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

Jason R. Swedlow[1,2]

1. Wellcome Trust Centre for Gene Regulation & Expression, University of Dundee, UK
2. Glencoe Software, Inc. Seattle, WA, USA

jason@lifesci.dundee.ac.uk http://ome-xml.org/, http://openmicroscopy.org/

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. 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 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 and the Bio-Formats file format library provide an easy-to-use set of 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 in third party tools like Fiji/ImageJ.

The Java-based OMERO platform includes server and client applications that combine an image metadata database, a binary image data repository and high performance visualization and analysis. The current release of OMERO (Beta4.3) 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). Support for large images from digital pathology is now included. This version of OMERO includes a number of new functions, including SSL-based secure access, distributed compute facility, filesystem access for OMERO clients, and a scripting facility for image processing.

Biography

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.