

# Program

Wednesday 8th of October

15:00-18:00 Registration

18:00-18:15 Welcome

18:15-20:15 **Session 1: High Throughput BioImage Analysis**

18:15 -18:45 Integrated pipeline for processing of multi-view SPIM data

**Pavel Tomancak**, MPI-CBG, Dresden, Germany

18:45 -19:15 3D Visualization-Assisted Analysis - BioImage Informatics Platform for High-Throughput Biology

**Hanchuan Peng**, Allen Institute for Brain Science, Seattle, US

19:15 -19:45 Uncovering genetic and chemical relationships using image-based profiling

**Anne Carpenter**, Broad Institute of MIT and Harvard, Cambridge, Massachusetts, US

19:45 -20:15      Cell mechanics analysis through  
physics-constrained optical flow

**Jean-Christophe Olivo-Marin**, Institut  
Pasteur, Paris, France

20:15 -22:00      **Welcome Reception and Poster Session 1**

# Program

Thursday 9th of October

09:00-10:30      **Session 2: Feature extraction**

09:00 -10:00      Multidimensional wavelets and invariance principles for the analysis of bioimages

**Michael Unser**, EPFL, Lausanne, Switzerland

10:00 -10:15      Defining global and local proximity of filamentous networks

**Liya Ding**, UT Southwestern Medical Center, Dallas, US

10:15 -10:30      Quantifying similarity among sets of biological images using wavelet compression

**Andrew Cohen**, Drexel University, Philadelphia, US

10:30-11:00      Coffee Break

11:00-12:30      **Session 3: Tracking and Dynamics**

11:00 -11:30      KNIME: Integrating Image Processing  
and Advanced Analytics

**Michael Berthold**, Konstanz University,  
Konstanz, Germany

11:30 -11:45      The Roles of Guanine Nucleotide  
Exchange Factors in Regulating  
Collective Cell Migration

**Assaf Zaritsky**, UT Shouthwestern  
Medical Center, Dallas, US

11:45 -12:00      A generic methodological framework  
for studying single cell motility in high-  
throughput time-lapse screening data

**Alice Schoenauer Sebag**, ParisTech,  
Paris, France

12:00 -12:30      Tracking and software

**Fred Hamprecht**, Heidelberg,  
Germany

12:30-14:00      Lunch and Poster Session 2

14:00-15:30      **Session 4: Validating and Storing Images**

14:00 -14:30      Adaptive Validation, a possible  
alternative to Cross-Validation

**Joseph Salmon**, Télécom ParisTech,  
LTCI, Paris, France

14:30 -14:45      Forget pixels: adaptive particle representation for processing and storage of fluorescence microscopy images

**Bevan Cheeseman**, MPI-CBG,  
Dresden, Germany

14:45 -15:15      The Open Microscopy Environment: Open Source Image Informatics for the Biological Sciences

**Jason Swedlow**, Wellcome Trust  
Biocentre, University of Dundee, UK

15:15 -15:30      SSBD: an open repository for quantitative data of biological dynamics

**Yukako Tohsato**, RIKEN Quantitative  
Biology Center, Kobe, Japan

15:30-16:00      Coffee Break

16:00-16:30      **Discussion on challenges**

16:00 - 16:30      Establishment of a benchmark for evaluation and comparison of cell segmentation and tracking algorithms

**Michael Kozubek**, Masaryk University,  
Czech Republic

16:30-18:00      **Session 5: Novel Tools**

16:30 -17:00      Tools for Multidimensional Image Visualization

**Kevin Elliceiri**, University of Wisconsin-  
Madison, Wisconsin, US

- 17:00 -17:15 Guided exploration of imaging mass spectrometry data using the Allen Mouse Brain Atlas
- Nico Verbeeck**, KULeuven, STADIUS, Leuven, Belgium
- 17:15 -17:30 Yeast Image Toolkit: A benchmark and evaluation strategy for yeast segmentation and tracking algorithms
- Szymon Stoma**, ETH, Zürich, Switzerland
- 17:30 -17:45 Supporting open source initiatives within ZEN
- Bernhard Weiss**, Carl Zeiss
- 17:45 -18:00 Addressing the HCS data analysis bottleneck within an advanced visual analytics environment
- Christian Schueller**, Perkin Elmer

# Program

Friday 10th of October

09:00-10:00      **Session 6: Classification and Screening**

09:00 - 09:30      Classification problems in biomedical imaging

**Jelena Kovačević**, Carnegie Mellon,  
Pittsburgh, US

09:30 -09:45      A genome-wide, multi-process high-content microscopy survey of cell shape, microtubule organization and cell cycle progression

**Anatole Chessel**, University of  
Cambridge, Cambridge, UK

09:45 -10:00      Automatic Quantification and Classification of Spatio-Temporal Dynamics of Human Mitotic Proteins

**Yin Cai**, EMBL, Heidelberg, Germany

10:00-10:30      Retrospective Illumination Correction for Optical Microscopy

**Kevin Smith**, Biozentrum - University of  
Basel, Switzerland

10:30-11:00      Coffee Break

11:00-12:30

**Session 7: 3-D Imaging and Modeling**

11:00 -11:30

Computer Vision & Computational Optics for BioImage Informatics

**Gene Meyers**, Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

11:30 -11:45

Three-dimensional modelling approach and software for data integration and statistical analysis of spatial distributions in bioimaging

**Philippe Andrey**, INRA, Versailles, France

11:45 -12:00

Improved Volume Assembly from Large Electron Microscopy Section Series

**Stephan Saalfeld**, HHMI Janelia Farm, Ashburn, US

12:00 -12:30

3D morphometry and context modeling for quantitative medical image computing

**Paul Suetens**, ESAT - Processing Speech and Images, KU Leuven, Leuven, Belgium

12:30-14:00

Lunch & Company Demos and Booths



14:00-15:30      **Session 8: Digital Pathology**

14:00 -14:30      Microscopic Image Analysis: Closing the loop

**Mefin Gurcan**, Ohio State University, Ohio, US

14:30 -14:45      Understanding ICU-acquired weakness through histological data mining

**Thomas Janssens**, KU Leuven, Leuven, Belgium

14:45 -15:15      Centralized Tma Digital Pathology Process with Distributed Expertise and Quality Control

**Olivier Debeir**, ULB, Brussels, Belgium

15:15 -15:30      Feature-Learning for understanding digital pathology slides

**Theofanis Karaletsos**, MSKCC, New York, US

15:30-16:00      Coffee Break

16:00-17:45      **Session 9: From Device to Signal Integration**

16:00 -16:30      Making novel microscope imaging strategies available through Open Source software

**Nico Stuurman**, Vale Lab, University of California, San Francisco, US

16:30 -16:45      To Measure or Not To Measure Terabyte-Sized Images?

**Peter Bajcsy**, NIST, Gaithersburg, US

16:45 -17:00      Image-based analysis of in vivo cardiac conduction

**Nico Scherf**, MPI-CBG, Dresden, Germany

17:00 - 17:45      Discovering cell biology by computer vision

**Gaudenz Danuser**, Harvard Medical School, Boston, US

17:45-18:30      Closing notes & remarks