

## The Open Microscopy Environment: Informatics and Quantitative Analysis for Biological Microscopy

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Over the years, many advances have been made in instrumentation for light microscopy, and image analysis algorithms. However, computational cell biology remains out of reach for many investigators because file formats are proprietary, there are few facilities store, analyze and query numerical data or analysis results, integration of new algorithms into proprietary packages is difficult at best, and there are inadequate standards for sharing image data and results with colleagues. We have developed an open-source software framework to address these limitations called the Open Microscopy Environment (<http://openmicroscopy.org>). 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.

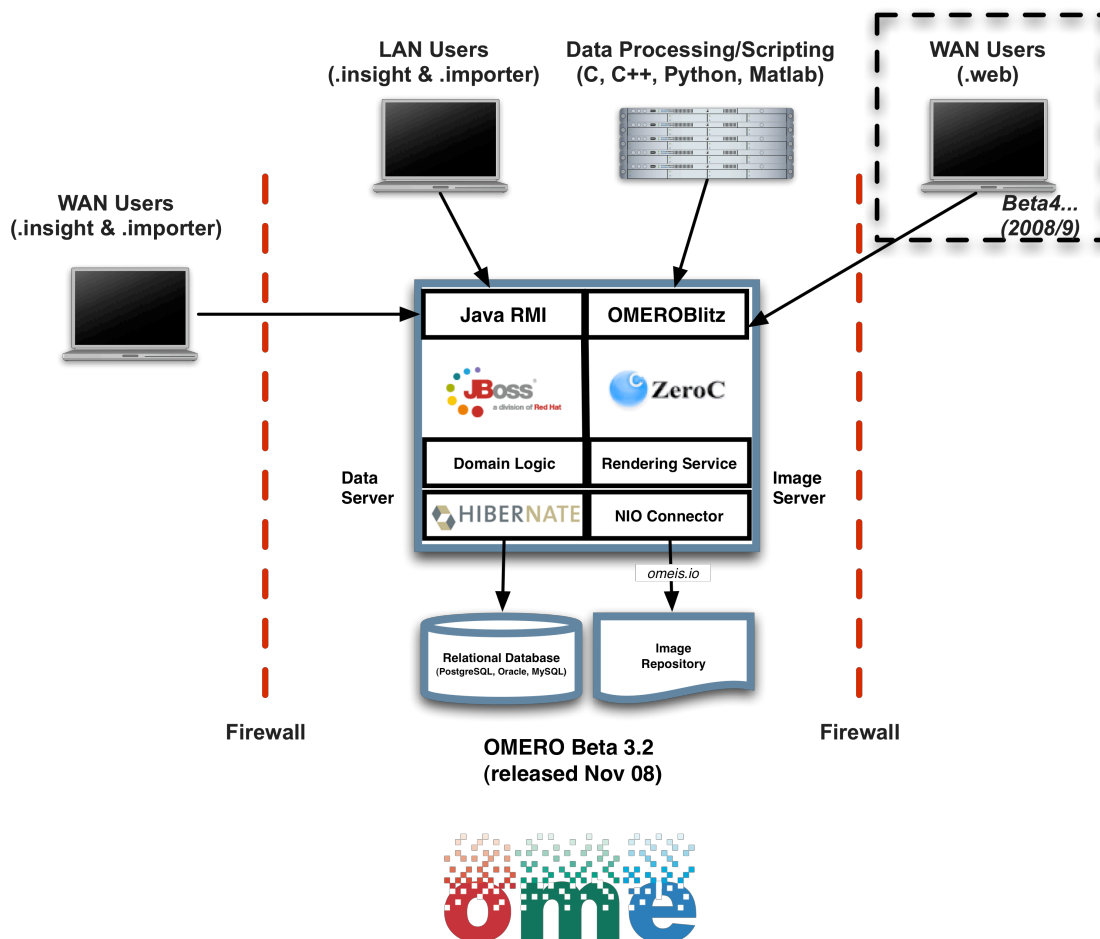
The OME Data Model (<http://www.ome-xml.org>) has recently been updated to more fully support fluorescence filter sets, the requirement for unique identifiers, including LSIDs, and screening experiments using multi-well plates.

The OME-TIFF file format (<http://www.loci.wisc.edu/ome/ome-tiff.html>) and the Bio-Formats file format library (<http://www.loci.wisc.edu/ome/formats.html>) provide an easy-to-use set of tools for converting data from proprietary file formats. These resources enable the access to data by different processing and visualization applications, and sharing of data between scientific collaborators.

The OMERO Platform is OME's Java-based server and client application suite that combines an image metadata database, a binary image data repository and an image rendering engine for a complete solution for image data management. OMERO includes OMERO.server, a Java application running inside a JBOSS application server, a web server OMERO.admin for user administration, OMERO.insight, a rich client developed in partnership with the Usable Image team (<http://www.usableimage.com>) for image data management, visualization, and analysis, OMERO.importer, a client application tool that uses Bio-Formats for proprietary data file import into an instance of OMERO.server, and OMERO.editor, an application for capturing and recording experimental protocols and other metadata. The Current release of OMERO.server (Beta3.2; <http://trac.openmicroscopy.org.uk/omero/wiki/MilestoneDownloads>) includes interfaces for C/C++ and Python to support a wider variety of client applications. This facility is achieved using the ICE library, which provides enables access from a wide variety of programming environments. Output analysis data can be stored as Structured Annotations—data structures that can be attached to any aspect of an Image or Experiment that can contain essentially any type of structured data in a defined namespace. Demos of OMERO functionality are available at

<http://www.openmicroscopy.org/site/videos>. Roadmaps and future work are available at <http://trac.openmicroscopy.org.uk/omero/roadmap>. Figure 1 shows the architectural outline of OMERO, emphasising the components of OMERO.server.

All of these tools are focussed on delivering interoperability between image software applications. Rather than focus our efforts on defined data standards that may or may not work in any given situation, OME builds software tools that function as interfaces between as many applications as possible ultimately with the goal of delivering the flexibility needed by experimental biologists.



**Figure 1. Architecture of OMERO.server and OMERO clients.** The layout of the OMERO.server is shown, with a range of different client applications using the same interface for communication. For a full description of the components of OMERO, see <http://trac.openmicroscopy.org.uk/omero/wiki/ServerDesign>.