Modelling and Simulation in Systems Biology using COPASI
January 21 - 23, 2013
Manchester Institute of Biotechnology
University of Manchester
Manchester, UK

Free registration!

This workshop, sponsored by the EU FP7 project BioPreDyn (http://www.biopredyn.eu), is aimed at current and prospective users of the COPASI modeling and simulation package for system biology. The workshop is directed both at beginners as well as advanced users and there will be sessions directed at each of these groups (in parallel if needed). The workshop will also be an important means for the COPASI development team to collect feedback from users about improving the software.

COPASI is a free, open-source, software package for creating and simulating systems biology models. COPASI runs on Windows, Mac, and Linux and it is a user-friendly software that allows for construction of kinetic models without much knowledge of mathematics. However COPASI is also equipped with advanced algorithms and is a powerful tool for modeling and simulation, with some features that are not available in other simulators. COPASI is available at http://www.copasi.org

The workshop will cover several features of modeling and simulation by using examples of previously published models. The set of topics covered:

- Basic Modeling and Simulation - How to create biochemical kinetic models, and find out their dynamic behavior and steady-state properties.
- Sensitivity Analysis - Study of the importance of parameters in determining the values of model variables. This includes local as well as global sensitivity analysis.
- Optimization - How to use numerical optimization methods to explore the properties of large and complex models. This includes the use of optimization in strategies for metabolic engineering.
- Parameter Estimation - How to use experimental data to calibrate models to represent real biological systems accurately. This includes analysis of enzyme kinetic experiments, and in vivo time courses of cell biology experiments, among other applications.
- Stochastic Simulation - COPASI's capabilities for running Gillespie's algorithm, as well as for automatically converting ODE-based models to the stochastic representation.
- Integration with other Software Packages - How to use COPASI together with other applications that support SBML (e.g. Biomodels database, CellDesigner and SBW)
- Advanced topics – several features such as the command line version, using COPASI on distributed computing, and web services.

The Workshop is led by Pedro Mendes and Kieran Smallbone.

BioPreDyn is a Cooperation project of the Knowledge Based Bio-Economy (KBBE) EU grant, with the number 289434. BioPreDyn partners are developing data-driven computational models to analyze multi-scale biological networks, creating tools to help design and optimize complex production processes.