

Fiji Is Just ImageJ – an Open Source platform for biological image analysis

Pavel Tomancak¹, Stephan Saalfeld¹, Johannes Schindelin¹, Albert Cardona²

¹Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG)

PfotenhauerStrasse 108, D-01307 Dresden, Germany

²Institute of Neuroinformatics, Uni/ETH Zurich Winterthurerstrasse 190 Bau 55, Zurich 8057

E-Mail: tomancak@mpi-cbg.de,

Web: <http://pacific.mpi-cbg.de>; License: GPL; Source code: <http://pacific.mpi-cbg.de/cgi-bin/gitweb.cgi>

KEY WORDS: Image Processing, Open Source development, biological image analysis

Substantial portions of primary data in biology are in the form of images. The volume of raw image data has increased dramatically in recent years with wider adoption of high-throughput and high-content imaging technologies. There is an urgent need for extracting quantitative information from these massive datasets in order to address important biological questions in particular from the systems biology point of view.

We contribute towards addressing this need by developing **Fiji** (Figure 1), an Open Source distribution of the popular biological image analysis software ImageJ written in Java. Fiji has recently gained substantial international recognition documented by almost 19,000 downloads from over 10,000 unique IP addresses over the past year and sustained increase in traffic on the Fiji Wiki reaching a record 37,000 hits in March [1]. The popularity of the platform comes from the fact that Fiji is developed according to modern software engineering practices, is extensively documented through active Wiki pages [2,3], offers a broad range of **scripting languages** (Python, Ruby, Javascript, BeanShell and Clojure) for algorithmic prototyping, provides transparent system for automatic updates and most importantly, because an active interdisciplinary community of developers has formed around Fiji who use the platform to solve real biological problems. Fiji developers come from all over the world yet they meet regularly at coding sprints called '**hackathons**' that dramatically speed up the development of the platform. The innovative Open Source development strategies of the Fiji community have been recognized by inclusion in the prestigious Google Summer of Code in 2009 [4].

The power of Fiji is highlighted by the **Fiji projects** that include rigid and elastic registration of large light and electron microscopy acquisitions, hardware accelerated 3d visualization, segmentation, neurite tracing, feature extraction and many more. The common denominators of Fiji projects are close connections to ongoing biological research and extensive sharing of algorithms and code through common software libraries. One example of such a shared code base is the dimension-, storage- and data type-independent image processing library that enables seamless manipulation of massive microscopy datasets in Java. We will describe the benefits of Fiji for users as well as developers interested in solving biologically motivated image analysis problems and hopefully attract more talent from the imaging community to this emerging Open Source platform.



Figure 1: Fiji logo

[1] Fiji Wiki statistics [http://pacific.mpi-cbg.de/awesome/index.html#Unique visitors in each month](http://pacific.mpi-cbg.de/awesome/index.html#Unique%20visitors%20in%20each%20month)

[2] Fiji Wiki pages : <http://pacific.mpi-cbg.de/>

[3] Fiji YouTube channel : <http://www.youtube.com/user/fijichannel/>

[4] GSoC Fiji <http://socghop.appspot.com/gsoc/org/show/google/gsoc2009/fiji/>