

OME: An Image Informatics Toolbox for Functional Genomics

Goldberg, I.G.¹, Hochheiser, H.¹, Johnston, J.¹, Orlov, N.¹, Sorger, P.², Creager, D.², Hughes, B.², Swedlow, J.R.³, Burel, J.³, Allan, C.³, Falconi, A.³, Brauner, E.O.⁴.

¹Laboratory of Genetics, NIA/NIH-IRP, Baltimore, MD, USA; ²Department of Biology, MIT, Cambridge, MA, USA; ³Wellcome Trust Biocentre, University of Dundee, Dundee, Scotland, UK; ⁴Institute for Chemistry and Cell Biology, Harvard Medical School, Cambridge, MA, USA

The Open Microscopy Environment (OME) is a system of open-source software and information standards for optical light microscopy (<http://openmicroscopy.org>). The standards defined by OME facilitate universal access to five-dimensional image data (XYZ, wavelength, time), acquisition parameters (light sources, filters, objectives), and computed results (statistics, derived images, extracted features, etc). OME provides two ways of representing this information: a database used by OME software and software-independent text-based XML files. These XML files allow exchange of imaging information between independent software platforms without data loss, far beyond the simple exchange of pixel data afforded by TIFF files. Extensibility of the types of data stored in OME is built into the system. OME software will automatically extend the database when encountering new data definitions in OME XML files. This file standard can be used together with proprietary formats to supplement the information stored in existing image files. OME XML files can also specify interfaces for existing image analysis utilities so that they can be used in user-constructed analysis chains. This allows OME to be used as a generalized image processing toolbox that brings together utilities from a variety of sources. These utilities (or modules) can be linked together into analysis chains to perform a complex series of image processing steps. OME uses semantic types to link modules together into analysis chains. Semantic types are a mechanism of assigning a meaning to a piece of data and allow the data to be shared by different modules that agree on a common meaning. Since the user is free to define new semantic types, an analysis chain can easily contain semantic types from microscopy, image analysis, and general biology. We believe that this flexibility will finally bring about the routine use of high-throughput quantitative microscopy for functional genomics.

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