OME

9th Annual OME User's Meeting
5th – 6th June 2014
Institut Pasteur, Paris

Acknowledgements

The OME Consortium would like to express our thanks to the Institut Pasteur for hosting the 9th Annual OME Meeting. We like to offer a special note of appreciation to Christiane Pacaud, Sebastien Simard, Sophie Gaudiard, Anne Danckaert, Nathalie Aulner and Spencer Shorte for all their work and support.

We are particularly grateful to the invited speakers for sparing their time and accepting our invitation to give an account of how they are using the project's tools in their respective fields of work.

Finally, our thanks to OME's funders, the Wellcome Trust and the BBSRC, for their continued support of our work, and in particular for their willingness to support the costs of the Annual OME User's Meeting.

About OME

OME is about sharing and access, and ultimately transparency and integrity. OME tools allow you to see and interact with image data, judge it for yourself, and communicate your ideas with others. OME is committed to the principles of open source software development and distribution, and collaboration with the community of scientists and developers who build tools to enable scientific discovery.

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Imperial College London

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Day 1 • Thursday 5th June 2014

13:00 – 14:00	*Buffet lunch*	
14:00 – 14:30	Registration	
14:30 – 14:40	Welcome and Introduction	*Spencer Shorte, Institut Pasteur*
14:40 – 15:30	OME Project Summary and Progress	*Jason Swedlow, University of Dundee*
15:30 – 16:00	'Bio-Imaging for the International Mouse Phenotyping Consortium'	*Gautier Koscielny, EBI*
16:00 – 16:30	*Coffee and Refreshments*	
16:30 – 17:00	'openBIS Importer Toolset (oBIT)'	*Aaron Ponti, ETH Zurich*
17:00 – 17:30	'Integrating OMERO into a correlative microscopy workflow: successes and struggles'	*Damir Sudar, Lawrence Berkeley Lab*
17:30 – 18:00	'Towards Precision Medicine: Translational Diagnostics, Feasability Research and OME'	*Karl Garsha, Ventana Medical Systems*
18:00 – 18:30	'The JCB DataViewer: Bringing new dimensions to published image data'	*Liz Williams, The Rockefeller University Press*
18:30 – 18:45	Poster Lightning Talks	
18:45 onwards	*Buffet Dinner and Poster Session*	

Day 2 • Friday 6th June 2014

09:00 – 09:15	Welcome	*Jason Swedlow, University of Dundee*

09:15 – 10:30 Workshops - Round 1

Room 1 - Working with OMERO.web
Presentation on customizing and extending OMERO.web with your own configuration and apps, followed by demonstrations of 'Virtual Microscope' and OMERO.figure

Room 2 - Administering OMERO in the real world
Troubleshooting your specific issues (note that our sysadmin will also be available for the rest of the day)

Room 3 - Acquisition and Analysis - how to integrate your tools
Presentations and demonstrations of integrated tools such as CellProfiler, FLIMfit, ImageJ, µManager, OMERO.webtagging and OMERO.searcher, as well as various MATLAB-based tools and Python scripting examples

10:30 – 11:00 *Coffee & Refreshments*

11:00 – 12:15 Workshops - Round 2

Room 1 - Working with OMERO.web Part 2
OMERO.web apps and further demonstrations as requested, see also the Acquisition and Analysis workshop

Room 2 - Managing imports with OMERO 5
Changes since OMERO 4 and discussion of import scenarios, migration and advanced admin issues

Room 3 - Acquisition and Analysis Part 2
Further demonstrations and discussion as requested, see also the OMERO.web workshop

12:15 – 13:30 *Lunch*

13:30 – 16:00 Workshops - Round 3

Informal software demonstrations and open discussion time. Your chance to meet and discuss with OME Consortium Developers or catch up on a demo you missed in the morning

14:45 – 15:15 *Coffee & Refreshments*

16:00 – 16:30	Summary & Close	*Jason Swedlow, University of Dundee*

Poster Abstracts

1. Data Organization in OMERO with OMERO.webtagging

Douglas Russell & Ilan Davis

University of Oxford, Department of Biochemistry

This poster describes the features and interface of OMERO.webtagging and how it benefits the biologist by matching (and extending) the organizational capabilities of a hierarchical filesystem within the OMERO framework.

OMERO is an excellent platform for storing imaging data, but the storage of data in a nearly flat hierarchy presents a challenge for users who traditionally make extensive use of many levels of hierarchy in a filesystem. Directory hierarchies are used to represent metadata of the contained images such as the fact that the images in a 'denoised' sub-directory have been denoised.

OMERO offers an alternative way of adding metadata to the images in the form of Tag Annotations. These are simple text labels that can be added to any Project, Dataset or Image. Many tags can be applied to one image and many images can have one tag applied to them.

Adding the tags manually can be a time consuming, manually exhaustive process that is usually a duplication of effort as this metadata is normally encoded into the directory structure and filenames of the originally imported data.

OMERO.webtagging [1] is an extension of OMERO.web [2] that streamlines the tag application process using automation and batch operation. The metadata encoded into the original path and filename of each image can be extracted and used to infer which tags should be applied to each image. OMERO.webtagging's interface also allows the user to create and apply new tags during this process as well.

A commonly expounded advantage of using a filesystem hierarchy is the ability to then browse the data; at each stage being offered a refined list of choices as an aide memoire. OMERO.webtagging also has a navigation component that offers this same capability, but for tagged data stored in OMERO. This is more powerful than navigating the filesystem because it avoids the problem of trying to find many identical directory names at different nested locations throughout the hierarchy.

OMERO.webtagging aims to improve OMERO usability by extending its organizational capabilities. This is driven by close user collaboration. OMERO.webtagging is developed at the University of Oxford, Department of Biochemistry in close collaboration with Micron Oxford [3], The Davis Lab, Oxford [4] and the Open Microscopy Environment.

[1] https://www.openmicroscopy.org/site/support/partner/omero.webtagging
[2] http://help.openmicroscopy.org/web-client.html
[3] http://www2.bioch.ox.ac.uk/microngroup/micron_home.php
[4] https://sites.google.com/site/davislaboxford/home

2. Omero and GigaScience for reproducible research

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Affiliation: GigaScience, BGI-HK Research Institute, 16 Dai Fu Street, Tai Po Industrial Estate, Hong Kong SAR, China.

GigaScience journal [1] is an Open Access, Open Data, scientific journal that aims "to revolutionize data dissemination, organization, understanding, and use." Beyond the traditional publication, GigaScience is linked to GigaDB [2], an Open Access repository for scientific data, and GigaGalaxy [3], a Galaxy Project [4] installation for sharing Open Source software tools and workflows. GigaScience is currently in the process of adding OMERO to this suite of knowledge sharing tools.

Originally, the journal was set up as a collaboration between BioMed Central [5] and the world's largest genomics research centre, BGI [6] specifically to promote reproducible research by opening data as well as access to publications. GigaDB, has acted as a repository for many genomics datasets produced by BGI e.g. the 40+ bird genomes recently released as part of the Avian Phylogenomic Project [7].

The evolution of the repository has seen the addition of imaging datasets such as micro-CT taxonomy of a novel centipede species [8] and it has recently recieved Optical Mapping data for some genomic sequences. To aid readers in visualising these images, OMERO has been chosen to present GigaDV (working title), a 'data viewer' for GigaDB image files. OMERO's ability to work with an extensive and growing variety of image formats meaning that GigaDV ought to be able to adapt to the changing technologies of contributors.

This poster presents a community announcement of GigaScience's OMERO based data viewer, describing the development and implementation of the web client, integration with existing repositories (GigaDB), challenges and future extensions.

[1] www.gigasciencejournal.com

[2] www.gigadb.org

[3] galaxy.cbiit.cuhk.edu.hk

[4] www.galaxyproject.org

[5] www.biomedcentral.com

[6] www.genomics.cn

[7] dx.doi.org/10.5524/101000

[8] dx.doi.org/10.5524/100063

3.   Community mining of high-throughput microscopy screens

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Despite the ground-breaking discoveries in genomics of the past decade, the genomes of most organisms remain black boxes with the function of the majority of genes and gene products still unknown. Moreover, many genes and proteins play roles in multiple biological processes themselves functionally linked, with those multiple roles and links still to be unravelled.

High-throughput/high-content microscopy-based (HT/HC) screening provides a powerful tool to discover and functionally annotate genes and biological pathways, and has led to several important discoveries, like the systematic identification of genes important for mitosis, endocytosis, and other fundamental processes. However, despite the power of this approach specialised large-scale image and data analysis methods are needed to produce phenotypic data, limiting such functional genomic annotation techniques to researchers of groups that possess that expertise. This means that the community at large is limited in their access to data and their ability to further mine HT/HC screens after publication, reducing the impact of those expensive projects. Overall, while technical advances led to an explosion in the amount of data being acquired, suitable data handling, visualization and analysis techniques are still lagging behind.

Here we propose a novel data visualization tool, which will allow the community to mine further the raw multidimensional feature data and knowledge from published HT/HC screens leading to a better exploitation of experimental results. The user interface allows the members of the community without any computational knowledge to extract meaningful information from the data. The web interface can be used for querying the data and the results are visualized as plots in real-time. The tool is based on a novel data model allowing the visualization and analysis of extremely large amounts of data. As a demonstrative example, we use phenotypic data extracted from a high-throughput fission yeast (*Schizosaccharomyces pombe*) screen carried out in our group.

4.   Integrating Woolz into OME

Bill Hill, IGMM, Edinburgh

Woolz, an open source image processing system, is used by IIP3D to allow the remote visualization of large 3D datasets with complex spatial annotation. We have integrated Woolz into Bioformats and IIP3D into OME; allowing Bioformats to read large Woolz memory mapped images and spatial annotation and OME to perform remote visualization of large 3D datasets with arbitrary sectioning, volumetric projection and morphological analysis.

5. Imaging for the International Mouse Phenotyping Consortium

Gautier Koscielny, EMBL-EBI

Authors: Ilinca Tudose [1], Jonathan Warren[1], Gautier Koscielny[1], Julian Atienza-Herrero[3], Andrew Blake[3], Chao-Kung Chen[1], Richard Easty[2], Armida Di Fenza[3], Tanja Fiegel[3], Mark Griffiths[2], Alan Horne[2], Neil Horner[3], Vivek Iyer[2], Natasha A Karp[2], Natalja Kurbatova[1], Thomas Lawson[3], Jeremy C Mason[1], Peter Matthews[2], Terrence F Meehan[1], Hugh Morgan[3], Asfand Qazi[2], Jack Regnart[2], Ahmad Retha[3], Luis A Santos[3], Duncan J Sneddon[3], Henrik Westerberg[3], Robert J Wilson[2], Gagarine Yaikhom[3], David G Melvin[2], Damian Smedley[2], Steve DM Brown[3], Paul Flicek[1], William C Skarness[2], Ann-Marie Mallon[3] and Helen Parkinson[1]

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[3] Medical Research Council Harwell (Mammalian Genetics Unit and Mary Lyon Centre), Harwell, Oxfordshire, OX11 0RD, United Kingdom

The International Mouse Phenotyping Consortium (IMPC) is building thefirst truly comprehensive functional catalogue of a mammalian genome. This global effort requires generating and characterising a knockout mutant strain for every protein-coding gene in the mouse. Data from a standardised, broad based phenotyping pipeline are collected and archived centrally by the IMPC Data Coordinating Center including imaging measurements in adult and mouse embryo at different developmental stages. Detection and quantification of morphological phenotypes in adult is achieved using high-throughput X-Ray phenotyping. Organ, tissue, substructure and cell type of gene expression is assessed by LacZ staining. Abnormalities in eye morphology are detected via non-invasive ocular imaging. Histology sections reveal pathological phenotypes and corroborate clinical phenotypes detected via other screens. Because 30% of the knockout mutant strains are expected to be embryoniclethal, a standardised pipeline for embryo has been developed to capture gross dysmorphology and more subtle defects. Three-dimensional volumetric imaging will help detect multi-organ abnormalities that single tissue or two-dimensional sections can easily miss. Imaging platforms include Optical Projection Tomography (OPT) at E9.5, High-resolution Episcopic Microscopy (HREM) and X-Ray Micro-Computed Tomography (μCT) at E14.5. Image annotation with biomedical ontologies allows biologists and clinicians to easily find mouse strains with phenotypic traits relevant to their research.

Users can freely access all data including new gene-phenotype associations and annotated images via APIs and an intuitive web portal. The community is invited to explore and provide feedback at:

www.mousephenotype.org

[1] The first 3 authors should be regarded as joint First Authors

6. **Adding Affine & Non-Linear 3D Reconstruction and IIP3D Visualization to OMERO 5**

J. Rao, N. Burton, B. Hill and R. A Baldock

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http://www.emouseatlas.org/

Here we demonstrate an use-case from the work of the eMouseAtlas group in Edinburgh developed to extend the new Open Microscopy Environment (OME) OMERO 5 image archive. A script, which can be used to build 3D volume from serial 2-D sections by rigid-body, full affine, or non-linear registration. We also, demonstrate the integration of the 3D image viewer (IIP3D), which enable an OMERO authenticated user to view sections of arbitrary orientation thought a 3D volume. The viewer extends the visualization option for the OMERO web-interface and allows the user to navigate through the volume using a WebGL implemented viewer. These extensions have been made possible by the integration of the image-processing system Woolz into bioformats and OMERO.

7. SSBD: an integrated database of spatiotemporal dynamics and microscopy data

Tohsato Yukako[1], Ho Kenneth H.L.[1], Kyoda Koji[1], Onami Shuichi[1,2] [1]RIKEN Quantitative Biology Center, Kobe, Japan , [2]National Bioscience Database Center, JST, Tokyo, Japan

Recent advances of imaging technology enable us to produce a large amount of quantitative data of spatiotemporal dynamics of biological objects such as molecules, cells, tissues, and organisms. This amount of data has created a need to provide a comprehensive approach for managing, visualising and analysing data and images. Systems Science of Biological Dynamics database (SSBD) is an open repository for quantitative data with spatiotemporal information and microscopic images used to produce them (http://ssbd.qbic.riken.jp). SSBD utilises OMERO.server internally to manage microscopic images and their metadata. Quantitative data are represented by using a unified data format, the Biological Dynamics Markup Language (BDML). BDML can represent spatiotemporal quantitative data from single-molecules to organisms. SSBD currently provides a wide variety of quantitative experimental data. There are 188 sets of quantitative data of nuclear dynamics in *C. elegans* (Kyoda et al., 2013; Bao et al., 2006) together with 33480 Z-stack microscopy images. There are also quantitative data of nuclear dynamics in zebrafish (Keller et al., 2008) and *D. melanogaster* (Keller et al., 2010). In addition, there are quantitative data obtained from computer simulation, e.g. microtubule-dependent nuclear dynamics in *C. elegans* (Kimura and Onami, 2005) and single- molecule dynamics in *E. coli* (Arjunan and Tomita, 2010). A web-based 4D viewer, which runs on any web browser with WebGL, allows easy access to visualise the quantitative data. A RESTful API allows 3rd party applications to access data directly from SSBD. SSBD provides a rich and useful resource of quantitative dynamics in BDML and microscopy data in OMERO.

8. Implementation of OMERO and PPMS on the basis of a central user database at a multi-user/system core facility

Tristan Nowak[1], Ralf Palmisano[1]

[1]Optical Imaging Center Erlangen, University of Erlangen-Nuremberg

The University of Erlangen-Nuremberg recently inaugurated a new central institute, the Opti- cal Imaging Center Erlangen (OICE), constituting a core facility where researchers are given the opportunity to perform professionally supported high- and super-resolution microscopy and image analysis on a multitude of systems. An OMERO server in combination with a PPMS booking system were chosen to provide a secure and flexible environment for users to store, share, analyze and remotely access their images as well as manage their bookings for OICE equipment. A web-based wiki system is also provided to introduce users to the on-site work- flow and regulations.

In order to give users the same account on all software modules, including the microscopy computers, a centralized user database was setup in the form of an LDAP directory and all relevant systems, including OMERO and PPMS were setup to authenticate with this directory. The LDAP directory is managed with the open source web frontend GOsa², which allows users to change their data centrally and makes it very easy for administrators to add new users to all modules that use the LDAP directory for authentication.

Overall, this approach provides a convenient way for users to work with the various IT solutions currently available at the OICE. New services can be easily added in the future without the users needing to create new accounts or remember any new passwords.

9. Combining the powers of ImageJ and OMERO

Curtis Rueden, University of Wisconsin

http://curtis.imagej.net/ImageJ-OME-Paris-2014-poster-abstract.pdf

ImageJ2 [1] is a new version of ImageJ for the next generation of scientific image data. Internally, it is a total redesign of ImageJ, but it is backwards compatible with ImageJ 1.x via a "legacy layer" including complete integration with the existing ImageJ user interface, as well as extensible support for new user interfaces. ImageJ2 has an Ndimensional data model driven by the powerful ImgLib2 library [2], which supports image data expressed in an extensible set of numeric and nonnumeric types, and accessed from an extensible set of data sources.

The ImageJ2 vision is to extend Java's mantra of "write once, run anywhere" to image processing algorithms. With that goal at its heart, ImageJ2 introduces extensible plugin and module frameworks [3] which make ImageJ commands richer, more powerful and easier to share across applications. ImageJ2 completely isolates the image processing logic from the graphical user interface (UI), allowing ImageJ2 modules to be used in many contexts; already, these modules are accessible from several software platforms including CellProfiler [4], KNIME[5], Alida [6] and OMERO.

This poster describes the basics of ImageJ's module framework while highlighting the integration of these modules from within OMERO on the server side. It also describes use of ImageJ as an OMERO client, including accessing and processing image data from an OMERO server. ImageJ is developed in close collaboration with related projects including Fiji [7], ImgLib2, SCIFIO [8] and OME, and strives to deliver a coherent software stack reusable throughout the life sciences community and beyond, so that scientists can truly "write once, run anywhere" and share with the world. For further details, see the SciJava web site: http://scijava.org/.

[1] http://developer.imagej.net/
[2] http://imglib2.net/
[3] http://github.com/scijava/scijavacommon
[4] http://cellprofiler.org/
[5] http://tech.knime.org/community/imageprocessing
[6] http://www2.informatik.unihalle.de/agprbio/alida
[7] http://fiji.sc/
[8] http://scif.io/

Technical details that the poster will discuss:

* Client side: Interacting with OMERO from inside the ImageJ application

* Server side: Executing ImageJ modules (including scripts!) from OMERO

* How it works: the SCIFIO-OMERO helper library

* How it works: adapting ImageJ modules into OMERO scripts

10.   Integrating OMERO and the Huygens Remote Manager

Niko Ehrenfeuchter [a], Aaron Ponti [b] and Daniel Sevilla [c]

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[c] Scientific Volume Imaging, Hilversum, NL

The Huygens Remote Manager (HRM) [1] is an Open Source, efficient multi-user web-based interface to the Huygens software for parallel batch deconvolutions. It is intended for centralizing computational resources for the 3D/4D/5D deconvolution of images from wide-field, confocal, spinning-disk fluorescent microscopes. Just recently, the capability for processing STED images was added to both, the Huygens core as well as the HRM.

Deconvolving microscopy images has become a standard restoration technique during the last decade, while it is still computationally expensive and thus a rate-limiting step in the analysis of the acquired data. However, it is an essential part of the workflow, allowing for increased resolution, better contrast and improved signal-to-noise ratio and is considered as a crucial element in quantitative and/or colocalization analysis. The Huygens software by Scientific Volume Imaging (SVI) [2] is one of the most advanced commercially available deconvolution and colocalization analysis packages available today. As one of its products, SVI offers Huygens Scripting, an engine that exposes all processing functionality of the Huygens Compute Engine for the automated restoration of datasets through scripts in a non-interactive way.

The HRM is a complementary tool providing a web-based interface that allows users to create jobs easily from their workstation and takes care of translating the job parameters into the scripts that are then passed on to the Huygens Compute Engine via a queue manager.

However, one of the most time-consuming manual steps is the actual transfer of the imaging data to a location where it can be processed by the HRM's queue manager. As the usage of OMERO is becoming more and more popular among scientists, especially in the context of imaging facilities, it is a natural decision to work on an integration of these two parts, OMERO for the data handling and HRM for processing and analysis. To keep the burden as low as possible, we decided therefore to develop an integration of OMERO's hierarchical user data tree into the HRM web interface, so scientists accustomed to using HRM in their workflow can use the integration with almost zero training. The HRM-OMERO connector is currently still work in progress [3] and will be integrated in the next HRM release 3.2.0.

It provides the user with an additional button in the files-related views of the HRM that can be used to log on to an OMERO server, which then shows the user's data tree and allows for transferring images directly from OMERO to the HRM for deconvolution as well as pushing back the processed results from the HRM into OMERO. The process is initiated and controlled by the user from its web browser, whereas the actual data transfer is running directly between the HRM and OMERO, this way providing maximum performance even when the user is logged on remotely to the HRM using a low bandwidth and/or VPN connection.

[1] http://huygens-rm.org/

[2] http://www.svi.nl/

[3] https://github.com/aarpon/hrm/tree/omero_remote

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