Latin America High Performance Computing Conference (CARLA)
Turrialba, Costa Rica
Conference Dates: 25-27 September, 2019
Tutorials and Workshops: 23-24 September, 2019

Tutorial: Modeling with COPASI

Time and Location: Sala 3, National High Technology Center (CeNAT), San Jose, Costa Rica. Monday September 23, 8:30am-5:30pm This event is free of charge and hosted in the context of CARLA 2019.

COPASI is a software application for simulation and analysis of biochemical networks and their dynamics. www.copasi.org. COPASI is a widely used software tool for creating, simulating and analyzing models of biochemical reaction networks. It is open source free software and available for all major operating systems. Its features include deterministic and stochastic simulation, steady state analysis, stoichiometric analysis, optimization and parameter estimation, time scale analysis, sensitivities and metabolic control analysis, Lyapunov exponents, linear noise approximation, etc. In the workshop we will provide and introduction to the modeling concepts as well as hands on experience using COPASI. We will also be available for the discussion of individual questions from the participants.A list of the many features can be found here.

Requirements: Laptop computer with COPASI installed. Download here:
http://copasi.org/Download/

SPEAKER

Stefan Hoops is a Research Associate Professor in the Network, System Science & Advanced Computing (NSSAC) division at the Biocomplexity Institute & Initiative at the University of Virginia. Before joining the institute in 2018, Dr. Hoops worked at the Biocomplexity Institute of Virginia Tech (2000-2018), and served as a software designer/developer for Schumann Consulting Corporation in Germany (1995-2000).

Dr. Hoops is a co-leader of the COPASI project. COPASI is a software application for simulation and analysis of biochemical networks and their dynamics. It is a stand-alone program that supports models in the SBML standard and can simulate their behavior using ODEs or Gillespie's stochastic simulation algorithm; arbitrary discrete events can be included in such simulations.

He was elected in 2006 as one of the 5 editors of the Systems Biology Markup Language (SBML), serving for the years 2007-2009 and continues to be engaged in this and other standard development effort for the life science community.
Further interest of Dr. Hoops is the integration of computational modeling and immunology experimentation to characterize the immunoregulatory mechanisms underlying immune responses to enteric pathogens.

For registration: https://www.carla2019.org/tutorials (tutorial 4)
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