27247 Computational Biology II: Sequence Modeling and Analysis (4 KP)

Spring 2025

Mihaela Zavolan (Mihaela.Zavolan@unibas.ch)

Theory - lectures: Thursdays, 11:15-13h, Room 02.094, Biozentrum. *(Not on 13.3, 17.4, 1.5., 29.5.)*

Practical sessions: Monday 13:15-14h, Biozentrum, 02.094 *(No lecture on 10.3., 21.4.)*

Contents:
The course introduces notions of molecular evolution and sequence comparison with practical implications for database searches, phylogeny reconstruction, functional annotation, quantification of gene expression, etc. The following topics are covered:
- Evolution: mathematical models for the evolution of DNA sequences.
- Describing relationships between sequences: sequence alignment.
- Phylogeny: inferring the evolutionary relationships between sequences.
- Functional annotation of genomes: finding genes and regulatory elements.
- Families of protein coding sequences: hidden Markov models of protein domains.

In the practical sessions, basic techniques and tools of bioinformatics are introduced.

Aim:
The aim is to provide the students with the fundamental concepts of computational sequence analysis. Computational models of molecular evolution and algorithms on strings and sequences were among the first applications of quantitative methods in molecular biology and revolutionized the field. They remain central to today's high-throughput approaches.

Format:
The lecture will introduce key topics in bioinformatics and will provide pointers to additional literature.
The lecture slides will be made available for download via ADAM.

Exercises:
The exercises will help deepen the understanding of theoretical concepts via implementation and analysis of simulations and real-life data. The topic of each week will be posted on ADAM, and the students are expected to be able to access these materials to carry out the exercises during the week. The exercise session will be used to resolve outstanding issues via group discussions (laptops needed).

Tutor of the programming exercises:
Mihaela Zavolan and members of the Zavolan group

Evaluation:
The course is evaluated in grades (1-6, half grades). Grading is based on the final exam, which will cover the material in the lectures as well as exercises.

Exam:
The exam takes place on Thursday 22.05.2024, 13:15-15:00h, Biozentrum, 02.094

Course Evaluation:
We value your opinion very much, and we will use your comments to improve this and future lectures. Please feel free to contact the lecturer and the tutors during the lecture time or outside of it. Please also let us know should you not have enough background for one of the topics or if a certain topic should have been covered already in another course.

Course Material: How can I access the lecture downloads and exercises?

The lecture space on ADAM is connected to the Belegliste of this course. If you have signed up for this course, you will have access to the ADAM space as well. (Synchronization of ADAM with the Belegliste overnight).

> ADAM » synchronisierte Mitgliederverwaltung » Philosophisch-Naturwissenschaftliche Fakultät » Departement Biozentrum » Frühjahrsemester 2025 » 27247-01 – Computational Biology II: Sequence Modeling and Analysis

You will then see the files you can download.

Lecture slides and exercises will be made available after the lecture.