Syllabus:

Bioinformatics 1 - Systems Biology

Lecture room: see [<< course page >>](#).

COURSE STAFF

For Systems Biology: Prof. Korsching
for the other lectures Prof. Makalowski, Prof. Gadau, Prof. Jiang.

OBJECTIVE

Introduction into systems biology and biological networks. Get into touch with the basic concepts and the methodological practice.

PREREQUISITES

none - introductory level

ABSTRACT

The (biological) cell is an enormous complex machinery based on the ordered interaction from atoms to huge macro molecules. All these chemical reactions and non chemical interactions are packed in specific environments which are in many respects separated from the surrounding environment. All these specific interactions are 'learned' over a long time span of about 3 billion years and conserved or saved in the cellular genome. Not everything of this huge development, or biological evolution, is preserved in this cellular machinery - but the main functionality. This course should enable the participants to understand important features of this system and try to join this knowledge with established biological or medical experience. Besides these conceptual aspects some exemplary methodological procedures in this field of research are presented as starting points for further explorations, e.g. microarray technologies / parallel measurements and their corresponding analysis strategies.

Extra curricular course [Biology/Medicine]

Course ID
bioinformatics 1

Class Start
see main << course page >>

Timeline
weekly

Estimated Effort
see main << course page >>

Class Size
unlimited

The RESEARCH COMMUNITY

This means we try to join learning and research as far as possible. We also encourage successful participants of the courses to consider projects / cooperations in our field of research.

Concept of the lecture Systems Biology

The course is designed to introduce the theoretical field of bioinformatics to students of the biology and life sciences including students from medical faculty.

The lecture on systems biology has the objective to introduce the students to some aspects of cellular function, their analyses and the concepts necessary to explore and understand complex systems.

The double period starts with an overview on the number of subjects which are involved in the field of systems biology a truly interdisciplinary profession. Some resources are given as starting points to explore further aspects of this field. A historical view presents these modern developments of theoretical biology in the light of similar developments in experimental and theoretical physics. The systems biology paradigm "the whole is more than the sum of the parts" is explained by a simple graph. This starting point is important because it opens the mind for a deeper understanding of what is a system. Further definitions of the term 'systems biology' out of the historical development of this field strengthen the field of associations bound to this term. A histological example from pathology - breast cancer - introduces a first real world example of a different system biology between normal and pathological breast cells due to different regulation based on the same cell type. The term 'high throughput' technologies is introduced and the paradigm shift from deconstructing a system into parts to analyzing the interaction of these parts finalizes this introductory section.

The following three sections are presenting exemplary work areas with some prominent details and concepts while the last seven fields are kaleidoscopically illustrating the diversity and depth of the field of systems biology.

The first example - measuring protein expression dependencies - is given in a very detailed and practical way, so students might associate at least some aspects to their a priory knowledge. Starting by a model of the cell and their histological representation in an ultra thin section of a specimen, the complexity of the cell is revisited. The terms 'expression', 'network' rsp. 'biological network', 'expression measurement' and associated methods are introduced. Tissue heterogeneity is discussed as well as other sources of variation for the measurement. The sampling type macro molecule extraction from tissue sample versus in situ measurement is illustrated. Overall the impact of sample and measurement procedure on the result is exemplified.

The complete workflow to measure protein expression in tissue samples is shown and explained. The first detailed analysis approach for such a data type is introduced: the multi step procedure to establish protein dependency pattern from tissue microarray data. The next example relates to differential gene expression analysis and the generation of pathway models from expression data. This step generalizes the expression approach to a universal tool for detecting dependencies in the context of an assumed network model of the biochemical cellular reactions. Petri nets as a very detailed version of network models are introduced. Finally another different co-expression approach, but orthogonal to the first one, is described. This example should train people to recognize the multitude of small but profound differences in theoretical approaches and their consequences.

With a final series of spotlights on several research topics the conclusion is pointing towards the necessity to precisely deal with complex matters and get not stuck in theory but interact actively with the experimental sciences and their perspectives.