

BioImageXD - a high performance free open source software framework for multi dimensional biological image visualisation, processing and quantitative analysis.

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Modern biomedical imaging methods such as time-lapse fluorescence microscopy and MRI/CT/PET produce gigabytes of data. These techniques have thousands of users. Scientists need cheap, simple and effective access to advanced multidimensional image visualisation, processing and analysis tools for making biological sense of this wealth of information. Commercial solutions cost tens of thousands of €/license, restricting availability to a few licenses at large institutions and core imaging facilities. Their use of proprietary algorithms make scientific interpretation of results near impossible as the algorithms are not disclosed in full as source code. In contrast, the BioImageXD project provides a software framework with a biologist friendly graphical user interface to access modern 2D/3D/4D/xD visualisation methods, quantitative image analysis algorithms, movie generation, scripting for batch processing of many datasets, and a simple development framework for addition of new visualisation and analysis methods. BioImageXD is free and open source (GPL), enabling all scientists, students and programmers to use it and to take part in a collaborative, rapid software development process, prioritise the most needed tools, contribute home-grown algorithms and methods, pool and share functionality, knowledge and discussion, and prevent duplication of effort. Further refinement and addition of required new functionality to BioImageXD, along with it's increased use in biomedical research, promises a leap in quantitative biomedical imaging output, greatly reduced software costs and better communication of 3D biomedical imagery to the public and other sciences. The BioImageXD project gives biologists easy access to those methods, increasing data throughput and scientific output.

BioImageXD runs on all modern operating systems, personal computers, super computers and clusters, and comes with a comprehensive user manual. Present features include: 3D, 4D, xD multidimensional data support, slices, MIP, orthogonal sections, gallery, and 3D views with hardware accelerated 3D volume rendering with 3 arbitrary clipping planes and multiple transparent surfaces rendering. Fully user defined colour and opacity look up tables for each data channel with colour merging, brightness - contrast - gamma adjustment, and data export. Native reading of Zeiss .lsm, Olympus .oif, Leica files and numbered image stacks. Quantitative analysis functions including calculation of colocalisation statistics, various filtering and segmentation methods, and object tracking over time. The sophisticated animator module allows generation of best in class free rotation / fly through movies of volume rendered multi channel 3D time series data. BioImageXD is in active development. We are implementing image deconvolution methods and parallel supercomputer/cluster support. BioImageXD is hardware accelerated with multithreaded execution for multiple processors/cores, vectorised binaries for SSE and AltiVec CPU extensions, and hardware accelerated 3D rendering on modern graphics cards. BioImageXD is written mostly in Python/xwPython for rapid development and simple implementation of new methods as python modules, with intensive calculations coded in python wrapped C++ for speed. BioImageXD relies heavily on the open source toolkits VTK.org and ITK.org for 3D graphics rendering and image processing/segmentation. The Windows beta version installer of BioImageXD is available at <http://www.bioimagexd.net> along with the user manual, mailing lists and other information. Linux and Mac OSX versions are in development, and already run from the source code. Read more about BioImageXD in the May 2006 issue of "Microscopy Today". The BioImageXD project is the future of open source collaborative software development in biomedical imaging.