COPASI systems biology software package now open source for all users

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(PhysOrg.com) -- A software package developed by a professor at the Virginia Bioinformatics Institute and his colleagues to help researchers better understand the workings of biochemical networks now features an open source license, offering an ever wider range of benefits to its users.

In development for over a decade, COPASI (Complex Pathway Simulator) involves an international collaboration between Virginia Bioinformatics Institute Professor Pedro Mendes' research groups at Virginia Tech and the University of Manchester and Professor Ursula Kummer's group at the University of Heidelberg. Allowing users with limited experience in mathematics to develop models and simulations of biochemical networks, COPASI supports the Systems Biology Markup Language (SBML) standard for systems biology software and provides researchers the computational tools needed to investigate how a system is working through the construction of biochemical models. COPASI is also used by advanced modelers since it includes sophisticated algorithms. One of COPASI's main features is the ability to automatically adjust model parameters to reproduce experimental results, which helps to justify the validity of the chosen model.

COPASI has always been available through an open source format for individual users, but the software's new license agreement, which is approved by the Open Source Initiative, allows commercial users to freely use the software. This enhanced availability is included with the release of the newest version (4.6.33) of the software.

“Through our new Artistic License 2.0 licensing scheme, everyone will have the opportunity to download and use future versions of COPASI free of charge,” explains Stefan Hoops, Virginia Bioinformatics Institute senior project manager and one of the technical leads of the project. “The new license is also compatible with more software libraries and other academic software programs, which will allow the development team to enhance the quality and functionality of COPASI. Third parties will now be able to develop and distribute software packages that use the program and it can also be included in other software bundles, such as Linux distributions. Researchers from across the globe will now be able to integrate COPASI in their own software projects and freely distribute results.”

The COPASI development team continues to make improvements to the software package, with the ultimate goal of helping to further the understanding of cellular and molecular behavior by facilitating the quantitative interpretation of modern experiments. COPASI is designed to meet the real needs of life scientists in a powerful package that every biologist can use, not just experts in systems biology. Development of COPASI has been funded by the National Institutes of Health, the German Ministry of Science, the Klaus Tschira Foundation, the Commonwealth of Virginia, and the British Biotechnology and Biological Sciences Research Council. The software may be freely downloaded.

COPASI (Complex Pathway Simulator) is a software package that allows the simulation and detailed analysis of biochemical networks. The package, which is available for use on Windows, Macintosh, Linux and Solaris operating systems, is based on original software developed by Pedro Mendes (Gepasi) and on the STODE software developed at EML Research. The main authors of COPASI are Stefan Hoops, Sven Sahle, and Ralph Gauges. COPASI incorporates a model editor, different simulation techniques (e.g. deterministic and stochastic), optimization

routines, sensitivity analysis and user-friendly visualization techniques. Some of the current features include: stochastic and deterministic time course simulation; steady state analysis (including stability); metabolic control analysis/sensitivity analysis; elementary mode analysis; mass conservation analysis; parameter scans; optimization of arbitrary objective functions; parameter estimation using data from time course and/or steady state experiments; sliders for interactive parameter changes; global parameters to change multiple kinetic rates at once; import and export of SBML; fully compatible with Gepasi files; command line version for batch processing.

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