





COMBINE Tutorial Modelling and Simulation Tools in Systems Biology

Participants will learn how to set up computer models of biological systems (e.g. metabolic or signalling networks) using experimental kinetic data and how to simulate them in different systems biology platforms. Hands-on sessions, lectures and software demonstrations will be included, providing attendees with the necessary skills to access experimental kinetics data from available resources, to assemble computer models with these data, and finally to simulate the generated models using simulation tools. Also handling and exchange of biological models based on existing community standards will be demonstrated along with the basic principles of the underlying standard formats.

The topics will include:

- 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

Target audience

Experimentalists and modellers with some very basic experience in modelling and simulation of biological networks and everybody who would like to learn more about the tools and standards. Attendees are expected to bring their own computer.

Date and Venue

Friday, September 16th, 2016 (8:30 - 13:30)

Barcelona, Spain

UPF (Universitat Pompeu Fabra, Campus Universitari Mar) building next to the PRBB (Biomedical Barcelona Research Park), about 15 min from the ICSB venue by taxi, or about half an hour by metro.



Carrer Dr. Aiguader 80. 08003 Barcelona, Spain







Covered tools, platforms and databases

• BioModels Database: http://www.ebi.ac.uk/biomodels/

• CellDesigner: http://www.celldesigner.org

COPASI: http://www.copasi.org/

• CombineArchive Toolkit: https://sems.uni-rostock.de/projects/combinearchive/

• JWS Online: http://jjj.biochem.sun.ac.za/

SABIO-RK: http://sabio.h-its.org/
 SEEK: http://fair-dom.org/seek

Introduced standard formats

Some commonly used community standards for model and modelling data exchange, as well as for model visualization will be introduced (SBGN, SBML and SED-ML) in practical examples using the covered tools. More information about the standards can be found on the COMBINE (Computational Modeling in Biology Network) website: http://co.mbine.org

Tutors

The list of tutors currently is preliminary and subject to change.

Akira Funahashi and Noriko Hiroi: Keio University (Yokohama, Japan)

Martin Golebiewski, Ron Henkel, Olga Krebs and Andreas Weidemann:

HITS, Heidelberg (Germany)

Ursula Kummer, Frank Bergmann, Jürgen Pahle and Sven Sahle:

University of Heidelberg (Germany)

Nicolas Le Novère: Babraham Institute (Cambridge, UK)

Jacky Snoep: Stellenbosch University (South Africa)

Natalie Stanford: University of Manchester (UK)

Tutorial Organization

Martin Golebiewski

Email: martin.golebiewski@h-its.org

Heidelberg Institute for Theoretical Studies HITS gGmbH

Schloss-Wolfsbrunnenweg 35 D-69118 Heidelberg (Germany)

Phone: +49-6221-533-281 FAX: +49-6221-533-298







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Agenda

8:30 - 10:30	Standards and Tools for Systems Biology Modelling
8:30 - 8:40	Introduction Martin Golebiewski (HITS, Heidelberg, Germany)
8:40 - 9:10	COMBINE and its Standards (BioPax, SBGN, SBML, SED-ML, CellML, SBOL, NeuroML) Nicolas Le Novère (Babraham Institute, Cambridge, UK)
9:10 - 9:30	SABIO-RK – Reaction Kinetics Database Martin Golebiewski & Andreas Weidemann (HITS, Heidelberg, Germany)
9:30 - 9:50	CellDesigner – Modeling Tool for Biochemical Networks Akira Funahashi and Noriko Hiroi <i>(Keio University, Yokohama, Japan)</i>
9:50 - 10:10	COPASI – Biochemical System Simulator Ursula Kummer, Frank Bergmann, Jürgen Pahle and Sven Sahle (University of Heidelberg, Germany)
10:10 - 10:30	JWS Online Jacky Snoep (Stellenbosch University, South Africa)
10:30 - 10:50	Coffee Break
10:50 - 11:40	Data and Model Management for Systems Biology
10:50 - 11:10	BioModels Database Nicolas Le Novère (Babraham Institute, Cambridge, UK)
11:10 - 11:30	Integrated Data and Model Management: FAIRDOM and SEEK Natalie Stanford (University of Manchester, UK) & Olga Krebs, Martin Golebiewski and Andreas Weidemann (HITS, Heidelberg, Germany)
11:30 - 11:40	COMBINE archive and OMEX format Ron Henkel (HITS, Heidelberg, Germany)

11:40 - 13:30 Parallel Demo and Hands-on Session

- 1) Integrated Modelling Workflow: COPASI, SABIO-RK, BioModels, JWS Online, SEEK, COMBINE archive Frank Bergmann, Martin Golebiewski, Ron Henkel, Olga Krebs, Ursula Kummer, Nicolas Le Novère, Jürgen Pahle, Sven Sahle, Jacky Snoep, Natalie Stanford and Andreas Weidemann
- COPASI Advanced Modelling & Simulation (only for attendees with advanced modelling experience!)
 Ursula Kummer, Frank Bergmann, Jürgen Pahle and Sven Sahle
- Modelling with CellDesigner
 Akira Funahashi and Noriko Hiroi

13:30 End of Tutorial Workshop