n pathlist

an: nit__(self, pathid): pathid = pathid self.nucs = ArrayList() self.nucs = ArrayList() self.ninby = 0 self.minby = 0 self.maxby = 0 self.binstack = ImagePlus() self.actualbx = 0 self.actualbx = 0 Self.actualbw = 0 Self.actualhw = 0 Self.actualhw

EUBIAS 2015

European Biolmage Analysis Symposium

Paris, January 5-6, 2015 Institut Curie

Biolmage Data Analysis Community: Status Quo Open Software Showcase Sponsor and commercial software bridging open source software Applications/ New Developments from Scientific Computing Cells and particles dynamics analysis Image Data management and visualization Open Community Panel Discussions

Sponsors:



Supporting Organisations :





Program

Day 1: Monday 5th of January 2015

Arrival of Delegates

10h00 - 10h15 Green Café

Coffee

10h15- 11h00 Burg Amphitheatre

Session 1: Biolmage Data Analysis Community: Status Quo (chair Perrine Paul-Gilloteaux)

- 10h15-10h30: Julien Colombelli, Sébastien Tosi :EUBIAS activity short report
- 10h30- 10h45: Jason Swedlow: Euro-BioImaging updates
- 10h45- 11h00: Jean Salamero: France Biolmaging and IPDM node

11h00 -11h30 Burg Amphitheatre

(chair Jean Salamero) Keynote 1: Stephan Saalfeld, Janelia Farm. Improving Volume Reconstruction from Large Electron Microscopy Data

11h30- 12h50 Burg Amphitheatre

Session 2.1: Open Software Showcase (chair Sébastien Tosi)

- 11h30- 11h50 Introducing the ImageJ OPS framework (Johannes Schindelin)
- 11h50- 12h10 ICY (Fabrice de Chaumont)
- 12h10- 12h30 CellCognition (Christoph Sommer)
- 12h30- 12h50 Knime for image Processing(Christian Dietz)

12h50 - 14h00 Green Café

Lunch

14h00 -15h20 Burg Amphitheatre

Session 2.2: Open Software Showcase (chair Perrine Paul-Gilloteaux)

(chair Perrine Paul-Gilloteaux)

- 14h00- 14h20 Cell Profiler (Carolina Wählby)
- 14h20- 14h40 Ilastik (Chong Zhang)
- 14h40- 15h00 ITK/VTK (Jérôme Velut)
- 15h00- 15h20 Tango (Julien Cochennec)

15h20 - 15h40 Green Café

Coffee break

15h40 -16h40

Session 3: Sponsor and commercial software bridging open source software session (*chair Julien Colombelli*)

- 15h40-15h55 AMIRA (FEI): Customizable 3D Processing Tool Application to Correlative Imaging
- 15h55-16h10 Arivis: fast and unlimited: Visualize, analyze and share microscopic image data without limitations

- 16h10- 16h25 Nikon Lim: Integrating Flexible and Efficient Image Acquisition with Open software
- 16h25- 16h40 Zeiss ZEN: Open Application Development Tools for Smart Microscopy

16h40- 17h40 ANNEXES BURG and META Room

(Contact: Lucie Sengmanivong, Heiligenstein Xavier, Ludovic Leconte) Meet the developers' session 1 Speakers interact with participants at computer/poster: questions, demos etc... See Room plan

17h40- 18h10 Burg Amphitheatre

(Chair Raimund Ober) Keynote 2: Berndt Rieger, TU Delft. Image processing for super-resolution microscopy

18h10-19h30 BURG Burg Amphitheatre

Session 4: Applications/ New Developments from Scientific Computing (Chair Bernd Rieger)

- 18h10-18h30 Marc Beal (BioSearch Technologies Inc) : StellarVision Commercial Breaking the Optical Resolution Barrier Novel Next Generation Synthetic Aperture Optic (SAO) based Fluorescent Microscopy
- 18h30-18h50 Y. Natai (Keio university, Japan) Development of high-speed 3D imaging system with electrically tunable lens
- 18h50-19h10 Jerry Chao (Texas A&M University) FandPLimitTool: An application for calculating limits of accuracy for parameter estimation in single molecule microscopy
- 19h10- 19h30 Jan Brocher (BioVoxxel Inc) The BioVoxxel Image Processing and Analysis Toolbox

19h30-21h Green Café

Dinner

Day 2: Tuesday 6th of January 2015

9h30-10h00 Burg Amphitheatre

(Chair Sébastien Tosi) Keynote 3 Ivo Sbalzarini, MPI-CBG, CSBD. Bioimaging requires novel computer vision approaches and open software

10h00-11h20 Burg Amphitheatre

Session 5-1: Cells and particles dynamics analysis (Chair Jean Salamero)

- 10h00-10h20 David Holcman (ENS Paris). BioNewMetrics and stochastics analysis of super resolution single particles trajectories
- 10h20-10h40 Thierry Pecot, (Inria Rennes). Space Time Representation Imaging and cellular dynamics of molecular complexes
- 10h40-11h00 Fabrice Cordelière (CNRS Bordeaux). Automated cell tracking and analysis in phase contrast videos (iTrack4U): Development of Java software based on combined mean shift processes
- 11h00- 11h20 David Kim, (College Station, Texas, USA). A Java implementation of MIATool for multidimensional image data analysis

11h20 - 11h50 Green Café

Coffee break

11h50 – 12h50 Burg Amphitheatre

Session 5-2: Cells and particles dynamics analysis (Chair Charles Kervrann)

- 11h50-12h10 Jean-Yves Tinevez (Institut Pasteur Paris). MaMuT: a software tool for visualization, tracking and lineaging in large multi-view SPIM images
- 12h10-12h30 Bo Shuang (Rice University, Houston USA). Fast Step Transition and state identification (STASI) for discrete single molecule data analysis
- 12h30-12h50 Zoltan Cseresnyes (DRFZ Berlin). Fourier transform-based fast characterization of cell shapes as a tool for intelligent classification of cells in intravital microscopy

12h50-14h00 Green Café

Lunch

14h00-15h40 Burg Amphitheatre

Session 6: Image Data management and visualization (Chairs Jason Swedlow and Julien Colombelli)

- 14h00-14h20 Jason Swedlow (Univ Dundee). The Open Microscopy Environment: Open Image Informatics for the Life and Biomedical Sciences
- 14h20-14h40 Raphaël Marée (Univ Liege). Cytomine for data scientists and image analysis software developers
- 14h40-15h00 Aaron Ponti (ETH Zurich). openBIS Importer Toolset (oBIT)
- 15h00-15h20 Jens Rittsher (Institute of Biomedical Engineering, University of Oxford). Zegami: A Platform for Image Centric Data Exploration
- 15h20-15h40 Elton Rehepaj (Institut Curie Paris) Integration of heterogeneous data sources for high content screening data exploitation and exchange

15h40-16h10 Green café

Coffee break

16h10 - 17h10 ANNEXES BURG and META Room (Contact: Lucie Sengmanivong, Heiligenstein Xavier, Ludovic Leconte)

(Contact: Lucie Sengmanivong, Heiligenstein Xavier, Ludovic Leconte) Meet the developers' session 2

17h10- 17h50 Burg Amphitheatre

(Animated by Philippe Gesnouin) Session 7.1 : Open Community Panel Discussion: Meaning of Open source licensing Patrick Moreau (Head of Inria assets), Jason Swedlow (Univ Dundee and Glencoe Software), Julien Velut (ITK/VTK and Kitware company), Johannes Schindelin (Fiji), Fabrice de Chaumont (Icy), Christian Goetze (Arivis founder)

17h50- 18h30 Burg Amphitheatre

Session 7.2: Open Community Panel Discussion : Reinforcing the Biolmage community Facility representative, image analyst, user (biologist focused on one topic), teachers... A community of users, analysts and developers: The expectations of each of us and how to work together in the most efficient way to conduct and disseminate cutting edge Biolmage analysis.

18h30 – 18h45 Burg Amphitheatre

Concluding remarks, summary of discussions and perspectives, organization of the next event.



Meet the developers'session

Additional place to hang out a poster or demo will also be available.

Monday	Room	Tuesday	Room
AMIRA (FEI)	annexe table 2	AMIRA (FEI)	annexe table 2
NIS JOBS (Nikon LIM)	META stand 2 + NIC	NIS JOBS (Nikon LIM)	META stand 2 + NIC
Arivis	annexe table8	Arivis	annexe table8
BitPlane	annexe table 5	BitPlane	annexe table 5
ImageJ	annexe table 1	OMERO	salle annexe table 1
ICY	annexe table 3	Cytomine	salle annexe table 3
CellCognition	annexe table 4	oBIT	salle META stand 3
Knime	annexe table 7	Zegami	salle annexe table 4
Cell Profiler	META stand 1	Rubies/iManage	salle META stand 1
llastik	META stand 3		
ΙΤΚ/VΤΚ	annexe table 9		
Tango	annexe table 6		



META room

Keynotes

Improving Volume Reconstruction from Large Electron Microscopy Data *Stephan Saalfeld HHMI's Janelia Research Campus, USA*

Connectivity analysis from Electron Microscopy images requires both efficient automation and manual proofreading. Current state-of-the-art automatic image analysis methods have high demands on data quality to deliver satisfying results within reasonable time.

We have developed methods to explicitly model and compensate for various artifacts that otherwise complicate automatic analysis. This includes joint distortion correction of multiple independent camera arrays, montaging sections from large sets of overlapping image tiles, elastic serial section alignment, local and global approaches to compensate intensity variation within and across sections, and an image based method for accurate local section thickness estimation and ordering.

Thanks to generic programming based on ImgLib2, our solutions transfer well to other applications, e.g. stitching Confocal image stacks or video processing.

All methods are available as plugins and protocols for the TrakEM2 software included in the ImageJ distribution Fiji. We are currently spending efforts to bring the best available methods to scale with a strong focus on making them accessible to the scientific community as Open Source Software. I will demonstrate the status of our joint efforts and outline perspectives.

Image processing for super-resolution microscopy

Dr. Bernd Rieger, Quantitative Imaging Group, Department of Imaging Physics Delft University of Technology, Lorentzweg 1, 2628CJ Delft, The Netherlands

Over the last decade a number of optical nanoscopy techniques have been proposed to bridge the resolution gap between electron (~1 nm) and conventional light microscopy (>200 nm). Localization microscopy is one of these nanoscopic techniques where, where fluorescent emitters are photochemically manipulated to switch on and off, such that at each instant in time only a sparse subset of all emitters is fluorescent. Recording thousands of frames thus provides a sequence of images of different random subsets nearly all fluorescent of emitters. Before a super resolved image can be visualized, however, a series of image processing steps needs to be undertaken. The first step in processing the raw frames consists of identifying and segmenting regions of interest (ROIs) that contain the emissions of single fluorescent emitters. Once ROIs in the raw data have been segmented, the next step is to estimate the positions of the emitting fluorescent molecules in these regions. Subsequently post-processing of the raw localizations takes place by filtering of the localizations to remove ones that do not represent trustworthy or accurate position estimates of single fluorescent emitters. The final step in the processing pipeline from raw data to super-resolution image is the actual visualization of the data.

In this presentation, I will discuss all the involved image processing steps and point to directions of further research with respect to image processing.

Bioimaging requires novel computer vision approaches and open software

Prof. Dr. Ivo F. Sbalzarini MOSAIC Group, Faculty of Computer Science, TU Dresden & Center for Systems Biology Dresden, Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Biological image data, especially from fluorescence microscopy, are very different from the photographs or satellite imagery traditionally considered in computer vision. Biological images are often three- or even higher-dimensional, and not standardized. Moreover, they frequently only become interpretable when considering additional prior knowledge, e.g., about the labeled structures or the optics of the microscope. We hence need to develop computer vision algorithms that provide principled ways of including prior knowledge in a modular fashion. This is necessary in order not to develop a separate "algorithm" for each problem. Microscopy and biological research are rapidly moving forward, and we cannot afford developing new methods from scratch every time the data change. This can only be achieved in a multi-disciplinary community effort and with user-friendly, open-source software to which everybody can contribute. As an example, we show how recent progress in computer vision enabled both user-friendly and optimal segmentation, as implemented in the open-source MOSAIC suite for Fiji and ImageJ.

Open Software Showcase

Introducing the ImageJ OPS framework

Johannes Schindelin, Tomancak group Dresden, Germany Christian Dietz, KNIME Konstanz, Germany Curtis Rueden, LOCI UW-Madison WI, USA

With increasing image sizes and modalities, scientists developing image processing and analysis software face a range of challenges: the software should be easy to use, easy to extend, easy to maintain, it should handle large amounts of data and it should be fast. Many individual developers attempted to tackle these challenges at a low level by developing reusable, generic frameworks, in general addressing up to two of the aforementioned challenges. The ImageJ OPS framework, still in an early stage, is already easy to use, extend and maintain, can handle data of almost arbitrary sizes and it sports a transparent optimization framework that makes its operation fast. Being based on the SciJava common framework, it is flexible enough to allow for already-existing algorithms to be accelerated simply by copying files that replace selected operations with machine-specific optimal ones. For example, a deconvolution algorithm making use of the Fourier Transform operation can run faster by providing a separate GPU-accelerated Fourier Transform operation – without touching the deconvolution algorithm at all. The architecture of ImageJ OPS was designed by three research groups, ensuring that it addresses a wide range of needs and that it is viable in the long term. As a further bonus, the ImageJ OPS framework is implemented in pure Java guaranteeing maximal interoperability, platform-independence and tapping into a vast number of software developers already familiar with that language. We predict that ImageJ OPS will be the standard framework to process and analyze images in bio-image informatics

Icy: an open community platform for bioimage informatics

Icy, Quantitative Image Analysis Unit at Institut Pasteur, Paris chaumont@pasteur.fr

Icy is a free and open-source image analysis software. Icy is a versatile tool that can be used

1. On desktop for final user requiring very rich and interactive dedicated client, offering a complete suite of more than 100 build-in functionalities plus 300 contributed online plugins that extend software functionalities seamlessly.

2. On cluster and cloud with its headless framework dedicated to deployment and schedulers calls, coupled with a new Icy-made streaming library for heavy data access, either stored locally and remotely. Icy also focus on a centralized repository, gathering plugins, scripts and graphical programming, but also support and now rating and plugin usage statistics, as its community asked !

Icy is used by 1000 regular (using at least 2 times a month Icy) users. Usage and statistics are refreshed every days and visible at http://icy.bioimageanalysis.org/index.php?display=icyStats

CellCognition – Analysis of live cell imaging data

Christoph Sommer, IMBA Vienna; Thomas Walter, Institut Curie, Paris;Rudolf Hoefler, IMBA Vienna;Daniel Gerlich, IMBA Vienna

CellCognition is a tool dedicated to the automatic analysis of live cell imaging data in the context of High-Content Screening (HCS). It contains algorithms for segmentation of cells and cellular compartments based on various fluorescent markers, features to describe cellular morphology by both texture and shape, tools for visualizing and annotating the phenotypes, classification, tracking and error correction. Events such as mitosis can be automatically identified and aligned to study the temporal kinetics of various cellular processes during cell cycle (Held et al. 2010). We also present how state-of-the-art outlier detection methods can be used to autonomously discover novel phenotypes in a large amount of high-throughput imaging data.

CellCognition can be used by novices in the field of image analysis and is applicable to hundreds of thousands of images by parallelization on compute clusters with minimal effort. The tool has been successfully applied to quantitative phenotypic profiling of cell division, yet machine learning enables CellCognition to be used for the analysis of other dynamic processes. CellCognition is based on VIGRA and python and is a common software project between the IMBA Vienna, Institut Curie, and EMBL Heidelberg.

KNIME for Image Processing: Integrative Open Source Image Analysis

Christian Dietz and Michael R. Berthold, Department of Computer and Information Science, University of Konstanz, Konstanz, Germany

State of the art high throughput microscopy calls for software solutions that can handle huge volumes of heterogeneous image data. These kinds of software solutions have to fulfill an extensive range of requirements (e.g. image analysis, machine learning, statistics, and visualization) and yet still be easy to use for the non expert. There are many monolithic platforms and some highly task oriented platforms that can process and analyze biological image data.

However, in view of the diverse nature of present problems, it is often necessary to integrate several applications. This involves going through many manual, time consuming and error prone steps, which are hard to document and therefore incomprehensible to others. This explains the increasing popularity of integrative workflow systems. 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. The KNIME Image Processing Extension is designed to extend KNIME by providing algorithms and datastructures, which enable KNIME users to process and analyze images. Combined with other existing KNIME extensions, non experts can easily compose complex domain comprehensive workflows. Further advantages directly inherited from KNIME include intelligent data caching strategy and fast prototyping of understandable workflows. Not wishing to reinvent the wheel, KNIME Image Processing integrates with ImageJ1, ImageJ2, OMERO, OpenCV and Tess4J, among others.

KNIME Image Processing is already used to solve several segmentation, classification and tracking problems in different areas of science, such as biology, chemistry and physics.

Analysis of microscopy data using CellProfiler and CellProfiler Analyst

Carolina Wählby Centre for Image Analysis and SciLifeLab, Dept. of Information Technology, Uppsala University, Uppsala, Sweden, and Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, MA, USA.

CellProfiler is free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically. It was launched in 2006 and has been cited in more than 1500 published papers. It interfaces with ImageJ/Fiji plugins, and Ilastik, broadening the possibilities of problem specific solutions.

I work part-time at the Imaging Platform of the Broad Institute in Boston, developing algorithms for CellProfiler. My own lab at Uppsala University in Sweden is focused on algorithm development for microscopy image analysis with applications in biomedicine. It is part of SciLifeLab, which is a national facility for advanced research in biomedicine. As such, researchers in need of ways to quantify their microscopy data often contact us. Here, CellProfiler has become the primary tool for helping non-computer-science researchers getting started with their own data analysis. At the same time, CellProfiler is a key tool in our own research on primary cell cultures from glioma patients, and our development of methods for spatially resolved gene expression profiling. Raw data and analysis results from our large-scale experiments are stored on a web-accessible database, allowing collaborators to explore and analyze the high-dimensional image-derived data without having their own local copies of the data. We use CellProfiler Analyst for this data exploration, including its machine learning tools for identifying complex and subtle phenotypes.

I will present some of our ongoing projects using CellProfiler, and discuss recent developments in CellProfiler and CellProfiler Analyst.

Interactive image analysis with ilastik

Stuart Berg, Markus Doering, Burcin Erocal, Luca Fiaschi, Carsten Haubold, Fred A. Hamprecht, Bernhard X. Kausler, John Kirkham, Jens Kleesiek, Anna Kreshuk, Thorben Kroeger, Ullrich Koethe, Christoph Straehle, Martin Schiegg, Buote Xu, Chong Zhang

The interactive learning and segmentation toolkit (ilastik) is a modular software framework, which allows for interactive visualization and analysis of very large datasets in up to 5 dimensions. Most analysis operations are performed lazily, which enables targeted interactive processing of data subvolumes, followed by complete volume analysis in offline batch mode. The main application, driving the development of ilastik, is large-scale automated processing of biomedical images. Our main interest lies in learning-based image processing, which allows the user to concentrate on the analysis task by providing examples, rather than tuning the algorithm parameters. Most common tasks performed with ilastik include - but are not limited to - image segmentation, classification, tracking and density estimation. In this talk, we will give an overview of ilastik and show the latest additions to its workflow stack on challenging biological data. ilastik is available as free and open source software at www.ilastik.org.

Open source tools for image analysis and visualization

Jérôme Velut, Kitware SAS

Bioimage computing involves a wide variety of software tools, from analysis to visualisation. We present a comprehensive framework of open source libraries and end-user graphical interfaces dedicated to image processing. We choose a set of tools that provides cross-platform and multilanguage support, essential conditions for a wide spread in the community. Combining these tools allows for developing applications that provide cutting-edge processing algorithms as well as complex yet user-friendly human interactions.

First we present the Insight Toolkit (ITK), an image segmentation and registration toolkit. We show how the open source community contributes with state-of-the-art algorithms and how it can be used in a user-speci_c application. ITK is highly extensible thanks to a generic coding approach and proposes several script languages bindings.

Then we present two visualisation solutions: VTK (Visualization Toolkit) and SlideAtlas. The former is a scientific visualisation library with 3D interaction capabilities while the latter is a web-based software dedicated to massive 2D images exploration. Visualisation is a critical task in the image processing field, as it stands at the interface between human, data and system.

Finally, we show several end-user applications harnessing the previous analysis and visualisation tools. These applications provide graphical user interfaces and are often seen as collaborative platforms for image analysis research. A short analysis of their architectures gives the keys to the design of personalised bioimage analysis tools.

TANGO Tools for Analysis of Nuclear Genome Organization

Cochennec, Ollion, Boudier, Escude <u>julien.cochennec@mnhn.fr</u> UMR CNRS 7196 - INSERM U1154 – MNHN, Paris

TANGO (Tools for Analysis of Nuclear Genome Organization) is an image analysis framework dedicated to the study of nuclear architecture (Ollion et al., 2013, Bioinformatics, 29-1840). This generic software includes tools to (1) process various types of signals,(2) quantify several features on signals, and (3) assist statistical analysis of quantifications.

The user interface allows to manage large datasets of images, visualize them in 3D and rapidly assess the quality of processing. Moreover, TANGO is interfaced with the statistical processing software R, which allows to easily apply all R tools to data generated by TANGO, and to define and access subpopulations of nuclei both in R and TANGO.

We will present the software through the description of a practical case in order to give an overview of its different concepts and functionalities.

Sponsors and commercial software bridging open source software session

AMIRA: Customizable 3D Processing Tool Application to Correlative Imaging

FEI Visualization Sciences Group , <u>Cornelia.Vacar@fei.com</u>

The increasing high performance in imaging techniques must be accompanied by software tools able to handle the high volumes of data and overcome the challenges specific to every type of technique (slice misalignment, high noise, artefacts...). Amira is a dedicated 3D image visualization and processing software for biomedical applications, which provides both generic and application-specific image processing tools, optimized for fast computation. Moreover, Amira has enhanced features for addressing the issue of correlative imaging, a topic of increasing interest in the field of biomedical image processing. Fusing data obtained through different imaging techniques is an increasingly current practice in many life science applications.

The Amira features will be illustrated on a correlative light and electron microscopy application, part of an academic research project in cell biology.

The second part of the talk focuses on the various options for customizing Amira. This can be achieved through either scripting, for automatizing the workflows using existing tools, or via the XPand extension, to add new functionalities. This extension enables the user to develop new features in C++ to respond to the specific needs of its application. Moreover, the user can bridge to existing C++ libraries, to directly exploit the available open source resources in the image processing community.

Fast and unlimited: Visualize, analyze and share microscopic image data without limitations

Christian Goetze, CIO, arivis AG

New imaging techniques hold many opportunities but also pose various challenges to those involved. And as optical engineers, biologists or data analysis specialists learn how to make use of, or even extend functions of novel hardware systems, also new scientific methods evolve rapidly. For instance, in the field of neuroscience one of the latest examples might be the development of tissue-clearing techniques imaged by state-of-the art SPIM and Light Sheet microscopes. This combination of methods allows high-resolution imaging of whole organisms and organs in a relatively short period of time. The data sets produced by these new techniques are often extremely large and can't be visualized and analyzed by standard software or without using very powerful and expensive computers. In our presentation at the EUBIAS we will show how arivis enables researchers to face these problems. We highlight on the arivis Vision approach to handle and analyze data sets of almost unlimited size, even on standard desktop PCs. We demonstrate the typical workflow when dealing with data sets of several hundreds of Gigabyte up to Terabyte of size. This involves the import and stitching of single stacks to one large volume, the fast and impressive 3D/4D-visualization techniques, image analysis in arivis Vision 4D and the arivis Vision solution to present and share image data and analysis results in a web based approach.

Integrating Flexible and Efficient Image Acquisition with Open Software

LIM (Nikon Software) ondrej.prazsky@lim.cz

Over the past twenty years there has been an increasing use of live-cell imaging to study dynamic processes in diverse biological preparations. One of the main challenges in fluorescent live-cell microscopy is reducing photo-damage. Others are coming from the fact that they are living: they undergo their live cycle, they move and morph. The acquisition must adapt to it (change focus, laser intensity, stage position or make some decision based on live analysis). The appearance of novel microscopy techniques (such as SMLM, SPT, SIM, SPIM) make the live-cell experiments even more complex. Such experiments are a challenge for acquisition hardware and software – it must be flexible on one hand to fulfill all these requirements and yet efficient in order to get most photons while inducing least possible photo-damage.

Recently, many open software platforms appeared alongside commercial software solutions enabling the researchers to implement their own algorithms relatively quickly and easily. As it becomes obvious that it is impossible to implement everything either in commercial or open software the necessity to bridge this gap is more and more imminent.

In this presentation two NIS Elements advanced acquisition modules are shown: the "Illumination Sequence" and "JOBS". Focus is put on integration with Open Source solutions.

ZEN Open Application Development Tools for Smart Microscopy

Sebastian Rhode, Carl Zeiss Microscopy, Business Unit BioSciences Kistlerhofstr. 75, D-81370 Munich

Microscopy has become much more than just assembling the correct lenses but a very demanding workflow integrating tools from various areas. To enable researchers to work effectively it is required to offer various tools to bridge and connect those workflow steps in an easy and open way. This is exactly what the Open Application Development (OAD) concept is aiming for. It currently has four core components. The CZI open image data format, the Python Macro Environment, the Experiment Feedback Engine and the Extension Concept. This talk will give a brief overview about the latest activities and advances on those topics and we will be happy to get your feedback regarding our ideas.

Examples:

- CZI File Format
- Python Macro Environment
- Experiment Feedback Engine
- Extension Concept
- Control via TCP/IP

Applications/ New Developments from Scientific Computing

StellarVision – Breaking the Optical Resolution Barrier Novel Next Generation Synthetic Aperture Optic (SAO) based Fluorescent Microscopy

Marc Beal M.B.A. Biosearch Technologies Inc. Email: marcb@biosearchtech.com

Synthetic Aperture Optics (SAO) technology is a fundamentally new optical detection paradigm that enables massively parallelized optical detection. The technique combines coherent interferometric illumination (similar to synthetic aperture radar) and computational image reconstruction (similar to computed tomography) to achieve ultra-high resolution that is far beyond the native resolution of the lens and the camera. Unlike conventional optical detection, resolution can be independently improved without affecting the field of view, working distance, and depth of field, thereby providing a unique mechanism to build a high-speed scanner for ultra-high density imaging. The SAO-based StellarVision gene expression analysis instrument can analyze hundreds of cells simultaneously within a single field of view using a 20x air lens, but with resolution comparable to 100x oil immersion lens or higher.

Development of High-Speed 3D Imaging system with electrically tunable lenses

Nakai Y1*, Boilot V3, Ozeki M1, Taniguchi A2, Clark J3, Hiraiwa T1, Shrestha R3, Tanimoto R1, Tamura N3, Oku H4, Nonaka S2, Draviam VM3, Hiroi N1**, and Funahashi A1, 1. Keio University, Japan, 2. National Institute of Basic Biology, Japan,

3. University of Cambridge, UK, 4. Gunma University, Japan Email: *nakai@fun.bio.keio.ac.jp, **hiroi@bio.keio.ac.jp

We evaluated an electrically tunable lens assembled with a fluorescence microscope to achieve 4D tracking of +TIPs (Microtubule plus-end tracking proteins) in mitotic cells. During mitosis, microtubules are regulated to coordinate several force generation tasks that are important to separate chromosomes accurately. The molecular mechanism of this fine control by microtubules remain a fascinating, but poorly understood area of biology. Since +TIPs contribute to regulating microtubules [1], tracking of these molecules have the potential to reveal this mechanism. The difficulty in tracking +TIPs in mitosis is that the rounded shape of a mitotic cell and the distribution of the +TIPs require 4 dimensional imaging (xyzt). Considering the velocity of +TIPs [2] and the pixel size of the images, transition of the focal plane must be achieved within a few milliseconds and at tens of nanometers spatial resolution, which cannot be performed even with piezoelectric zfocusing device [3]. We are trying to solve this problem by using ETL (EL-10-30, Optotune, Switherland), whose focal length can be controlled by supplied current. We attached the ETL to a fluorescent microscope and measured axial focus shift and settling time of the focal plane. We confirmed ETL could satisfy the required spatiotemporal resolution. We further analysed its effect to the optical performance. We measured the change of the magnification and resolution. These data shows that it does not affect the 3D imaging within a cell.

[1]V.M.Draviam,I.Shapiro,B.Aldridge,andPK.Sorger, EMBO J. 25, 2814–2827 (2006)

[2]A. Matov, K. Applegate, P. Kumar, C. Thoma, W. Krek, G. Danuser, T. Wittmann, Nat. Methods, 7 761-768 (2010)

[3]B.F. Grewe, F.F. Voigt, M. van't Hoff, and F. Helmchen, Biomed. Opt. Express, 2, 2035–2046 (2011)

FandPLimitTool: an application for calculating limits of accuracy for parameter estimation in single molecule microscopy

Anish V. Abraham, Amir Tahmasbi, Jerry Chao, Sripad Ram, Raimund J. Ober Department of Electrical Engineering, University of Texas at Dallas, Richardson, TX 75080

In single molecule microscopy, the accurate estimation of the location of a single fluorescent particle plays a central role in the analysis of image data, especially in the context of high-accuracy molecule tracking and superresolution image reconstruction. The achievable estimation accuracy, however, depends on a multitude of factors ranging from the wavelength of the photons detected from the fluorescent particle to the pixel size of the detector that is used to capture the image data. It is therefore useful to be able to determine, for a given experimental setup, the best possible accuracy with which a parameter such as the particle location can be estimated from the acquired images. To this end, the FandPLimitTool [1] software program was developed for the calculation of Cramer-Rao lower bound-based limits of accuracy [2] for the estimation of parameters from single molecule microscopy image data. FandPLimitTool is a GUI-based application [3] written in MATLAB, and it currently enables calculation of limits of accuracy for estimating, among other parameters such as the number of photons detected from the molecule(s) of interest, the location of a single molecule and the distance between two single molecules in both two-dimensional and threedimensional space. For a given estimation problem, options are available in terms of the model for the point spread function, the detector type (e.g., CCD or EMCCD camera), and calculation settings such as the step size for the evaluation of various integrals.

 A. V. Abraham, S. Ram, J. Chao, E. S. Ward, and R. J. Ober, "Quantitative study of single molecule location estimation techniques," *Optics Express*, vol. 17, no. 26, pp. 23352–23373, 2009.
 R. J. Ober, S. Ram, E. S. Ward, "Localization accuracy in single-molecule microscopy," *Biophysical Journal*, vol. 86, no. 2, pp. 1185-1200.

[3] Ward Ober Lab, "FandPLimitTool Software Download." [Online]. Available: http://www.wardoberlab.com/software/fandplimittool/.

The BioVoxxel Image Processing and Analysis Toolbox

Jan Brocher , BioVoxxel , Kurpfalzstrasse 13, 67112 Mutterstadt, Germany

The "BioVoxxel Toolbox" is a collection of plugins and macros for Fiji and ImageJ which is designed to assist in various image processing and analysis tasks such as lighting and background correction, image filtering, high quality feature extraction as well as binary object analysis. The "Filter Check" for example allows to test several image filter conditions in one step to easier pinpoint suitable preprocessing to improve consecutive analyses. The "Threshold Check" [1] enables to semiquantitatively assess automatic binarization methods available in Fiji to achieve a high quality feature extraction. Tools working on binary images to split up connected cells or other features in a adaptive fashion or like the "Speckle Inspector" enable an object wise comparison of small features contained in bigger objects such as biomarker spots in cells or nuclei. Object extraction by secondary features is facilitated by the "Binary Feature Extractor". Analysis and classification of objects by size and shape descriptors is facilitated by the "Extended Particle Analyzer" and color-coded "Shape Descriptor Maps". The toolbox is rounded up with differential intensity plots and methods for object distribution analyses.

In addition to the described toolbox, a huge variety of further methods already available in the Fiji distribution are the basis on which BioVoxxel as bioimaging analyst aims to bridge the gap between software development and a broad application by the end users in the area of life sciences. To this end BioVoxxel further offers transmission of experience through courses and customized tool development.

Reference:

[1] Qualitative and Quantitative Evaluation of Two New Histogram Limiting Binarization Algorithms Jan Brocher, 2014, IJIP 8(2), pp. 30-48.

Cells and particles dynamics analysis

BioNewMetrics and stochastics analysis of super resolution single particles trajectories

David Holcman (ENS Paris)

Recent advanced mathematical analysis of SPTs of superresolution microscopy is based on massive amount of data. New algorithms allow reconstructing the physical properties of the dynamics but also neuronal surfaces.

BioNewmetrics created in 2009 (http://bionewmetrics.org/) is our platform for disseminating algorithms, classes and videos.

This talk will summarize recent progress in analyzing trajectories and reconstruction procedures.

Mobyle@SERPICO: Image processing methods for the temporal analysis of moving particles on a Mobyle Web Portal

Thierry Pécot and Charles Kervrann

Centre INRIA Rennes – Bretagne Atlantique Campus de Beaulieu, 263 Avenue Général Leclerc, 35042 Rennes, France The SERPICO team (INRIA Rennes – Bretagne Atlantique), in collaboration with UMR 144 CNRS

Institut Curie ("Subcellular Structure and Cellular Dynamics" Unit / PICT – IbiSA) and Nikon Imaging Centre@Institut Curie, has developed mathematical tools and algorithms to analyze the dynamic coordination and organization of molecular complexes at the single cell level. Several of these methods are accessible through a Mobyle web portal (http://mobyle-serpico.rennes.inria.fr/). This platform allows any user to apply state-of-the-art denoising, segmentation, object/background separation and optical flow algorithms to their own image/volume sequences in the cloud.

Automated cell tracking and analysis in phase-contrast videos (iTrack4U): Development of Java software based on combined mean-shift processes

Fabrice P. Cordelières ^{1,*}, Valérie Petit ^{2,*}, Mayuko Kumasaka ², Olivier Debeir ³, Véronique Letort ⁴, Stuart J. Gallagher ² and Lionel Larue ²

¹ Bordeaux Imaging Center, UMS 3420 CNRS - Université de Bordeaux - US4 INSERM, Pôle d'imagerie photonique, Institut François Magendie, Bordeaux, France.

² Institut Curie, CNRS UMR3347, INSERM U1021, Normal and Pathological Development of Melanocytes, Orsay, France.

³ Université Libre de Bruxelles (ULB), Laboratory of Image Synthesis and Analysis (LISA), Faculty of Applied Sciences, Brussels, Belgium.

⁴ Ecole Centrale Paris, Laboratory of Applied Mathematics, 92290, Chatenay-Malabry, France

Cell migration is a key biological process with a role in both physiological and pathological conditions. Locomotion of cells during embryonic development is essential for their correct positioning in the organism; immune cells have to migrate and circulate in response to injury. Failure of cells to migrate or an inappropriate acquisition of migratory capacities can result in severe defects such as altered pigmentation, skull and limb abnormalities during development, and defective wound repair, immunosuppression or tumor dissemination. The ability to accurately analyze and quantify cell migration is important for our understanding of development, homeostasis and disease. In vitro cell tracking experiments, using primary or established cell cultures, are often used to study migration as cells can quickly and easily be genetically or chemically manipulated. Images of the cells are acquired at regular time intervals over several hours using microscopes equipped with CCD camera. The locations (x,y,t) of each cell on the recorded sequence of frames then need to be tracked. Manual computer-assisted tracking is the traditional method for analyzing the migratory behavior of cells. However, this processing is extremely tedious and time-consuming. Most existing tracking algorithms require experience in programming languages that are unfamiliar to most biologists. We therefore developed an automated cell tracking program, written in Java, which uses a meanshift algorithm and ImageJ as a library. iTrack4U is a user-friendly software. Compared to manual tracking, it saves considerable amount of time to generate and analyze the variables characterizing cell migration, since they are automatically computed with iTrack4U. Another major interest of iTrack4U is the standardization and the lack of inter-experimenter differences. Finally, iTrack4U is adapted for phase contrast and fluorescent cells.

A Java implementation of MIATool for multidimensional image data analysis

David Kim, Anish V. Abraham, Jerry Chao, Raimund J. Ober Department of Electrical Engineering, University of Texas at Dallas, Richardson, TX 75080

Modern microscopy imaging experiments are capable of producing complex image data sets. When performing a data analysis task, the images in a data set are arranged by attributes such as the time and focus levels at which they were acquired. Importantly, the different tasks comprising an analysis are often facilitated by the use of different arrangements of the images. To support such data analyses, a software framework has previously been proposed [1] which enables the use of different logical image arrangements to analyze a physical set of images. Called the Microscopy Image Analysis Tool (MIATool), the framework realizes the logical arrangements of images using arrays of references to the images, thereby avoiding the need to physically arrange the images in their storage medium. To allow customization based on the specific requirements of different analysis tasks, these logical arrangements may vary, without limit, in size and dimensionality, and have no restrictions placed on the meaning of each dimension. MIATool additionally offers data processing flexibility, mechanisms for incorporating new processing capabilities, and storage management of images and associated information. The currently available implementation [2] of MIATool is written in MATLAB and used in-house. We present here a new implementation of MIATool using Java.

MIATool now takes full advantage of class hierarchies to programmatically associate attributes and parameters to the images. The use of Java also provides program portability across platforms, memory footprint reduction, as well as compatibility with MATLAB for prototyping.

[1] J. Chao, E. S. Ward, and R. J. Ober, "A software framework for the analysis of complex microscopy image data," *IEEE Trans. Inf. Technol. Biomed.*, vol. 14, no. 4, pp. 1075–1087, 2010.
[2] Ward Ober Lab, "MIATool Software Download." [Online]. Available: http://www.wardoberlab.com/software/miatool/.

MaMuT: a software tool for visualization, tracking and lineaging in large multiview SPIM images.

Jean-Yves Tinevez¹, Tobias Pietzsch², Carsten Wolff³, Spencer Shorte¹, Pavel Tomancak² and Anastasios Pavlopoulos^{2,4}.

¹ Institut Pasteur, PFID, Imagopole, 75015 Paris, France

² Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden, Germany.

³ Humboldt-Universität zu Berlin, Institut für Biologie, AG Vergleichende Zoologie, Philippstr.13, 10115 Berlin, Germany.

⁴ Howard Hughes Medical Institute, Janelia Farm Research Campus, 19700 Helix Drive, Ashburn, VA 20147, USA.

Multi-view Selective Plane Illumination Microscopy (SPIM) is now a prominent and powerful tool to investigate multiscale phenomena, and has the potential to link subcellular molecular events to large scale tissue remodeling occuring during development. It proves particularly useful for instance in the investigation of tissue remodeling caused by infectious diseases or in developmental biology, where a developing embryo can be followed over several days, with a subcellular resolution in a non-invasive manner.

These abilities of SPIM raise several new challenges in image analysis and data handling. The exquisite temporal and spatial resolution offered by multi-view imaging combined with long timelapse observation can generate a torrent of data, which classical visualization and annotation tools cannot handle. MaMuT is a software tool that addresses these unique challenges, by providing the BioImaging community with an interactive tool for the visualization, annotation, tracking and lineaging of very large, multi-view image data sets. We will present the rationale for such a tool, introduce its functionality, and demonstrate its utility in the study of arthropod appendage development in crustacean amphipod *Parhyale hawaiensis*.

Fast step transition and state identification (STASI) for discrete single-molecule data analysis

Bo Shuang[†], David Cooper[†], J. Nick Taylor[‡], Lydia Kisley[†], Jixin Chen[†], Wenxiao Wang[§], Chun Biu Li[‡], Tamiki Komatsuzaki[‡], and Christy F. Landes^{*†}[§]

+ Department of Chemistry, Rice University, MS 60, Houston, Texas 77251-1892, United States
+ Molecule & Life Nonlinear Sciences Laboratory, Research Institute for Electronic Science, Hokkaido University, Sapporo 001-0020, Japan

§ Department of Electrical and Computer Engineering, Rice Quantum Institute, Rice University, MS 60, Houston, Texas 77251-1892, United States

We introduce a step transition and state identification (STaSI) method for piecewise constant single-molecule data with a newly derived minimum description length equation as the objective function. We detect the step transitions using the Student's *t* test and group the segments into states by hierarchical clustering. The optimum number of states is determined based on the minimum description length equation. This method provides comprehensive, objective analysis of multiple traces requiring few user inputs about the underlying physical models and is faster and more precise in determining the number of states than established and cutting-edge methods for single-molecule data analysis. Perhaps most importantly, the method does not require either time-tagged photon counting or photon counting in general and thus can be applied to a broad range of experimental setups and analyses.

Fourier transform-based fast characterization of cell shapes as a tool for intelligent classification of cells In intravital microscopy

Zoltan Cseresnyes¹, Fabian Kriegel¹, Jannike Bayat-Sarmadi¹, Simon Bayerl², Anja E. Hauser^{1,2}, Raluca Niesner¹

¹Deutsches Rheuma---Forschungszentrum (DRFZ) Berlin, Charité platz 1, 10117 Berlin ²Charité Universitätsmedizin Berlin, Charité platz 1, 10117 Berlin

In numerous tissue types, the kinetic behavior of cells as well as the complexity and the aspect ratio of their shapes adjust to short- and long-term changes in the actual physiological and pathological conditions of the tissue. Generally, the kinetic behavior of cells is characterized by the so called "cell tracks", i.e. the time course of the 3-D location of the centroids of the cells, as well as by various parameters characterizing the volume of the tissue occupied by the cell and those describing the surface corresponding to the outer membrane of the cell. Cells are then often classified based on a number of these parameters, often guided by *a priori* knowledge provided by expert biologists or medical professionals. Whilst such approach will provide an excellent starting point for analyzing complex intravital image data, ultimately we will need faster methods for automated characterization and more intelligent tools for unbiased analysis that may also reveal hidden correlations amongst the track- and shape-describing parameters.

Here we propose the use of Discrete Fourier Transform (DFT) applied on multiple---angle cross sections of cells prepared automatically by a set of ImageJ/Fiji macros.

We find that the first 10 DFT parameters (F0–F9) are sufficient to describe even the complex shape of microglia in the healthy or cancerous tissue of the mouse brain, or that of the macrophages in the mouse gut under physiological or pathological conditions, imaged via two-photon intravital microscopy. After normalizing the DFT components (using the amplitude Fi=SQRT{Re(Fi)2+Im(Fi)2}) so that they are independent of the cell size (by dividing Fi (i={2..9}) by F1), we were able to find clusters in the Fourier parameter space by using methods of Artificial Intelligence (AI), e.g. Self-Organizing Maps (SOM).

These AI methods have also been successfully applied here to identify correlated cell tracks by training SVMs as well as SOMs on a selected group of cell tracking parameters.

In more complex cases, a 3-D SOM was necessary in order to provide adequate separation of track groups; however, for visualization purposes the 2-D version may be preferred in order to make comprehension easier for the observer. We further propose that such automated and unbiased methods may be used as part of the design of intelligent microscopes, where the actual flow of experiments can be continually adjusted based on the instantaneous analysis of the recorded 3-D and 4-D image stacks.

Image Data management and visualization

The Open Microscopy Environment: Open Image Informatics for the Life and Biomedical Sciences

Jason R. Swedlow¹ and the OME Consortium² ¹Centre for Gene Regulation & Expression, University of Dundee, Dundee, Scotland, UK ²http://www.openmicroscopy.org/site/about/who-ome

Despite significant advances in biological imaging and analysis, major informatics challenges remain unsolved: file formats are proprietary, storage and analysis facilities are lacking, as are standards for sharing image data and results. The Open Microscopy Environment (OME) [1] is an open-source software framework developed to address these challenges. OME has three components—an open data model for biological imaging: OME data model; standardised file formats (OME-TIFF) and software libraries for file conversion (Bio-Formats [2]); and a software platform for image data management and analysis (OMERO [3]).

The Java-based OMERO client-server platform [3] comprises an image metadata store, an image repository, visualization and analysis by remote access, enabling sharing and publishing of image data. OMERO's model-based architecture has enabled its extension into a range of imaging domains, including light and electron microscopy, high content screening and recently into applications using non-image data from clinical and genomic studies [4]

Our current version, OMERO-5 improves support for large datasets and reads images directly from their original file format, allowing access by third party software.

OMERO and Bio-Formats run the JCB DataViewer [5], the world's first on-line scientific image publishing system and several other institutional image data repositories (e.g. [6], [7]).

- [1] http://openmicroscopy.org
- [2] http://openmicroscopy.org/site/products/bio-formats
- [3] http://openmicroscopy.org/site/products/omero
- [4] http://www.openmicroscopy.org/site/products/partner
- [5] http://jcb-dataviewer.rupress.org/
- [6] http://odr.stowers.org
- [7] http://emdatabank.org/

Cytomine for data scientists and image analysis software developers

R.Marée^{1,2}, L. Rollus¹, B. Stévens¹, G. Louppe¹, J.-M. Begon¹, R. Vandaele¹, L.Wehenkel¹ ¹Systems and Modeling, Dept. EE&CS & GIGA-Research, University of Liège, Belgium ²Quantitative Image Analysis Unit, Institut Pasteur, France

Cytomine (http://www.cytomine.be/) is a rich internet application for remote visualization of highresolution bioimages (à *la* Google Maps), collaborative and semantic annotation of regions of interest using user-defined ontologies [Marée et al., Diagnostic Pathology 2013], and semiautomated image analysis using machine learning, web services, and proofreading [Marée et al., ISBI 2014].

In this talk, we will first present latest applications of the software as it is now being actively used by a dozen of research groups (more than 15000 images are stored and annotated by tens of users) in several application domains as illustrated below.

Then we will describe our latest developments to allow data scientists and image analysis software developers to use and extend the platform in various ways. In particular we will first show how to import/export data through our HTTP based RESTful API which ensures interoperability. We will also show how to integrate novel modules and third-party softwares/algorithms by leveraging web communication mechanisms and database software templates.

Cytomine will be available under an open-source software license early 2015.

Acknowledgments

Cytomine (2010-...) is funded by Wallonia research grants n°1017072/1217606.

openBIS Importer Toolset (oBIT)

Aaron Ponti Single Cell Unit Department of Biosystems Science and Engineering ETHZ Basel (Switzerland)

openBIS¹ is an extensible, open source software framework for constructing user-friendly, scalable and powerful information systems for data and metadata acquired in biological experiments. It enables users to collect, integrate, share, publish data and to connect to data processing pipelines. The openBIS Importer Toolset² (oBIT) is a tightly integrated collection of tools that allows for the semi-automated, semi-unsupervised registration of annotated datasets into openBIS directly from the acquisition stations.

oBIT aims at optimizing the usage of shared acquisition machines in centralized facilities by offering a workflow for moving annotated data from the acquisition stations into openBIS in a simple but quick and robust way. In addition, oBIT provides an extensible framework that facilitates integrating the registration of new classes of hardware and data types into openBIS. Indeed, one of the strengths of oBIT/openBIS is the way it transparently allows co-registration of data from different acquisition modalities into one, common environment. oBIT is being developed at the Department of Biosystems Science and Engineering ³ of the ETH Zurich and in its current state it supports flow cytometers, cell sorters and microscopes for the Single Cell Facility⁴ and will in a later stage also address the needs of the Laboratory Automation Facility⁵.

openBIS is developed by the Scientific Software and Data Management group (part of Scientific IT Services⁶) at the ETH Zurich.

In this talk I will introduce openBIS and then the current state of oBIT.

1 http://www.cisd.ethz.ch/software/openBIS 2 http://www.scs2.net/next/index.php?id=150 3 http://www.bsse.ethz.ch 4http://www.bsse.ethz.ch/research/facilities/single---cell---facility.html 5 http://www.bsse.ethz.ch/research/facilities/laboratory---automation---facility.html 6 https://www1.ethz.ch/id/about/sections/sis/index_EN

Zegami: A Platform for Image Centric Data Exploration

Stephen Taylor, Computational Biology Research Group, Weatherall Institute of Molecular Medicine, University of Oxford

Jens Rittscher, Institute of Biomedical Engineering, University of Oxford

Enabled by automated platforms bioimaging and associated informatics is generating an unprecedented amount of data. Sophisticated imaging techniques yield large, heterogeneous, multidimensional data sets that need to be viewed, analysed, annotated, queried, and shared.

The resulting image data sets pose a number of challenges that are very distinct from conventional clinical imagery in their size and abundance.

Like computational tools enabled large scale gene sequencing, there is a need for advanced analytical tools for biological imagery in order to advance biomedical research. The key requirement is for automated tools that characterize the phenotype of images and extract higher level information content. Given the amount of data that is being generated we believe that there is a growing need for open tools that enable the efficient exploration of the image space.

We are developing a platform, Zegami, which facilitates an interactive image centric exploration of large collections of biological imaging data. Building upon the concept of the PivotViewer we designed a system that will help users to explore complex image data sets efficiently. Users are able to simultaneously view traditional data visualization, the corresponding descriptive statistics simultaneously with the underlying image data. Since any type of data visualization relies on a set of features that has been extracted from the images, we view the development of selected image analysis algorithms to be a core component of this research programme. The resulting interface will allow users to interactively analyse, sort, and annotate images.

Integration of heterogeneous data sources for high content screening data exploitation and exchange

Authors: Dmitri Voitsekhovitch, Elton Rexhepaj, Francois Prudhomme, Aurianne Lescure, Elodie Anthony, Sarah Tessier, Philippe Benaroch, Jacques Camonis, Franck Perez, Jean Salamero, Perrine Paul-Gilloteaux, Elaine Del Nery

High Content Screening produces large amounts of data. Images alone can go into the terabytes per month, and other data types must also be considered (e.g. lab experiment reports). Existing solutions may not be deemed satisfactory either because they may be proprietary, making it difficult to extend its functionalities or because they define restrictive data models, the evolutions of which make component maintenance difficult.

As part of France Bio-Imaging network, we are developing the Real-time Unified Bio-Imaging Exploitation System. RUBIES uses open source tools and widely-known paradigms to create a collaborative platform to visualise and exchange HCS data. Heterogeneous data from HCS is analysed in real-time in order to enrich databases which are exposed through a web service layer.RUBIES relies on the WebLab integration framework, which is based on Service Oriented Architecture where individual components are encapsulated as web services with common interfaces and communication protocols. It proposes a taxonomy of web service interfaces and a Resource Description Framework (RDF)-based common data exchange format to ease service interoperability. RDF is a web standard which represents any kind of information statements as collections of (subject, predicate, object) triples.

RUBIES can then interoperate with other data management systems, such as iManage Curie Data base.

Further work will include user-added annotations and exploitation of image and metadata in order to create cell image dictionaries.

Page 44

Participants Contacts

Amazit Larbi Faculté de Médecine Paris-Sud --INSERM U693 Le Kremlin-Bicètre-France larbi.amazit@u-psud.fr **Arganda-Carreras** Ignacio INRA Versailles-France Ignacio.Arganda@versailles.inra.fr Arpon Javier INRA IJPB Paris-France javier.arpon@versailles.inra.fr Asselbergh Bob VIB - University of Antwerp Antwerp-Belgium Bob.asselbergh@molgen.vib-ua.be Baecker Volker INSERM Montpellier-France volker.baecker@mri.cnrs.fr Beal Marc Biosearch Technologies Inc. Petaluma-USA marcb@biosearchech.com Bhatia Dhiraj Institut Curie Paris-France dhirajbhatia1@gmail.com Brocher Jan BioVoxxel - Scientific Image Processing and Analysis Mutterstadt-Germany jan.brocher@biovoxxel.de Burguet Jasmine INRA Versailles-France jasmine.burguet@versailles.inra.fr Calderon Chris Ursa Analytics Denver-USA chris.calderon@ursaanalytics.com Texas A&M University Chao Jerry College Station-USA vchao@tamu.edu **Chong Zhang** Bioquant Univisity of Heidelberg Heidelberg-Germany chong.zhang@bioquant.uni-heidelberg.de Cochennec Julien UMR CNRS 7196 - INSERM U1154 - MNHN Paris-France julien.cochennec@mnhn.fr **Contremoulins Vincent** Institut Jacques Monod Paris-France contremoulins.vincent@ijm.univ-parisdiderot.fr Cordelières Fabrice Bordeaux Imaging Center, UMS 3420 CNRS - Université de Bordeaux - US4 INSERM, Pôle d'imagerie photonique Bordeaux-France fabrice.cordelieres@u-bordeaux.fr **Cseresnyes Zoltan** *DRFZ* Berlin-Germany zoltan.cseresnyes@drfz.de Dallongeville Stephane Institut Pasteur Paris-France stephane.dallongeville@pasteur.fr Danckaert Anne Institut Pasteur Paris-France anne.danckaert@pasteur.fr Danglot Lydia Inserm, Institut Jacques Monod Paris-France lydia.danglot@inserm.fr Dauphin Aurélien IMAGERIE CELLULAIRE PICPS - Inserm Paris-France aurelien.dauphin@upmc.fr de Chaumont Fabrice Institut Pasteur Paris-France chaumont@pasteur.fr Del Nery Elaine Institut Curie Paris-France edel@curie.fr Delestro Matos Felipe IBENS / ENS Paris-France delestro@biologie.ens.fr Delobel Hélène NIKON Paris-France helene.delobel@nikon.fr University of Konstanz **Dietz Christian** Konstanz-Germany dietzc85@googlemail.com Ehrenfeuchter Niko University of Basel Basel-Switzerland nikolaus.ehrenfeuchter@unibas.ch Eirinopoulou Theano INSERM Paris-France theano.eirinopoulou@inserm.fr Espinosa Leon CNRS Marseille-France leon.espinosa@imm.cnrs.fr Floyd Hayley The University of Birmingham Birmingham-UK

hxf750@bham.ac.uk

Fouquet Stephane Institut de la Vision Paris-France stephane.fouquet@inserm.fr **Gelman Laurent** Friedrich Miescher Institut **Bâle-Switzerland** laurent.gelman@fmi.ch Genoud Christel Friedrich Miescher Institute for Biomedical Research Basel-Switzerland christel.genoud@fmi.ch **Genovesio Auguste** Ecole Normale Superieure Paris-France auguste.genovesio@ens.fr Gesnouin Philippe Inria Paris-France Philippe.Gesnouin@Inria.fr Gilloteaux Perrine Institut Curie/ CNRS UMR144 Paris-France perrine.paul-gilloteaux@curie.fr **Goehlmann Dieter** Bitplane AG Zürich-Switzerland goehlmann@bitplane.com Goetze Christan arivis AG Munich-Germany christian.goetze@arivis.com Golani Ofra Weizmann Institute of Science Rehovot-Israel ofra.golani@weizmann.ac.il Goudin Nicolas INSERM Paris-France nicolas.goudin@inserm.fr **Guggenheim Emily** University of Birmingham **Birmingham-UK** ejg843@Bham.ac.uk Hiroi Noriko Keio University Yokohama-Japan hiroi@bio.keio.ac.jp Hoang Thai V. IGBMC Illkirch-France hoang@igbmc.fr Holcman David ENS Paris-France david.holcman@ens.fr Hurbain Ilse Institut Curie Paris-France ilse.hurbain@curie.fr Incardona Pietro Max Planck Institute of Molecular Cell Biology and Genetics Desden-Germany incardon@mpi-cbg.de

Irondelle Marie Institut Curie Paris-France marie.irondelle@curie.fr Jugé Romain LBMC UMR5239 CNRS/ENS Lyon/UCBL/HCL Lyon-France romain.juge@ens-lyon.fr Julien Colombelli IRB Barcelona Barcelona-Spain julien.colombelli@irbbarcelona.org Kervrann Charles Serpico Inria Rennes-France charles.kervrann@inria.fr Kim David Texas A&M University College Station, Texas-USA ddukki@tamu.edu Klein Christophe INSERM U1138 Paris-France christophe.klein@crc.jussieu.fr Lagache Thibault Institut Pasteur Paris-France thibault.lagache@pasteur.fr Le Baccon Patricia UMR3664 CNRS/Institut *Curie* Paris-France lebaccon@curie.fr Leconte Ludovic Institut Curie Paris-France ludovic.leconte@curie.fr Leroy Olivier Institut Curie Paris-France olivier.leroy@curie.fr Li Yingbo ENS Paris-France vingboli@ens.fr Loménie Nicolas Université Paris Descartes Paris-France nicolas.lomenie@parisdescartes.fr Lonnen Emma University of Birmingham Birmingham-UK exl208@bham.ac.uk Louvet Émilie Gustave Roussy Villejuif-France louvetemilie@yahoo.fr Majer Peter Bitplane AG Zürich-Switzerland peter@bitplane.com Manuelian Tamara arivis AG Munich-Germany tamara.manuelian@arivis.com Marée Raphaël Institut Pasteur and University of Liège Paris and Liège-France and Belgium raphael.maree@ulg.ac.be

Martins Gabriel G. Instituto Gulbenkian de Ciencia Oeiras-Portugal gaby@igc.gulbenkian.pt Moreau Patrick Inrig Paris-France patrick.moreau@inria.fr Morichon Romain UMS-30 Paris-France romain.morichon@upmc.fr Nakai Yuichiro Keio Univ. Yokohama-Japan nakai@fun.bio.keio.ac.jp Nevo Reinat Weizmann Institute of Science Rehovot-Israel Reinat.Nevo@weizmann.ac.il **Ober Raimund** Texas A&M University College Station, Texas-USA raimund.ober@tamu.edu Pavie Benjamin VIB Leuven-Belgium Benjamin.Pavie@cme.vib-kuleuven.be Pécot Thierry INRIA Rennes-France t pecot@yahoo.fr University of Birmingham Pike Jeremy **Birmingham-UK** jap161@bham.ac.uk Ponti Aaron ETH Zurich Basel-Switzerland aaron.ponti@bsse.ethz.ch Prazsky Ondrej LIM, Nikon Prague-Czech Republic ondrej.prazsky@lim.cz Racine Victor QuantaCell Pessac-France victor.racine@quantacell.com Ramos Magalhaes Jose FEI Paris-France Jose.RamosMagalhaes@fei.com Rexhepaj Elton Institut Curie Paris-France elton.rexhepaj@curie.fr Rhode Sebastian Carl Zeiss Microscopy GmbH Munich-Germany sebastian.rhode@zeiss.com **Rieger Bernd** Quantitative Imaging Group TU Delft Delft-Netherlands b.rieger@tudelft.nl **Rittscher** Jens Institute of Biomedical Engineering, University of Oxford Oxford-UK jens.rittscher@eng.ox.ac.uk

Rossberger Sabrina Max Planck Institute for Intelligent Systems Heidelberg-Germany rossberger@is.mpg.de Ruszczycki Błażej Nencki Institute of Experimental Biology Warszawa-Poland blazej13@yahoo.com Saalfeld Stephan HHMI's Janelia Research Campus, USA Ashburn-USA saalfelds@janelia.hhmi.org Salamero Jean Institut Curie CNRS Paris-France salamero@curie.fr Salvaire Fabrice None Paris-France fabrice.salvaire@orange.fr Saxon Peter University of Birmingham Birmingham-UK pas115@bham.ac.uk Sbalzarini Ivo TU Dresden & Center for Systems Biology Dresden, Max Planck Institute of Molecular Cell Biology and Genetics Dresden-Germany ivos@mpi-cbg.de Schindelin Johannes LOCI University Wisconsin-Madison/Tomancak Lab Dresden-Germany schindelin@wisc.edu Schorb Martin EMBL Heidelberg-Germany schorb@embl.de Sedlak Roman LIM, Nikon Prague-Czech Republic roman.sedlak@lim.cz Sengmanivong Lucie Institut Curie Paris-France lucie.sengmanivong@curie.fr Shuang Bo Rice University Houston-USA bs16@rice.edu Signolle Nicolas Institut Curie Paris-France Nicolas.Signolle@curie.fr Sommer Christoph Institute for Molecular Biotechnologie (IMBA) Vienna-Austria christoph.sommer@imba.oeaw.ac.at Stavru Fabrizia Institut Pasteur Paris-France

fabrizia.stavru@pasteur.fr

Svoboda Miroslav LIM, Nikon Prague-Czech Republic

miroslav.svoboda@lim.cz

Swedlow Jason University of Dundee Dundee-UK

j.r.swedlow@dundee.ac.uk

Sylvain Prigent *Bio Genouest* Rennes-France sylvain.prigent@univ-rennes1.fr

Tanimoto Ryuichi Keio University Yokohamashi-Japan

tanimoto@fun.bio.keio.ac.jp

Taylor Stephen University of Oxford, UK Stephen.taylor@imm.ox.ac.uk

Tinevez Jean-Yves Institut Pasteur Paris-France

jean-yves.tinevez@pasteur.fr

Tosi Sébastien IRB Barcelona Barcelona-Spain sebastien.tosi@irbbarcelona.org

Vacar Cornelia *FEI* Paris-France cornelia.vacar@fei.com

Velut Jérôme Kitware SAS Villeurbanne-France

jerome.velut@kitware.com

Wählby Carolina Centre for Image Analysis and SciLifeLab, Dept. of Information Technology, Uppsala University, Uppsala, Sweden, and Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, MA Uppsala and Cambridge-Sueden and USA

carolina@cb.uu.se

Whitehead Lachlan Walter and Eliza Hall Institute of Medical Research Melbourne-Australia

whitehead@wehi.edu.au

Wiegraebe Winfried Stowers Institute for Medical Research Kansas City-USA

WIW@stowers.org

WilsonRhodriHeriot-WattUniversityEdinburgh-UK

rsw31@hw.ac.uk

Organizing committee:

Kota Miura (EMBL Heidelberg, Germany) Sébastien Tosi (IRB Barcelona, Spain) Julien Colombelli (IRB Barcelona, Spain) Perrine Paul-Gilloteaux (Institut Curie Paris, France) Jean Salamero (Institut Curie Paris , France)

Local organisation committee :

PICT IBISA Institut Curie : Lucie Sengmanivong Nicolas Signolle Irondelle Marie Xavier Heiligenstein Ludovic Leconte Ilse Hurbain

Both Eubias conference and QBI conference are strongly supported by France Bio Imaging (FBI). Eubias conference is supported by the french microscopy society (sfmu). We are also very thanksful to our sponsors, Bitplane, Nikon, FEI, Roper and Arivis.

We also thank the Quantitative BioImaging Conference Organizing committee for this joint meeting and contributing to reinforce the links between our two communities.

INSTITUTE FOR RESEARCH IN BIOMEDICINE