

MPA2019 tutorials

On the first day of MPA we will be offering tutorials where you will be able to learn about the newest software in use and get advice from skilled professionals. Since the number of participants is limited for each tutorial, please only attend the tutorial that you have registered for. Tutorials will happen on the 3rd floor.

12.08.2019

10:00 - 13:00 Tutorials 1

1.1. R334 "Modelling Dynamic Systems in Python" Oliver Ebenhöh

Description: The goal of the workshop is to teach students how dynamic systems based on ordinary differential equations can be simulated and analyzed with Python. Depending on the background, we will recapitulate some basic programming elements of the programming language Python and repeat some basics about differential equations. In the hands-on tutorial, we will use the well-documented Python package 'modelbase', which is designed to support the model construction and analysis process as a fully integrated part of the Python programming language. We will implement some simple systems, integrate these, and visualize the results for analysis. Participants are strongly encouraged to install Python and modelbase beforehand. Please see <http://doi.org/10.5334/jors.236> and <https://modelbase.readthedocs.io/en/latest/> on information on the modelbase software and the (simple) instructions on how to install.

1.2. R335 "Metabolic Modeling in the Department of Energy Systems Biology Knowledgebase (KBase)", José P. Faria, Janaka Edirisinghe

Description: The Department of Energy Systems Biology Knowledgebase (KBase; <http://kbase.us>) is a knowledge creation and discovery environment designed for both biologists and bioinformaticians. KBase integrates a variety of data and analysis tools, from DOE and other public services, into an easy-to-use platform that leverages scalable computing infrastructure to perform sophisticated systems biology analyses. KBase is freely available and a developer extensible platform enabling scientists to analyze their own data within the context of public data and share findings across the system. The Workshop will focus on the genome-scale modeling tools available in KBase. Participants will learn how to reconstruct and analyze metabolic models for microbes, plants, and communities.

1.3. R336 "Merlin - Software for Reconstruction of Genome-Scale Models", Isabel Rocha, Oscar Dias

14:00 - 17:30 Tutorials 2

2.1. R334 "Reproducibility and Standards in Metabolic Kinetic Modeling", Herbert Sauro

Description: The vast majority of published models in systems biology cannot be reproduced. In this tutorial, we will use Tellurium, a Python-based simulation environment that supports all current modeling standards. We will show users how to retrieve models from biomodels, turn such models into a readable form, simulate, change, then convert them back into SBML. The tutorial will also discuss other aspects of Tellurium including creating new models using the highly readable Antimony syntax, metabolic control analysis, bifurcation analysis, and parameter estimation. The tutorial will also demonstrate the new structural python package that can be used to compute conservation laws and elementary models. It is recommended that users download and install the software before the tutorial from tellurium.analogmachine.org. The software can run on Windows, Mac OS, and Linux.

2.2. R336 "Analyzing Metabolic Networks with CellNetAnalyzer", Axel von Kamp, Philipp Schneider, Steffen Klamt

Description: CellNetAnalyzer (CNA) is a MATLAB package for analyzing biological (metabolic, signalling and regulatory) networks and supports both command-line based operations, as well as a graphical user, interface with embedded network visualizations. In the first part of the tutorial (1,5h), we will demonstrate key features of CNA for stoichiometric and constraint-based modeling of metabolic networks (including flux (balance) analysis, flux, and yield optimization, elementary mode analysis, computational strain design with minimal cut sets and others). The second part of the tutorial (1,5h) will consist of hands-on exercises where the participants will learn how to use CellNetAnalyzer in practice.