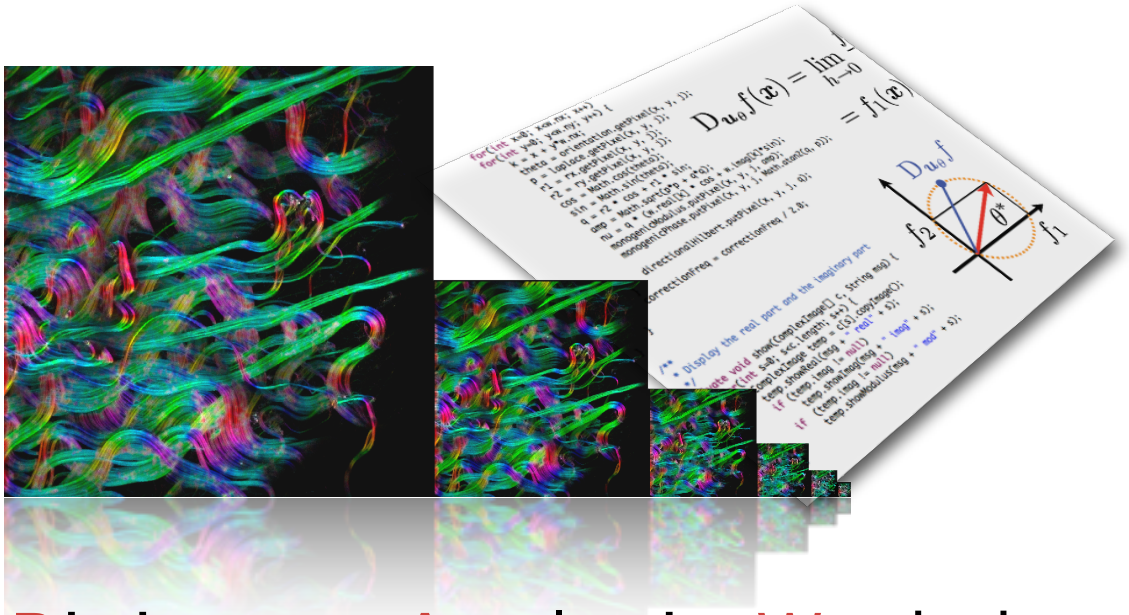
EURO-BIOIMAGING

ÉCOLE POLYTECHNIQUE FÉDÉRALE DE LAUSANNE

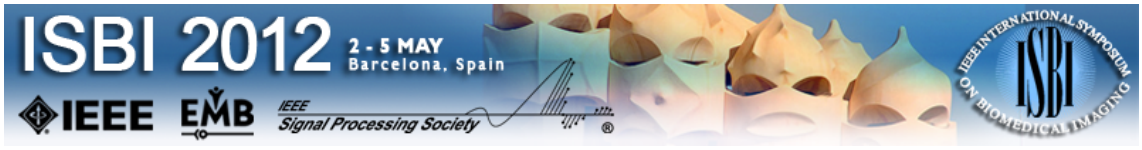
Bioimage analysis software: is there a future beyond ImageJ?



Bioimage Analysis Workshop

April 30–May 1, 2012

Barcelona



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Preface

The workshop will 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 will be on JAVA-based open-source solutions–in particular, ImageJ–and other open architectures that facilitate the development of plugins and community-driven projects.

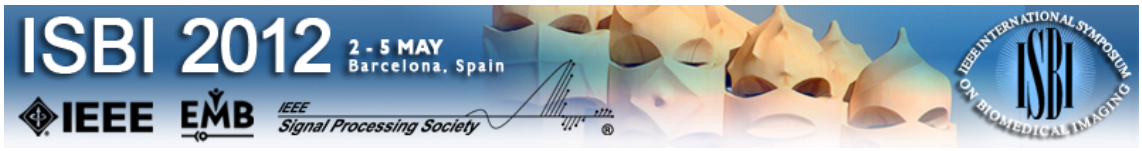
Bioimage Analysis Workshop

The program will feature a series of invited talks by software developers and researchers who have significantly contributed to the field. In addition to the presentations, there will be 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 includes 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 computating
- Standardization mechanisms and accreditation of software
- Benchmarking and testing
- Web-based resources

Organisation

- Prof. Michael Unser, Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland
- Dr. Arrate Muñoz-Barrutia, Center for Applied Medical Research, Pamplona, Spain
- Dr. Andreas Jahnen, CRP Henri Tudor, Luxembourg
- Dr. Daniel Sage, Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland



Support

- Euro-BioImaging Project
  http://www.eurobioimaging.eu/
- Ecole Polytechnique Fédérale de Lausanne, Biomedical Imaging Group
  http://bigwww.epfl.ch/
- Centre de Recherche Public Henri Tudor, Luxembourg (ImageJ Conference)
  http://imagejconf.tudor.lu/
- Conference IEEE ISBI 2012, Barcelona
  http://biomedicalimaging.org/

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18:30	*Closing of the doors*

Abstracts of speaker

Image Registration and Segmentation Paradigms in Fiji

Ignacio Arganda-Carreras

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Abstract

Automatic image registration and segmentation tools are two of the most demanded features of any bio-imaging software. Image registration is understood as the alignment of multiple 2D or 3D images based on a simple (translation, rigid-body, affine) or not that simple (non-linear, elastic) transformation model. This search of a common coordinate system is vital in order to integrate or compare image data obtained from different measurements. Image segmentation involves the automatic labeling or detection of the structures of interest in our images —complete objects or often just their boundaries—, which simplifies the image representation and facilitates the posterior analysis. In that sense, Fiji has proven to be a very popular platform for bio-medical users and developers, with a very wide spectrum of state-of-the-art algorithms in both areas. The integration of such methods along with the need of a robust and straightforward workflow to deal with large data sets originated TrakEM2, one of the most powerful Fiji plugins. TrakEM2 allows the user to process the massive amount of image data (Tera byte scale) that modern microscopes produce nowadays in affordable personal desktop computers. Moreover, TrakEM2 integrates all the software pieces for volumetric reconstruction, visualization and analysis of objects from 2D sections in a very coherent and flexible way. The challenge now consists of progressively incorporating novel and more sophisticated methods and adapt them to function on such a large scale. A very representative example is the on-going integration of machine learning based segmentation algorithms using the Weka and Knime toolboxes.

Biography

Ph.D. on Computer Science and Electrical Engineering for the Escuela Politécnica Superior (Universidad Autónoma de Madrid). Currently, working as a postdoctoral fellow at Sebastian Seung's lab (Massachusetts Institute of Technology, USA). Prior to that, I worked during my PhD at the Ortiz-de-Solorzano lab, at the Bioimaing Group (Lawrence Berkeley National Laboratory, California, USA), the Biocomputing Unit (National Centre for Biotechnology, Madrid, Spain), the Biomedical Signal Processing group in the Escuela Politécnica Superior (Universidad Autónoma de Madrid) and collaborated with the IRB Barcelona, in the Cell & Developmental Biology group. Right after obtaining my PhD, I worked as a researcher in the Institute of Neuroinformatics (University and ETH, Zürich) and as a consultant at the Image Processing Facility in the Max Planck Institute of Molecular Cell Biology and Genetics (Dresden, Germany).

My research interests include image processing, graphics, biomedical image registration and segmentation, computer vision, machine learning and neuroscience. I am currently working on applying machine learning methods to improve the segmentation of neural structures in EM images. My specific focus centers on studying the performance of convolutional neural networks in contrast to more classical algorithms using pre-computed features.

Open Source BioImage Informatics: Tools for Interoperability

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Abstract

Biological imaging has greatly advanced over the last thirty years with the now unprecedented ability to track biological phenomena in high resolution in physiologically relevant conditions over time and in space. As these imaging technologies mature and become main stream tools for the bench biologist there is great need for improved software tools that drive the informatics workflow of the imaging process from acquisition and image analysis to visualization and dissemination. To best meet the workflow challenges, these tools need to be freely available, open source, and transparent in their development and deployment. In particular it is clear that given the complexity, and heterogeneity of the modern image dataset, there can not be a single software solution. Different imaging processing and visualization approaches need access not only to the data but to each other. There needs to be compatibility not only in file import and export but interoperability in preserving and communicating what was done to the image. There is a great opportunity in achieving this interoperability, tools that can talk to each other not only enable new biological discovery but also efficiencies in sharing code and in many cases more precise workflows. We present our efforts towards interoperability in the FIJI and Open Microscopy Environment consortiums. The consortiums are actively developing key software libraries like ImgLib and Bio-Formats that are utilized in dozens of software applications to parse and visualize biological image data, to the developmental benefit of not only of the applications but the libraries themselves.

Biography

Kevin Eliceiri received his undergraduate and graduate training in Microbiology and Biotechnology at the University of Wisconsin in Madison. He worked in the R.M. Bock laboratory developing imaging approaches for the model nematode C. elegans. He received further post-graduate training at the National Integrated Microscopy Resource (Madison, Wisconsin) in the area of computer science and microscopy. Since 2000 he has been at the Laboratory for Optical and Computational Instrumentation (LOCI) at the University of Wisconsin at Madison. He is currently director of the LOCI and a Principal Investigator in the Laboratory of Molecular Biology at the University of Wisconsin in Madison Graduate School. He holds research investigator appointments in the Departments of Biomedical Engineering and Medical Physics and is a full investigator in the University of Wisconsin Comprehensive Cancer Center. His current research focuses on the development of novel optical imaging methods for investigating signaling and cell interaction in development and disease processes, and the development of software for multidimensional image informatics.

BioImageXD Image Processing, Analysis and Visualization Platform

Pasi Kankaanpää

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Abstract

We present BioImageXD (manuscript under revision), a new open source software project for bioimage analysis, processing, visualization and animation, written in Python and C++. Software comparison tests show BioImageXD to be faster, more versatile, and capable of dealing with more complex image processing tasks than most other similar programs (both open source and proprietary), while remaining intuitive to use and offering a graphical user interface also for batch processing. BioImageXD aims at being a single large package for processing images inherently in 3D/4D, leveraging the power of the VTK and ITK libraries, and being suitable for high throughput applications without requiring programming skills. Thus it differs in design philosophy from projects such as ImageJ. However, as ImageJ and many other projects are highly important and useful, it would be advantageous for the projects to work together and benefit from synergy. BioImageXD has therefore been designed to be extendable and to interoperate with other open source projects, as currently exemplified by its support for VTK, ITK and the Open Microscopy Environment. This interoperability is further enhanced in the next BioImageXD version, which is currently under development. It is written in Java, supports Bio-Formats, and it is planned to interoperate with ImageJ both "externally" (by seamlessly transferring data between the two programs) and "internally" (by directly running selected ImageJ plugins). Specific attention is being paid to high throughput and performance aspects. We hope that these qualities would enable BioImageXD to play a role in the future European bioimaging software scheme.

Biography

Pasi Kankaanpää started specializing in microscopy and image processing while studying cell biology at the University of Jyväskylä in Finland. In 2001 he was one of the first to work extensively with 4D confocal microscopy of living cells in Finland. In 2005 he initiated a new open source software project, BioImageXD, for analyzing and visualizing multi-dimensional microscopy image data, aimed at solving the bioimaging bottle-neck of software unavailability. He has been the design lead and coordinator of the large, international, multi-disciplinary project since then. The software has been in active use since 2006, and is currently one of the largest and most versatile available in the field, with an extensive manuscript currently under revision. In 2005 Kankaanpää moved to the University of Turku (Turku, Finland) to pursue PhD studies, and in 2008 he became a special/senior researcher, establishing and running a new confocal and atomic force microscopy facility. In the beginning of 2012 Kankaanpää was appointed coordinator of the Cell Imaging Core facility of the Turku Centre for Biotechnology, which is one of the major imaging facilities of Northern Europe. Kankaanpää regularly visits many European universities, lecturing and teaching about microscopy and image analysis. He is also one of the key members of the Turku BioImaging umbrella organization, developing bioimaging on a national and pan-European level.

Prototyping Complex Microscopy Imaging Pipelines

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Abstract

In this talk, I will discuss our efforts to integrate and customize commercial and open source tools for acquiring, processing, and analyzing images to study developing organisms in vivo. While many constraints that guided implementation choices were directly related to system performance, such as speed, scalability, portability, stability, or cost, others were linked to programmer skills or end-user preferences. Modular software tools, capable of interfacing with multiple software packages proved particularly useful for rapid system prototyping. I will illustrate these points with examples from digital holography, tomography, and in vivo high-speed and time-lapse imaging of the developing heart.

Biography

Michael Liebling is an Assistant Professor in the Department of Electrical and Computer Engineering at the University of California, Santa Barbara (UCSB) since 2007. He graduated from École Polytechnique Fédérale de Lausanne, Switzerland, with an MS in Physics (2000) and a PhD for a dissertation on Digital Holography and Image Processing that he completed under the advisory of Prof. Michael Unser (2004). From 2004 to 2007, he was a Postdoctoral Scholar in the lab of Prof. Scott E. Fraser at the Biological Imaging Center, Beckman Institute, California Institute of Technology.

At UCSB, his research focuses on biological image acquisition, reconstruction, processing, and analysis. His lab develops microscopy instrumentation and imaging protocols along with the computational tools to observe and analyze embryonic morphogenesis in vivo.

Robust Cell Segmentation: Half a Century Between Hope and Reality

Erik Meijering

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Abstract

A central problem in many areas of bioimage analysis is cell segmentation. Cellular morphology is an important phenotypic feature and is indicative of the physiological state of a cell. But also for the study of intracellular processes (single particle analysis), or of cell sociology (in embryogenesis or histopathology), segmentation of cells is often the premier step in the image processing pipeline. First examples of computerized cell analysis date back more than half a century. Since then, the field of light microscopy has undergone a series of revolutions, giving rise to a wide variety of imaging modalities, which are greatly challenging the development of generic and robust cell segmentation methods. While research in this area has intensified exponentially in the past decade, and new solutions are proposed in the literature every month, it turns out that the majority of the methods are still based on a small set of classical image segmentation approaches, whose limitations are well known. More powerful data processing concepts will need to be developed to finally bridge the gap between hope and reality. In addition, to accelerate and steer these developments, it is highly desirable to improve the possibility to easily and fairly peer-evaluate new methods and compare them to the state of the art. To this end, the availability of a single, open-source image processing software platform, supported as widely as possible by researchers in image processing as well as in biology, will be of key importance.

Biography

Erik Meijering is an Associate Professor of Bioimage Analysis at the Erasmus University Medical Center Rotterdam in the Netherlands. He received a MSc degree (cum laude) in Electrical Engineering from Delft University of Technology (1996), and a PhD degree in Medical Image Analysis from Utrecht University (2000), both in the Netherlands. During 2000-2002, he worked as a postdoctoral fellow at the Biomedical Imaging Group of the Swiss Federal Institute of Technology in Lausanne (EPFL), Switzerland. In 2002 he returned to the Netherlands to join the new Biomedical Imaging Group of the Erasmus University Medical Center Rotterdam. His research interests are in the areas of computer vision, image processing, and image analysis, with applications in cellular and molecular imaging. He published more than 60 peer-reviewed articles in this area. He is a Senior Member of the Institute of Electrical and Electronics Engineers (IEEE), its Signal Processing Society (SPS), and Engineering in Medicine and Biology Society (EMBS). He was Technical Program Chair for the IEEE International Symposium on Biomedical Imaging (ISBI) in 2006 and 2010. He was/is an Associate Editor for the IEEE Transactions on Medical Imaging (since 2004), the International Journal on Biomedical Imaging (term 2006-2009), and the IEEE Transactions on Image Processing (term 2008-2011), and was a Guest Editor for the September 2005 Special Issue of the latter journal, which focused on Molecular and Cellular Bioimaging. He also served/serves in a great variety of scientific conference, advisory, and review boards.

Icy – An Open-Source Community Image Processing Software

Jean-Christophe Olivo-Marin

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Abstract

We present Icy (http://icy.bioimageanalysis.org), a GNU GPL open source software providing an integrated and innovative multi-platform development environment for image analysis applications. It offers a common platform both for image analysis scientists developing new algorithms and biologists seeking for a powerful and intuitive tool for image analysis applications. Icy includes a flexible framework designed around a plugin architecture, offers rich data structures for images and output data, enhanced data visualization and communication layers. Icy kernel has been designed to manage multidimensional images as a 5D structure able to store data in 3D, time, and an unlimited number of channels. Icy provides a rich API of 80 functions to perform pixel transfer, conversions and assignments that are designed to access directly the data and are compatible with the native Java objects, ensuring fast transfers and visualizations. A number of functionalities are delegated to dedicated libraries: 3D rendering is done by VTK, loading and saving files by BioFormats, live acquisition by microManager, while Substance and Flamingo are used for interface look and feel and ribbon management. Icy now features more than 100 applicative plugins covering such diverse tasks as image enhancement, filtering, active contours, cell segmentation and tracking, particle detection and tracking, available on the web site and ready for use in biological applications.

Biography

Jean-Christophe Olivo-Marin is the head of the Quantitative Image Analysis Unit and the Chair of the Cell Biology and Infection Department at Institut Pasteur, Paris. He holds a Ph.D. and an HDR in Optics and Signal Processing from IOTA, University of Paris-Orsay. His research interests are in cell and particle tracking, cellular dynamics and computational microscopy. He is an IEEE Fellow, the Past Chair of the Bio Imaging and Signal Processing Technical Committee (BISP-TC) and member of the Editorial Board of Medical Image Analysis and BMC Bioinformatics. He was the General Chair of IEEE ISBI'08 and has organized several special sessions dedicated to biological imaging at international biomedical conferences (ELMI'02, ISBI'04, ICASSP'06, SPIE Wavelets'09 & '11, EMBO'11).

Introduction to ImageJ

Wayne Rasband[1,2]

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Abstract

ImageJ is a public domain, Java-based image analysis program that can be easily extended via recordable plugins (written in Java), macros or JavaScript. I will briefly describe the history of ImageJ, including the two programs it evolved from, "Image" and NIH Image. I will also demonstrate some newer and lesser-known ImageJ features, including sub-pixel resolution, interpolated selections, custom cursors, "Live" histograms and profile plots, 3D gaussian blurring, the Control Panel, toolbar menus and custom tools. In addition, I will demonstrate the new Image>Transform>Bin command, which exemplifies how to write a plugin that handles all supported ImageJ data types (8-bit, 16-bit, float and RGB) and dimensions (up to 5D).

The first imaging program I developed, starting in the late 70s, was called simply "Image". It was written in Pascal, ran on PDP-11 minicomputers and ran in only 64KB of memory! I started work on the second, NIH Image, in 1987 when the Mac II became available. I was a Mac enthusiast, and the Mac II had card slots just like the PDP-11. I started work on ImageJ in 1997, when Java was becoming popular. I was intrigued by the idea of creating a version of NIH Image that would "run anywhere", including as an applet in Web browsers.

Biography

I was a software developer at the National Institutes of Health (NIH) for 40 years. I retired in 2010 but continue to work on ImageJ as an NIH volunteer. I fix bugs, answer questions and add features based on user feedback. I also manage the ImageJ Website and mailing list.

I developed three image analysis programs while at the NIH.

The first, from the late 70s, was called "Image". It ran on PDP-11 minicomputers, was written in Pascal, and was used to analyze autoradiographs and 2D electrophoresis gels. It had many of the capabilities we now take for granted in ImageJ, such as regions of interest, contrast stretching, thresholding and color lookup tables. "Image" did all this on computers with only 64KB of memory (images were stored in a 512x512 frame buffer/display).

I started work on NIH Image in 1987 when the Mac II was introduced, with the goal of creating a smaller, less expensive and more approachable imaging system. Unlike "Image", NIH Image was widely used outside of the NIH and it benefited greatly from suggestions, bug fixes, code and documentation contributed by dozens of users.

ImageJ came to life in 1997 when I started experimenting to see if I could recreate NIH Image in Java. Java was attractive because, in theory, I could develop a program on my Mac that would "run anywhere". ImageJ has continuously improved over the last 15 years based on user feedback and the contributions of hundreds of users.

ImageJ2 – ImageJ for the Next Generation of Biological Image Data

Curtis Rueden

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Abstract

Any successful software project, after a period of sustained growth and the addition of functionality outside the scope of the program's original intent, will benefit from a subsequent period of scrutiny and refactoring, and ImageJ is no exception. ImageJ2 is a new version of ImageJ seeking to strengthen both the software and its community. Internally, it is a total redesign of ImageJ, but it is backwards compatible with ImageJ 1.x via a "legacy layer" and features a user interface closely modeled after the original. Under the hood, ImageJ2 completely isolates the image processing logic from the graphical user interface (UI), allowing ImageJ2 plugins to be used in many contexts, including headless in the cloud or on a server such as OMERO, or from within another application such as KNIME, ICY or CellProfiler (a Python application). ImageJ2 has an N-dimensional data model driven by the powerful ImgLib2 library, which supports image data expressed in an extensible set of numeric and non-numeric types, and accessed from an extensible set of data sources. ImageJ2 is driven by a state-of-the-art, collaborative development process, including version control, unit testing, automated builds via a continuous integration system, a bug tracker and more. We are collaborating closely with related projects including Fiji, Bio-Formats and OMERO, and are striving to deliver a coherent software stack reusable throughout the life sciences community and beyond. The result is well-designed, community-driven software accessible to users yet powerful enough for programmers.

Biography

Curtis Rueden is a software architect, and lead programmer of the software projects at the Laboratory for Optical and Computational Instrumentation (LOCI). He is the technical lead for ImageJ2, the next-generation version of ImageJ, and is actively involved with the ImageJ, Fiji and Open Microscopy Environment (OME) software communities. In 2005 he started the Bio-Formats project to address the growing number of proprietary microscopy file formats. Before that, Curtis was also one of the principal programmers on the VisAD Java component library for interactive and collaborative visualization and analysis of numerical data, developed at the UW's Space Science and Engineering Center. He has an M.S. in Computer Sciences from the University of Wisconsin-Madison.

ImgLib2 – Generic Image Processing in Java

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Abstract

Re-usability of implemented computational methods is crucial for both algorithmic advancement and scientific progress. ImgLib2 is an open-source Java library for multidimensional data representation and manipulation with focus on image processing. It aims at minimizing code duplication by being agnostic to data type, dimensionality, and memory layout.

The ImgLib2 interface architecture clearly separates pixel-algebra, data access, and data representation in memory. On one hand, this architecture enables fine-grained control in specifying the minimal requirements of an algorithm to facilitate maximum re-usability. On the other hand, it provides great flexibility to developers when adding new data representations and types. ImgLib2 illustrates that an elegant high-level programming interface can be achieved without sacrificing performance. It provides highly efficient implementations of common data types, memory layouts, and algorithms.

ImgLib2 serves as the core data model underlying ImageJ2, KNIP (KNIME Image Processing toolbox), and an increasing number of Fiji-Plugins. The Open Microscopy Environment (OME) plans to make use of the ImgLib2 API in the Bio-Formats library as well as the OMERO server. ImgLib2 is licensed under BSD. Source code is available in public git repositories at http://fiji.sc/srv/git/imglib.git and https://github.com/imagej/imglib. ImgLib2 is a core part of the scijava effort http://scijava.github.com. In this talk, we will describe the core concepts of ImgLib2, discuss its performance, and demonstrate a number of practical examples.

Biography

Stephan Saalfeld is a grad student in Pavel Tomancak's Lab at the Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany, funded by the PhD program of the International Max Planck Research School for Molecular Cell Biology and Bioengineering. He holds a Diploma (German MSc equivalent) in Computer Science and Media (Technische Universität Dresden, 2008).

His current research focus is image registration and interpretation in the context of biological microscopy, particularly serial section Electron Microscopy of neuronal tissue.

Stephan is an experienced software designer and developer with particular focus on web-applications and image processing. He contributes to the open source projects ImgLib2, Fiji, TrakEM2 and CATMAID.

Fiji – A ImageJ Distribution for the Bioimaging Community

Johannes Schindelin

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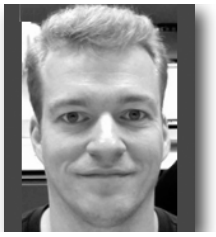
Abstract

The ImageJ distribution Fiji ("Fiji Is Just ImageJ") was conceived to address the need of an easy-to-install image processing package for biologists, based on ImageJ. Always inspired by researchers' needs, Fiji bundles many ImageJ plugins and offers tutorials and documentation in the ever-growing Fiji Wiki. To facilitate the interaction between biologists and programming experts, Fiji has an update function that allows for a rapid turn-around time between development and usage of Fiji components.

Fiji not only caters for regular users but also for advanced ones, offering powerful scripting languages in addition to the ImageJ macro language. Expert programmers benefit from Fiji's Script Editor which allows to edit and run not only scripts but also Java plugins without the need to leave ImageJ. To avoid duplication of efforts and to provide better separation of concerns, Fiji collaborates closely with other projects such as Bio-Formats, ImageJ2 and ImgLib. The ever-growing number of website visits and downloads, as well as a growing number of contributions, suggests that Fiji addresses a need in the scientific community.

Biography



Johannes Schindelin is maintainer of Fiji (Fiji Is Just ImageJ, (http://fiji.sc/). While he worked as a professional software designer in industry, his formal training is in pure mathematics (Dipl.) and genetics (Dr.) obtained at the Julius-Maximilians-University of Wuerzburg, Germany. He was PostDoc at the school of psychology at the University of St Andrews, Fife, UK, and was visiting scientist and leader of the image processing facility at the Max-Planck Institute of Molecular Cell Biology and Genetics in Dresden, Germany. He is currently a senior programmer on the FIJI and ImageJ2 projects at the Laboratory for Optical and Computational Instrumentation at the University of Wisconsin-Madison, USA.

Hybrid C++ / ImageJ Visualization System: An Example in Xmipp

Carlos Óscar Sorzano

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Abstract

We present an example of how to use ImageJ as a set of useful libraries for visualization in C++. C++ classes can be exposed in Java through JNI and a hybrid Java-C++ application can be developed exploiting the visualization capabilities of ImageJ. In this case, ImageJ is used as an external library instead of as the main program. In this way, ImageJ classes can be integrated into visualization components providing extended functionalities.

Biography

Carlos Óscar Sorzano is technical director of the Instruct Image Processing Center. This center provides service and infrastructure for image processing in Structural Biology. His research interests include image processing for electron microscopy. He is the coordinator of the Biomedical Engineering degree at Univ. San Pablo - CEU.

MicroManager – An Open Software Platform for Control of Motorized Microscopes and Cameras

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Abstract

Image analysis starts with image acquisition. Taking images with modern microscopes requires software capable of interfacing with the camera and many other parts, such as shutters, filter wheels, motorized stages, lasers, etc. The sequence in which these parts change state as well their timing is critical to successful experiments, and the operator needs a comfortable yet simple to understand interface to carry out complex experiments. Although several commercial solutions existed when we started, none of these were cross-platform, extendable to new hardware, or easy to integrate with other software and hardware. We therefore developed an Open Source image acquisition platform called µManager. Its core, written in C++, has a simple interface to device adapters (interfaces between µManager and devices). Device adapters are discovered and loaded at run-time. This plugable device support has encouraged companies and scientists to write code for a wide array of equipment, (currently more than 20 camera companies, all major microscopes, many peripherals, more than 120 device adapters). An upper level API exposes device control to environments such as Matlab, Java and Python. We developed a user interface running as an ImageJ plugin. Written in our lab with continuous feedback by biologists, it is easy to use and has facilities for configuring complicated, multi-dimensional acquisitions. An API at the UI level makes the µManager extensible through scripts and plugins. Plugins for photo-bleaching/photo-conversion and super-resolution are being developed now. µManager runs on more than 2,500 microscope systems world-wide.

Biography

Nico Stuurman grew up in the Netherlands and studied Chemistry at the University of Amsterdam. He obtained a Ph.D. in Cell Biology at the same University in 1991, based on his studies of the nuclear matrix with Dr. Roel van Driel.

He then studied the structure and function of nuclear lamins in Drosophila as a post-doc, first with Paul Fisher at SUNY Stony Brook, and then with Ueli Aebi at the BioZentrum in Basel, Switzerland.

Nico was a staff scientist at the University of Leiden from 1997-2001 and then joined the laboratory of Ron Vale at the University of California San Francisco where he combines his interest in computer programming and microscopy in various projects including the Open Source software Micro-Manager. He taught microscopy in the Physiology and Neurobiology courses at the MBL in Woods Hole and is co-organizer of the Bangalore Microscopy course in India.

The Open Microscopy Environment: Open Image Informatics for the Biological Sciences

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Abstract

Despite significant advances in cell and tissue imaging instrumentation and analysis algorithms, major informatics challenges remain unsolved: file formats are proprietary, facilities to store, analyze and query numerical data or analysis results are not routinely available, integration of new algorithms into proprietary packages is difficult at best, and standards for sharing image data and results are lacking. We have developed an open-source software framework to address these limitations called the Open Microscopy Environment. OME has three components—an open data model for biological imaging, standardised file formats and software libraries for data file conversion and software tools for image data management and analysis.

The OME Data Model provides a common specification for scientific image data and has recently been updated to more fully support fluorescence filter sets, the requirement for unique identifiers, screening experiments using multi-well plates.

The OME-TIFF file format and the Bio-Formats file format library provide an easy-to-use set of tools for converting data from proprietary file formats. These resources enable access to data by different processing and visualization applications, sharing of data between scientific collaborators and interoperability in third party tools like Fiji/ImageJ.

The Java-based OMERO platform includes server and client applications that combine an image metadata database, a binary image data repository and high performance visualization and analysis. The current release of OMERO (Beta4.3) includes a single mechanism for accessing image data of all types–regardless of original file format–via Java, C/C++ and Python and a variety of applications and environments (e.g., ImageJ, Matlab and CellProfiler). Support for large images from digital pathology is now included. This version of OMERO includes a number of new functions, including SSL-based secure access, distributed compute facility, filesystem access for OMERO clients, and a scripting facility for image processing.

Biography

Jason Swedlow earned a BA in Chemistry from Brandeis University in 1982 and PhD in Biophysics from UCSF in 1994. After a postdoctoral fellowship with Dr T. J. Mitchison at UCSF and then Harvard Medical School, Dr Swedlow established his own laboratory in 1998 at the Wellcome Trust Biocentre, University of Dundee, as a Wellcome Trust Career Development Fellow. He was awarded a Wellcome Trust Senior Research Fellowship in 2002 and named Professor of Quantitative Cell Biology in 2007. His lab focuses on studies of mitotic chromosome structure and dynamics and has published numerous leading papers in the field. He is co-founder of the Open Microscopy Environment (OME), a community-led open source software project that develops specifications and tools for biological imaging. In 2005, he founded Glencoe Software, Inc., a commercial start-up that provides commercial licenses and customization for OME software. In 2011, Prof Swedlow and the OME Consortium were named BBSRC's Social Innovator of the Year and Overall Innovator of the Year. In 2012, He was named Fellow of the Royal Society of Edinburgh. Prof Swedlow is Co-Director of the Analytical and Quantitative Microscopy Course, an annual course that covers the latest developments in advanced quantitative light microscopy at Marine Biological Laboratory, Woods Hole, USA.

TurboReg and Other ImageJ Plugins at the Biomedical Imaging Group of EPFL

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Abstract

We briefly present a non-exhaustive digest of some of the ImageJ plugins that were developed through the years by many authors at the Biomedical Imaging Group. While these plugins rely on advanced mathematical and algorithmic tools, we believe their user interface to be friendly enough that even non-experts can feel comfortable using them. We then focus on the specific plugin named TurboReg, which has been well received by many users. We look at it from a historical perspective, from its inception to its current state, discussing issues like development, coding, testing, deployment, documentation, update, extension, and user support. We draw a few lessons gained during its life cycle

Biography

Philippe Thévenaz was born in 1962 in Lausanne, Switzerland. He graduated in 1986 from the École polytechnique fédérale de Lausanne (EPFL), Switzerland, with a diploma in microengineering. He joined the Institute of Microtechnology (IMT) of the University of Neuchâtel, Switzerland, where he obtained his Ph.D. in 1993. He then worked as a Visiting Fellow with the Biomedical Engineering and Instrumentation Program, National Institutes of Health (NIH), Bethesda MD, USA, where he developed research interests that include splines and multiresolution signal representations, geometric image transformations, and biomedical image registration. Since 1998, he is with the EPFL as senior researcher.

A Biologists Perspective on the Challenges in Biological Image Analysis and how the Fiji Platform Attempts to Meet them

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Abstract

Most primary data in biological research are in the form of images and recent advances in microscopy have brought about orders of magnitude increase in the volume of biological imagery. Since it is no longer possible to draw meaningful conclusions on these vast image datasets by simply inspecting them, computer assisted image analysis is increasingly becoming an indispensable tool for discovery in biological research. Several fields of computer science, in particular computer vision, deal with analysis of image data, however the biology application domain poses unique challenges necessitating adjustment of existing algorithms and development on entirely novel approaches. Therefore biologists need to engage in productive collaboration with computer scientists to enable computer assisted reasoning on top of vast biological image datasets. The necessary pre-requisite for such interdisciplinary collaboration is an Open Source software platform that offers on one hand advanced programming facilities to computer scientist and at the same time is broadly accepted by biologists. We have been, over the past few years, investing a lot of effort into making Fiji (Fiji Is Just ImageJ) such a platform that enables collaborative, interdisciplinary research in the area of biological image analysis. I will demonstrate the fruits of these efforts on applications connected to my research agenda that focuses on imaging of tissue specific gene expression patterns in developing biological systems. In particular, I will show how Fiji facilitates the acquisition, processing and analysis of massive image datasets from an emerging microscopic imaging modality, the Selective Plane Illumination Microscopy (SPIM) of large, living biological specimen.

Biography

2005 - present: Group leader at the Max Planck Institute of Molecular Cell Biology and Genetics, Dresden focusing on live imaging of gene expression patterns and evolution of gene regulation.

2000 - 2004: Postdoctoral work at the Dept. of Molecular and Cell Biology, University of California in Berkeley at the laboratory of Dr. Gerald M. Rubin focusing on functional genomics of gene expression patterns in Drosophila embryogenesis

1995 - 1999: PhD work at EMBL Heidelberg, Germany at the laboratory of Dr. Anne Ephrussi working on establishment of polarity during oogenesis.

Poster Abstracts

Parametric Snakes in Microscopy

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Abstract

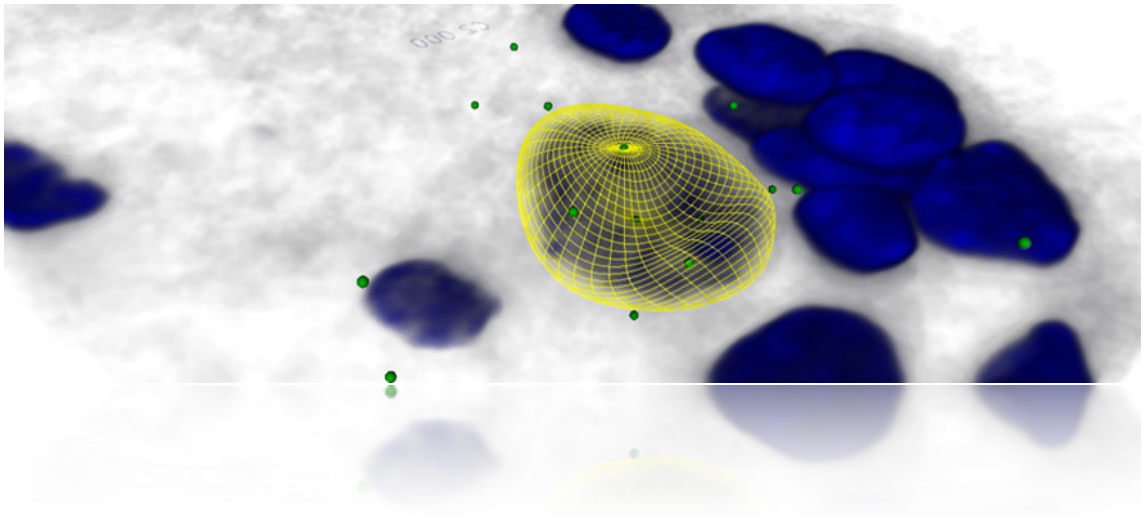
Snakes are effective tools for image segmentation. Within a 2D image, a snake is a 1D curve that evolves from an initial position, which is usually specified by a user, toward the boundary of an object. Within a 3D image, a snake is represented by a 2D surface. In the literature, these methods are also known as active contours or active surfaces. The snake evolution is formulated as a minimization problem. The associated cost function is called a snake energy.

Snakes have become popular because it is possible for the user to interact with them, not only when specifying their initial position, but also during the segmentation process. This is often achieved by allowing the user to specify anchor points the curve or surface should go through.

We have developed a JAVA framework for the design of 2D and 3D snakes that are parameterized by a set of control points compatible with ImageJ and ICY. It provides fast 2D and 3D filters for image preprocessing, several snake energies, different snake topologies (e.g., spherical and tubular in 3D), and efficient optimization routines. We have also designed a dedicated user interface for ICY that features numerous possibilities for user interaction through a mouse-based manipulation of control points in synchronized 2D and 3D views. High-quality data rendering is performed thanks to VTK. Moreover, the snake surface can be overlaid to the original data during the optimization process. Stereo rendering is provided in order to make the visualization of the 3D objects more effective.

Keywords

Segmentation, active contours, active surfaces, VTK



Segmentation of EM Images of Neuronal Structures Using CellProfiler

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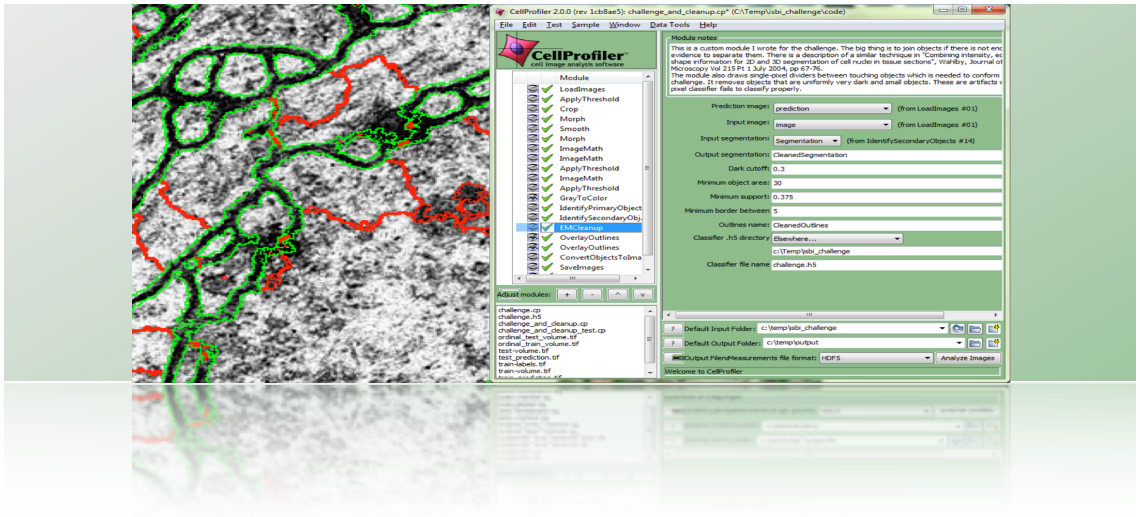
Abstract

CellProfiler is a flexible, open-source tool designed to analyze microscopy images. CellProfiler's primary focus is on analysis of fluorescently labeled cells, but it can be adapted to other uses. This poster describes the analysis of the ISBI 2012 EM challenge images using CellProfiler in conjunction with custom software written for the challenge. The images are first scored with a custom pixel-based classifier trained on the ground truth. This scoring is then used as the input for CellProfiler. I first identify potential centers within tissue surrounded by membrane, and then grow these using a seeded watershed. Finally, I use a module that was custom-designed for the challenge to clean up artifacts in the resulting segmentation.

The CellProfiler EM Challenge entry demonstrates techniques for analyzing neuronal structures. It also demonstrates how CellProfiler can be used as an algorithm development platform. CellProfiler can run ImageJ and ImageJ 2.0 plugins written in Java as well as native modules written in Python. An analysis method can be distributed as a CellProfiler pipeline, contributing to the reproducibility and documentation of the method and allowing researchers to easily integrate both their algorithms and others to arrive at a production-quality and scale solution.

Keywords

CellProfiler, machine Learning, ISBI 2012 EM challenge



KNIP – KNIME Image Processing and Analysis

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Abstract

The increase in high-throughput microscopy in recent years has resulted in much richer data being available for image analysis. This calls for software solutions that are able to handle the huge amounts of image data produced in a high-throughput environment. Such a software must provide a wide range of functionality (e.g. image analysis, machine learning, statistics and visualisation), and yet still be easy to use by non-experts.

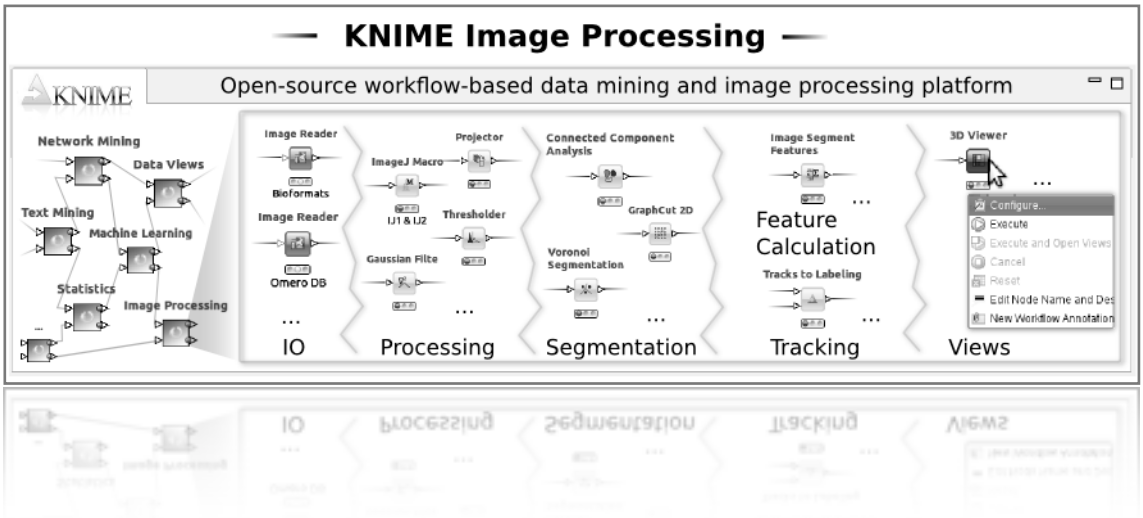
KNIME is a user-friendly and comprehensive open-source data integration, processing, analysis, and exploration platform designed to handle large amounts of heterogeneous data. It therefore satisfies the aforementioned requirements. As an integration platform, KNIME directly combines functionality from several different domains.

More recently the image processing plugin KNIP has been developed. It is designed to extend KNIME by providing algorithms and data structures that can easily process and analyse images and videos on a large scale. 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. Further advantages directly inherited from KNIME, amongst many others, are the handling of large amounts of images and fast prototyping of understandable workflows.

Avoiding redundant development, KNIP in turn uses and integrates state-of-the-art libraries like ImageJ1 and ImageJ2, Bioformats, OMERO and ImgLib2. Additionally KNIP provides powerful functionality itself. Currently KNIP is used to solve several segmentation, classification and tracking problems in different areas of science, such as biology, chemistry and physics.

Keywords

High-throughput analysis, image processing, image analysis, screening, imagej, imagej2,



ALIDA – Automatic Generation of User Interfaces for Data Analysis Algorithms

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Abstract

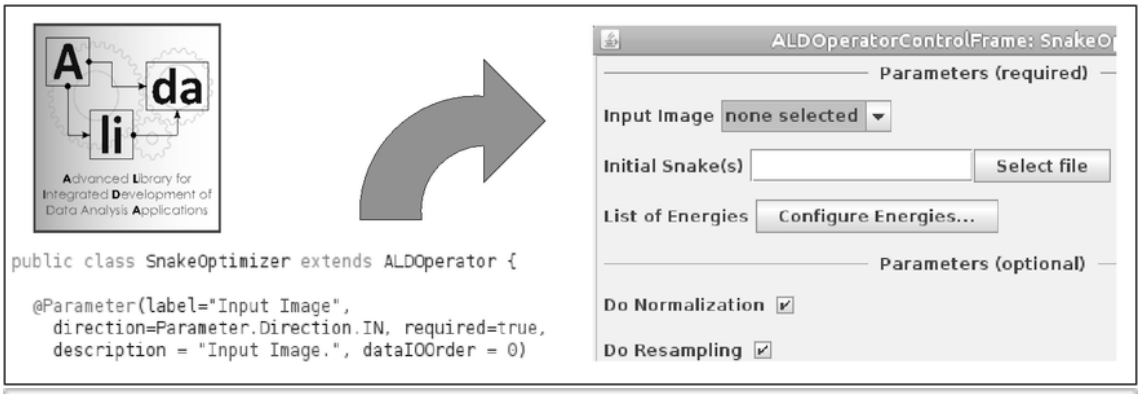
Analysis of biomedical data may be interpreted as a flow of objects through an analysis pipeline. The Java framework Alida defines the concept of operators as the single places of these manipulations. Typically, operators may be invoked sequentially or in parallel, and often also nested. Besides invocation on the programming level their functionality should also be available directly to users, including developers of algorithms and non-experts. This calls for graphical as well as command line interfaces. Eliminating the need to explicitly code these interfaces, Alida features fully automated generation of graphical and command line user interfaces for each operator implemented in the Alida framework.

The basis is a formalism for an operator to define all input and output data objects and parameters to control processing. Automatic generation of interfaces is based on the model view presenter design pattern to achieve maximal independence between the operators, interfaces, and I/O of data objects. For implementation Java's annotation mechanism is used. The programmer is only required to properly annotate classes and member variables. Out of the box this facilitates I/O for a wide variety of Java objects including primitive data types, enumerations, arrays, and collections. In a generic way Alida handles also operators as parameters of other operators and inheritance. Only specialized classes like images require additional data providers to be implemented.

While Alida is devised for data processing in general, it is used in our image analysis toolbox MiToBo (http://www.informatik.uni-halle.de/mitobo) for biomedical image analysis which is based on ImageJ and compatible to it.

Keywords

User interface, automatic generation, data analysis, ImageJ



BudJ – Cell Size Computation During the Cell Cycle

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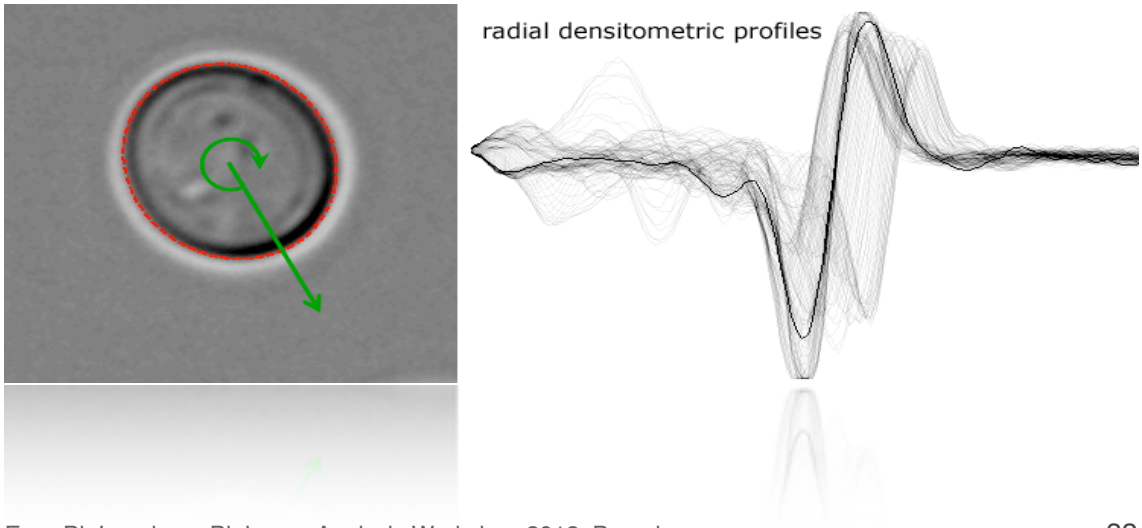
Abstract

Coordination of cell growth and DNA replication is a universal mechanism that ensures size adaptation and homeostasis. Budding yeast cells, as most eukaryotic cells, exert this coordination essentially during G1, where a critical size is assumed to be attained. However, a molecular mechanism that acts as a "sizer" is yet to be uncovered. In order to tackle this problem, we decided to analyze cell growth kinetics during the cell cycle at a single-cell level by time–lapse microscopy. We have developed a specialized plugin for ImageJ that allows semi-automated computation of cell sizes from bright field images and, at the same time, provides with precise data of cell-cycle landmarks from fluorescence images. The algorithm first obtains a densitometric profile along a radial axis from a seed point within the cell (initially provided by the user) to establish the optical cell boundary. Then, all cell boundary pixels are iteratively defined by full rotation of the radial axis and a preliminary prolate object is fitted. Outliers are rigorously eliminated and missing boundary pixels are estimated by fitting ellipsoidal segments. Finally, different molecular and cellular events are analyzed from fluorescent distribution and levels within cell boundaries. Cell volumes obtained with BudJ are fully comparable to other methods that only produce data at a population level. With this tool, we have found that the critical size is set as a result of the individual growth potential by specific proteins of the network that controls entry into the cell cycle.

Keywords

Cell size, cell cycle, time-lapse analysis



WIDE – Web Image and Data Environment

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Abstract

WIDE is an open source project that aims at providing a centralized image database solution for the use at microscopy and imaging facilities. A client software and a service component are installed on the computers of the facility. Users can initiate the upload of images and documents. The service executes the upload. It continues to work after the user logged out. It can be configured to work fast or slower using less resources in order not to interfere with an ongoing image acquisition.

Once uploaded, the images are stored on a file server and indexed in the database system. The original file format is kept in order not to loose any metadata.

Users can access the images via a web-interface. The data is presented in a virtual filesystem view with thumbnails. Other, for example project based views will be added later. WIDE currently allows to manage data in the virtual filesystem, to download it, to share it with other users of WIDE and to create download links that can be accessed by anyone.

A plugin system will allow to run image analysis jobs, for example deconvolution or ImageJ macros on dedicated processing machines from the web interface. Further planned features are a history function, a tagging system and the import and export of metadata.

WIDE is based on Java EE and runs on the glassfish server. It can be accessed from other software using EJB (Entreprise Java Beans) clients or web services.

Keywords

Image database, web-application, open source software, image analysis, batch processing, ImageJ, data centralization, image management, data sharing

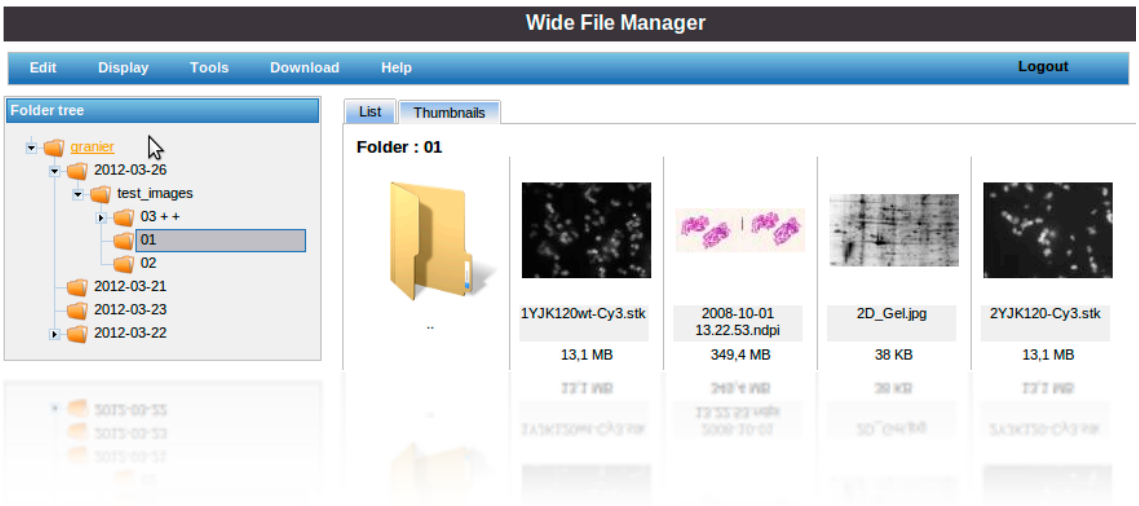

Image Analysis Tools within an Integrated Development Environment for Ecological Modeling at Various Scales

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2. Dept. of Experimental and Systems Ecology, University of Bielefeld, Germany

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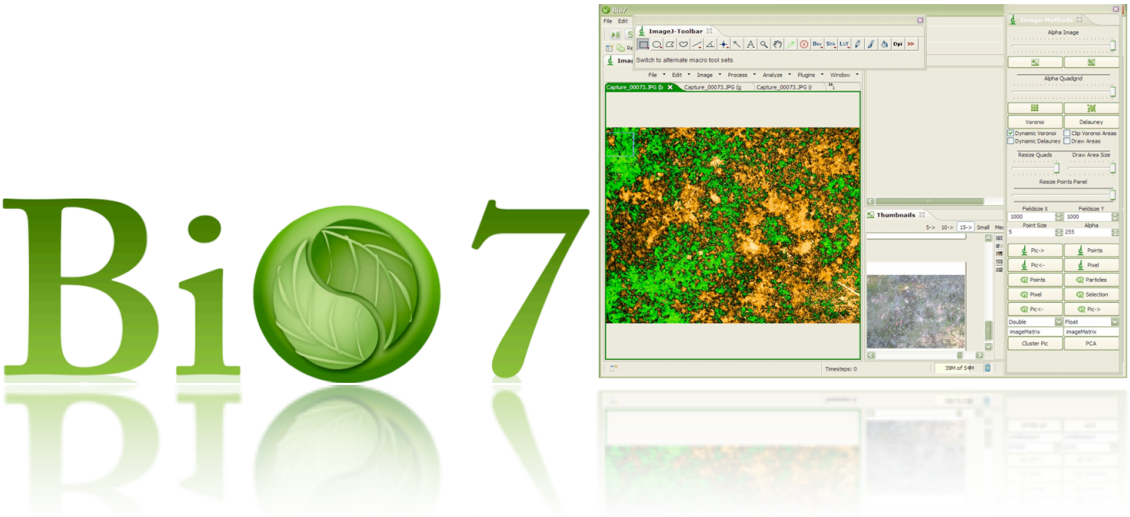
Abstract

The integrated development environment Bio7 is an ongoing effort to simplify the modeling and analysis of complex ecological systems. The application itself is based on the Eclipse Rich Client Platform (RCP) and contains several different plugins for special simulation and analysis tasks. One of these plugins is an adaption of the scientific image application ImageJ embedded in a Graphical User Interface within the Bio7 application. Furthermore a bidirectional Java connection to the statistical software R is available and can be used to analyze image, matrix and vector data which can easily be transferred from and to ImageJ.

In this presentation the Bio7 RCP framework and the use of ImageJ in combination with R for image analysis tasks will be demonstrated. It will also be shown that Bio7 can be useful for disciplines beyond ecological modeling in order to describe complex biological processes at various scales. Possible future developments of the platform will be discussed.

Keywords

Rich client platform, ImageJ, R, ecological modeling



SynapCountJ – an ImageJ Plugin to Analyze Synaptical Densities in Neurons

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Abstract

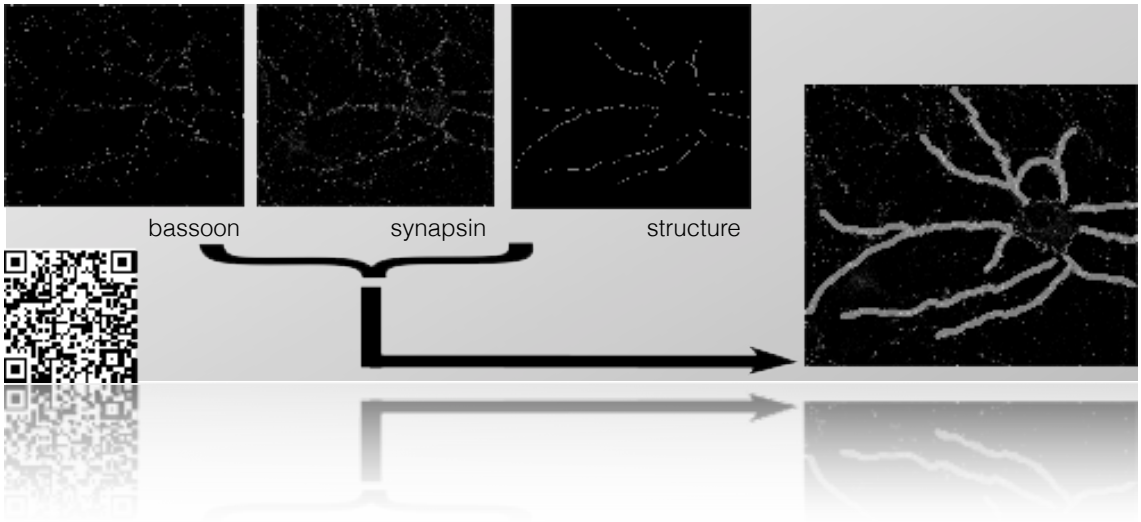
Synapses are dynamic structures subject to changes depending on their development and activity. There are direct relationships among the number of synapses, memory processes and some neuropathologies such as Alzheimer. Quantification of synapses in both, neuronal cultures and tissue is based on morphological or immunocytochemical criteria. The procedure to identify and quantify synapses needs a huge time effort, it is a task performed, mainly, manually by the researcher.

The aim of our work is the development of a software system that allows determining the synaptic density from immunofluorescence images. To achieve this goal, we have implemented SynapCountJ, an ImageJ plug-in, based on topological and geometric algorithms. The main hindrance in automating such a process consists in discriminating between the actual synapses and irrelevant information; for instance, the background or other structures such as axonal vesicle transport. In order to only count the synapses into neuronal dendrites, the plug-in uses a triple criterion: two images with two different synaptic markers and the identification of the neuronal structure by immunostaining or by manual tracing. The analysis of big data volumes can be performed, without external interaction, by a batch job subroutine.

The comparative study using cultured rat hippocampal neurons, after manually and automatically counting, indicates a high reliability obtaining a counting error of less than 2% and a time saving among 90%.

Keywords

Synaptic density, algebraic topology



ImageJ-Driven Intelligent High Content Screening

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Institute for Research in Biomedicine, Barcelona

Spain

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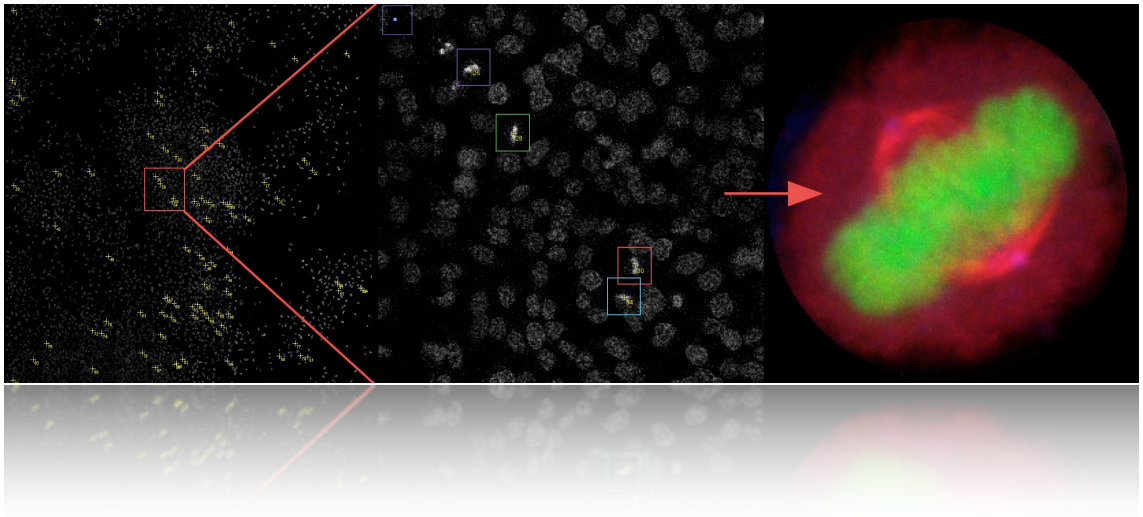
Abstract

High content screening at high resolution can generate an overwhelming amount of data and a prohibitive acquisition time, especially for 3D multispectral scans which became routine work in life science. However only a small fraction of the information acquired is often useful to the experimenter, interested in inspecting some particular, potentially rare events. As a faster alternative, we propose to re-organize the acquisition in two scans: a primary scan at lower resolution to detect events of interest and a secondary scan with optimal settings, but with dramatically fewer views centered only on the positions of interest. We developed a software interface in JAVA/ImageJ-macro-language that allows the communication of a workstation running ImageJ with a Leica SP5 confocal microscope, through the recently available High-Content-Screening HCS-A software module from Leica. The program is modular so that the image analysis section can be easily edited by the user to detect virtually any custom targets. The only requirement is that the analysis returns points of interest from the large map of the primary scan, to be sent back to the microscope to trigger the secondary scan. The program launches the scans, accesses, processes and presents the images to the user. User interactions, for instance to refine the secondary targets' selection, can also be easily handled in the program, which keeps all ImageJ functionalities at any time. We demonstrate intelligent scans with automated detection of fixed samples (e.g. cells in mitosis, cells on micropatterns, tissue sections) and show automated time-lapse imaging of rare events.

Keywords

High content screening, ImageJ, image analysis, event detection, user interaction



A Generic Solution for Tile-Based Histological Image Analysis

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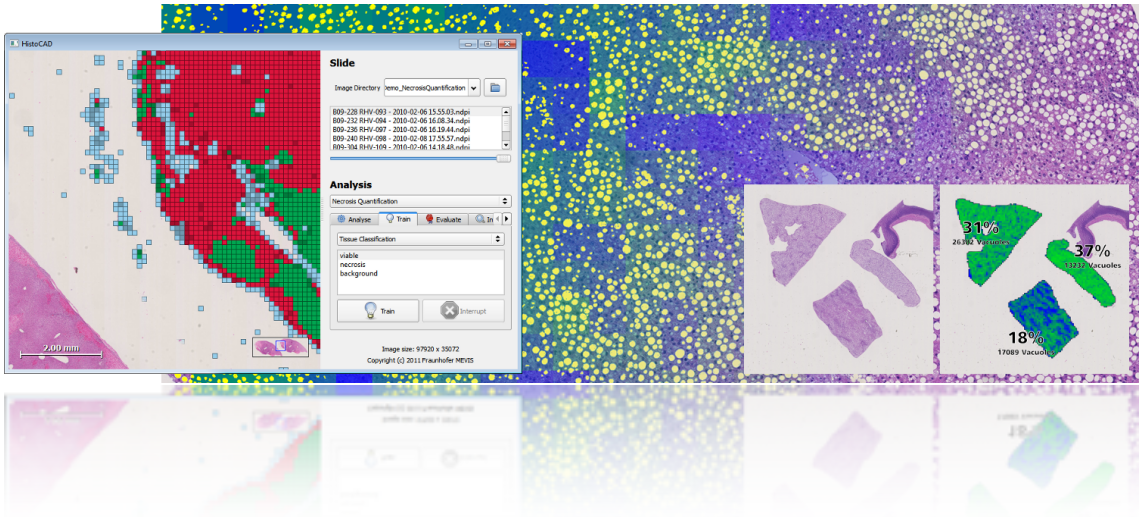
Abstract

With the rising availability of digital slide scanners, histology is experiencing a rapid trend toward digitization. This opens the door for the automatic quantification of tissue parameters, with the potential to greatly improve the speed, accuracy and reproducibility of biomedical observations. The huge size and variability of histological whole-slide images are still major challenges to their automated analysis. A common approach is to subdivide the image into a lattice of square tiles and to automatically classify each tile into different tissue categories. We will present an efficient tile-based image analysis solution for generic tissue classification problems. By considering tissue structures on multiple scales, the software can quickly process Gigabyte-sized images on standard computers. We will demonstrate how the software can be easily adapted to the huge complexity and variance of histological images. Instead of being forced to set any abstract parameters, all the user has to do is to point out examples of the relevant tissue structures in an intuitive microscope-like user interface. The software incorporates a relational data model for image analysis results, that can efficiently handle large volumes of data and be comprehensively queried on the basis of SQL. Since this data model is very generic and entirely founded on open-source technologies, it will be applicable in other scenarios of biomedical image analysis as well.

Keywords

Histological image analysis, whole-slide image analysis, classification



Developing Open Source Image Analysis Software in Plant Sciences

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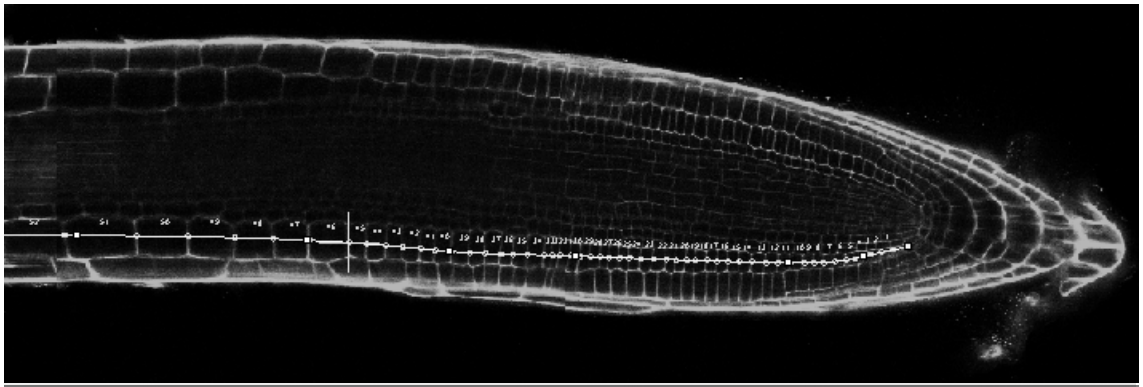
Abstract

At the Centre for Plant Integrative Biology, we have developed a number of software tools for use by biologists. Some of our tools have been developed in ImageJ and Fiji, as both macros and plugins, while others have been written from the ground up in languages such as C++ and C#. Here, we present an overview of our image analysis tools, which include automated plant root measuring, co-localization, confocal cell measuring, and 3D segmentation. Additionally we will discuss the benefits and challenges we have experienced developing this software both with ImageJ and using other languages.

Keywords

Image analysis, plant sciences, ImageJ



CytoSurfer – Deal with Large Data Sets Generated by Image Segmentation Using ImageJ

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Abstract

High Content Screening (HCS) technologies are used in drug discovery to identify hits and characterize lead candidates from large compound libraries. In HCS, cells grown multi-well plates are imaged using automated microscopes resulting in the production of very large sets of images.

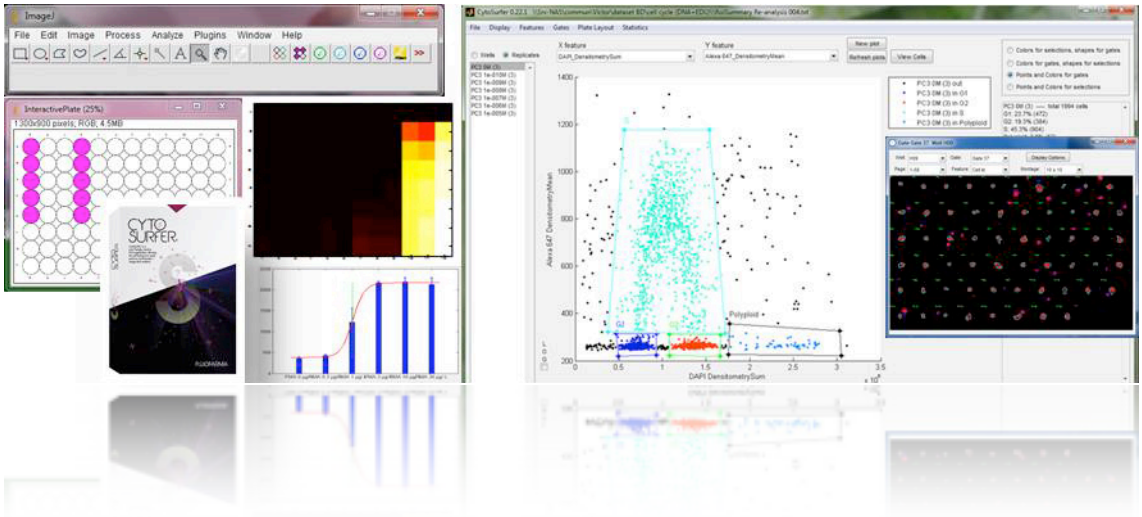
Handling and interpreting such image datasets are recurrent bottlenecks in the HCS workflow. HCS analysis is composed of (i) an image analysis step intended for segmentation of the cellular objects, followed by (ii) a feature extraction/data processing step meant for profiling the compound's biological effects. In addition to the dedicated HCS platform softwares, ImageJ is a perfect environment to proceed to customized cell segmentation and feature extraction. This solution allows to easily automate complex image analyses using ImageJ tools and macros.

ImageJ's segmentation and feature extraction results in millions of cells depicted by dozens of quantitative features. To correlate these data with compound effects, population analysis and visualization can be easily performed in CytoSurfer®. This user-friendly software allows datasets to be visualized as population scattergrams, histograms and density maps.

Subpopulations of cells can be defined by drawing polygons in scattergrams or histograms. Cells within the gates (defined polygon) are then analyzed in all samples. Images of the cells within the gates can be directly visualized. CytoSurfer includes 96/384 wells plates capability, heatmap, dose response, IC50, ZFactor, t-test and multi-plates processor. ImageJ brings a flexible segmentation toolbox to CytoSurfer®, leading to a modular and versatile HCS profiling application.

Keywords

High content screening, data processing, large data set, population analysis, cytometry



ImgLib2 – Concepts and Features

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Abstract

ImgLib2 is an open-source library for representing and manipulating image data. It is the core data model underlying ImageJ2. ImgLib2 aims at minimizing code duplication by being agnostic to the image data type, dimensionality, and storage format.

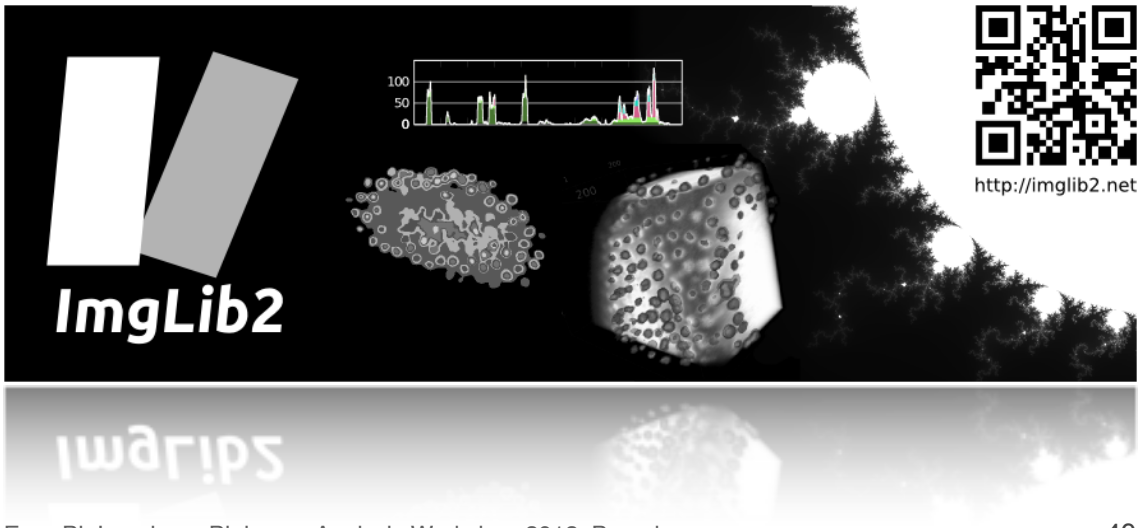
The prominent feature of ImgLib2 is an interface architecture that clearly separates pixel-algebra, data access, and data representation in memory. On the one hand, the interface hierarchy provides fine-grained control in specifying the requirements of image processing algorithms to facilitate maximum re-usability. On the other hand, it provides great flexibility to developers when adding new image data types and representation. ImgLib2 illustrates that an elegant high-level programming interface can be achieved without sacrificing performance. It provides highly efficient implementations of common data types, storage models, and generic algorithms.

In this demonstration I will showcase ImgLib2 using small example programs. The demonstration consists of several short independent parts, where each part gives a hands-on introduction into one of the features of ImgLib2. Small example codes are developed step-by-step, visualising and explaining intermediate results.

The demonstration highlights type and dimensionality independence,on-the-fly value and coordinate transforms, as well as representation and access to sparse data sets.

Keywords

ImgLib2, image representation, image processing, generic algorithms



Icy: One Year Old but Already Grown-Up!

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Abstract

Icy (http://icy.bioimageanalysis.org) is a GNU GPL platform that bridges the gap between the life science, bio imaging and image processing communities. This platform provides a modern Java-based plug-in oriented software framework that fits today and tomorrow's needs in biological imaging from acquisition to analysis. Central to the concept of community work, a collaborative web-site offers a centralized platform to gather and exchange ideas and know-how while fostering interactions and collaborations between researchers from all backgrounds.
Icy will celebrate its first anniversary at ISBI 2012. One year of existence during which Icy has been continuously improved thanks to the efforts of a growing community. To celebrate this event, we will briefly showcase the 100+ plugins developed during that period. We will also present the new features available in the desktop application and in the back office provided for developers.

Keywords

Icy, image processing software, bioimage analysis

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Remote Visualization, Collaborative Annotation, and Automated Analysis of High-Resolution Bioimages Through Internet

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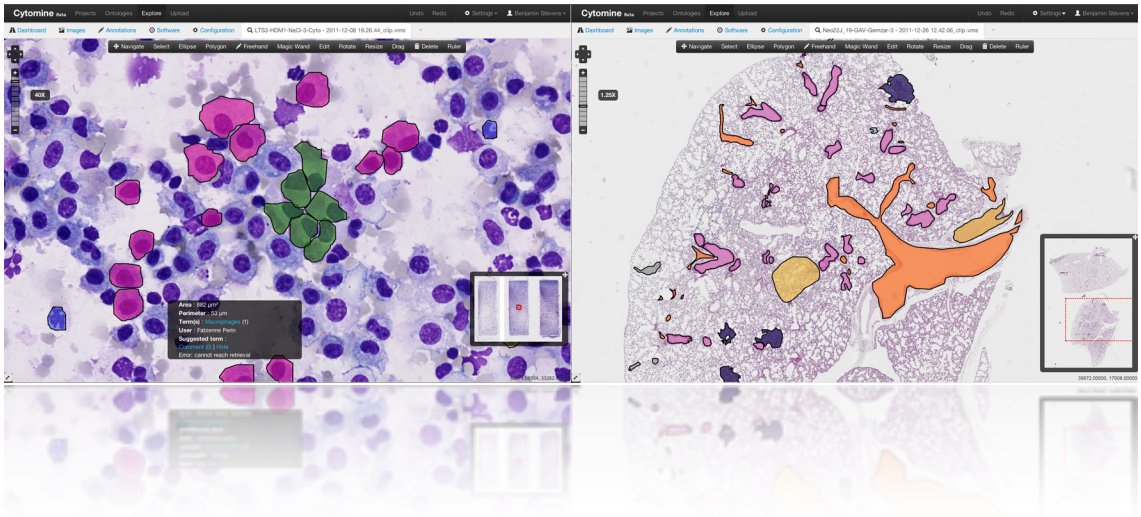
Abstract

We will present the development of a rich internet application for remote visualization, collaborative annotation, and automated analysis of high-resolution, high-throughput biological images. With our application, high-resolution images in various formats (e.g. from whole-slide scanning devices) that are usually too big to fit into traditional computer memory can be visualized at multiple resolutions in web clients through fully Javascript interfaces, caching mechanisms and distributed image tile servers. Our underlying relational data model allows to create projects which contain users with permission lists, images, ontologies with domain-specific terms, and layers of annotation geometries (e.g. polygons) drawn on top of original images. All project data are stored in a relational database and can be visualized and edited through the web interface, and they can also be retrieved or updated by third-party softwares through a RESTful API (two client libraries in Java and Python have been developed). In addition, we are integrating ImageJ/Fiji/OpenCV image processing routines and our general-purpose machine learning algorithms to facilitate image annotation and quantification.

At this stage of development, our application already delivers about one thousand whole-slide images (roughly 1.5Tb of data) and more than six thousand regions of interest were annotated by our collaborators in the context of ongoing studies on lung cancer and inflammation, and Zebrafish toxicology. Overall, the proposed web software is generally applicable and its methodological choices open the door for large-scale distributed and collaborative image annotation and exploitation projects. Acknowledgments: This work is funded by the research grant n°1017072 of the Walloon Region (DGO6).

Keywords

Bioimage, high-resolution, visualization, tiling, rich internet application, web-based, REST, annotation, collaborative, machine learning, decision trees



Extending Imaris Using Java and Launching Fiji Plugins From Within Imaris

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Abstract

In this presentation we show Imaris' Java programming interface in operation and demonstrate the interacts with Fiji. The demonstration will include extensions of popular applications, namely cell tracking and dendritic neuron detection, and is equally targeted for biologists and computer scientists.

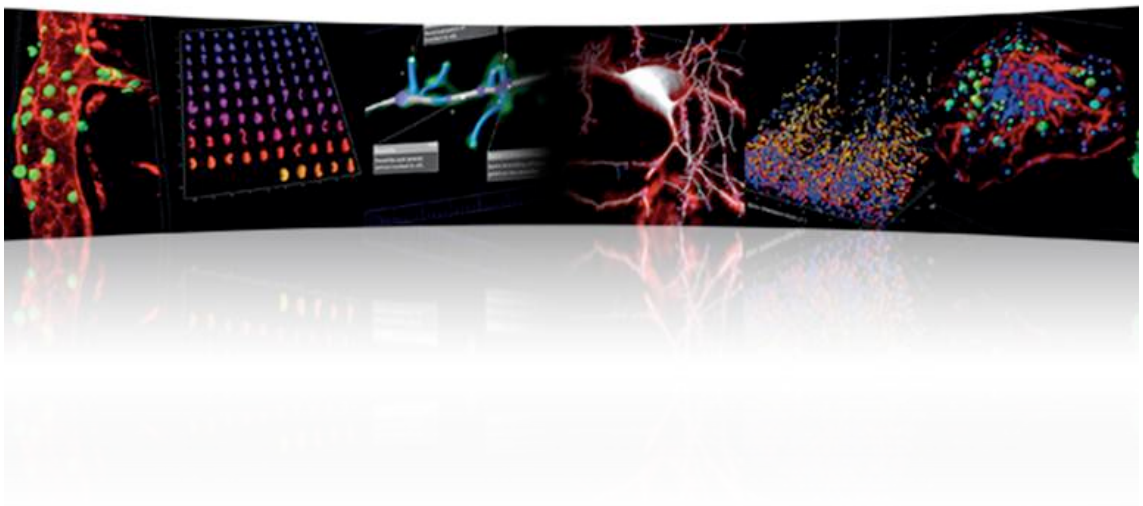
Imaris is commercial image analysis software designed for the analysis of multi-dimensional fluorescent images. It was launched in 1993 and has grown continuously responding to user needs and instrument innovations. In 2004 the first version of the programming interface, called ImarisXT, has been released.

ImarisXT enables software developers to use Imaris as a framework offering an extensive collection of microscopy file readers, an image management subsystem fit for GB size images combined with advanced visualization, interaction, and statistics display subsystems.

Based on the fact that Imaris faces the same end-user challenges as ImageJ we would like to discuss the future role of commercially supported software frameworks in bio labs and are keen to learn how to expand the programming interface to best support the community.

Keywords

Programming interface, imaging framework, huge images, commercial software, plugin



ImageJ Tools for STED Performance Analysis

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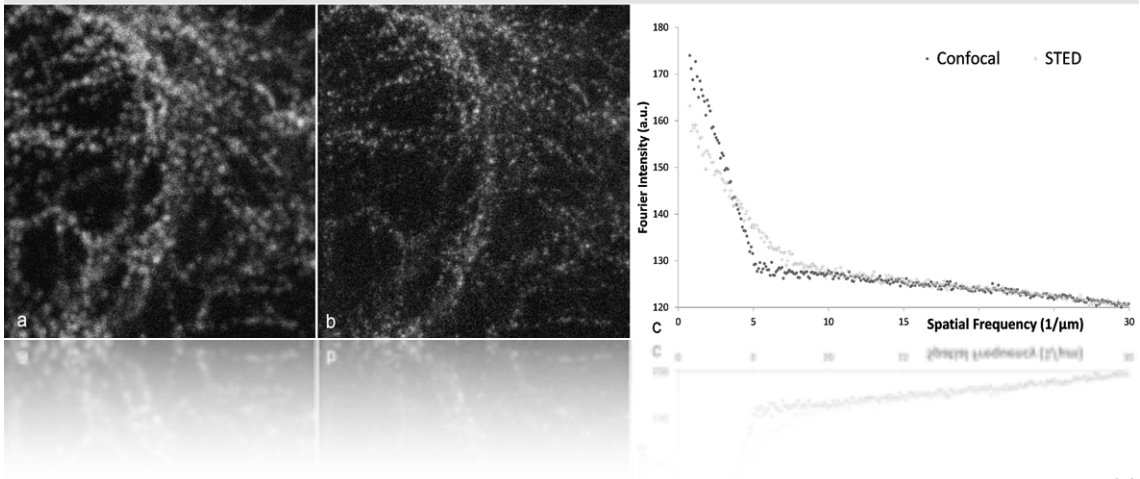
Abstract

Stimulated emission depletion (STED) microscopy is a super-resolution fluorescence-based technique where the diffraction limit is overcome. A ring shaped beam is used to inhibit fluorescence in the outer regions of the excitation point. The size of the resulting emitting point can be reduced, virtually, without any limitation. As the performance of STED is based on superimposing the STED beam to the excitation beam, the system is very sensitive to misalignments. In addition, other factors such as image exposure time and dwell time (travel's duration of the scanning laser on the area corresponding to a pixel in the final image), as well as temperature changes or small vibrations can produce important effects on the alignment of the setup and that compromise the resolution efficiency. Therefore, it is not easy to determine when the performances of the system are at its best. In this work we present an ImageJ plugin which implements an analysis of the image quality, based in the Fourier transform (FT) formalism. This quantify the performance of our STED microscopy in order to determine the actual imaging conditions. In order to determine the increase of resolution, we use the build-in functions of ImageJ to calculate the dispersion of the FT of the image of nano-sized fluorescent beads. To be able to compare single values, we perform the average in the angular direction of the FT. We can, then, make use of the one-dimensional dispersion obtained, which is directly related to the resolution of the system.

Keywords

STED microscopy, Fourier transform analysis, super resolution

HeLa cells' vimentin labeled with Horizon V500. a. Confocal Image b. STED image c. Fourier analysis



A KNIME-Based Workflow for the Distinction of S-Phase Stages in Cells Immunolabeled for PCNA Detection

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Abstract

Most physiological processes in eukaryotic cells are regulated in a cell-cycle specific manner. Assigning cellular phenotypes to distinct cell cycle phases enables to detect subtle effects that appear only transiently, and improves the understanding of their regulation. In S-phase, cells duplicate their genome in a spatially and temporally precisely regulated fashion. Open, active regions of the genome are replicated first, while inactive, compacted areas mostly located at the nuclear periphery lag behind. PCNA is an essential factor for eukaryotic DNA replication and a marker of replication activity. Its distribution in the cell nucleus, which is conveniently visualized via immunocytochemistry, reflects the location of actively replicating genomic regions. This PCNA staining pattern yields information about the stage of S-phase the cell has reached at the time point of fixation. Here, we present a KNIME workflow which enables to automatically assign cells to early-mid-or late S-phase in stationary images of PCNA-labeled nuclei obtained by epifluorescence or confocal microscopy. This workflow uses KNIP, the KNIME Image Processing framework along with the KNIME data mining tools. To correctly segment cell agglomerates a cluster splitting method was developed that separates nuclei based on the criterion of maximum contour concavity. The 110-dimensional feature vector is a combination of histogram features and Haralick texture features. Using this feature set the KNIME decision tree is the classifier with the best performance. In sum, we present a general tool for classifying S-phase stages with high accuracy in fluorescence images lacking the temporal information provided by time-lapse recording.

Keywords

KNIME, cell cycle, antibody-labeling, fluorescence microscopy, segmentation, classification, features, clump splitting

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Open-Source Software for Single-Molecule Localization Microscopy

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Abstract

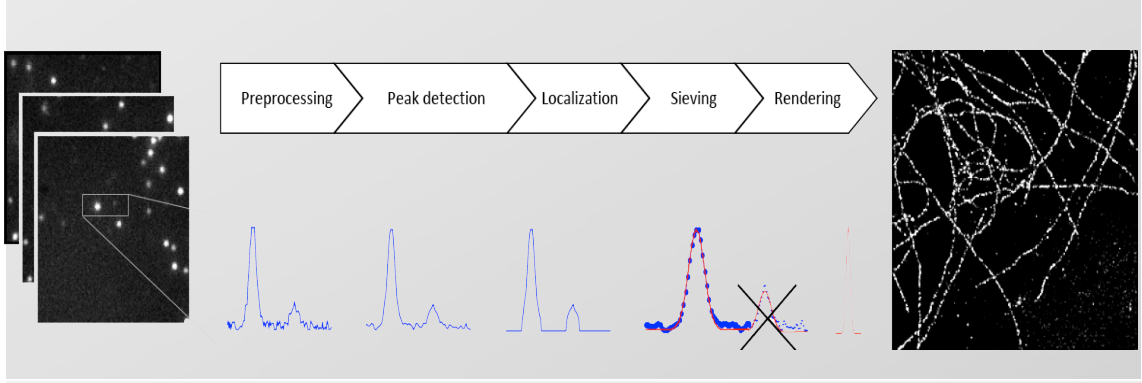
The increasing adoption of single-molecule localization microscopy techniques such as PALM and STORM has spurred the development of a number of software packages to perform the localization and rendering of the data. Each software package differs in a number of aspects, which makes the comparison of the different algorithms non-trivial. Here, we present a summary of the algorithms used in the literature and a number of open-source software packages which implement them.

The process from the raw data to the final localized particles can be divided into five steps: preprocessing, peak detection, localization, sieving and rendering. Each software package has been described according to these different steps. The performance of the different algorithms has been compared on synthetic data, highlighting specifically: precision and recall of the peak detection, localization accuracy of detected peaks, and precision and recall of the entire process.

Algorithms have been tested under selected signal-to-noise-ratio conditions, varying particle densities and sample depth. The particles have all been simulated using a Gibson and Lanni model, which gives a good balance between accuracy and speed, while taking into account optical aberrations commonly present in PALM/STORM setups.

Keywords

Super-resolution microscopy, localization, PALM



Endrov – An Open Source Framework for Image Processing and Analysis

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Abstract

The software is becoming more and more important for biological research but has been greatly overlooked compared to the hardware. Commercial software is hard to extend as the source code is not provided. The expense and format lock-in makes it hard to spread to other labs. ImageJ, the defacto-standard image software, is not designed for modern needs and has become only a patchwork trying to add the missing features. To solve these problems we have developed a new platform - Endrov - that covers the entire microscopy chain. It is a plug-in framework consisting of 140 000 lines of Java with a tight coherent design, running on all operating systems and covers a range of different functionality. Endrov has advanced control of the microscope hardware (via Micro-manager). It can view, annotate, process and analyze recordings using 130 image processing filters and 80 plugins. New applications are introduced with the graphical programming language (flows), interpreted Java or new plugins. Endrov can also be used as a library, making heavy data analysis simple. We have developed a new schema for data storage which handles arbitrary metadata, 6D recordings, mixed resolutions and compression (both lossy and lossless). Large datasets are handled gracefully. Moreover, the speed of most operations is unaffected by the size of datasets. Most file formats are supported via Bio-formats and it can access the OMERO image server. Our framework is open and free of charge. It is highly flexible and can be adopted to any needs in current research. Endrov has for example been used to quantify a large number of genes' expression levels.

Keywords

Image processing, image analysis, microscopy, imagej, c elegans, particle tracking, hcs, hts, micro-manager, omero, metadata, annotation, visualization

Visualization Tool for the Examination of 3D Tracking Results

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Abstract

In a project for studying cell movement during embryonic development, I realized that a particular painful task after tracking biological objects in 3D is the evaluation of tracking results. Many tracking packages claim their their high precision in following objects. When such packages are applied to "my data", we cannot refrain ourselves from checking if the package really did the tracking. This evaluation process is in general not so easy hindered by multi-dimensional nature of 3D time series. For this reason, a tool was made by extending the 3Dviewer plugin of ImageJ / Fiji created by Benjamin Schmid (Uni. Wuerzburg). The tool loads tracking results data text file and visualizes 3D tracks in OpenGL to compare them with the original 4D sequences.

Keywords

3D viewer, 3D tracking, visualization

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Image (15 cm x 5 cm)
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Multiview 3D Image Tiling for OPT and SPIM Data

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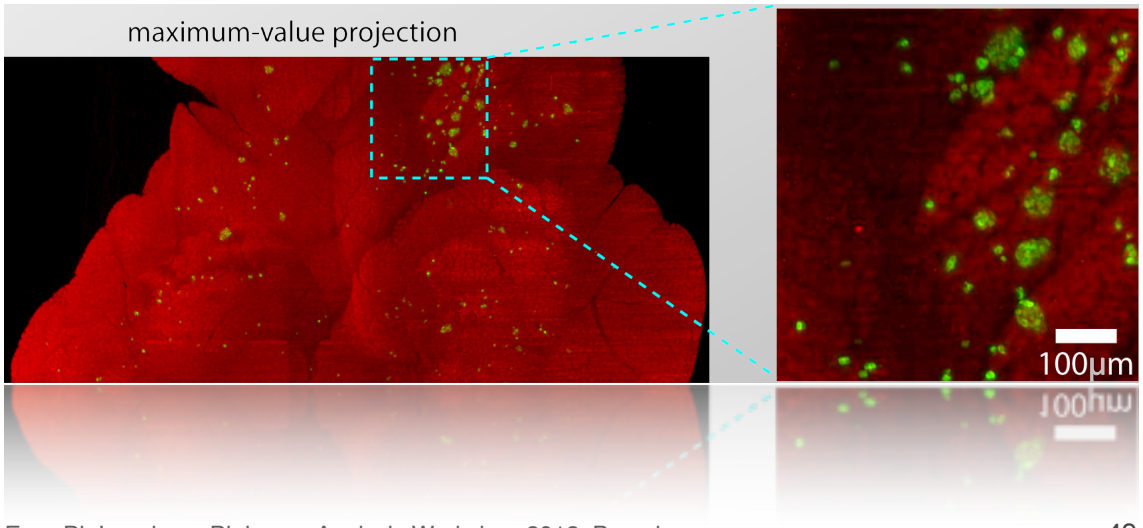
Abstract

Imaging mesoscopic samples in OPT (Optical Projection Tomography) and SPIM (Selective Plane Illumination Microscopy) has intrinsic optical limits when trying to acquire high resolution for the entire specimen. To reach high resolution without loosing the global perspective, we want to achieve automated registration and tiling of our multiview 3D datasets. Automation is the key for processing high throughput data. The idea is to embed existing tools and adapt them to our needs, or develop a new approach in case the previous does not work.

The tools that we are using right now are: a) Matlab, where we have a variety of programs dealing with the data we acquired, such as general processing and reconstruction. b) FIJI/ imageJ and XuVTools to do the semiautomated stitching and blending of our high resolution 3D image data and c) LabView to control our setup and log approximate positions of the tiles.

Keywords

Tiling, stitching, 3D-data, automization, OPT, SPIM, mesoscopic imaging



Applications of Novel Cellular Diagnostics

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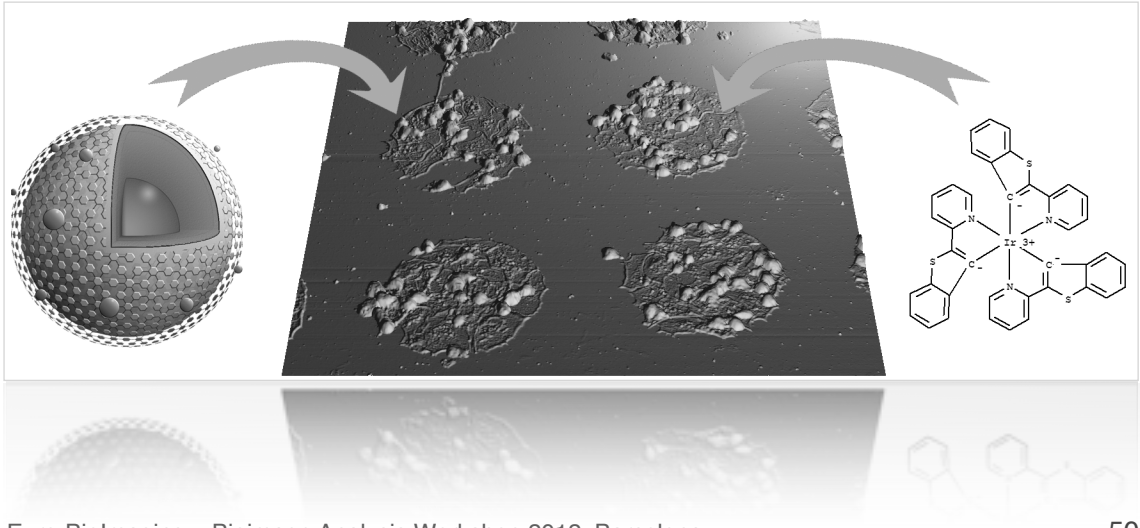
Abstract

The National Biophotonics Imaging Platform of Ireland provides a research and training framework applied to the field of advance imaging within the life sciences. Two independent research streams at Dublin City University focus on the development of novel fluorescent based sensors for cellular diagnostics. Divergent applications range from complex 3D cell-cell interactions, pattern recognition, nanoparticle based detection, to cell organelle recognition, advanced photophysical characterisation and subcellular environmental sensing.

Here we present two examples of our work. Firstly, the use of highly fluorescent silica nanoparticles as detection agents for platelet cell membrane receptors responsible for maintaining haemostasis. Secondly, we detail the use of custom synthesised environmentally sensitive fluorescent probes for subcellular labelling within a number of established cell lines (SP2, CHO and Hela cells). Each example presents specific challenges in resolving key features in order to establish protocols for automatic image analysis. The combination of customised probes, tailored imaging platforms and automatic analysis protocols will be applied to the development of new diagnostics device.

Keywords

Nanoparticle, intracellular sensing, diagnostics, automated analysis



PureDenoise – An ImageJ Plugin for Denoising Multidimensional Fluorescence Microscopy Images

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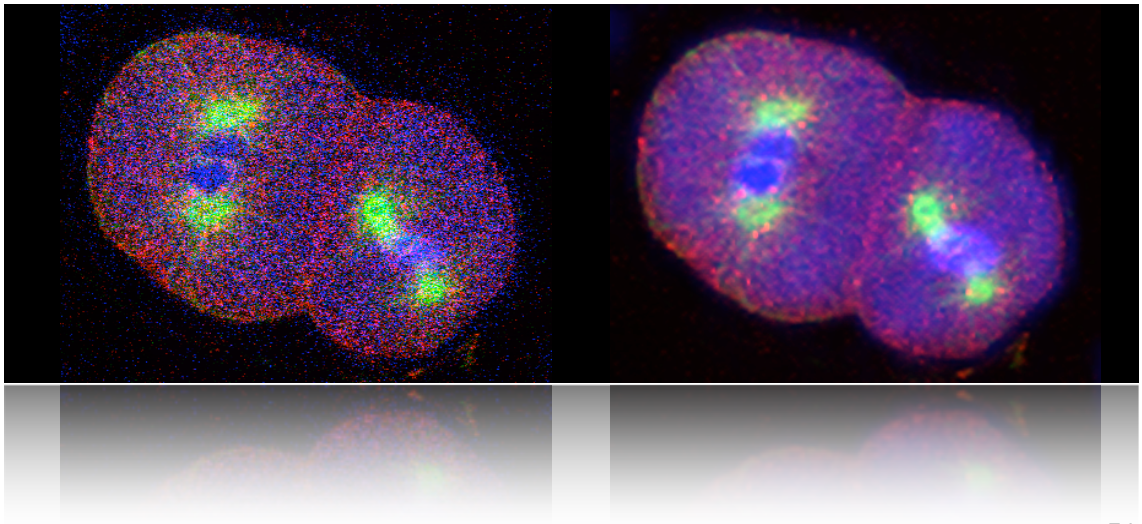
Abstract

Thanks to the development of improved microscopy imaging techniques and the advent of highly selective fluorescent dyes, fluorescence microscopy imaging has allowed the precise identification of tagged molecules in biological specimen. Of particular interest are the visualization and the study of living cells, which induce tight constraints on the imaging process. To avoid the alteration of the sample and to achieve a high temporal resolution, low fluorophore concentration, low-power illumination and short exposure time need to be used in practice. These stringent imaging conditions generate undesirable random distortions, called noise, that have a negative impact on the signal-to-noise ratio (SNR) of the resulting images. We have thus developed PureDenoise, an ImageJ plugin for the efficient, fast, and automatic denoising of multidimensional fluorescence microscopy images. This Java plugin is based on the Poisson Unbiased Risk Estimate-Linear Expansion of Thresholds (PURE-LET) denoising approach. Assuming a mixed Poisson-Gaussian noise model, an unbiased estimate of the mean-square error (MSE) is used to optimize the parameters of a linear expansion of Haar wavelet-domain thresholding functions. These data-adaptive thresholding rules take into account the high redundancy between neighboring slices (resp. frames) in 3D (resp. 2D-timelapse) fluorescence microscopy images. The proposed plugin features an automatic noise parameters estimator and two cursors for balancing the denoising quality and the computation time. A multithreaded implementation allows to denoise several slices or frames in parallel, which drastically reduces the overall execution time. For instance, a 400x400x10 data set can be efficiently denoised within a couple of seconds.

Keywords

Fluorescence microscopy, denoising, risk estimation, ImageJ, Java, multithreading, Haar wavelet, Poisson-Gaussian noise



Digital Phantoms as a Tool for Benchmarking and Testing in Cell imaging

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Abstract

This contribution tackles the problem of assessing the quality of cell image analysis results for benchmarking purposes. As the ground truth for cell image data (and measurements on them) is not available in most experiments, the outputs of different image analysis methods can hardly be verified or compared to each other. Images are often strongly affected by degradations (caused by cell preparation, optics and electronics) that cause high variation of the results computed using different algorithms.

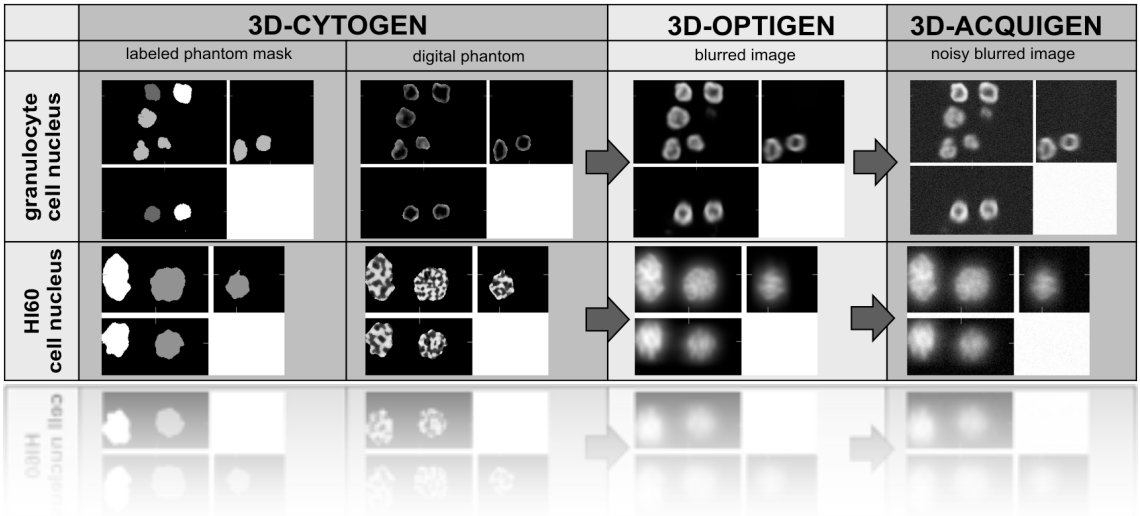
Some papers solve this problem partially using estimates of ground truth by experts in the field (biologists or physicians). However, in many cases, such a ground truth estimate is very subjective and strongly varies between different experts.

In order to overcome these difficulties, we created a web-based toolbox [1] that can generate 3D digital phantoms of specific cellular components along with their corresponding images degraded by specific optics and electronics. The user can then apply image analysis methods to such simulated image data. The analysis results (such as segmentation or measurement results) can be compared with ground truth derived from digital phantoms of input objects (or measurements on them). In this way, image analysis methods can be compared to each other and their quality (based on the difference from ground truth) can be computed. Simulated benchmark data sets will be available soon for download.

[1] D. Svoboda; M. Kozubek, and S. Stejskal, “Generation of Digital Phantoms of Cell Nuclei and Simulation of Image Formation in 3D Image Cytometry,” Cytometry Part A, 75A, 6, pp. 494-509, 2009.

Keywords

Digital phantom, synthetic image, 3D cell imaging, fluorescence microscopy, benchmarking, web-based resources



Graph-Cut library for Biomedical Image Analysis

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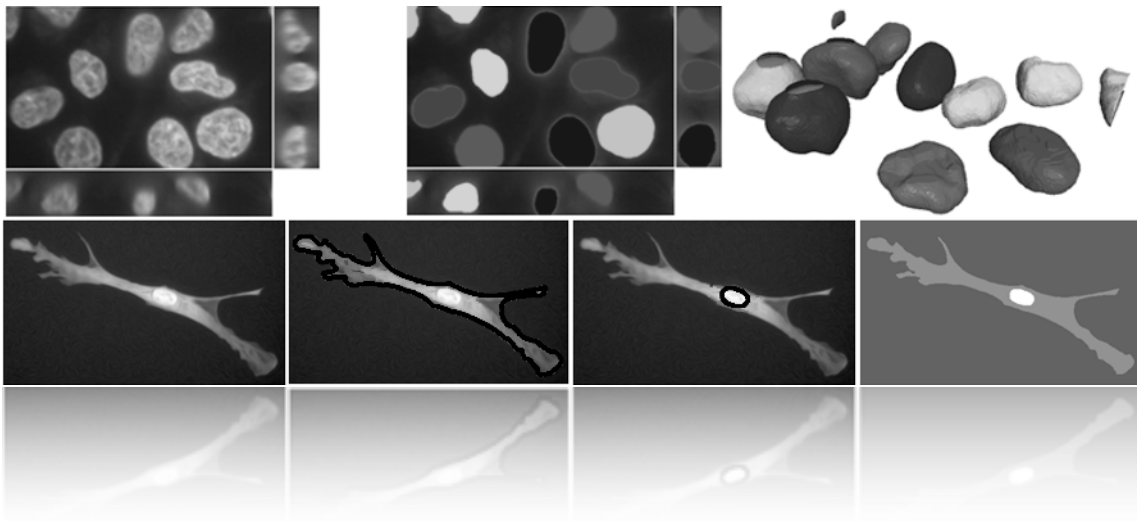
Abstract

We have developed an open-source cross-platform library focusing on combinatorial optimization via graph cuts. It can be used in many digital image analysis tasks; especially for finding optimal solutions to energy minimization based discrete labeling problems such as image segmentation (e.g. Chan-Vese or Mumford-Shah segmentation model or geodesic active contour model). The library is being developed in C++ and places emphasis especially on speed and low memory usage as well as clean and extensible object-oriented design. It considers the aspects typical for biomedical image analysis, e.g. anisotropy, n-dimensionality, large images. MATLAB interface for all segmentation algorithms in the library is also available. We will present the library and examples of its usage in fluorescence microscopy image analysis.

Keywords

Graph-cuts, image segmentation, C++ library, energy minimization



Creating Faster, More Expressive ImageJ Scripts and Plugins with Scala

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Abstract

ImageJ libraries and plugins are traditionally developed using Java. Java provides execution speed and a programming environment suitable for creation of large code bases.

Smaller, more expressive, code is created using ImageJ macros and scripting in dynamic languages like JavaScript or Groovy. Macros/scripts help quickly create specialized code with minimal boiler-plate, in syntax more expressive than Java. Main drawbacks are a much slower execution speed and a need to learn/use two different types of syntax for scripting and plugin/library code.

Scala is a statically-typed general purpose language that has a feel of a dynamic language. You can create code that is as expressive as a dynamic language but executes at the speed of compiled Java code. It can be used both for scripting, without loss of execution speed, and for "regular" library code. Scala code integrates with existing Java libraries like ImageJ. Java can also call Scala libraries. Scala builds on strength of Java, adding many advanced language features like closures, traits, type inference, powerful generics and concurrency support, and many more.

This presentation will show how Scala can be used to create image analysis libraries and scripts that are more expressive (smaller number of lines and characters) then existing Java code, at the same time being at least as fast or faster. Scala annotations can be used to actually generate code that is more computationally efficient than equivalent Java code. Specialized compiler plugins can be used to further optimize the byte code and to take advantage of dedicated hardware, like GPUs.

Keywords

Image analysis, image processing, ImageJ, Scala, scientific computing, software development

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Image (15 cm x 5 cm)
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ITK Warper for Fiji

Fethallah Benmansour[1], Mark Longair[2], Engin Turetken[1], Johannes Schindelin[3], Pascal Fua[1]

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Abstract

The Insight Segmentation and Registration Toolkit (ITK) is a powerful open-source, cross-platform image analysis toolkit that employs leading-edge algorithms for registering and segmenting multidimensional data. In the past, several open-source applications, such as Paraview and 3D Slicer, based on ITK have been used for analysis and visualization purposes. Fiji is another open-source solution that possibly targets a wider community ranging from image processing and computer vision to bioengineering and neuroscience. In this work, we propose to bridge the gap between these solutions by making the ITK-based functionalities accessible from within the Fiji environment. This is achieved through the use of the Java Native Interface (JNI), which enables ImageJ to load C++ libraries. We tested our approach on the problem of semiautomated neuron tracking by extending the publicly available Simple Neurite Tracer plugin to improve tracing quality.

Keywords

ITK warper, ImageJ/Fiji, neuron tracking

Free space for an optional illustration
Image (15 cm x 5 cm)
Coming soon

FucciJ – Semi-Automatic Tracking of FUCCI Cells to Build Lineage Trees Based on Fluorescence Images

Daniel Schmitter[1,2], Marta Roccio[1], Matthias Lutolf[1], Daniel Sage[2]

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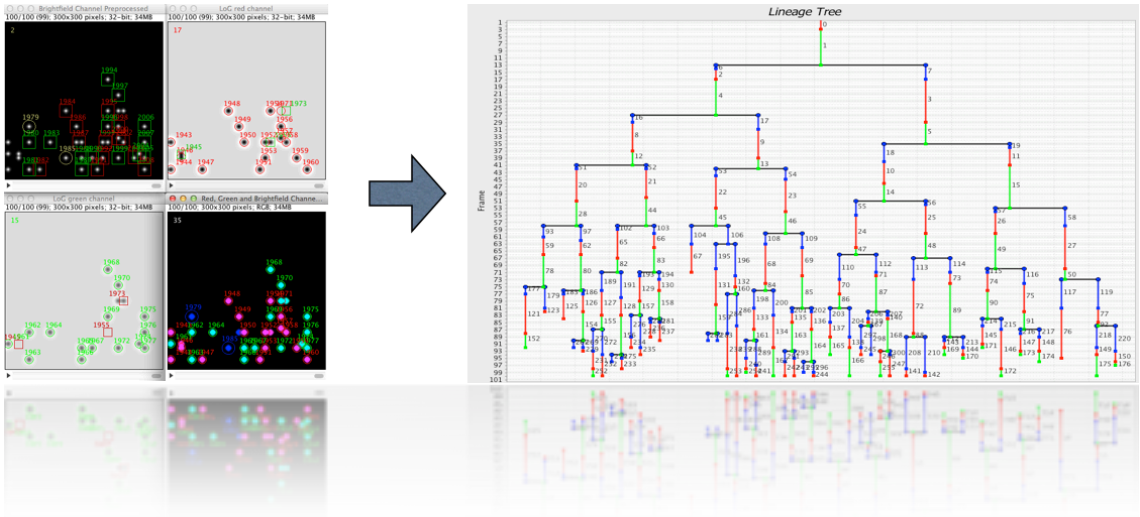
Abstract

The Fluorescence Ubiquitination dependent Cell Cycle Indicator (FUCCI) reporter is based on the specific expression of two fluorescent tagged proteins during G1 (red) and G2 (green), due to phase specific expression of their respective ubiquitin ligases during the cell cycle [1]. To study the cell cycle time-lapse movies are recorded in three different channels: brightfield, red and green . We have developed two ImageJ plugins that are distributed under the name “FucciJ” to detect and track the cells simultaneously in the three different channels in a semi-automatic way in order to establish cell lineage trees to study cell fate and the cell cycle itself.

FucciJ is able to compute the most probable lineage trees only based on the detection of cells in G1 (red channel) and G2 (green channel) phase even in the case of unreliable detection of cells in M phase.

Keywords

FUCCI, fluoresence images, tracking, cell lineage



TANGO – A Customizable Tool for High Throughput for Images Analysis of Nuclear Signals

Jean Ollion[1], Philippe Andrey[2], Christophe Escudé[1], Thomas Boudier[3]

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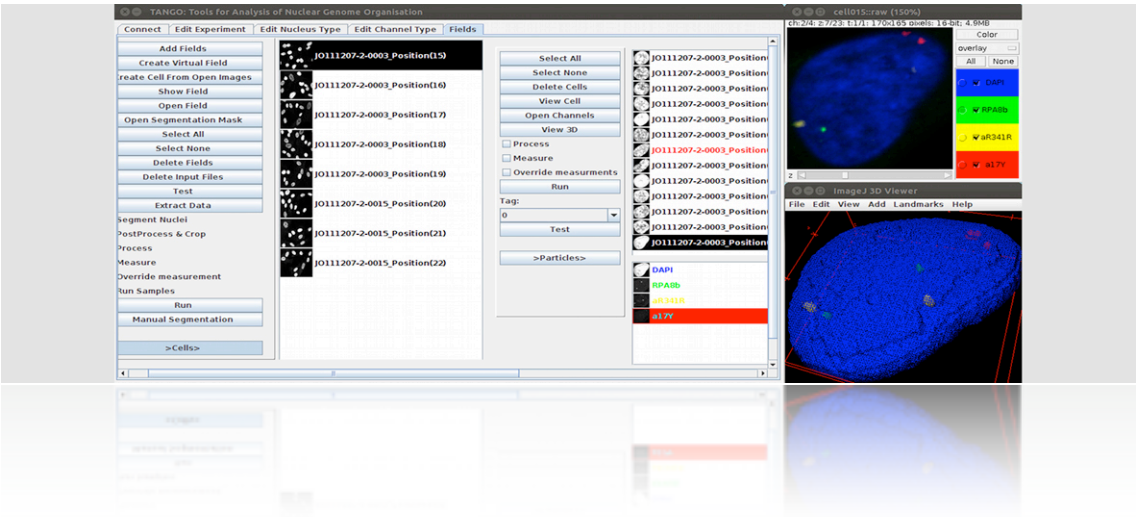
Abstract

The nucleus is a highly structured and organized cellular compartment. The genome is not randomly organized inside the nucleus, each chromosome occupies a particular space called the chromosomal territory (CT). Within CTs genes of particular interest may occupy particular localization and move during expression. Repeated DNA sequences located in the centromeric regions of mammalian chromosomes are thought to organize the genome by interacting with each other or with specific nuclear compartments such as the nucleolus or the lamina. In order to analyze nuclear organization, a statistical study needs to be run on a large population of cells. Modern microscopes allows to acquire a large amount of fields. Thanks to software such as ImageJ it is possible to automate analysis including filtering and quantitative measurements. Unfortunately in ImageJ available processing and measurements are only for 2D images. Furthermore since different users may need different settings for filtering and analyses, the use of macros has its limitation. We have developed TANGO (Tool for Analysis of Nuclear Genome Organization) to analyze thousands of nuclei in 3D. All images, settings and results are stored in a database (mongo-DB, powerful multi-platform object-oriented DB), a customizable processing chain can be set up for each different experiments using available plugin in ImageJ and new ones have been developed like 3D spatial statistics. The visualization of the 3D images and results benefits from the development of powerful 3D interfaces such as Image5D and 3D Viewer.

Keywords

ImageJ, database, 3D, nucleus, processing, analysis, measurements



From Acapella to ImageJ

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Abstract

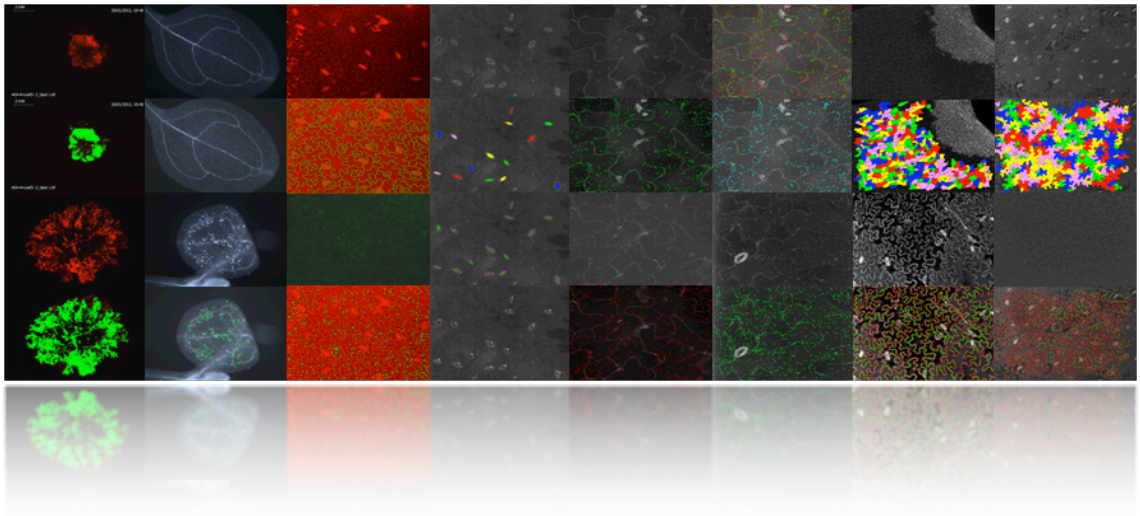
In the last two years, we developed several high-throughput image processing algorithms to detect and quantify plant cellular objects on the basis of PerkinElmer's Acapella image analysis software and Opera high content screening system. With one year's development, our algorithms can precisely detect fluorescently labelled plant cells, plasma membrane, stomata, plasmodesmata (PDs), vesicles co-localisation, and different types of membrane compartments. Furthermore, whilst processing tens of thousands images, cellular traits (e.g., size, roundness, width, length, and fluorescence signal intensity) can also be calculated in output fields, which are impossible to be manually identified and scored.

More recently, we have advanced our Acapella scripts to batch process images obtained by conventional confocal microscopy (e.g., TIFF files). Some successful examples of this new application of Acapella are callose detection, calculating pathogen infected area, coloured spots recognition, PDs and cell wall detection, etc.

With an aim of sharing our image analysis algorithms and analysis workflows with the cell research community, we are genuinely interested in translating our Acapella algorithms and scripts into plugins for the JAVA based open-source solution – ImageJ. Hence, we want to make a start on participating Bioimage Analysis Workshop 2012 so that we could commence involving in the ImageJ development from now on.

Keywords

Acapella, high-throughput image processing, confocal microscopy



Web-based collaborative neuronal reconstruction with CATMAID

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Abstract

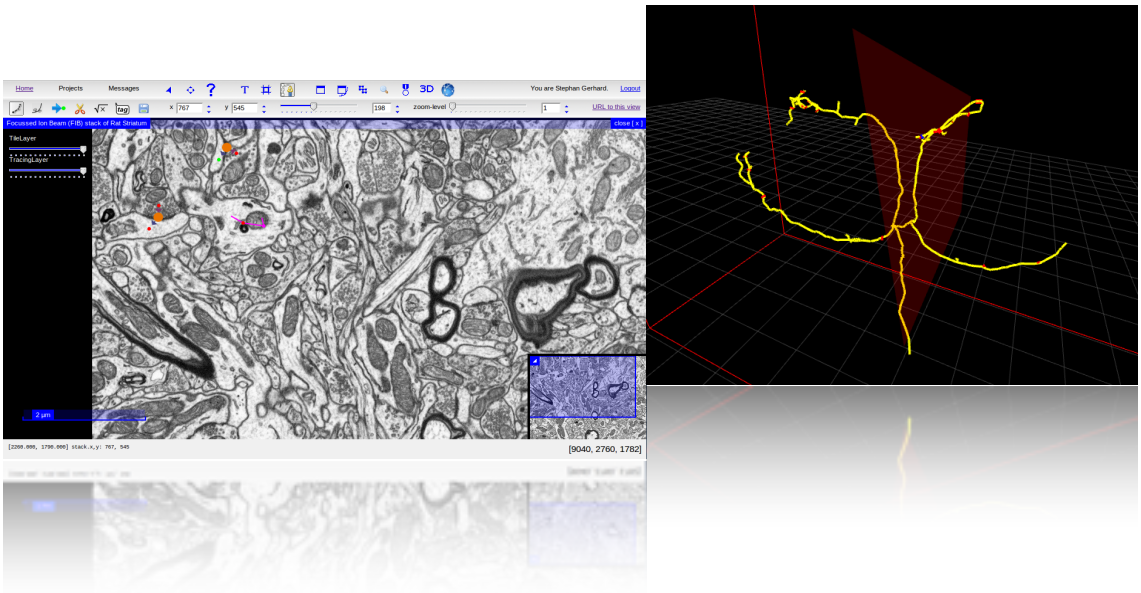
CATMAID, the Collaborative Annotation Toolkit for Massive Amounts of Image Data (www.catmaid.org), is a web-based platform suitable for the annotation of very large 3D data sets, such as those produced by serial section transmission electron microscopy. Manual and automated methods are required to segment and extract meaningful information from these images. Automated methods for segmentation are certainly improving, but much annotation and segmentation still needs to be done by human operators. A fast and proven way to extract neural circuits is by by skeletonizing neurons and their synaptic connectivity. We implemented in CATMAID such an annotation and tracing interface, and means to semantically group and tag neurons in a hierarchical manner. Every new or changed annotation is immediately reflected in a remote centralized database. The utilization of a client-server architecture enables crowd-sourcing approaches to neural circuit reconstruction with hundreds of annotators or researchers within a lab, no duplication of large image datasets, automatic incremental backup, client-side browser caching, and making data available via web services.

We also have added to CATMAID WebGL-based 3D visualization of neural morphologies, text tagging of skeleton nodes and connectors, statistics of the tracing progress, a review system and a logging system.

Future plans aim at integrating segmentation workflows on the server through standardized protocols that supports the manual segmentation task and enables dense neural circuit reconstruction in a collaborative, interactive and incremental manner.

Keywords

Collaborative tool, large image, segmentation, annotation, web-based



Improving Acquisition Skills Using Continuous Image Quality Assessment

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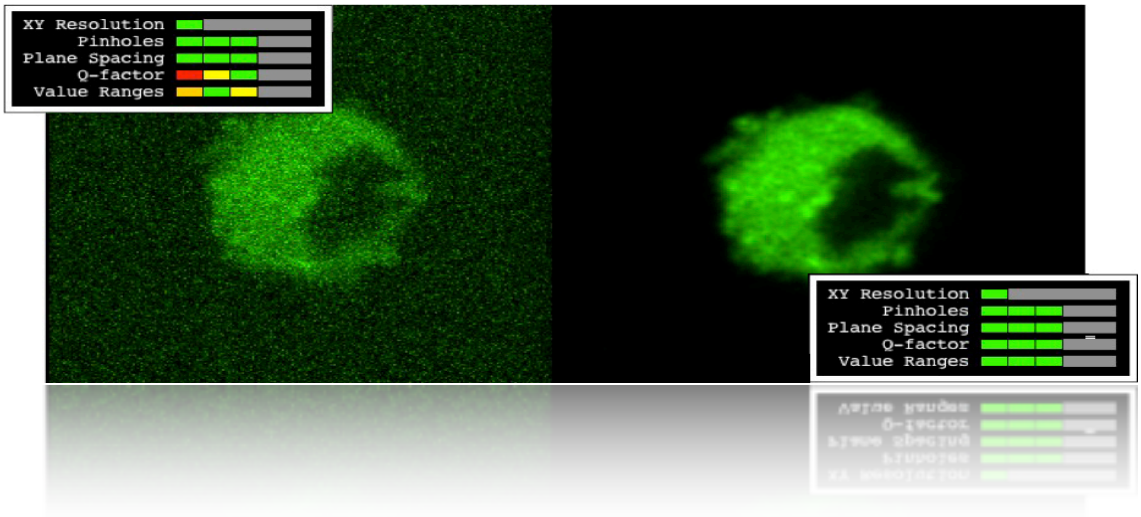
Abstract

A system is presented that performs continuous assessment of images acquired on confocal microscopy devices. A background-running system task monitors the acquisition software's current directory. Recent files are sampled at user defined time interval and subjected to a set of image acquisition quality measurements. Synthetic results of these procedures are unobtrusively presented to the workstation user through a series of red/green scaled indicators. Based on issues detected, targeted advices can be obtained that aim at improving next-image quality, and image acquisition skills in the long term. Administrator warnings can be set on a threshold basis, enabling remote alerting of the device or facility manager. The simple design involves Windows scheduled tasks, image metadata access though the LSM Toolbox library, basic image statistics accessed with ImageJ running in the single instance listener mode and the Twitter4J library for the optional quality alert messages.

Keywords

Image quality, facility management



CUDA-based massively parallel implementation of gray-scale Mathematical Morphology operations in Java

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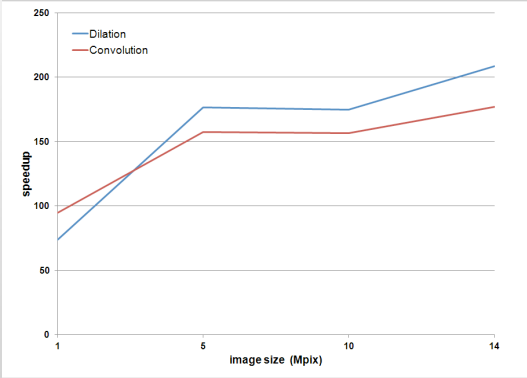
Abstract

Parallelization of image processing algorithms can be achieved either on the Central Processing Unit (CPU) or on the Graphics Processing Unit (GPU) side. High level support of parallelization schemes is still minimally developed in Java, which is a definite disadvantage compared to C++ and C#. The support of GPU parallel image processing in Java is still minimal and depends on custom libraries. The availability of image processing frameworks in Java, such as ImageJ, together with the potential of GPUs to offer high performance at low cost makes it attractive to bridge this gap. On the other hand, the advantages of GPU parallel architecture are penalized by the memory transfer overheads, which make GPU implementation of certain classes of algorithms not useful. In this work we demonstrate a combined Java and CUDA based implementation for the basic morphological operations and spatial convolution. It is demonstrated that the overhead of Java is negligible, which presents a viable option for integration of GPU code into Java programs. The CUDA-enabled GPUs have four types of memory, notably global memory, constant memory, texture memory and shared memory. The results indicate that the most advantageous GPU implementation is by using texture memory. Our results show an advantage of GPU parallelization over sequential implementation on the CPU for both convolutions and mathematical morphology operations. Using 3x3 kernel, on a NVIDIA GeForce GTX 470 platform the speedup of the CUDA processing was ranging from 177 to 208 times for convolution and dilation respectively .

Keywords

Convolution, morphology, dilation



Runtime speedup on NVIDIA GeForce GTX 470 as a function of image size

CellFileAnalyzer – Automatic Plant Cell File Length Estimator

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Abstract

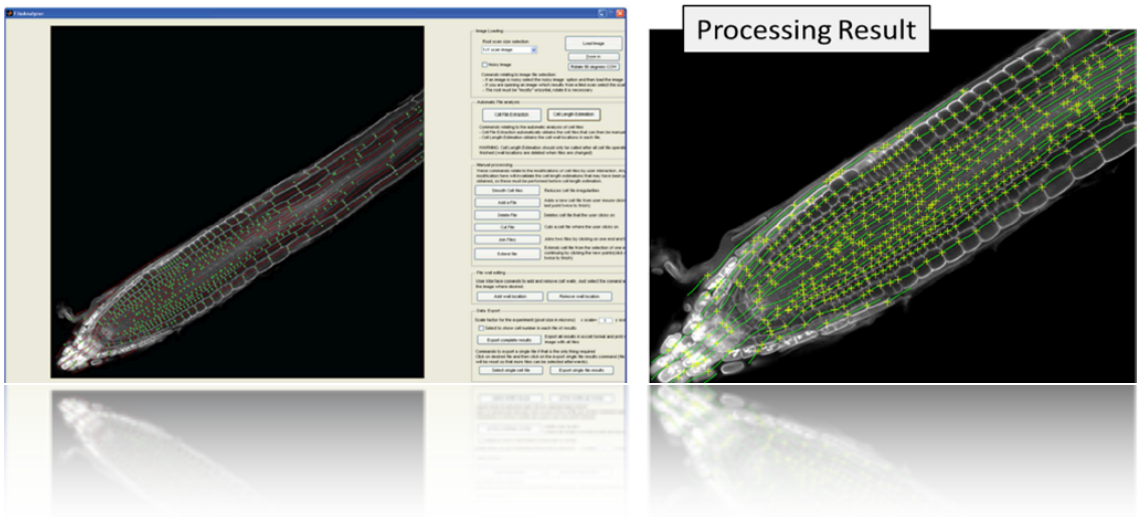
CellFileAnalyzer is an automatic tool for cell file detection and cell length estimation, developed without using explicit image segmentation. Most analysis of plant structure is performed through manually measurement. In these conditions, researchers spend large amounts of time performing measurements which may not be reliable due to varying bias. This need to analyze a large amount of images from many replicate roots motivates the development of automatic tools for root structure analysis.

CellFileAnalyzer enables the detection of cell files, the main structure in plant roots, and extracts the length of the cells in those files. Contrary to most automatic plant root analysis applications it does not use image segmentation to detect cells and analyze their properties. Through the use of image symmetry analysis, cell files can be detected without requiring segmentation. Furthermore, after the detection of a cell file, the cell length estimation problem becomes a one dimensional problem with a much easier solution than that of cell segmentation. In both cases we use the phase based image symmetry.

CellFileAnalyzer reduces analysis time in more than 90%, improving the biologist work and more data to be analyzed. While the software implements a fully automatic approach, it is well known that fully automated solutions are unlikely to have zero errors. Manual editing is provided to the user for error correction, enabling the verification of results given by the approach. Users did not correct more than 20% of all automatically detected structure, taking no more than 10% of manual analysis time to do so.

Keywords

Plant cell structure analysis, image symmetry, user interaction



Massive Stitcher – Integrating Plugins for New Tasks

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Abstract

The main intention of the plugin is to facilitate the assembly of a large amount of 3D stacks, taken at multiple time-points. Even though several software (MosaicJ, Stitching, Grid Assembly and TrackEM2) existed in order to perform the operation, none of them met all of the needed requirements. We are aiming for a simple to use interface that could open and manipulate typical microscopy formats (e.g. Leica LIF and Zeiss LSM files), stitch the data using acceptable memory requirements and register multiple stacks from a time-lapse experiment.

The resulting plugin is based on the assembling of several available plugins built for ImageJ, wrapped around a simple classic ImageJ interface. The LOCI BioFormats reader plugin and its metadata structure were used to extract position data, as well as selectively load planes onto memory. The Stitching of each timepoint was performed on a maximum intensity projection (MIP) of a given slice range by using code from Stephan Preibish's "Stitch Grid Collection" plugins. By adapting code from the StackReg plugin, the stitched MIPs were then registered in 2D. The stitching and registration are then propagated to the individual slices and timepoints. Memory-wise, a maximum of two complete images are simultaneously loaded, the required data and results being directly read and written to disk. This approach allows for the plane-by-plane stitching of very large datasets on desktop machines with acceptable speeds.

Keywords

Stitching, registration, plugins, ImageJ, StackReg, LOCI, microscopy

Free space for an optional illustration
Image (15 cm x 5 cm)
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