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

Jason R. Swedlow[1,2] and the OME Consortium[3]
[1]Centre for Gene Regulation & Expression, University of Dundee, Dundee, Scotland, UK.
[2]Glencoe Software, Inc. Seattle, WA, USA
[3]http://www.openmicroscopy.org/site/about/who-ome

***Abstract*—**Despite significant advances in cell and tissue imaging instrumentation and analysis algorithms, major informatics challenges remain unsolved: file formats are proprietary, facilities to store, analyze and query numerical data or analysis results are not routinely available, integration of new algorithms into proprietary packages is difficult at best, and standards for sharing image data and results are lacking. We have developed an open-source software framework to address these limitations called the Open Microscopy Environment [1]. OME has three components—an open data model for biological imaging, standardised file formats and software libraries for data file conversion and software tools for image data management and analysis.

The OME Data Model [2] provides a common specification for scientific image data and has recently been updated to more fully support fluorescence filter sets, the requirement for unique identifiers, screening experiments using multi-well plates.

The OME-TIFF file format [3] and the Bio-Formats file format library [4] are easy-to-use tools for converting data from proprietary file formats. These resources enable access to data by different processing and visualization applications, sharing of data between scientific collaborators and interoperability with third-party tools like Fiji/ImageJ.

The Java-based OMERO platform [5] includes server and client applications that combine an image metadata database, a binary image data repository and visualization and analysis by remote access. The current stable release of OMERO (OMERO 5.0; [6]) includes a single mechanism for accessing image data of all types-- regardless of original file format-- via Java, C/C++ and Python and a variety of applications and environments (e.g. ImageJ, Matlab and CellProfiler). OMERO includes SSL-based secure access, distributed compute facility, filesystem access for OMERO clients, and a scripting facility for image processing. An open script repository allows users to share scripts with one another. A permissions system controls access to data within OMERO and enables sharing of data with users in a specific group or even publishing of image data to the worldwide community. OMERO 5.0 includes updates and resources that specifically support large datasets that appear in digital pathology and high content screening. Importing these large datasets is fast, and data are stored in their original file format, so they can be accessed by 3rd party software. Several applications that use OMERO are now released by the OME Consortium, including FLIMfit, a fluorescence lifetime analysis module; u-track, an object tracking module; image-based search applications, OMERO.searcher and WND-CHARM; an automatic image tagging application, and also a biobanking application [7].

OMERO and Bio-Formats run the JCB DataViewer [8], the world's first on-line scientific image publishing system and are used to publish 3D EM tomograms in the EMDataBank [9]. They also power several large institutional image data repositories (e.g. [10], [11]).

All OME software is available at http://openmicroscopy.org.

[1] http://openmicroscopy.org

[2] http://openmicroscopy.org/site/support/ome-model/

[3] http://openmicroscopy.org/site/support/ome-model/ome-tiff

[4] http://openmicroscopy.org/site/products/bio-formats

[5] http://openmicroscopy.org/site/products/omero

[6] http://downloads.openmicroscopy.org

[7] http://www.openmicroscopy.org/site/products/partner

[8] http://jcb-dataviewer.rupress.org/

[9] http://emdatabank.org/

[10] http://odr.stowers.org

[11] http://lincs.hms.harvard.edu/