

Programme

Training course June 1-3 2015

Monday 2pm – 6pm

Tuesday 10am – 6pm

Wednesday 10am – 6pm

VIBE-Z

- Principles and potential of the method
- Installation of the software
- Queries in the current database
- Processing of new data
- Integration of new data in the atlas
- Preparation of Posters to be presented on June 4th (for those willing)

BioEmergences

- Principles and potential of the methods
- Installation of the standalone WKF
- Access to the webservice
- Data sheet, data upload, processing
- Center select software for parameter optimization
- Mov-IT for cell tracking validation and analysis
- Preparation of Posters to be presented on June 4th (for those willing)

MecaGen

- Principles and potential of the method
- Software installation
- Case studies
- Parameter space exploration
- Confronting simulations and real data
- Preparation of Posters to be presented on June 4th (for those willing)

Computational Biology For ZF-Health Training Course

Registration & Information

Dr. Jana Maier

European Zebrafish Resource Center

jana.maier@kit.edu

The aims of the course are to disseminate some of the computational biology tools, resources and concepts built during the course of the EU FP7 Integrated Project ZF-Health "Zebrafish Regulomics for Human Health" (2010-2015). We expect to foster an e-community that will synergize through the use of common databases and software. The training course is organized for three different groups of attendees willing to manipulate respectively the functionalities of the software platforms:

VIBE-Z for the construction and querying of protein and gene expression in the zebrafish embryonic brain <http://vibez.informatik.uni-freiburg.de/>

BioEmergences workflow for the reconstruction of cell lineages from *in vivo* imaging and for *in silico* experimentation <http://www.bioemergences.eu>

MecaGen, agent based framework to couple gene regulation and cell behaviours in embryonic morphogenesis modelling [mecagen](http://mecagen.org)

Attendees are welcome to bring their own data. We will provide computers although attendees are welcome to bring their personal laptop.



ZF-Health resources For *in silico* experimentation

TRAINING COURSE

VIBE-Z
BioEmergences Wkf
MecaGen

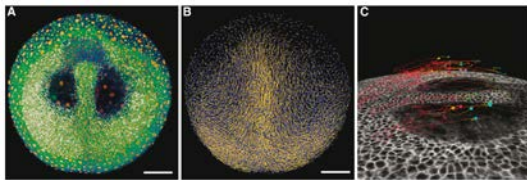


Gif-sur-Yvette

June 1-3 2015

The BioEmergences workflow for the cell lineage reconstruction

The BioEmergences workflow spans from the acquisition of microscopy images to the interactive visualization of reconstructed data. Two-photon microscopy datasets obtained from developing embryos are processed to reconstruct cell lineage trees. The processing workflow includes original algorithmic steps for image filtering, nucleus center detection, nucleus and membrane segmentation, and cell tracking. Subsequent validation, correction, annotation, and analysis are carried out using Mov-IT, a custom-made interactive visualization software. The BioEmergences cell-tracking pipeline and Mov-IT functionalities are available both as a standalone software and as a web service, offering a unique set of tools for *in silico* experimental embryology.



Snapshots, zebrafish, tailbud stage. **A:** Raw data section at 100 μm from animal pole. **B:** Display of detected nuclei and cell trajectories. Scale bar 100microns. **C:** Selected clones (colored cubes) and their trajectories raw data orthoslice in white (Faure et al. Nature Comm. 2015 in press).

Instructors:

Sylvia Dyballa

Dimitri Fabrèges

Mark Hammons

Nadine Peyri ras

Adeline Rausch

Thierry Savy

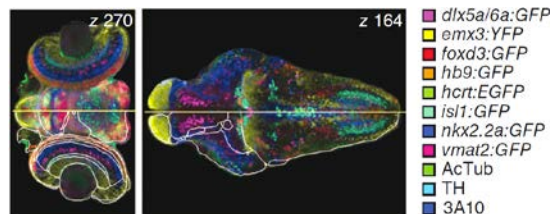
bioemergences@inaf.cnrs-gif.fr

VIBE-Z Virtual brain explorer for zebrafish

ViBE-Z the "Virtual Brain Explorer for Zebrafish" is an imaging and image analysis framework for virtual colocalization studies in larval zebrafish brains.

ViBE-Z contains a database with precisely aligned gene expression patterns ($1\mu\text{m}^3$ resolution), an anatomical atlas, and a software. This software creates high-quality data sets by fusing multiple confocal microscopy image stacks, and aligns these data sets to the standard larva. The full ViBE-Z software is available through a web interface that allows all interested users to use it without the need for complicated setup of own hard- and software.

The training course will show the preparation of the data sets for ViBE-Z using ImageJ/Fiji, the interaction with the server, and how to perform quality control on each step in the processing pipeline. For interested users we can also teach the usage of the elastic registration software on a local Linux machine.



Digital 3D anatomical atlas and qualitative colocalization analysis (From Ronneberger, O. et al. Nature Methods 2012)

Instructors:

Pierre Affaticati

Carlos Castro

 zg n Cicek

Olaf Ronneberger

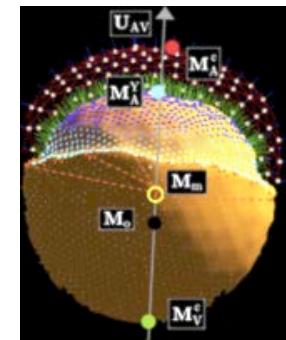
ronneber@informatik.uni-freiburg.de

MecaGen a cell-based computational model of embryogenesis

MecaGen is an integrative modeling platform enabling the hypothesis-driven simulation of morphogenetic processes with a focus on the coupling between mechanical and chemical variables.

The training course will address the deployment of the platform under Linux and the modeling and simulation of case studies:

- Notch-Delta signaling and formation of compartments in 3D tissues
- response to morphogen gradients in 3D tissues
- zebrafish epiboly and confrontation to real data



Macroscopic landmarks of the epibolic deformation in simulated specimens

(From Delile, J. Doursat, R. Peyri ras, N. Chapter 16, Computational Systems Biology (Second Edition) 2013.

Instructors:

Julien Delile

Ren  Doursat

Mathieu Herrmann

rene.doursat@inaf.cnrs-gif.fr