FIJI (ImageJ)

Cell Profiler

Cell Profiler Analyst

Bio Image XD
FIJI (ImageJ)

- http://fiji.sc/

- „Fiji Is Just ImageJ." (ImageJ2 – beta1 at 9.4.2012)
- „Fiji is an image processing package."
- „It can be described as a distribution of ImageJ."
- „Fiji compares to ImageJ as Ubuntu compares to Linux."

- easy to install (just extract and run)
- has an automatic update function
- bundles a lot of plugins
- offers comprehensive documentation, tutorials
FIJI (ImageJ)

- Linux
- Linux (64-bit)
- Windows
- Windows (64-bit)
- MacOSX
  (only limited support for PowerPC (G4/G5) Macs)
FIJI (ImageJ)

- Fiji is released under the General Public License.

- Each component has its own license:
  - GPL: General Public License (latest) as specified at http://www.gnu.org/licenses/gpl.txt
  - GPL 2: General Public License version 2
  - LGPL: Lesser General Public License as specified at http://www.gnu.org/licenses/lgpl.html
  - AGPL: Affero General Public License as specified at http://www.gnu.org/licenses/agpl.html
  - PD: Public Domain
  - CPL 1.0: Common Public License 1.0 (http://eclipse.org/legal/cpl-v10.html)
  - PSF 2: Python Software Foundation Version 2
  - JSF 2.1: Jython Software License 2.0, 2.1
  - JPSL: JPython 1.1.x Software License
  - SPL: Sun Public License
  - MPL: Mozilla Public License as specified at http://www.lowagie.com/iText/MPL-1.1.txt
  - BSD: Berkeley Software Distribution
  - BSDR: BSD-like license allowing use for research
  - EPL: Eclipse Public License (http://opensource.org/licenses/eclipse-1.0.php)
  - AL: Apache License (http://xmlgraphics.apache.org/batik/license.html)
  - ?: UNKNOWN
FIJI (ImageJ)

- Extract and run

- Interactive affine transform
FIJI (ImageJ)

- File - File input/output, new files
- Edit - Selection/ROI handling
- Image - Visualization, stack manipulation
- Process - Image filters (noise, FFT, …)
- Analyze - Statistics (histogram, scale, …)
- Plugins - Plugins, Macros and Utilities
- Window - Windows
- Help - Help & Links
FIJI (ImageJ) - Segmentation

- Advanced Weka Segmentation
- Auto Local Threshold
- Auto Threshold
- Dithering
- Graph Cut
- Gray Morphology
- Level Sets
- Maximum Entropy Threshold
- Minimum Splits and Mergers Warping error
- Mixture Modeling Thresholding
- Multi Otsu Threshold
- Nuclei Watershed Separation
- RATS: Robust Automatic Threshold Selection
- SIOX: Simple Interactive Object Extraction
- Segmentation of neuronal structures in EM stacks challenge - ISBI 2012
- Simple Neurite Tracer
- Topology preserving warping error
- TrackMate

(30 plugins)
FIJI (ImageJ)

- Java
- Scripting with Macros
  - Beanshell
  - Javascript
  - JRuby
  - Jython
  - Clojure
- Using Interpreters
  - Beanshell
  - JRuby
  - Jython
  - Clojure

Image processing group
FIJI (ImageJ)

- Script Editor
CellProfiler

- Free open-source software.
- Enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically.

CellProfiler Analyst

- Free open-source software.
- SW for exploring and analyzing large, high-dimensional image-derived data.
- Includes machine learning tools for identifying complex and subtle phenotypes.

http://www.cellprofiler.org/

based on Python 2.7
CellProfiler \(^{(r11710)}\)
- MAC
- Win32
- Win64
- Linux

Analys 2.0 \(^{(r11710)}\)
- MAC
- Windows
- Linux (only V1.1 – Java 1.6)

PDF and Video documentation
Fly Images tutorial

- Images
- Modules pipe
- Settings
- Analyze
Fly Images tutorial

• a few outputs
CellProfiler

- Free open-source software.
- Enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically.

CellProfiler Analyst

- Free open-source software.
- SW for exploring and analyzing large, high-dimensional image-derived data.
- Includes machine learning tools for identifying complex and subtle phenotypes.
Used for

- visualization and exploration of high-throughput data
- visualizations are interactive and linked to the image data
- visualization of quality-control results from a screen
- normalization of results to correct systematic errors

- requires MySQL database
- Classifier
- Table, Image, Plate viewer
- Scatter, Histogram, Density, Box plot
Classifier

- allows to train the computer to identify objects
Plate viewer

- tool for browsing image-based data laid out on multi-well plates common to high-throughput biological screens.
Table, Image viewer
- display tables, images
Scatter, Histogram, Density, Box plot

- allows to create plots
• For Developers

https://github.com/CellProfiler/CellProfiler/wiki

- Source code - CP, CPA
- Bugs and Feature Requests
- Installation (Linux, Mac, PC)
  (Python, CellProfiler's libraries and dependencies)
- Writing a CellProfiler module
BioImageXD

- [http://www.bioimagexd.net](http://www.bioimagexd.net)
- Version 1.0 Release Candidate 3 (r1789) 05/2012
  - first beta at 02/2006
- free open source software project for analyzing, processing and visualizing of multi dimensional microscopy images
- written in Python and C++,
- using wxPython for the GUI,
- uses ITK and VTK
- Mac OS X 10.6/10.7, Windows 32b/64b, Linux 64b
  - *old documentation* (2007)
Features

- Supports many file formats (tiff, png, jpg, VTK xml, mrc, ...)
- Image viewing modes (slices, gallery, orthographic sections, intensity projection, 3D rendering)
- 3D modules (ray casting, texture mapping, surface rendering, warping, ...)
- Animator (videos, animations, keyframes, ...)
- Image processing (color, brightness, contrast, noise, registration, deconvolution, ...)
- Batch processing (multiple parallel processing pipelines)
- Quantitative analysis (3D segmentation, object analysis, motion tracking, ROI analysis, ...)

BioImageXD
BioImageXD

Gallery
BiolmageXD

3D mode
BioImageXD

Merge 3D
Batch processor
BioImageXD

Animator
- video
Examples

**ORIGINAL IMAGES** vs **COLOCALIZATION IMAGES**

- **5 min**
  - 2.0% volume colocalized
  - M1 = 0.14
  - M2 = 0.42
  - p-value = 0.05

- **10 min**
  - 2.2% volume colocalized
  - M1 = 0.20
  - M2 = 0.43
  - p-value = 1.00
That's All Folks !