



**Euro-BiImaging**  
European Research Infrastructure for Imaging Technologies in Biological  
and Biomedical Sciences

WP11  
Data storage and analysis

**Task 11.2**  
The image processing, modelling and computing challenge:  
Architecture, tools and construction planning

**Deliverable 11.4**  
Software for biological image analysis:  
Present state and future requirements

**Task leaders**  
EPFL

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**Executive summary:**

This report provides a review of the current state of public-domain bioimage analysis software and a preliminary (unfiltered) list of requirements and proposed actions for future developments. A good part of this information was gathered during a two-day workshop that we organized in Barcelona April 30- May 1, 2012. It brought together the major developers and users of imaging software for the analysis of biomedical images (cf Section 3). The focus was on open-source solutions—in particular, ImageJ—and other open architectures that facilitate the development of plugins and community-driven projects.

The three primary outcomes of the workshop, which are reported in the present document, are:

An up-to-date list of currently available open-source solutions with a documentation of usage (Section 2)

The summary of the panel discussions that were held on future requirements and efforts to federate the community with special attention to issues such as technology, strategy, community, and inter-disciplinarity (Section 4)

The creation of a new consortium: "Open Bio Image Alliance" which brings together the primary actors in the field (software and algorithm developers, biologists, and bioimaging scientists).

The mission of OBIA is summarized in Section 5. Its next task will be to draft a road map for Euro-Biolmaging based on data and ideas collected in the present document. The federating idea that emerges right away from the discussions is the necessity to create a web portal that would provide a common entry points for all users and developers of open-source software for bioimage analysis.

In the next six months, WP11 will run proof-of-concept studies. This will comprise the set-up of a web-portal in beta-version, which offers access to a limited number of interoperable plugins from different platforms (e.g. Fiji together with Icy plug-ins on PCS SPIM data from Dresden facility, offering restoration, registration and quantification tools to demonstrate user guidance). For the WP11 PCS, 4-8 users from the PCS run in WP6, 7 and 8 will be offered the possibility to test this web portal and to run the offered tools on their PCS data. This concept would make a very strong use-case for the future Euro-Biolmaging infrastructure regarding data analysis.

# 1. Introduction

## 1.1 Background

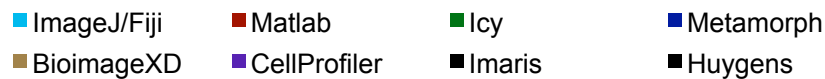
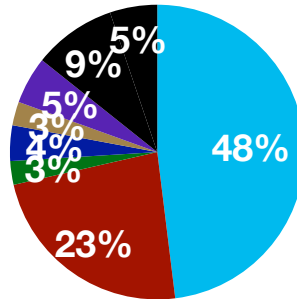
Bioimaging devices generate a huge amount of high-dimensional data in high-resolution format. The sheer amount of data is such that it generally becomes infeasible to visually inspect them all; moreover, it is highly desirable to automatize the extraction of objective quantitative features. These two issues highlight the importance of validated software tools as critical assets in the context of advanced light microscopy.

Currently, the software named *ImageJ* (<http://rsbweb.nih.gov/ij/>) is a major player in the context of bioimaging, so much so that it has become the *de facto* standard in the field. However, it is at a critical transition phase in terms of conceptual design and in terms of the manpower involved in its development. While this software is immensely useful, its current incarnation has numerous limitations that need to be addressed in order to secure its future usability. Fortunately, there are new versions on the way, as well as a number of alternative solutions (cf. Section 2) which have emerged during the past few years. While this plurality of solutions is a positive reflection of the dynamism of the community, it raises the important issue of interoperability of bioimaging software in general, which is still lacking in many respects. Euro-Biolmaging is a great chance to federate the efforts of the community by encouraging good practices, compatibility and by helping the users to find solutions that meet their needs.

## 1.2 Challenges

The improvement of ImageJ—and/or the development of alternative open-source imaging software—makes sense only if one is able to ensure the long-term continuation of the underlying community-driven efforts. Additional tasks involve modernization and enhancement to handle ever increasing amounts of multi-dimensional data, the facilitation of dissemination, and the offering of much needed resources to the existing large base of users and developers. Meanwhile, it is crucial to retain the capacity of an open community of independent contributors to participate. The main challenges will be to seek (rather than to impose) a consensus among developers, and to maintain backward compatibility.

So far, there has been little direct funding directly dedicated to the development of bioimage analysis software. The current offering, which is rather extensive, is largely the result of a grassroots effort entirely driven by the needs of the users. This is a rather unique situation in science. While this is highly commendable, the need for these tools has been growing steadily (if not exponentially); at the same time, more and more scientific projects crucially depend on them. The field is now ripe for some consolidation and organization which, at a minimum, would require some institutional funding to support a large-scale documentation and curation effort, the setup of some common web resources, and the launching of initiatives to promote good practices and software interoperability.

**Question: your main image-analysis software****1.3 Outcome**

This document provides a survey of the present state of open-source bioimage analysis software, and a detailed account of the discussions that were held on this topic at the European and international level during a workshop organized in Barcelona to address this specific purpose with an (unfiltered) list of propositions/ideas. The main outcome was the creation of a new consortium, OBIA (Open Bio Image Alliance), which brings together all the main players in the field. We consider this an important success because the participants in our discussions have agreed upon a common mission and strategy for the future, which was not obvious at the onset given the diversity of the community and the potential competition between various software packages.

**2. Open bioimage analysis software: present state****2.1 Statistics of usage**

For monitoring the usage of various software packages, we can use two surveys:

1. Survey of the workshop, April 30-May 1, 2012, 51 participants, 77 answers;
2. Survey of the Euro-Biolmaging, 2011, 128 participants, 393 answers.

The two surveys show clearly that ImageJ is the preferred software for end-users and developers alike. ImageJ comes first in both categories combined: open-source and commercial. Cell Profiler comes second in the open-source category and Matlab is first in the commercial category.

The majority of the participants to the Euro-Biolmaging survey are part of core facilities in microscopy, which explains the high score of the manufacturers' software.

## 2.2 Position of ImageJ (IJ)

Different image-analysis software packages have been implemented in the last decade. Nevertheless, one software has emerged and plays a particularly important role: ImageJ. It has overpassed all others in term of usability and diffusion in the biological community. ImageJ is the *de facto* imaging software and defines standards for extensibility through plugins.

1. ImageJ has an open-architecture which allows for the development of third-party plugins. A large part of the success of ImageJ is due to some popular plugins.
2. ImageJ has found a good balance between addressing the needs of users (mainly biologists and microscopists) and those of developers (mainly programmers and engineers). ImageJ is a platform for interdisciplinary research.

The omnipresence of ImageJ is confirmed by several facts: existence of various distributions of ImageJ, incorporation of ImageJ in software packages, presence of ImageJ in the majority of the core facility of microscopy, and presence of ImageJ in scientific publications.

ImageJ has also some drawbacks and limitations which make the future uncertain.

- limited model for the data;
- unclear separation between the GUI and data;
- old-style user interface;
- one-man development;
- lack of quality control of plugins.

## 2.3 List of software

Numerous software packages have been developed to analyze biological images. Hence, it may be impossible to list them exhaustively. The list of packages that we have retained was established based on the following criteria:

1. image-processing and image-analysis general purpose;
2. large basis of daily users, mainly biologists and microscopists;
3. framework for the development of specific tasks, perhaps extensible by adding plugins;
4. open-source to achieve the goal of reproducibility;
5. multi-platform, in particular Java-based software.

Most of the developers of packages fulfilling those criteria were present at the workshop.

The software are ordered by their relevance and their impact to the user community.

### ***ImageJ***

ImageJ is a public-domain, Java-based image-processing program developed at the National Institutes of Health. ImageJ was designed with an open architecture that provides extensibility via Java plugins and recordable macros. Custom acquisition, analysis, and processing plugins can be developed using ImageJ's built-in editor and a Java compiler.

- Author: Wayne Rasband, NIH, Bethesda MD, USA
- Type: End-user application
- Relation IJ: Classic ImageJ
- Language: Java
- License: Open-source
- Users: Very large base of user in biology and microscopy, also in other field

### ***ImageJ2***

ImageJ2 is a federally funded, multi-institution project to develop the next-generation version of ImageJ, an image-processing program widely used for scientific research. It wishes to strengthen both the ImageJ software itself and its community by pursuing a unified vision of ImageJ and associated community resources, including website, code and plugin repositories, and user and developer documentation.

- Author: LOCI, University of Wisconsin, Madison, USA
- Type: End-user application
- Relation IJ: Try to revamp ImageJ
- Language: Java
- License: Open-source
- Users: Few because ImageJ2 is very new, first beta version is dated of 9th of April 2012. ImageJ2 should be the successor of ImageJ.

### ***Fiji***

Fiji is an image-processing package. It can be described as a distribution of ImageJ (and soon ImageJ2) together with Java, Java 3D, and numerous plugins organized around a coherent menu structure. The main focus of Fiji is to assist research in life sciences. For users, Fiji is easy to install and has an automatic update function, bundles a lot of plugins, and offers comprehensive documentation. For developers, Fiji is an open-source project hosted in a Git version-control repository, with access to the source code of all internals, libraries, and plugins. It eases the development and scripting of plugins.

- Author: Multisite contribution (LOCI, University of Wisconsin, Madison, USA)
- Type: End-user application
- Relation IJ: Distribution of ImageJ and well known plugins
- Language: Java
- License: Open-source
- Users: Rapid expansion of the number of users in biology and microscopy

### **µManager**

µManager is a software package for the control of automated microscopes. Together with the image-processing application ImageJ, µManager provides a comprehensive, freely available, imaging solution. It has a simple and clean user interface, through which it lets you execute common microscope image acquisition strategies such as time-lapses, multichannel imaging, z-stacks, and combinations thereof. µManager works with microscopes from all four major manufacturers (Leica, Nikon, Olympus, and Zeiss), most scientific-grade cameras, and many peripherals (stages, filter wheels, shutters) used in microscope imaging.

- Author: Vale lab University of California, San Francisco, USA
- Type: End-user application
- Relation IJ: Work together with ImageJ
- Language: Java
- License: Open-source
- Users: Very large number of users in microscopy

### **CellProfiler**

CellProfiler is a free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically.

- Author: Broad Institute Imaging Platform, Boston, USA
- Type: End-user application
- Relation IJ: Enable to call ImageJ's macros
- Language: Python
- License: Open-source
- Users: Large number of users in biology

### **Biolmage XD**

Biolmage XD is a free open-source software project for analyzing, processing, and visualizing multidimensional microscopic images. It is a collaborative project designed and developed by microscopists, cell biologists, and software engineer.

- Author: Cell Imaging Core, Turku Centre for Biotechnology, Turku, Finland
- Type: End-user application
- Relation IJ: Plan to interoperate with ImageJ
- Language: Python
- License: Open-source
- Users: Large number of users in biology

### **OME**

OMERO is a client-server software for the visualization, management, annotation, and analysis of biological microscopic images. From the microscope to publication, OMERO handles all images in a secure central repository. You can view, organize, analyze, and share data from anywhere you have Internet access. Work with images from a desktop app (Windows, Mac, or Linux), from the web, or from third-party software.

- Author: Multisite collaborative effort among academic laboratories, Wellcome Trust

Centre for Gene Regulation & Expression, University of Dundee, UK

- Type: Web-client for imaging
- Relation IJ: Available plugin to access to OME server
- Language: Java
- License: Open-source
- Users: Large number of users

### ***Imaris***

Imaris is Bitplane's core scientific software module that delivers all the necessary functionality for data visualization, analysis, segmentation, and interpretation of 3D and 4D microscopic datasets. Combining speed, precision, and ease-of-use, Imaris provides a complete set of features for working with three- and four-dimensional multichannel images of any size, from a few megabytes to multiple gigabytes. It can conveniently load, process and visualize data and images acquired from almost any confocal and wide-field microscope to gain new and groundbreaking insight from image data.

- Author: Bitplane AG (Andor Group), Switzerland
- Type: End-user application
- Relation IJ: Enable to call ImageJ's macros
- Language: C++
- License: Commercial
- Users: Large number of users in biology

### ***ICY***

Icy provides an integrated platform that aims at bridging the gap between developers and users, by combining: a) an open-source image-analysis software, offering a powerful and flexible environment for developers such as applied mathematicians to write algorithms fast and efficiently; b) a common set of tools to view and manipulate data, and a set of plugins to perform specific quantification or analysis on images; c) a community-based website centralizing all plugins and resources to facilitate their management and maximize their visibility towards users.

- Author: Institut Pasteur, Paris, France
- Relation IJ: Interoperate with ImageJ
- Type: End-user application
- Language: Java
- License: Open-source
- Users: Fast growing number of users in biology and microscopy. Promising software

### ***Endrov***

Endrov is an open-source plugin architecture aimed at image analysis and data processing. Being based on Java, it is portable and can both be run locally and as an applet. It was designed to overcome the lack of support for spatiotemporal image data in common applications, and has since grown to become a full-featured platform for image analysis.

- Author: Johan Henriksson, Karolinska Institute, Stockholm, Sweden
- Type: End-user application
- Relation IJ: Nothing



- Language: Java
- License: Open-source
- Users: Few users

### ***ilastik***

Interactive Learning and Segmentation Tool Kit. *ilastik* is a simple, user-friendly tool for image classification and segmentation in up to three spatial and one spectral dimension. Using it requires no experience in image processing.

- Author: Christoph Sommer, Christoph Straehle, Ullrich Köthe and Fred A. Hamprecht
- Type: End-user application
- Relation IJ: Nothing
- Language: Python
- License: BSD

### ***Essential Java open-source libraries for bioimaging***

**BioFormats** is a standalone Java library for reading and writing life-sciences image file formats. It is capable of parsing both pixels and metadata for a large number of formats, as well as writing to several formats. Most of the packages of the OBIA consortium use BioFormats to read and write image files..

**ImgLib2** is a general-purpose, multidimensional image-processing library. It provides an interface-driven design that supports numeric and nonnumeric data types in an extensible way. It implements several data sources and sample organizations, including one single primitive array, one array per plane, N-dimensional array "cells" cached to and from disk on demand, and planes read on demand from disk.

### ***Other Java projects related to ImageJ***

**KNIME** is a user-friendly and comprehensive open-source data integration, processing, analysis, and exploration platform designed to handle large amounts of heterogeneous data. As an integration platform, KNIME directly combines functionality from several different domains. The addition of image-processing capabilities to KNIME means that complex domain-comprehensive workflows can be designed without difficulty, enabling for instance the analysis of images with machine-learning algorithms or the completion of image data with chemical information.

**Bio7** is an integrated development environment for ecological modeling. In terms of interoperability, Bio7 offers and embeds also powerful and well proofed third-party tools which are capable to support image analysis (ImageJ), statistical analysis (R), and an easy-to-learn scripting language (BeanShell). Furthermore an advantage of Bio7 is its plugin structure which can be extended with all kinds of third-party plugins.

**CATMAID** is a Collaborative Annotation Toolkit for Massive Amounts of Image Data. It is designed to navigate, share, and collaboratively annotate massive image data sets of biological specimens. The interface is inspired by GoogleMaps, with which it

shares basic navigation concepts, enhanced to allow the exploration of 3D biological image data acquired by optical- or physical-sectioning microscopy technique.

**TrakEM2** is an ImageJ plugin for morphological data mining, three-dimensional modeling, as well as for image stitching, registration, editing, and annotation.

**WIDE** is an open-source project that aims at providing a centralized image-database solution for the use at microscopy and imaging facilities.

### 3. Workshop on Bioimage Analysis Software

In Barcelona, Spain, from April 30 to May 1, 2012, Euro-Biolmaging held a workshop titled "Bioimage Analysis Software: Is There a Future Beyond ImageJ?"

#### 3.1 Goal

The goal of the workshop was to bring together developers and users of imaging software for the analysis of biomedical images. Its purpose is to review the state of the art and to establish requirements for future developments. The focus was on Java-based open-source solutions—in particular, ImageJ—and other open architectures that facilitate the development of plugins and community-driven projects.

#### 3.2 Program

The program featured a series of invited talks by software developers and researchers who have significantly contributed to the field. In addition to the presentations, there were special slots for posters and demos, as well as roundtable discussions for drafting a roadmap for future resource developments in the context of Euro-Bioimaging. The workshop did include the following topics:

- Description of novel open-source image-analysis software
- Solutions for the analysis of biological and biomedical images
- Issues in parallel implementations, multidimensional data, scripting, large data sets, distributed computing
- Standardization mechanisms and accreditation of software
- Benchmarking and testing
- Web-based resources

#### 3.3 Organization

The workshop was organized as a satellite event of the IEEE International Symposium of Biomedical Imaging (ISBI 2012) at Barcelona on April 30 and May 1, 2012. IEEE has taken care of the registration to the workshop. It has been hosted by the International Center of Convention of Barcelona (CCIB).

### 3.4 Attendance

The announcement of the workshop was done through the Euro-Biolmaging channel and using the forums of ImageJ and Fiji. It was based on a call for abstracts: <http://bigwww.epfl.ch/eurobioimaging/call-for-abstracts.pdf>.

- 90 participants to the workshop (85 people did register in advance, 5 people joined the workshop later)
- 15 talks of invited speakers (1 special guest was Wayne Rasband, the developer of ImageJ)
- 36 posters (all posters had at least one presenter at the workshop)
- 4 discussion panels: strategy, technical, interdisciplinary, and community
- 1 round table
- 1 survey <http://bigwww.epfl.ch/eurobioimaging/doc/survey.pdf>

Most people playing an important role in open-source bioimage software were present to the workshop. All known software packages were represented at the workshop, giving an unique opportunity to establish contacts and to draw the future of the field.

### 3.5 Proceedings

A 66-page conference booklet was printed and distributed to the participants. It contains the abstract of each talks and each poster. It will be available on the main website: <http://bigwww.epfl.ch/eurobioimaging/doc/booklet.pdf>

### 3.6 Finances

The financial status will be provided in a separate financial report.

## 4. Panel discussions on future needs

In addition to the technical contributions, several discussion panels took place, with the goal of exploring the following four key elements that will impact the future of the field:

- Technology (hosted by Johannes Schindelin)
- Strategy (hosted by Michael Unser)
- Community (hosted by Erik Meijering)
- Interdisciplinary Aspects (hosted by Jean-Christophe Olivo-Marin)

What follows is a digest of the discussions that were conducted during and after these panels, in a plenary round table.

## **4.1 Technology**

The technological discussion panel focused on the benefit and usage of a (as yet non-existing) web-based portal where would be collected and centralized the resources that are most useful to anyone working with images in a biological context. The panel consensus was that anybody ought to be allowed to submit to the portal freely, in an unmoderated and unrestrained way. In particular, no criterion for quality or suitability (such as interoperability) ought to be enforced at submission time. In return, a mechanism of ratings would be the main guidance to visitors of the portal. These ratings need not be monolithic; in particular, the scientific content (which impacts the biological issues) may be rated independently from the engineering content (which impacts the algorithmic issues) and from the degree of openness of every contribution, a topic which is typically germane to software components. The main purpose of the portal would be to serve as a central repository of publications, software, and data. In addition, the portal would be the natural place for the sharing of tutorials, for accessing a user forum where the lessons learned from a successful or unsuccessful experiment could be discussed, and for advertising conferences and workshops within the focus of Euro-Biolmaging. The portal would promote the reproducibility of experiments by giving access not only to the latest version of submitted softwares, but also to all previous ones. It would encourage authors to also mention the associated hardware components. Moreover, it would facilitate the submission of validation data and organize them in such a way that even non-authors can validate and report the success or failure of every validation attempt. Finally, the portal would additionally accommodate for the submission of ground-truth data and their associated metrics, to provide challenges for algorithms. To every item stored in the portal, one could associate tags and keywords, for instance work-in-progress, segmentation, analysis, and so on.

In conclusion, this portal would serve several of the essential needs of the two communities that have being brought together during the workshop: scientists (biologists), and engineers (computer scientists, along with specialists in image processing and analysis). It is a crucial resource that does not exist until now, and that would certainly foster progress in the field.

## **4.2 Strategy**

Biologists need to quantify and analyze their imaging data while engineers strive to develop and provide the appropriate tools. One task of this work package is to document and give credit to the services provided by the engineering community to the scientific community. Several reporting mechanisms can be used for this task, such as surveys conducted by Euro-Biolmaging, citations, acknowledgments, number of users, or download figures for web-based resources like software components.

Indeed, there is already overwhelming evidence that interdisciplinary research is of paramount importance in this field, bringing together biologists, microscopists, software developers, specialists in signal processing, specialists in machine vision, and industrial partners. It is a feeling shared by all involved parties that a formal body would be required to federate and coordinate the various efforts taking place. A

concrete outcome of the workshop has been the founding of a steering committee, the first ever of its kind. Seven transitional members have been appointed. They are

- Kevin Eliceiri (ImageJ 2.0)
- Erik Meijering (Image processing)
- Jean-Christophe Olivo-Marin (ICY)
- Johannes Schindelin (FIJI)
- Jason Swedlow (Open Microscopy Environment)
- Pavel Tomancak (FIJI, biologist)
- Michael Unser, Chair
- In addition to this steering committee, which has given itself the name of Open Bio Image Alliance, an advisory board has been selected. Its first members are:
  - Marius Messerli (Industry, Bitplane)
  - Wayne Rasband (Founder of the present version of ImageJ)
  - Nico Stuurman (MicroManager: Hardware/Software interfaces in microscopy)

And the list is going to be expanded.

It has been argued in the panel that the breadth of the community of biologists in need of engineering resources, along with the visibility afforded by the committee born out of this workshop, will both contribute to strengthen the future funding requests that may be forwarded to institutions like Euro-Biolmaging, NSF, NIH, and other state or local agencies. This will become particularly true once the portal that will unite the various players will be itself funded and online.

In addition to the portal, other items requiring funding have been discussed. A few proposals are

- Hackathons, during which software developers meet and, in close interaction with one another, efficiently produce useful tools
- Co-developments, where important problems are identified and solved
- Student exchanges
- Targeted software developments
- In-depth software developments of core infrastructures and platforms
- Education
- Training
- User meetings
- Developer meetings, preferably held in alternation at venues dedicated to biologists and venues dedicated to engineers

It was recognized during the panel discussion that it would be reasonable to ask for a financial support that would be in proportion to the current impact, as measured by the reporting mechanisms mentioned above.

As compared to the scientific side resting with biologists, the merit of the engineering side appears to be less recognized. This, in part, is due to the dearth of conduits for publications centered on softwares for biologists and applications thereof. It was proposed during the discussion that the steering committee would encourage members to contact journals and editors to suggest a suitable format to remedy this

issue and make software amenable to citations. The community could supply an editorial board to this effect. A typical target would need to be an open-access journal, perhaps with ties with biology; the series of journals published by the Public Library of Science (PLOS) have been mentioned as a possible venue. Other possibilities would be The Open Source Journal (OneSci Scholarly Journal), the Journal of Mathematical Biology (Springer), or The Insight Journal (MIDAS). Although it is not open-access, Bioinformatics (Oxford Journals) has also been mentioned.

#### *4.3 Community*

Today, the community in our field is a fragmented, loose knitting of individuals. The discussion panel that was focused on community affairs also felt that the most efficient means to tighten the knots will be to build the portal that was already mentioned. It was perceived as particularly important to acknowledge and recognize the fact that this portal must cover broad interests; in particular, it must address not only the needs of developers and users, but also those of laboratories, facilities, and industry.

On one hand, the portal will provide a sustained drive to build the community. On the other hand, meetings will provide an event-based opportunity to cement it. They should be held regularly, as satellites of either technical conferences like the International Symposium on Biomedical Imaging (ISBI) or biological conferences like the annual meeting of the American Society For Cell Biology (ASCB). To promote cohesion, it was suggested to have them alternate between sites. A smaller-scale possible venue could be the BioImage Informatics conference, which already deals with many of the issues relevant to our community. Other conferences suggested at the workshop were the International Conference on Pattern Recognition (ICPR), the meetings of the European Light Microscopy Initiative (ELMI), the meetings of the International Society for Computational Biology (ISCB/ISMB), and the meetings of the European Molecular Biology Organization (EMBO). In addition to satellite meetings, a powerful mechanism to tighten our links could be the organization of special sessions within the main body of any of those conferences.

Cross-training, particularly of students, is yet another possibility to unite the members of this community and to improve the mutual awareness of the features inherent in each subfield. By providing a medium where existing course material could be assembled, the centralized portal would help join forces and avoid part of the repetition of the training material set up today by various institutions, thus streamlining the teaching efforts and reducing the workload. Meanwhile, courses or tutorials could be organized at biological conferences.

#### *4.4 Interdisciplinary aspects*

A quick poll revealed the variety of disciplines represented at the workshop. There were people from image vision, image processing, biologists, computer scientists, microscope builders, physicists, and people from the industry. This tends to show that the goal to bring together people from various fields has been reached in the

workshop. When asked for their motivations, a clear need for integration emerged. The portal could combine several of the elements that would fulfill this need:

- Easier access to information, such as documentation and availability of solutions
- Encouragement of software interoperability
- Ratings pertaining to the fitness of a solution from the image-processing perspective
- Ratings pertaining to the fitness of a solution from the biological perspective
- Ratings based on a peer-review mechanism
- User ratings

Another need impinging on interdisciplinary aspects was recognized during the workshop. It is modeling, the next frontier beyond the availability of software for the analysis of biological images. It consists in the integration of the information gained by image analysis into the larger vision of the biologist's global project. As of today, the groups that are confronted to this question are working in their lab, on their own. It unfortunately looks like they are going to reproduce the dispersion of efforts that plagued the early years of image processing/analysis. In the present case, building a strong interdisciplinary community may be one way to promote efficiency in research.

When it comes to perform interdisciplinary research, mutual understanding is the key, along with mutual respect. Gradually, by working and publishing together, biologists, physicists, mathematicians, and engineers will build a network while collaborating on a given project. The evolution of this project will find applications in the next project. Training and teaching of students and scientists alike is a necessary condition for for this to happen but, while tutorials and web-based forums do exist and are popular for microscopy, the same cannot be said for image analysis. So, it was found that the portal already discussed at large by the other panels would be essential to the community.

The exchange of students (or more generally, researchers), either within or between institutions, is an invaluable mechanism to stimulate mutual understanding. It could complement an extended curriculum where biologists would be exposed to the engineering point of view, and vice versa. A variant is to draw together interdisciplinary teams for a limited-time project, for instance in the context of a summer camp. This variant has been organized several times in the US already; the general outcome is that the resulting spirit, network, and building of a community is very strong. We would like to recommend Euro-Biolmaging to jump start this kind of summer camps in Europe, too.

In terms of objectivity of the information served by the portal, it would be preferable that it not be associated with any given laboratory. Instead, a neutral umbrella such as Euro-Biolmaging would be best and would guarantee a voice to a large diversity of opinions.

## **5. OBIA consortium: "Open Bio Image Alliance"**

As outcome of the open-source workshop, the "Open Bio Image Alliance" was created.

It is a consortium that brings together the primary developers and users of open-source software for the analysis of biological images.

### ***Mission***

The primary mission of OBIA is:

- to provide biologists and researchers in the life sciences with the highest-quality public-domain software resources and a corresponding knowledge base to analyze and quantitate their image data in a sound and reproducible fashion.
- to strengthen the interaction between biologists, imaging scientists, and developers of bioimage analysis software and algorithms.

OBIA capitalizes on the existence of highly successful software packages such as **ImageJ**, which have a huge base of users. However, it also faces substantial challenges relating to the long-term support of existing software, its improvement, the quantity and diversity of available macros/plugins, the documentation and organization of the modules, as well as compatibility issues. OBIA will meet these challenges by implementing mechanisms and initiating actions in order to

- facilitate the diffusion of bioimaging software and guide the choice of image analysis tools with special attention to quality (curation), long-term availability and (backward) compatibility;
- federate the harmonious community-based development of interoperable software and promote good practices, including the careful validation of tools;
- reinforce interactions between imaging scientists/developers and create a sense of community;
- be a catalyst for new software development projects, advanced image-analysis initiatives, and interdisciplinary collaborations in the computational and biological sciences.

### ***General principles***

The software resources that are being supported should be open-source, freely available on the web, platform-independent, and easy to install. While OBIA is open to different technical solutions and resolutely inclusive, it puts a strong emphasis on ease of use, response to the needs of the users, interoperability, algorithm validation, reproducibility, and viability of solutions in the long term.

### ***Steering committee***

It consists of seven prominent members who represent the different orientations of the community and who act as spokesmen for OBIA

- Prof. Kevin Eliceiri
- Prof. Erik Meijering
- Dr. Jean-Christophe Olivo-Marin
- Dr. Johannes Schindelin



- Prof. Jason Swedlow
- Dr. Pavel Tomancak
- Prof. Michael Unser, Chair

### *Advisory board*

The steering committee is helped by an advisory board whose role is consultative. The current list of advisory members, all of whom have extensive experience in the development and deployment of bioimage software, is:

- Wayne Rasband (creator of ImageJ): <http://rsbweb.nih.gov/ij/>
- Nico Stuurman (Micro-manager): [www.micro-manager.org/](http://www.micro-manager.org/)
- Marius Messerli (Imaris): <http://www.bitplane.com/go/products/imaris>
- Michael Berthold (KNIME): <http://www.knime.org/>
- Anne Carpenter (CellProfiler): <http://www.cellprofiler.org/>
- Daniel Gerlich (CellCognition): <http://www.cellcognition.org/>

### ***Immediate action items for OBIA***

1. To have the current document endorsed by the steering committee.
2. To create a web-based portal that should serve as a common entry point for all the currently available public-domain software resources for bioimage handling and analysis.  
*Current status:* A minimal web site "[openbioimage.org](http://openbioimage.org)" with mission statement, steering committee, and links to current bioimaging software resources is being put on line in June 2012.
3. To get in contact with several journal editors in order to lobby for a special place and format to publish papers describing some useful and carefully tested software (or plugins) for bioimage analysis. Members of OBIA—with a mixed representation of developers (computer scientists), advanced users (biologists), signal processing/computer vision researchers, and microscopists—could help in ensuring the quality control (*e.g.*, reviewing, membership of editorial board).  
*Current status:* A contact was initiated with Dr. Alfonso Valencia (Editor-in-Chief, *Bioinformatics*) in May 2012 at ISBI in Barcelona. He was receptive to the idea and pointed out that the current “application note” category may be appropriate for such submissions, assuming that the volume is reasonably small and the quality high.
4. Letter to the editor announcing the formation of OBIA and its long-term goals. The chair of OBIA has currently received two invitations: one by *Bioinformatics* and one by the *IEEE Transactions of Medical Imaging*. In the latter case, the Editor-in-Chief, Milan Sonka, would be willing to write a three-page editorial on open-source software with an equal representation of medical (EBIR) and bio (OBIA).
5. The organization of a meeting of the steering committee in order to draft a roadmap for Euro-bioimaging.
6. *Current status:* The meeting has been scheduled in Frankfurt airport, July 24, 2012.

Lausanne, 14 June 2012

Michael Unser, EPFL Switzerland

with the editorial help Dr. Daniel Sage and Dr. Philippe Thévenaz

and approval of OBIA

Prof. Kevin Eliceiri

Prof. Erik Meijering

Dr. Jean-Christophe Olivo-Marin

Dr. Johannes Schindelin

Prof. Jason Swedlow

Dr. Pavel Tomancak

Prof. Michael Unser, Chair