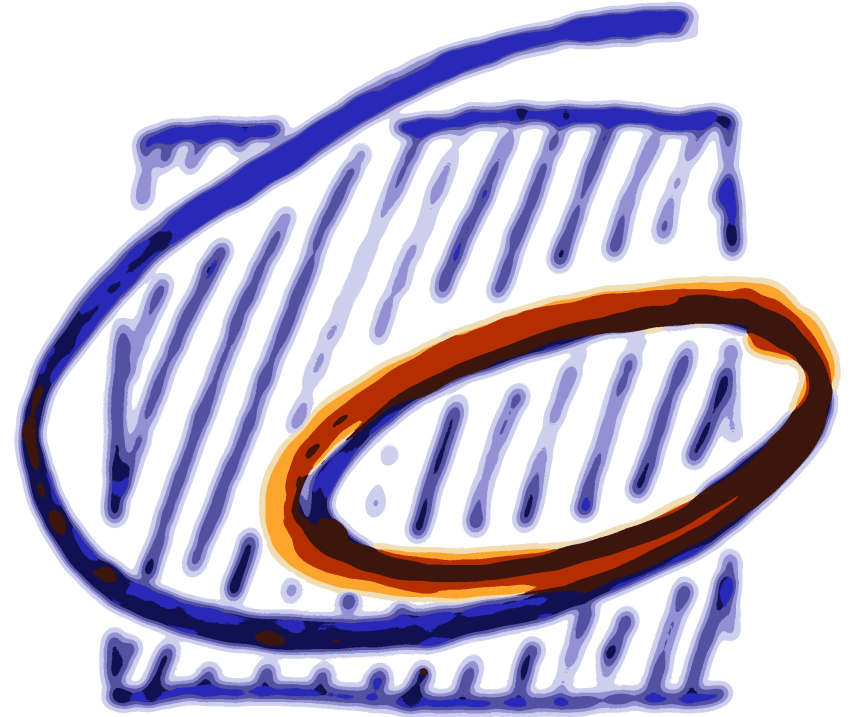


COPASI

Complex Pathway Simulator



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Abt. Modellierung biologischer Prozesse

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, Solaris**), easy to install

COPASI is free for academic use.

New features of the current release

- Assignment rules and ODE rules for metabolites (species) and compartments
- Initial assignments (sbml support has to wait for a release with new libsbml)
- Model debugging
- new optimization/parameter fitting algorithms

Support for rules

	Metabolites	Compartments	global Quantities
	Species	Compartments	global Parameters
reactions	✓	-	-
assignment rules	✓	✓	✓
ode rules	✓	✓	✓
const / „boundary“	✓	✓	✓

coming next: events

Model „debugging“

- Identify common problems with reactions and kinetic functions
- symbolic analysis of the mathematics
- check if a reversible reaction can be split into two irreversible reactions

Release schedule

- Stable release without new features soon
- Public development releases after that (also soon)

New features in upcoming releases (Overview)

- Events
- Display of Layouts
- MIRIAM support

MIRIAM support

- Display of all rdf contents
- Editing of a subset of this
- using libraptor

new user support forum

on

www.copasi.org

The COPASI Team

Blacksburg: Stefan Hoops, Aejaaz Kamal, ..

Manchester: Pedro Mendes, Joseph Dada

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Anton Ruff, Ursula Rost, Paul Willy

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

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