Computational Systems Biology, 3.0 credits

Beräkningssystembiologi, 3.0 hp

Third-cycle education course

6FIFMA4

Department of Physics, Chemistry and Biology

Valid from: First half-year 2025

Approved by **Approved**

Registration number

Entry requirements

Entry requirement for studies on third-cycle education courses

- second-cycle degree,
- 240 credits in required courses, including at least 60 second-cycle credits, or
- acquisition of equivalent knowledge in some other manner

Specific information

This course offers a comprehensive introduction to systems biology, combining theoretical knowledge with practical applications, making it ideal for students interested in the intersection of biology, medicine, mathematics, and computational science.

Learning outcomes

By the end of the course the students will be able to:

- Gain knowledge about the fundamental concepts and mathematical frameworks of systems biology.
- Understand the application of computational methods in biomedical research.
- Comprehend the differences between small-scale and large-scale models in systems biology.
- Learn about network science and its applications in disease modules and network medicine.
- Apply computational tools for gene regulatory network (GRN) inference and analysis.
- Utilize mathematical modeling techniques for systems biology in the context of drug discovery and repurposing.
- Perform network enrichment analysis and transfer learning using deep neural networks.
- Analyze and interpret biological data using multi-omics approaches.
- Critically evaluate and discuss recent advancements in systems biology.
- Integrate knowledge from various datasets to address complex biological questions.
- Assess the relevance and applicability of computational methods in solving medical challenges.
- Formulate and present solutions to problems in systems biology using computational techniques.

Contents

This one-week on-site course is held at Valla Campus in Linköping, with preparatory assignments and post-course tasks. Students will delve into the fundamental concepts and mathematical frameworks of systems biology, focusing on its application in biomedical research and medical challenges. The course distinguishes between small-scale and large-scale models through biomedical research examples, emphasizing large-scale systems biology methods. Due to the field's dynamic nature, the course content evolves annually and features a diverse array of instructors. The current topics include:

1. Introduction to Computational Systems Biology and Network Science
2. Introduction to Disease Modules and Network Medicine with Hands-on Session
3. Introduction to linear Gene Regulatory Network (GRN) Inference
4. Introduction to non-linear GRN inference
5. Analysis of GRNs
6. Biological Interpretation of GRNs
7. Mathematical Modeling for Systems Biology of Drugs
8. Computer Exercise – Mechanistic Models
9. Systems Medicine Using Multi-Omics for Drug Repurposing
10. Introduction to Disease Network Modules
11. Transfer Learning Using Deep Neural Networks for Systems Biology
12. Network Enrichment Analysis
13. Dissemination of a Recent Systems Biology Article

Educational methods

Lectures, laboration

Examination

Active presence and presentation of a systems biology article
Active participation and submission of lab and practical assignments during the course

Grading

Two-grade scale

Course literature

"Network Medicine: Complex Systems in Human Disease and Therapeutics" by Joseph Loscalzo, Albert-László Barabási, and Edwin K. Silverman, Harvard University Press, 2017.
Handouts, Articles, and Videos
Updated annually, the following article materials were used in previous years in addition to instructuive vidoes:

1\. Morselli Gysi D, do Valle Í, Zitnik M, Ameli A, Gan X, Varol O, Ghiassian SD, Patten JJ, Davey RA, Loscalzo J, Barabási AL. "Network medicine framework for identifying drug-repurposing opportunities for COVID-19." *Proc Natl Acad Sci U S A*. 2021 May 11;118(19):e2025581118. doi: 10.1073/pnas.2025581118. PMID: 33906951.
2. Menche J, Sharma A, Kitsak M, Ghiassian SD, Vidal M, Loscalzo J, Barabási AL. "Disease networks: Uncovering disease-disease relationships through the incomplete interactome." *Science*. 2015 Feb 20;347(6224):1257601. doi: 10.1126/science.1257601. PMID: 25700523.
3. Gawel DR, Serra-Musach J, Lilja S, Aagesen J, Arenas A, Asking B, Bengnér M, Björkander J, Biggs S, Ernerudh J, Hjortswang H, Karlsson JE, Köpsen M, Lee EJ, Lentini A, Li X, Magnusson M, Martínez-Enguita D, Matussek A, Nestor CE, Schäfer S, Seifert O, Sonmez C, Stjernman H, Tjärnberg A, Wu S, Åkesson K, Shalek AK, Stenmarker M, Zhang H, Gustafsson M, Benson M. "A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases." *Genome Med*. 2019 Jul 30;11(1):47. doi: 10.1186/s13073-019-0657-3. Erratum in: *Genome Med*. 2020 Apr 28;12(1):37. PMID: 31358043; PMCID: PMC6664760.

General information

The course is planned and carried out according to what is stated in this syllabus. Course evaluation, analysis and suggestions for improvement should be fed back to the Research and PhD studies Committee (FUN) by the course coordinator.