

Saturday, March 1, 2014

17:00 - 18:30	<i>Pre-course pick up of badge & course material</i>	<i>Lobby</i>
20:00 - 22:00		

Sunday, March 2, 2014 – Pre Courses

08:30 – 09:00	<i>Pre-course pick up of badge & course material</i>		<i>Lobby</i>
09:00 – 10:30	4 parallel pre-courses - part I		In groups
	PC-01	David Fell Mathematical Biochemistry in a nutshell	Room 051
	PC-02	Marcel Schilling Computing in a nutshell	Room 052
	PC-03	Ursula Klingmüller Cell Biology in a nutshell	Room 053
	PC-04	Karl Kuchler Molecular Genetics in a nutshell	Room EXL 3
10:30 – 11:00	<i>Coffee break</i>		
11:00 – 12:30	4 parallel pre-courses - part II		Rooms EXL 3, 051, 052, 053
12:30 – 13:30	<i>Lunch</i>		<i>Restaurant</i>
13:30 – 15:00	4 parallel pre-courses - part III		Rooms EXL 3, 051, 052, 053
15:00 – 15:30	<i>Coffee break</i>		
15:30 – 17:00	4 parallel pre-courses - part IV		Rooms EXL 3, 051, 052, 053

ABSTRACTS

PC-01 Mathematical biochemistry in a nutshell

David Fell

Biological & Medical Sciences, Oxford Brookes University, Gipsy Lane, Oxford OX3 0BP, UK

This precourse is designed for those less familiar with the mathematical aspects of modelling and systems biology. The aim is not to improve anyone's competence in mathematics, but to provide a basic introduction to some of the main mathematical concepts and computational techniques used to represent and model biological systems. The selection of topics is designed to underpin the main course and consists of:

Functions, parameters and variables

Calculating time courses from ordinary differential equations

Matrices and vectors

Mathematical representation of cellular systems

Sensitivity analysis - illustrated with metabolic control analysis

PC-02 Computation in a Nutshell

Marcel Schilling, PhD

Systems Biology of Signal Transduction, German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, 69120 Heidelberg, Germany, +49 6221 42 4485, m.schilling@dkfz.de

Biological processes such as signal transduction and subsequent target gene expression are governed by highly complex molecular mechanisms. Mathematical models consisting of ordinary differential equations (ODEs) are a frequently used approach that facilitates systematic network analyses. These models allow to test hypothesis about the biological processes and to predict cellular properties that are not accessible by experiments.

In this precourse, students and researchers with a biological background will be introduced to quantitative dynamic modeling of biological systems. We will start with describing simple examples of molecular interactions based on mass action kinetics. Then, more complex enzyme kinetics will be explained and we will introduce the establishment of ODEs. Finally, the basics of numerical integration and deterministic and stochastic simulations will be discussed. The introduced concepts will allow the participants to formulate the ODEs and describe the dynamics of exemplary signaling pathways.

The examples will be established and simulated interactively using the freely available software Copasi (www.copasi.org). Participants are encouraged to bring their own laptops and to pre-install the software. A background in mathematics or computational biology is not required for this precourse. Basic knowledge in biochemistry and signal transduction is of advantage.

ABSTRACTS

PC-03 Cell Biology in a Nutshell

Ursula Klingmüller

DKFZ, Im Neuenheimer Feld 280, Heidelberg 69120, Germany

The lecture will cover principle concepts in cell biology and will introduce relevant techniques used for experimental data generation for modeling purposes. Specifically, structural differences of cells and the function of organelles will be introduced. An overview of extracellular signals such as growth factors and hormones will be given and principal mechanisms facilitating signal transduction from the cell surface to the cell nucleus will be summarized. Key cellular responses and the underlying mechanisms will be illustrated.

To explain differences in time and spatial scales the impact of cellular decisions on reactions at the tissue up to organ level will be described. Furthermore, an overview of specific techniques for data generation and strategies for data processing as well as suitability of experimental data for different modeling approaches will be provided.

PC-04 Molecular genetics in a nutshell

Karl Kuchler

Medical University Vienna, Department of Medical Biochemistry, Dr. Bohr-Gasse 9/2, 1030 Vienna, Austria

Systems biology (SysBio) aims to gain a systems-level understanding of organismic, cellular or even subcellular pathway behaviour to identify novel as well as emerging principles of a living system. The long-term hope is to be able to better predict and cure diseases of complex genetic origin. One of the key features of SysBio is the integration of a multitude of quantitative biological data (deep-sequencing, SNP and mutations, genetic interactions, microarrays, proteomics, metabolomics, etc.) with various applicable mathematical modelling approaches. While modelling and the use of proper algorithms depends on the question and hypothesis to be addressed, the generation of quantitative biological data often poses unsurmountable technical problems or are even impossible with the current methodologies. This is especially true for measuring the dynamics and time-scale of biological processes from transcription, translation to post-translational modification as well as the kinetics of intracellular biomolecule trafficking. Likewise, pathway architectures and features often result from complex genetic interactions, which respond to various types of input, making parameter estimation for modeling a difficult task. In this pre-course teaching on molecular genetics for theoreticians and modellers, I will try to use simple model systems such as yeast as an example to explain how and which kind of experimental (genetic) data can be obtained from eukaryotic cells in a (near)-quantitative manner and which technical issues and pitfalls apply to the some of the current state-of-the-art technologies to study the dynamics of biological processes related to signal transduction.