COMBINE Tutorial
Modelling and Simulation of Biological Models

Focus

Participants will learn setting-up computer models of biological networks and simulating them in different systems biology platforms, as well as using databases and applying modelling standards. Hands-on sessions, lectures and software demonstrations will be included providing attendees with the necessary skills.

Topics:
- Model setup using different software tools and systems biology platforms
- Using experimental data for setting up quantitative models
- Parameter estimation, optimization and model fitting
- Simulation, analysis and visualization of biochemical models
- Database supported modelling: Integrated data management and model databases
- Community standards and formats for systems biology models

Standards (http://co.mbine.org/)**:** CellML, SBGN, SBML, SED-ML

Databases: BioModels, JWS Online, Physiome Repository, SABIO-RK, SEEK

Modelling tools: CellDesigner, COPASI, OpenCOR, SBGN-ED, SYCAMORE, Virtual Cell

Target audience
Experimentalists and modellers with basic experience in modelling and simulation

Date
Saturday, September 13, 2014 – Sunday, September 14, 2014 (1.5 days)

Tutors (confirmed)
- David Nickerson (Auckland Bioengineering Institute, New Zealand)
- Nicolas Le Novère (Cambridge, UK)
- Mike Hucka (Caltech, USA)
- Ion Moraru (Univ. Connecticut, USA)
- Akira Funahashi (Keio University, Japan)
- Jacky Snoep (Stellenbosch University, South Africa)
- Falk Schreiber (IPK Gatersleben and University of Halle, D)
- Ursula Kummer, Jürgen Pahle (University of Heidelberg, D)
- Pedro Mendes, Natalie Stanford, Neil Swainston (University of Manchester, UK)

Tutorial coordinator
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