

Conference Programme

9h00 -10h00 Welcome coffee

10h00 -10h40 **Francesco Argenton**

In vivo Imaging of Developmental Signalling Pathways

10h40 - 11h20 **Michael Richardson**

The Zebrafish Larva as an Alternative Screening Model

11h20 -11h40 **Coffee Break**

11h40 -12h20 **Olaf Ronneberger**

A U-shaped Deep Convolutional Network for Biomedical Image Segmentation

12h20 -13h00 **Wolfgang Driever**

Integrating Anatomy and Function in 3D

13h00 - 15h00 **Buffet lunch and poster presentation by the trainees**

15h00 -15h40 **Owen Randlett**

Mapping Neural Activity and Anatomy in a Larval Zebrafish Reference Brain

15h40 -16h20 **Claire Wyart**

Optical Probing of Sensory Motor Integration During Active Locomotion *in Vivo*

16h20 -16h40 **Coffee Break**

16h40 - 17h10 **Nicolas David**

Collective Prechordal Plate Migration

17h10 -17h40 **Nadine Peyri ras**

A Vertebrate Model Organism for the Multilevel Integration of Quantitative Data

17h40-19h00 **Cocktail**

The Zebrafish: A Vertebrate Model Organism for Biological and Biomedical Investigations

Registration deadline May 31st

Free registration online

http://www.ezrc.kit.edu/zf_health_symposium_2015.php

The EU FP7 Integrated Project ZF-Health "Zebrafish Regulomics for Human Health" (2010-2015) proposes this one day conference that follows the training course "ZF-Health resources for *in Silico* Experimentation" advertised in this flyer (June 1-3, 2015).

The conference programme is expected to cover some of the achievements of the ZF - Health project and provides an overview of the potential of the zebrafish model for biological and biomedical investigations.

We will emphasize the efforts of an interdisciplinary community to tackle the complexity of biological processes with quantitative approaches and the integration of multiscale data in predictive and explanatory models.



The Zebrafish: A Vertebrate Model Organism for Biological and Biomedical Investigations

Francesco Argenton (Univ. Padova)
Nicolas David (ENS Paris)
Wolfgang Driever (Univ. Freiburg)
Nadine Peyri ras (CNRS Gif-sur-Yvette)
Owen Randlett (Cambridge USA)
Michael Richardson (Univ. Leiden)
Olaf Ronnerberger (Univ. Freiburg)
Claire Wyart (ICM Paris)

June 4th 2015

Auditorium Building 21

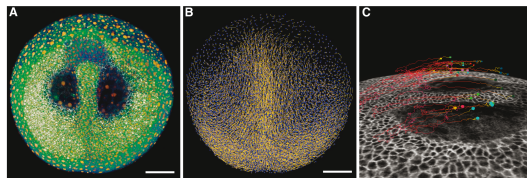
Gif-sur-Yvette

CNRS Campus

The BioEmergences workflow for the cell lineage reconstruction

<http://www.bioemergences.eu>

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 webservice, 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 100 μm . **C:** Selected clones (colored cubes) and their trajectories raw data orthoslice in white (Faure et al. Nature Comm. 2015 *in press*).

Instructors:

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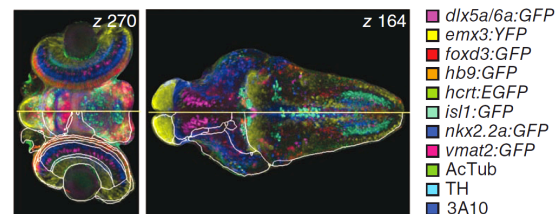
VIBE-Z Virtual Brain Explorer for Zebrafish

<http://vibez.informatik.uni-freiburg.de/>

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:

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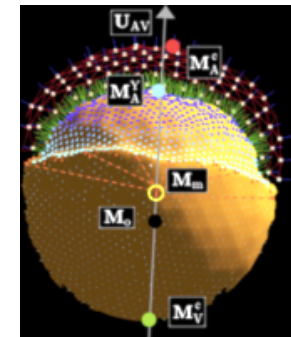
MecaGen A Cell-based Computational Model of Embryogenesis

Modeling with MecaGen

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:

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