Demuxed (Scarpa.LSa65)
- 5: Demuxed
- 4: Check for index read on data 1
- 3: Sample sheet for /SHARE/USERFS/els7/users/sequencing/var/galaxy/files/004/dataset_4948.dat
- 2: Qseq

The URL at the bottom of the browser window is: `seq.galaxy.crs4.it/history/list?f-sharing=All&sort=-update_time&f-name=All&f-tags=All&f-deleted=False&operation=Switch&use_panels=False&id=94e2ba1f861e6..`



OMERO & BIO-FORMATS: Pathology Instruction/Dundee VM

The screenshot displays the OMERO web client interface. The top navigation bar includes 'OMERO', 'Data', and 'History'. The main content area is divided into a left sidebar for navigation, a central image gallery, and a right-hand details panel.

Left Sidebar (Anatomy):

- BS21007 Introductory Anatomy 2
 - BS21007 Practical 3 Epith CT Muscle 13
 - 14_Tendon.svs**
 - 15_Breast non lactating.svs
 - 16_Elastic artery.svs
 - 18_Mesentery.svs
 - 1_Lung.svs
 - 26_Heart.svs
 - 2_Kidney.svs
 - 3_Gall bladder.svs
 - 4_Trachea.svs
 - 5_Urinary bladder.svs
 - 6_Tongue.svs
 - 7_Oesophagus.svs
 - 8_Skin.svs
 - BS21007 Practical 5 Nervous System 6
- BS31002 Histology 8
 - BS31002 Practical 1 7
 - BS31002 Practical 2 5
 - BS31002 Practical 3 7
 - BS31002 Practical 4 4
 - BS31002 Practical 5 2
 - BS31002 Practical 6 4
 - BS31002 Practical 7 7
 - BS31002 Practical 8 5
- Orphaned images



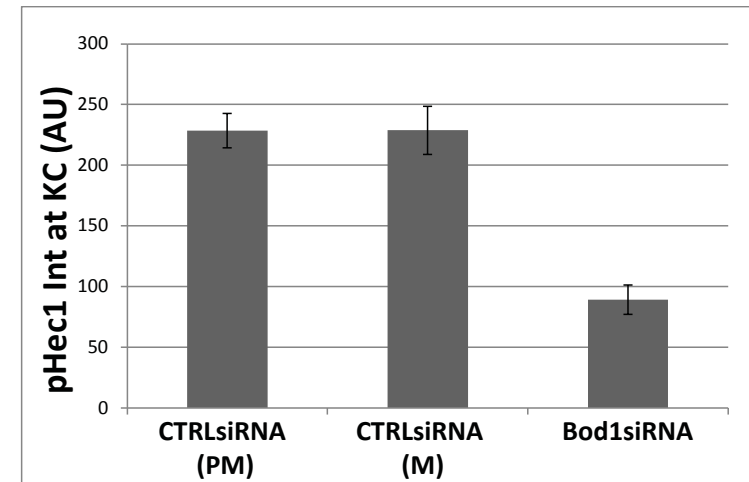
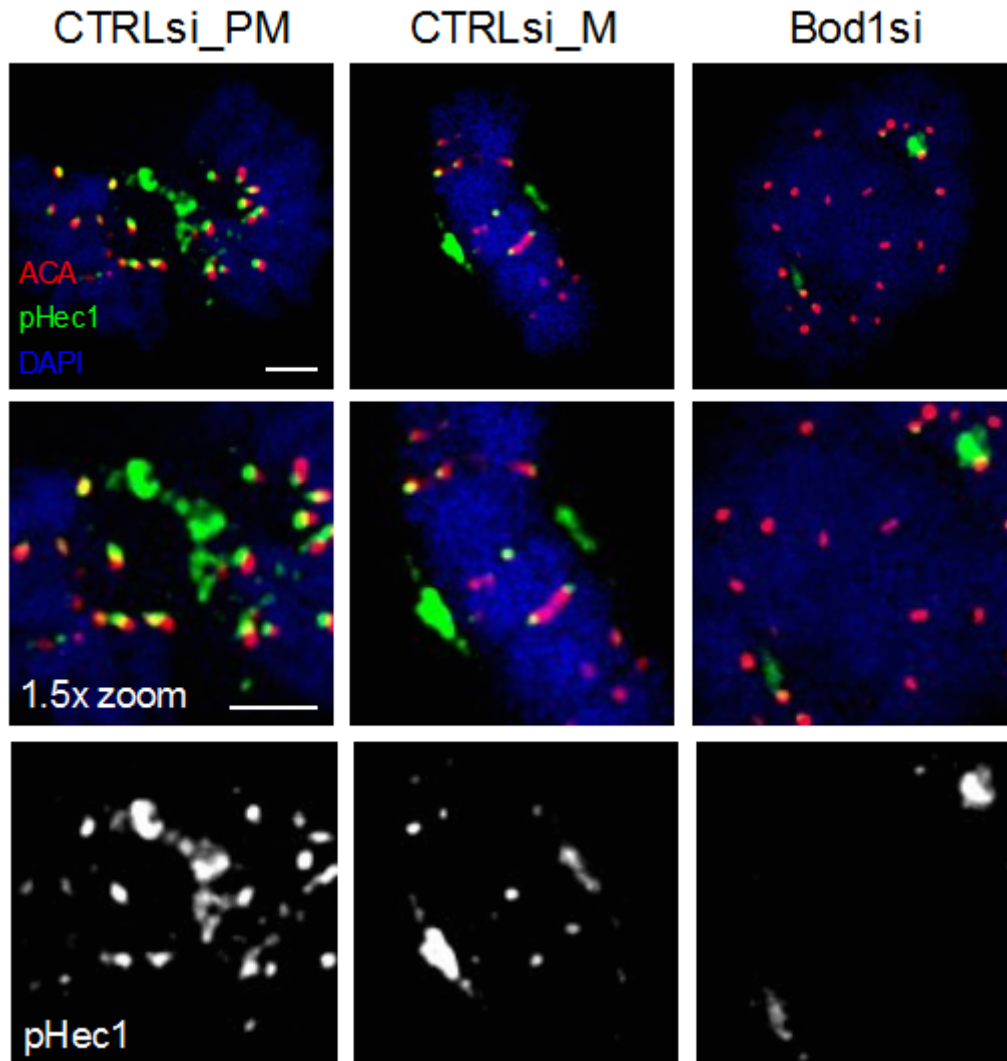
OMERO & Auto-Tagging

The screenshot shows the OMERO webclient interface. The browser address bar displays <https://omero1.bioch.ox.ac.uk/webclient/>. The user is logged in as Douglas Russell. The interface includes a navigation menu with 'Data', 'History', and 'Admin' options. A search bar and user profile are visible in the top right. The main content area shows a table of image processing results with columns for 'sqdGFP01', 'R3D', 'GLScy3', 'D3D', and 'Contrasted'. The 'selected' column is highlighted in green. The 'Image Name' column contains file names and their IDs.

sqdGFP01	R3D	GLScy3	D3D	Contrasted	selected	Image Name
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	020710_GLScy3_sqdGFP01_2_R3D_D3D.dv (19660)
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	020710_GLScy3_sqdGFP01_2_R3D_D3D_Contrasted.dv (42336)



Bod1 depletion reduces Hec1(Ser55) phosphorylation at the kinetochore



n = 10 cells per condition
(1000 kinetochores)





OMERO.figure



The screenshot shows a YouTube video player displaying a web browser window. The browser window is titled "OMERO.web Figure" and shows the OMERO.figure interface. The interface includes a navigation bar with "OMERO", "Figure", and "About" links. The main content area displays a grid of microscopy images. The grid is organized into two rows: "Control siRNA" and "Bod1 siRNA". Each row has four columns: "DNA", "Aurora B", "tubulin", and "merged". The "merged" column shows the combination of the other three channels. Below the grid, there are two larger images showing a zoomed-in view of the merged data. On the right side of the browser window, there is a "Labels" panel with tabs for "Info", "Preview", and "Labels". The "Labels" panel shows a "Scalebar" with a value of "10 μm" and a "Pixel Size" of "0.063 μm". There is also an "Add Labels" section with a dropdown menu set to "Bod1 siRNA" and a value of "12". Below the browser window, the video player shows a progress bar at "9:07 / 14:48" and the video title "Introducing OMERO.figure" by "William Moore · 61 videos". The video has "315 views" and a "Subscribe" button with "2" notifications. There are also "Like" (1) and "Dislike" (0) buttons.

Will Moore, Dundee (Google: "OMERO figure")

OME Community & Documentation

OME Community

Contact Us



You can contact us for help and advice by using the forums or mailing lists. Using these public feedback options means the whole community can take part and benefit.

Forums



Our [forums](#) allow the whole OME community to share their expertise and offer solutions.

Mailing Lists



We have two [mailing lists](#) for support-related requests and discussions.

Report a Bug



You can submit a bug report via our [QA system](#) for feedback and support.

Submit Files



Bio-Formats relies on the community to [submit example files](#) to improve support for different formats. Your data will never be shared unless you give us permission.

Sales Queries



Our commercial spin-out company, [Glencoe Software](#), handles [commercial licensing](#) and support contracting. If you are looking for a quotation for these services, please [contact them directly](#).

Project News

News and Events



Keep up with all the main project announcements and events via our [News feed](#).

Meeting Minutes



As an open source project, we are dedicated to openness. You can read all our [minutes](#) to keep up-to-date on what we are working on.

OME Help

Getting Started with OMERO.insight v. 5.0.2

[Download PDF](#)



User Help

[User Help Home Page](#)

▼ Quickstart User Guides

[Getting Started v. 5.0.2](#)

[Getting Started v. 4.4.11](#)

[Using ImageJ with OMERO](#)

[Try the OMERO Demo Server](#)

▼ Workflow User Guides

[Sharing Data](#)

▶ OMERO.insight

▶ OMERO.web

▼ Other OMERO Applications

[OMERO.figure](#)

[Virtual Microscope](#)

[OMERO.dropbox](#)

[OMERO.editor](#)

▼ More

[Guides for Previous Versions](#)

[Resources](#)

[Contact Us](#)

[Main OME Website](#)

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The Open Microscopy Environment

OMERO stores image data on a central server. You can use the OMERO.insight client to upload, view and download data from any personal computer.

Your institution's OMERO server administrator will provide you with the server address to use when connecting from OMERO.insight. They may have set up a user name and password for you too. Alternatively your username and password may be your standard login for the institution's networked computers.

Installing

1. Download OMERO.insight client at: <http://downloads.openmicroscopy.org/latest/omero5>



OMERO 5.0.2 Downloads

[Clients](#) | [Plugins](#) | [Additional](#) | [Servers](#) | [VirtualAppliance](#) | [API](#) | [Code](#) | [Artifacts](#) | [Legacy](#)

- Information on this release of OMERO is in the [release announcement](#)
- Full documentation is available as [web documentation](#) or [PDF documentation](#) and there are user guides for the clients on our [Help website](#)
- A standard OMERO user just needs to download the client package with the same major version as their institutional server e.g. 5.0 clients with the 5.0 server

OMERO client downloads

Clients	Size	File Name	Checksum
Windows	70.29 MB	OMERO.clients-5.0.2-ice35-b21.win.zip	3fb156 (MDS)
Mac OS X	205.68 MB	OMERO.clients-5.0.2-ice35-b21.mac.zip	55f177 (MDS)
Linux	68.44 MB	OMERO.clients-5.0.2-ice35-b21.linux.zip	a6e1a6 (MDS)

- Each client package includes [OMERO.insight](#), [OMERO.importer](#) and [OMERO.editor](#) and requires Java Version 1.6 or higher. OMERO.web is part of the server package, so individual users do not need to install it locally.

THE PRIORITIES

OME 4 & 5: 2012 -2014

OME 4.4.x & OME 5.0.x

- New UI Features
 - Permissions
 - Data Sharing & Publication
 - Tagging
- Performance....
- Analysis...
- Search...
- All bugs
- Consortium requirements
- *No API Breakage*
 - API Additions Possible
 - » OMERO.tables (for .searcher, WND-CHRM, .biobank, ...)
 - » Modulo (for FLIM, LSFM, OPT...)
- Aim: Supported, maintained API to end of current project

OME 5 and beyond: 2014→...

OME 5.1.x ...

- Decoupling Bio-Formats and OMERO releases
- *API Breakage*
 - Units
 - Map Annotations
 - New detectors
 - Rendering Settings
 - “New” imaging modalities (SRM, LSFM, OPT, ...)
 - ...
- Extended Metadata support
 - ROIs, Features, etc.
 - Graphs: (trajectories, provenance, ...)
- Data Sharing & Publication
 - Lab, Institute, Resource
 - National/Worldwide Repositories

Are these correct? Tell us what you think!!!!

What OME Means to You...

It's funding time....

- Written feedback is hugely valuable
 - Lists
 - Forums
 - Email to Jason
- Used to support requests for funding
- Defines our priorities

Without your feedback, we can't justify continuing our work.

OME Consortium

- Dundee – Jason Swedlow, Colin Blackburn, Jean-Marie Burel, Mark Carroll, Gus Ferguson, Helen Flynn, Kenny Gillen, Roger Leigh, Simon Li, Dominik Lindner, June Matthew, Josh Moore, Will Moore, Andrew Patterson, Blazej Pindelski, Balaji Ramalingam, Aleksandra Tarkowska, Petr Walczysko, Wilma Woudenberg
- University of Wisconsin, Madison (LOCI) - Kevin Eliceiri, Curtis Rueden, Mark Hiner
- UT Southwestern – Gaudenz Danuser, Sebastien Besson
- Oxford – Ilan Davis, Douglas Russell
- CRS4 - Gianuigi Zanetti, Gianmauro Cucurru, Simone Leo, Luca Lianas
- Edinburgh – Richard Baldock, Bill Hill, Jianguo Rao
- Carnegie-Mellon – Robert Murphy, BK Cho, Ivan Cao-Berg
- Imperial – Paul French, Chris Dunsby, Ian Munro
- NIA, NIH – Ilya Goldberg, Chris Coletta
- Pasteur – Spencer Shorte, Sebastien Simard, Julien Jorde
- EBI – Gerard Kleywegt, Ardan Patwardhan, Ingvar Lagerstedt
- Glencoe Software – Chris Allan, Joshua Ballanco, Andreas Knab, Melissa Linkert, Chris MacLeod, Josh Moore, Carlos Neves, Liza Unson, Wilma Woudenberg