**The Open Microscopy Environment: Open Image Informatics for the Biological Sciences**

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**OME Overview**

Since 2000, the Open Microscopy Environment Consortium (OME; openmicroscopy.org) has developed software infrastructure—file formats, applications, and interfaces to enable interoperability between the myriad data formats and processing tools developed by academic and commercial developers-- for analysis, management and sharing of biological light microscopy data [1-5]. OME has successfully released:

- OME Data Model & OME-TIFF -- data specifications for imaging used by a large and increasing number of academic and commercial entities (openmicroscopy.org/site/support/file-formats);
- Bio-Formats-- a plugin for translating >120 proprietary file formats, used by >43,000 sites worldwide (openmicroscopy.org/site/support/bio-formats);
- OMERO-- an enterprise data management application used at >3,500 sites worldwide for managing scientific image data used as the foundation for a growing number of applications and image data repositories (openmicroscopy.org/site/support/omero4).

**Current Status**

With the tools provided by OME, we standardize data access interfaces, enabling interoperability while allowing data formats and analytic tools to evolve as necessary. Bio-Formats enables a single image processing application to access data from many different imaging systems—adapting to new data formats simply requires updating to a new version of Bio-Formats—and write OME-TIFF. OMERO reads images using Bio-Formats and provides access control, image viewing, and a standardized cross-platform programming interface, allowing users to access and process large sets of image data, all over standard internet connections. Both tools are used heavily worldwide. OMERO has been developed and released under funding from the Wellcome Trust and the BBSRC. Versions of OMERO have been released since 2007 (www.openmicroscopy.org/site/about/project-history/omero-version-history) with 2-3 releases of OMERO per year. OMERO is now installed and running in >3,500 sites worldwide, and a large community provides substantial feedback and commentary on its functionality and planned directions. OMERO is the foundation for a number of commercial products and community projects including the JCB DataViewer (jcb-dataviewer.rupress.org), the world’s first on-line scientific image data publication system.

**OMERO Technical Description**

OMERO.server (Figure 1) is a Java server application that mediates communication with a number of databases based on PostgreSQL, Lucene, HDF5, and an image file store. OMERO.server uses Hibernate for object-relational mapping, Lucene for text indexing, PyTables for accessing its HDF5-based tabular store, and...
ICE for object remoting. The simplicity, stability and cross-platform support in ICE means that this single framework defines a single OMERO application programming interface (API). This single API supports simultaneous access from Java, C++ and Python clients and can be extended to many other frameworks. OMERO was originally built to serve image data, but is increasingly used to serve non-image types of data as well. The core of the OMERO system consists of several representations of the OME-XML specification ([ome-xml.org](http://ome-xml.org)) transformed into source code using code generators (Figure 2). These are custom classes that generate Python, Java, and C++ code and SQL. This generated code is then compiled and used to build the OMERO.server application and store metadata in the relational database and to transmit the metadata to remote clients. This set-up facilitates model updates and corresponding client adaptations to support new and complex imaging modalities. A recent example is the inclusion of data types for describing high-content screening (HCS) experiments.

**OMERO Clients**

We have two main OMERO client applications. The first, OMERO.insight is a Java application (requiring Java 1.5 or higher) that enables data management, annotation, visualization and analysis. The second, OMERO.web is a web browser-based client application that provides access to OMERO’s data hierarchies, and enables annotation and visualization of data. A full list of the functionality in these clients is available at [www.openmicroscopy.org/site/products/feature-list](http://www.openmicroscopy.org/site/products/feature-list). To demonstrate OMERO’s flexibility and interoperability, we have built specific bridges between OMERO and ImageJ and CellProfiler, two popular open image processing tools, thereby making these tools clients of OMERO. Moreover, we have used an existing Java gateway in Matlab, the popular scripting tool for data analysis, to read and write data from OMERO. This allows any of the functionality within Matlab to be directed towards data within an OMERO installation.

**Recent Enhancements to Bio-Formats & OMERO**

Recent updates to Bio-Formats and OMERO have improved support for digital pathology images (so-called “Big Images”), high content screens, and large tabular arrays. Our latest release, v4.4, includes major updates to OMERO.web and improved access control facilities. We have positioned the OME team to work with satellite development sites to drive integration of complementary software or analytical tools with OMERO. Overall, our goal is to build great software tools that catalyse access and analysis of large, complex datasets.

**References**

ABOUT THE AUTHOR(S)

Jason Swedlow earned a BA in Chemistry from Brandeis University in 1982 and PhD in Biophysics from UCSF in 1994. After a postdoctoral fellowship with Dr T. J. Mitchison at UCSF and then Harvard Medical School, Dr Swedlow established his own laboratory in 1998 at the Wellcome Trust Biocentre, University of Dundee, as a Wellcome Trust Career Development Fellow. He was awarded a Wellcome Trust Senior Research Fellowship in 2002 and named Professor of Quantitative Cell Biology in 2007. His lab focuses on studies of mitotic chromosome structure and dynamics and has published numerous leading papers in the field. He is co-founder of the Open Microscopy Environment (OME), a community-led open source software project that develops specifications and tools for biological imaging. In 2005, he founded Glencoe Software, Inc., a commercial start-up that provides commercial licenses and customization for OME software. In 2011, Prof Swedlow and the OME Consortium were named BBSRC's Social Innovator of the Year and Overall Innovator of the Year. In 2012, He was named Fellow of the Royal Society of Edinburgh. Prof Swedlow is Co-Director of the Analytical and Quantitative Microscopy Course, an annual course that covers the latest developments in advanced quantitative light microscopy at Marine Biological Laboratory, Woods Hole, USA.