COPASI

Complex Pathway Simulator

Pedro Mendes, Sven Sahle

General info

COPASI is a software tool for editing, simulating, and analyzing models of biochemical reaction networks.

COPASI is available for all major platforms (**Linux, Windows, OS X**), easy to install

COPASI is free and open source software.

General info (continued)

COPASI is a joint project of the groups of Ursula Kummer (Heidelberg) and Pedro Mendes (Blacksburg, VA and Manchester)

COPASI is designed to be robust and user friendly, intended for general use not only by experts. Powerful numerical algorithms.

Widely used (1000s of downloads)

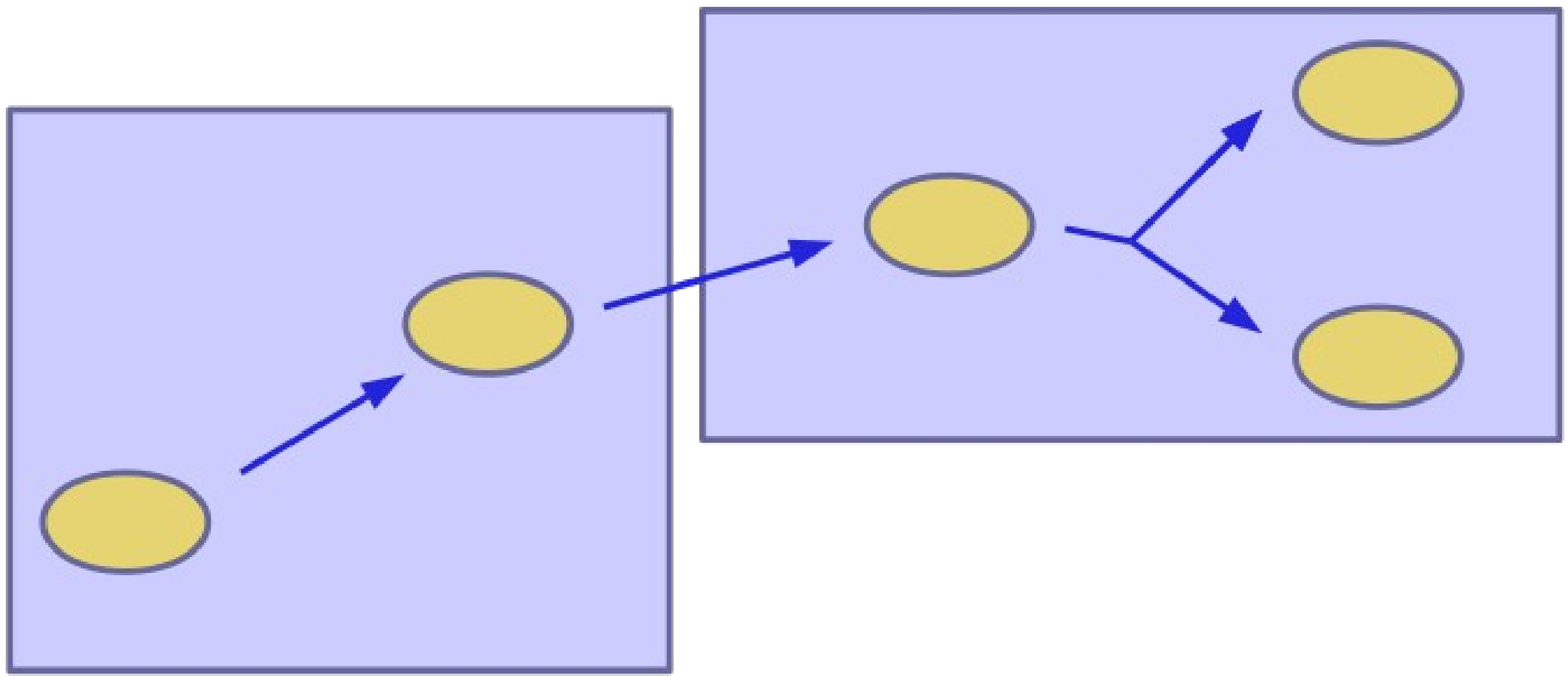
Download from **www.copasi.org**

Outline

- What kind of models can COPASI handle?
- Some examples of COPASI‘s features
- Demonstrations

The model

Compartments – Species - Reactions



The model (continued)

The basics, classical biochemical model:

- The **compartments** have a volume and contain metabolites
- The **species** have a concentration
- **Reactions** consume and produce metabolites and have a reaction rate (arbitrary kinetic functions)

The model (continued)

- Arbitrary ordinary differential and algebraic equations
- Discrete events

SBML support

SBML is an XML file format to exchange biochemical models between different tools.

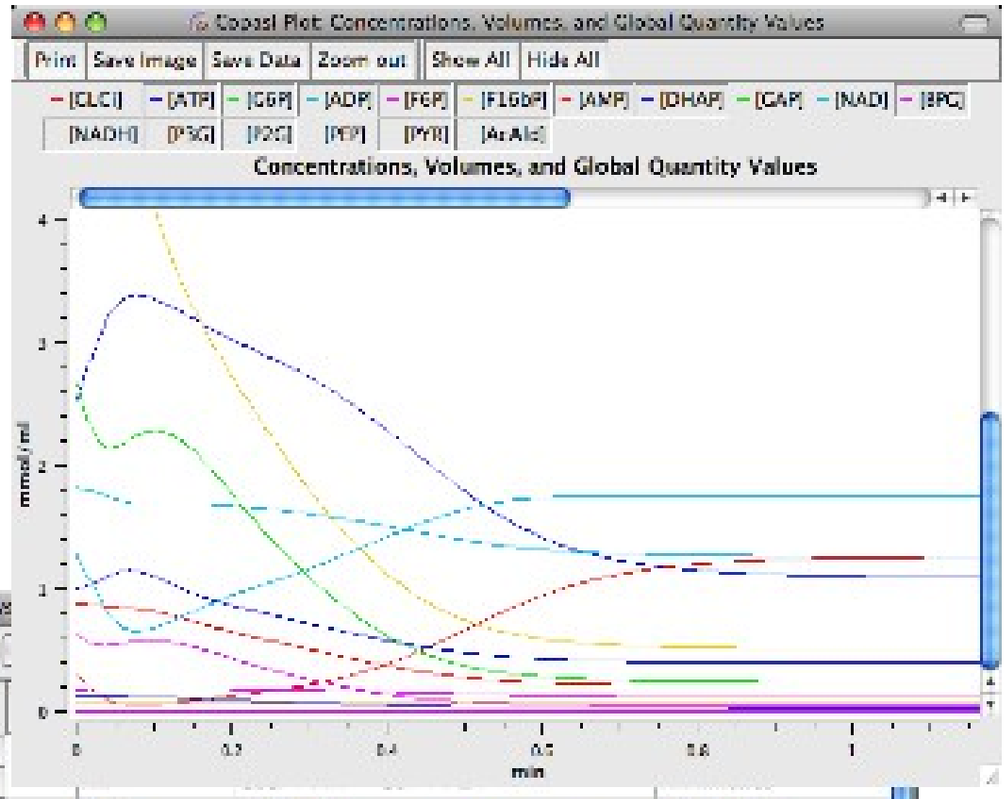
www.sbml.org

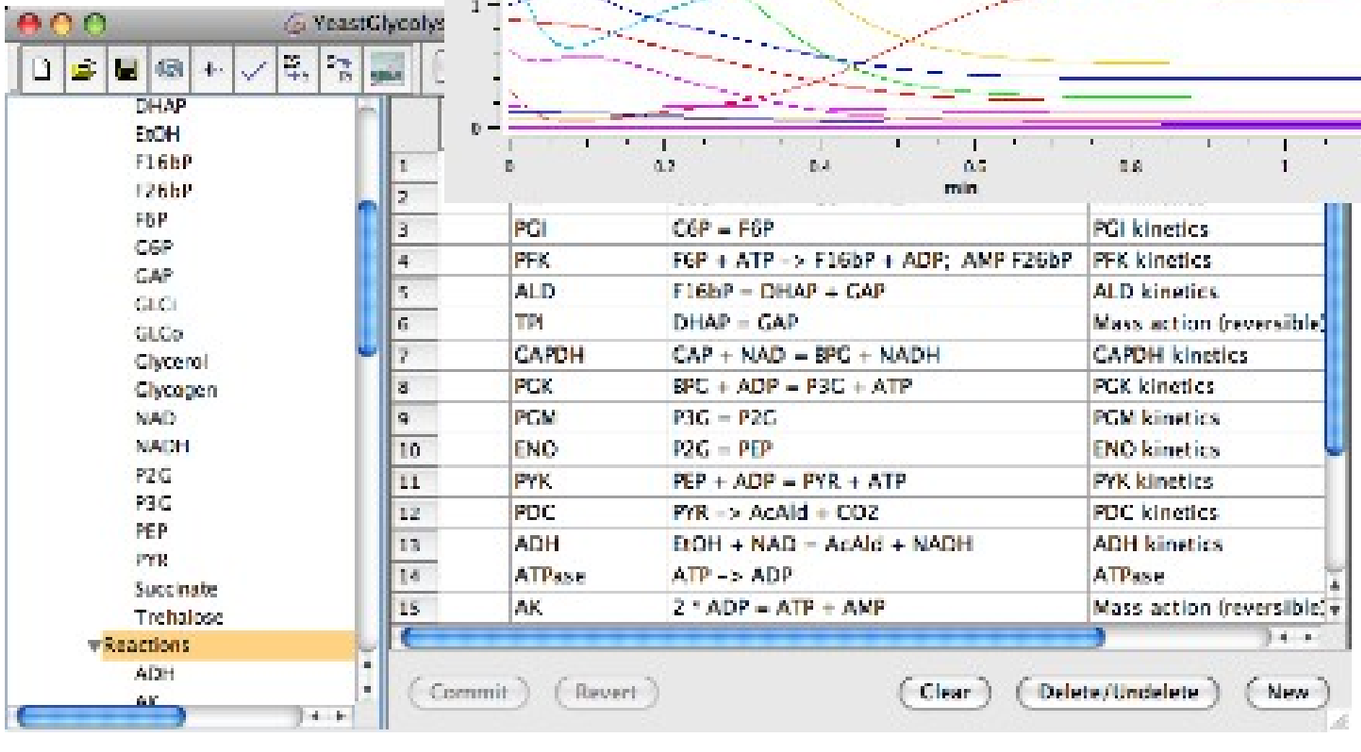
COPASI implements a large subset of the SBML specification. SBML complience is well tested. The COPASI team is actively involved in the development of SBML

Simulation

COPASI can do the usual things with a model:

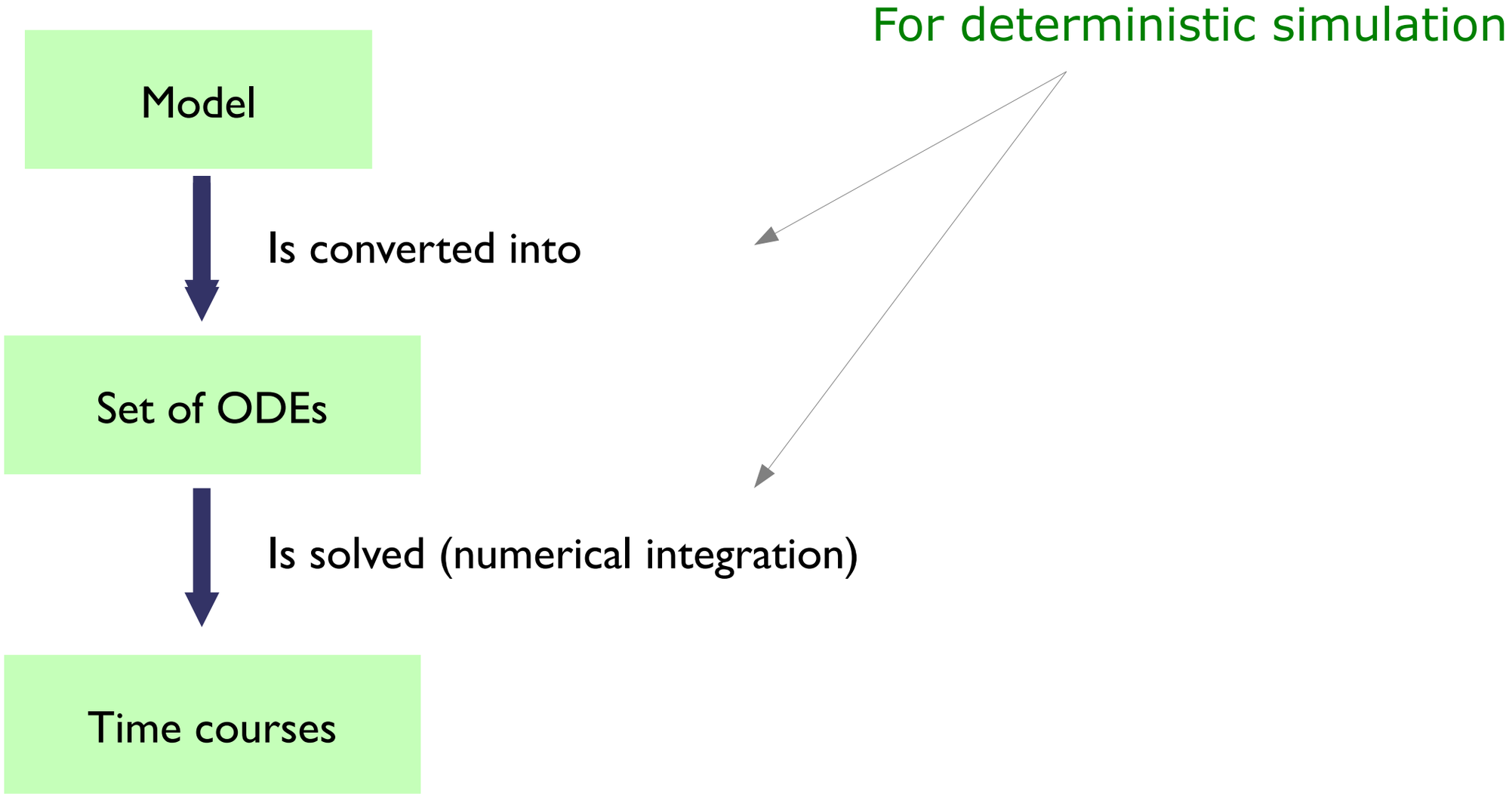
- Simulation
- Steady state analysis
- Metabolic control analysis
- Elementary flux modes
- …





Simulation

Simulation means the computer calculates the time course of the variables of the system



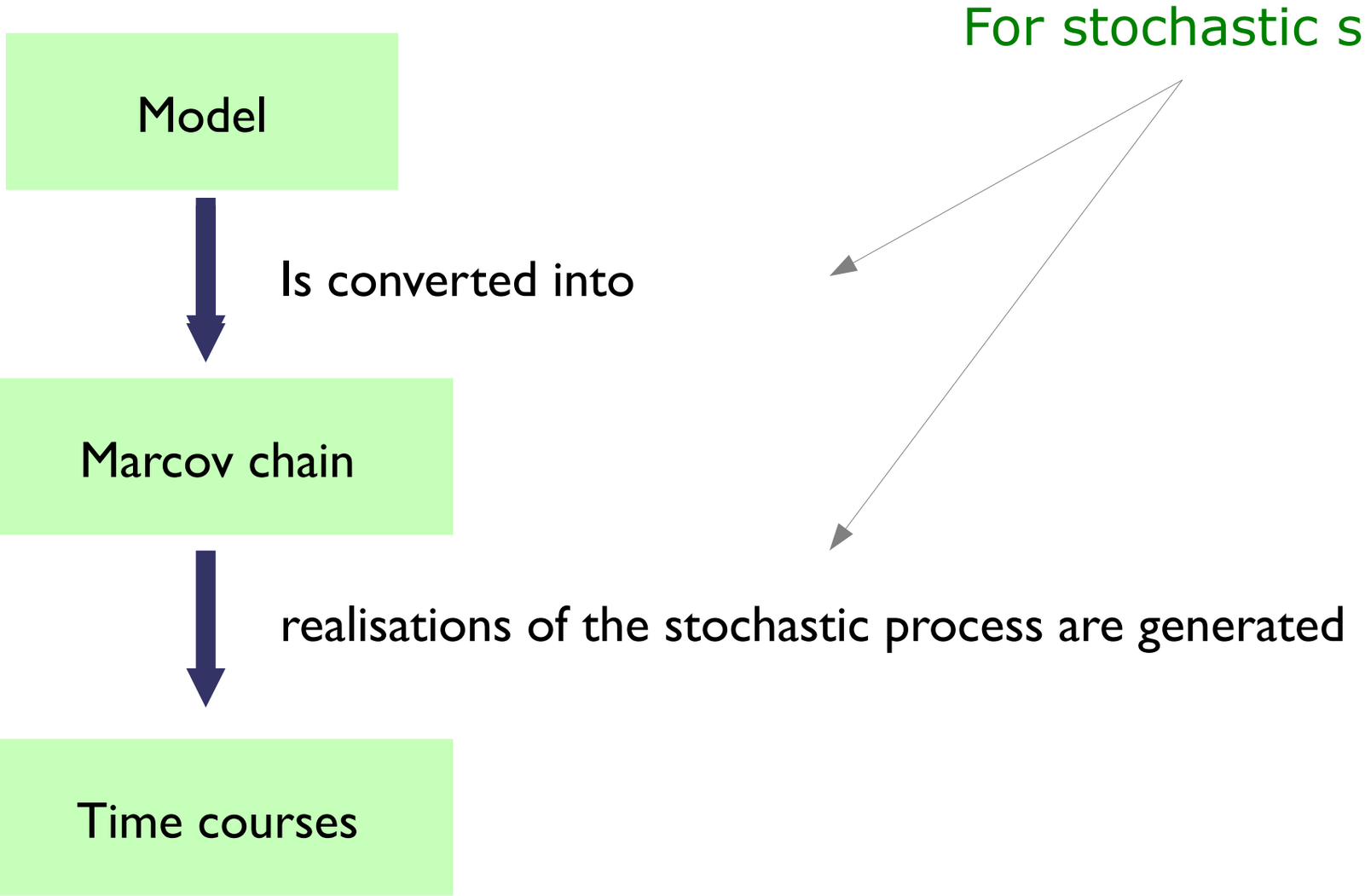
different mathematical interpretations of a model

A key feature of COPASI is the ability to switch transparently between a deterministic and a stochastic model interpretation

- Deterministic: ODEs are automatically generated and solved using LSODA
- Stochastic: Reaction rates are converted to reaction probabilities. Exact simulation with Gibson/Bruck or hybrid simulation

Stochastic Simulation

Simulation means the computer calculates the time course of the variables of the system



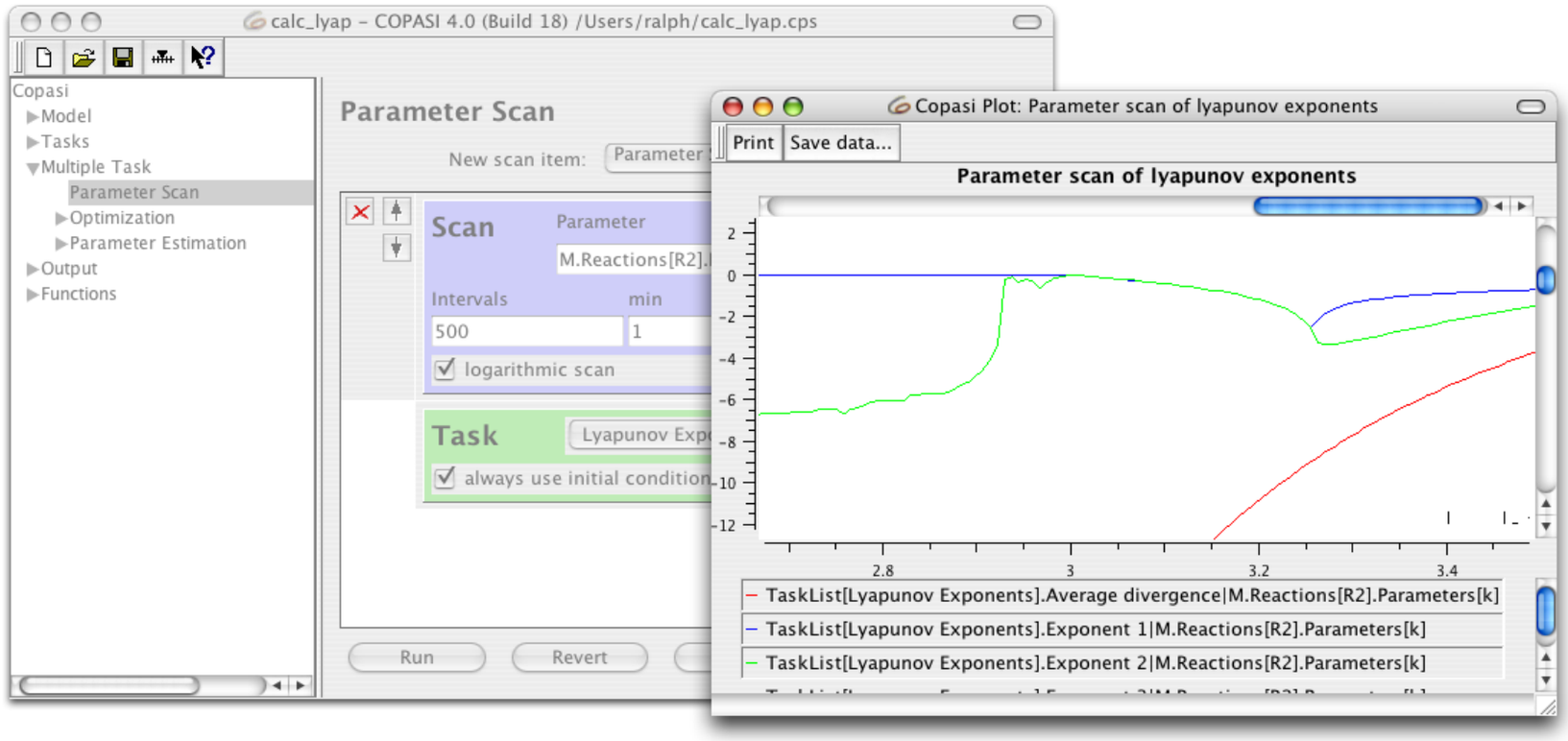
Deterministic/stochastic simulation

A key feature of COPASI is that it can transparently switch between deterministic and stochastic simulation framework.

- Important with small particle numbers, e.g. signalling networks
- Qualitatively different model behaviour, even if the curves look smooth (no visible noise)

Other analysis features

- Lyapunov exponents
- Parameter scan



- General sensitivities (first and second order)
- Optimization
- Parameter fitting
- Time scale analysis

Parameter fitting

- flexible input of experimental data
- arbitrary number of experiments
- simultaneously fitting of steady state and time course data
- potentially large number of parameters (takes a long time -> use command line version of COPASI)

The COPASI team

Blacksburg: Stefan Hoops, Brian Klahn

Manchester: Pedro Mendes, Joseph Dada, Jürgen Pahle

Heidelberg: Frank Bergmann, Ralph Gauges, Ursula Kummer, Natalia Simus, Sven Sahle

For support: **User forum at www.copasi.org**

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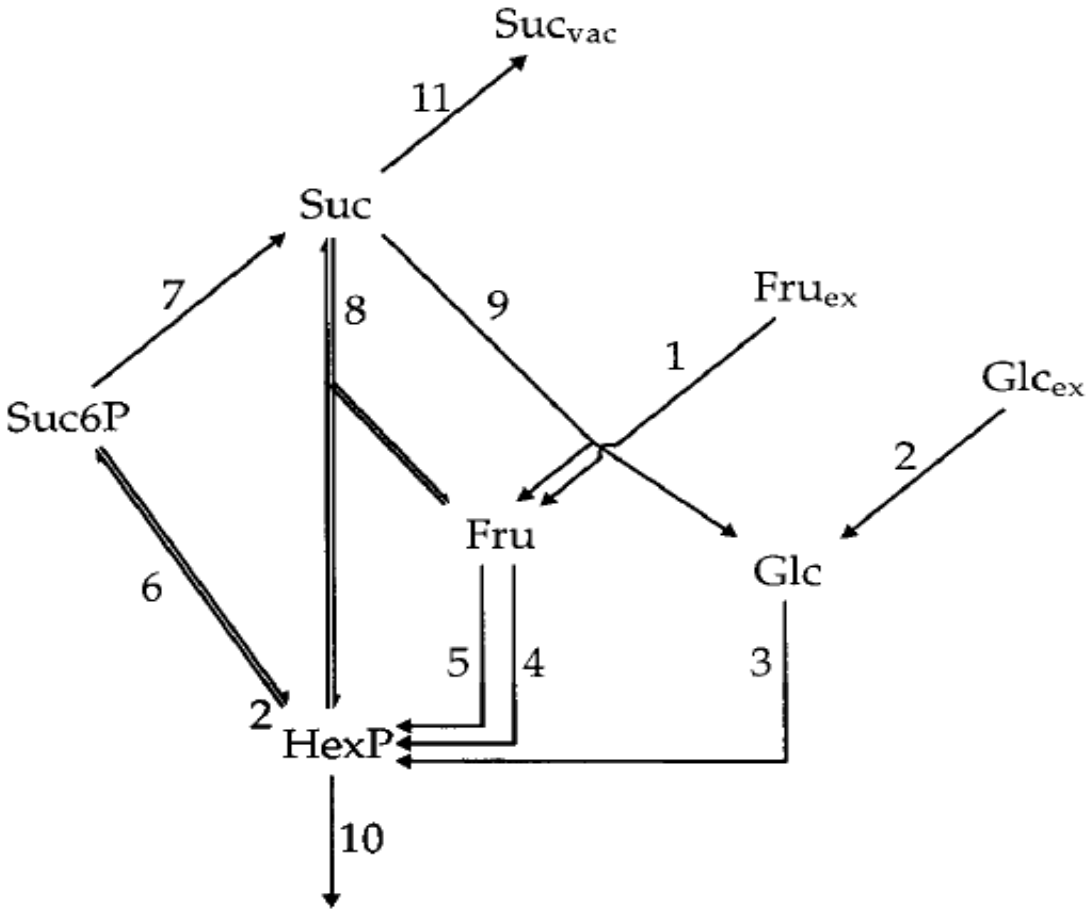
Biomodels 23



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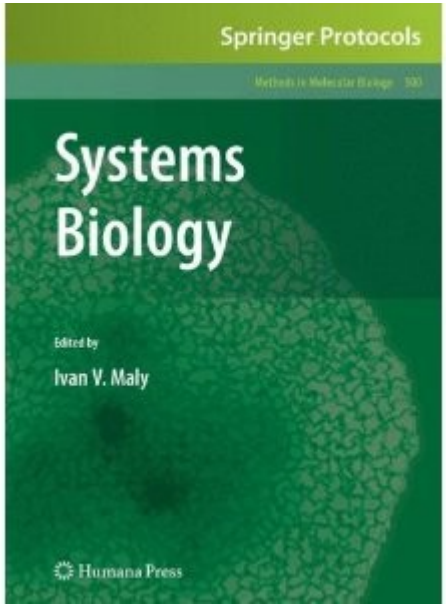

Mendes, P, Hoops, S, Sahle, S, Gauges, R, Dada, J, Kummer, U (2009) Computational Modeling of Biochemical Networks Using COPASI. Methods Mol. Biol. 500, 17-59.

Chapter 2

Computational Modeling of Biochemical Networks Using COPASI

Pedro Mendes, Stefan Hoops, Sven Sahle, Ralph Gauges, Joseph Dada, and Ursula Kummer

Summary

Computational modeling and simulation of biochemical networks is at the core of systems biology and this includes many types of analyses that can aid understanding of how these systems work. COPASI is a generic software package for modeling and simulation of biochemical networks which provides many of these analyses in convenient ways that do not require the user to program or to have deep knowledge of the numerical algorithms. Here we provide a description of how these modeling techniques can be applied to biochemical models using COPASI. The focus is both on practical aspects of software usage as well as on the utility of these analyses in aiding biological understanding. Practical examples are described for steady-state and time-course simulations, stoichiometric analyses, parameter scanning, sensitivity analysis (including metabolic control analysis), global optimization, parameter estimation, and stochastic simulation. The examples used are all published models that are available in the BioModels database in SBML format.

Team

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- ◇ Pedro Mendes
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- ◆ Ed Kent

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- ◇ Natalia Simus
- ◇ Ralph Gauges

+ many testers in several institutions

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