Workshop on Systems Biology using COPASI

Time and Space: Monday July 16th, Auditorio de Física Matemática, University of Costa Rica. Find the location here: https://goo.gl/maps/Xz54WB24ivP2
This event is free of charge and hosted in the context of IWOBI 2018.

COPASI is a software application for simulation and analysis of biochemical networks and their dynamics. www.copasi.org. COPASI 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.
A list of the many features can be found here.

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

SPEAKER

Pedro Mendes is a professor of the University of Connecticut (University of Connecticut Health Center, Center for Quantitative Medicine, Department of Cell Biology, and Center for Cell Analysis and Modeling.). His backgroun is in Biochemistry at the University of Lisboa and obtained his PhD at the University of Wales Aberystwyth, the Computer simulation of the dynamics of biochemical pathways), under the supervision of Douglas B. Kell. Mendes has published more than 120 manuscripts having a total of 17734 citations and h-index of 49 according to Google Scholar. His background is in Biochemistry and computer science. He has interest and research in both areas and their joint application. His area of research is in computational systems biology, where he has demonstrated leadership in biochemical modeling and simulation; he was the author of Gepasi, a popular and pioneering software package for modeling biochemical networks, which then became COPASI, now one of the top simulators for systems biology.

PROGRAM

8 am – 12 md. Basic Module:

- Construction of Mathematical Models and visualization.
- Construction of data files for parameter estimation.
- Steady State Analysis.
- Time Course Simulations.
- Parameter Scans.
- Sensitivity Analysis.

1 pm – 6 pm: Advanced Module:

- Metabolic Control Analysis.
- Lyapunov Exponents.
- Time Scale Separation.
- Cross Section.
- Parameter identifiability.
- Cloud COPASI.
- ManyCell.
- Large scale modeling and reverse engineering.

For more information please contact: **rodrigo.morarodriguez@ucr.ac.cr**