Cycle E: Computational and Systems Biology

Coordinator: Torsten Schwede

The lecture series “Genomics in Drug Discovery Research”, “Proteomics in Drug Discovery Research” and the seminar series “Current Research in Bioinformatics” are suited for listeners without computational background.

“Programming for life sciences” consists of lectures and exercises, where students are expected to acquire programming skills to be able to solve data analysis problems in life sciences.

“Computational Structural Biology” and “Computational Systems Biology” consist also of lectures and exercises, which should make the students familiar with current topics in these two computational sub-fields. Basic programming skills and a solid mathematical background are required.

For students interested in computational biology, but without a background in computational sciences, the lectures Computational Biology I and II are recommended, both taking place every spring semester. They do not belong to the graduate teaching program, but are described below as well. Similarly, the block course in Synthetic Systems Biology is recommended to students with basic molecular biology skills and interest in this topic.

E1: Genomics in Drug Discovery Research - 13185
(2 hrs/week, 2CP)

Paul Herrling, Torsten Schwede
Lecture series with invited speakers

Computational biology and bioinformatics have emerged as key disciplines in the use of genome-wide data for disease gene discovery and molecular epidemiology. These disciplines are increasingly important in the biopharmaceutical industry for the discovery of novel, more effective, and safer medicines. This course discusses the application of genomics research in drug discovery in the pharmaceutical industry.

E2: Proteomics in Drug Discovery Research - 12422
(2 hrs/week, 2CP)

Paul Herrling, Torsten Schwede
Lecture series with invited speakers

The availability of genome sequences and high-throughput sequencing data sets for many species, including human, has brought with it tremendous opportunities as well as many challenges. One of the immediate goals has been the determination of the structure, function and expression of all of the proteins that are encoded in the sequenced genomes. The field of proteomics aims at understanding of how the structure and function of such proteins and their post-translational modifications contribute to life processes. This course introduces potential applications of proteomics to the finding of new drugs.
**E3: Computational Systems Biology - 25661**  
(3 hrs/week + exercises, 6CP)

Richard Neher, **Erik van Nimwegen**, Mihaela Zavolan  
Lecture and exercises

Systems Biology has established itself in the past ten-fifteen years as the field in which large-scale quantitative measurements at multiple levels are analysed in the context of mathematical models to reach a better, more predictive understanding of biological systems. This lecture provides an introduction to current topics and methods in Computational Systems Biology. It will introduce the student to topics ranging from evolution and scaling laws in biological systems to quantitative approaches that employ biophysical methods with the aim of building an understanding of how the behaviour of biological systems can be described quantitatively. Pre-requisites are a good mathematical background (e.g. acquired through the Computational Biology I and II lecture series) as well as basic training in biology.

**E4: Computational Structural Biology - 24169**  
(3 hrs/week + exercises, 6CP)

Markus Meuwly, **Torsten Schwede**  
Lecture and exercises

The course will cover concepts of protein structure bioinformatics, modelling and simulation methods, their application to protein structures and their interactions with other molecules. In particular: protein structure comparison and classification, principles of molecular interactions, molecular mechanics simulations, in silico and structure based drug design, de novo and comparative protein modelling techniques.

During the course, the students will gain an overview of the theoretical concepts underlying modelling and simulation methods. The theoretical lectures are complemented by practical tasks, aiming to challenge the level of understanding of the students, e.g. by programming low-level implementations of certain algorithms. Practical applications of modelling and simulation methods will involve critical evaluation and assessment of the reliability and accuracy of the applied methods.

**Prerequisites:**
- Knowledge in structural biology, e.g. Bio4 ("Strukturbiologie") and Blockkurs or equivalent.
- Basic programming skills (preferably in Python).
**E5: Current research in Bioinformatics I - 22830**  
(2 hrs/week, 1CP)

**E6: Current research in Bioinformatics II - 21563**  
(2 hrs/week, 1CP)

Attila Becskei, Torsten Schwede, Mihaela Zavolan, Erik van Nimwegen
Lecture series with invited speakers

Computational biology and bioinformatics methodologies have become integral to molecular biology research in the post-genomics era. Developments are taking place at a staggering pace in all areas, from genomic sequence analysis to the analysis of phenotypes with imaging techniques. This course aims to expose the students to current directions of active research in computational and systems biology and bioinformatics.

**E7: Programming for Life Sciences - 43513**  
(2 hrs/week, 4KP)
Torsten Schwede, Mihaela Zavolan, and sciCORE  
Praktikum with exercises to be solved at home

Together with new measurement technologies, the use of computational and mathematical approaches that exploit modern information technology in the study of biological systems have brought about a deep transformation in the practice of molecular biology research. To take advantage of the new opportunities, the new generation of biologists should be highly competent not only in their experimental work but also in the development and use of mathematical and computational methods. This course aims to train the students into the proficient use of programming in analyzing data derived from projects in life sciences. The course is focused on the widely used Python programming language, with a few examples from other commonly used languages such as R and Matlab. Basic knowledge of computing systems, programming languages and algorithms are required.

**E8: Introduction to R/Bioconductor - 45038**  
(2 hrs/week, 2KP)
Sarah Carl, Florian Geier, Robert Ivanek, Helene Royo, Michael Stadler  
Lecture and exercises

The R/Bioconductor framework is the most widely used analysis tool for sequence based bioinformatics. The lecture gives an overview of typical Bioconductor based analysis pipelines including:
- Microarray and NGS data processing  
- Differential gene expression analysis  
- Working with sequence and annotation packages  
- Programmatic access to public databases  
- Visualization of genomic data  
Each lecture is organized around one analysis question using publicly available data. It consists
of 1 hour lecture and 1 hour hands on practical. Participants should bring along their laptops. Basic R knowledge is of an advantage.

**Recommended lectures outside the graduate teaching program:**

**Block course on synthetic systems biology:**

12469 – Praktikum: Biotechnologische Mikrobiologie II
(2 week block course, 6KP)
Attila Becskei
2 week block course, every fall semester
1-2 BZ students could take part, depending on space availability. Contact Attila Becskei if you are interested.

The course covers concepts of synthetic gene regulatory networks in microorganisms. The relevant molecular biological mechanisms are discussed, followed by the kinetic description of these mechanisms. Subsequently, experiments are performed that demonstrate network behaviour including cellular memory, bell-shaped response and stochastic gene expression.

By the ends of the course, the students will be able to write up, solve and analyse basic equations describing gene regulatory mechanisms. Furthermore, students will be able to construct synthetic gene regulatory networks for specific behaviours.

**Computational Biology I - 23605**

Erik van Nimwegen
every spring semester
→ for those who did not take it during their BSc Biology / Computational Sciences program at UniBas

This course provides a general introduction into quantitative analysis of data. Students will be introduced to the modern view of probability theory as a general method for reasoning with incomplete information and, guided by practical examples taken from computational biology, will get acquainted with the most important concepts and methods used in statistical analysis and modeling of data. By the end of the course students should have gained a solid understanding of the fundamentals of probabilistic analysis, and how to apply it to analyze biological data. The course also acts to introduce the probabilistic methods which are used in the more sophisticated computational biology applications that are presented in the course Computational Biology II.

Students should fulfil the following prerequisites:

- **Mathematics Background:**
  Although no formal requirements are made, the course assumes that students are comfortable with mathematical methods including analysis, calculus, and linear algebra, at a fairly advanced level.
• Computer Science Background
  Although not necessarily required, familiarity with the basics of programming is helpful.

Computational Biology II - 27247
Mihaela Zavolan
every spring semester

The course is the continuation of the Computational Biology I lecture. Students are introduced to more sophisticated computational biology applications. The following topics are usually covered:
• Evolution: Mathematical models for the evolution of DNA sequences.
• Phylogenies: the evolutionary relationships between sequences.
• Alignment of sequences: finding corresponding positions.
• Functional annotation: Finding genes and regulatory sequences.
• Families of coding sequences: Hidden Markov models of protein domains
• Gene expression networks
• Metabolic networks

Students should fulfil the following prerequisites:
Mathematics background
• Advanced Calculus (multi-dimensional functions, differentiation, integration, series, etc.)
• Linear algebra (matrices, vectors, etcetera).
• Differential equations.
• Discrete mathematics/combinatorics.
• Probability theory/stochastic processes

Computer Science background
• Programming languages
• Data structures
• Algorithms and their complexity

Physics/Chemistry/Molecular Biology background
• Laws of physics: energies, forces
• Chemistry: molecular interactions, reactions and their rates
• Thermodynamics
• Molecular components of biological systems: Cells, DNA, RNA, proteins, etc.

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