CB2320 Artificial Intelligence in Precision Medicine 7.5 credits

Artificiell intelligens i precisionsmedicin

This is a translation of the Swedish, legally binding, course syllabus.

Establishment

The official course syllabus is valid from the autumn semester 2026 as decided by the Faculty Board decision PA-2025-0010. Date of decision: 2025-10-01.

Grading scale

A, B, C, D, E, FX, F

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

Completed bachelor's degree project 15 credits, 20 credits in cell biology, biochemistry, microbiology and genetic engineering/molecular biology, 15 credits in mathematics, numerical analysis and computer technology, and courses in programming equivalent to at least 5 credits.

Intended learning outcomes

After completing the course, the student should be able to:

- explain the core concepts of precision medicine and its relevance to modern healthcare,
- explain the importance of different types of systems biology data in relation to disease biology,
- analyze and interpret multi-omics and patient data using quality control, visualization and integrative methods,
- integrate multi-omics datasets to identify biological patterns and disease mechanisms,
- apply machine learning and modeling methods to build predictive models for cancer subtypes, biomarker identification and prediction of clinical outcomes,
- reflect on limitations and ethical considerations when working with human-based data in precision medicine.

To achieve a higher grade, the student should also be able to:

- evaluate AI-based tools and multi-omics approaches in personalized medicine
- design a small data-driven study for a biomedical question.
- communicate results from data analyses clearly and effectively in both written and oral form.
- demonstrate insight into how computational models can support decision-making in clinical practice and translational research.

Course contents

The course covers the fundamentals and applications of artificial intelligence in precision medicine, with a particular emphasis on data-driven and systems-level understanding of human diseases. Students will gain knowledge of key concepts in multi-omics data analysis, including genomics, transcriptomics, proteomics, epigenomics, metabolomics and metagenomics, and how these can be integrated to provide insight into disease mechanisms and patient-specific responses. Furthermore, genome-scale metabolic models and methods such as Flux Balance Analysis (FBA) are used to investigate metabolic function in health and disease, including cancer, liver diseases and neurodegenerative diseases.

The course includes lectures and workshops covering:

- RNA-seq, copy number analysis,
- Metabolic modeling
- Machine learning methods for data integration, prediction and identification of biomarkers.
- AI-driven modeling methods, including dimensionality reduction, feature selection and predictive modeling (e.g. Cox models and survival analysis), in relation to real-world medical challenges.

The course also includes critical perspectives on the use of clinical and patient-derived data, with regard to data quality, bias, and interpretation. During the course, students are also expected to write a short reflective essay.

Examination

- TEN1 - Written exam, 5.0 credits, grading scale: A, B, C, D, E, FX, F
- UPP1 - Assignment, 1.0 credits, grading scale: P, F
- DEL1 - Participation, 1.5 credits, grading scale: P, F

Based on recommendation from KTH's coordinator for disabilities, the examiner will decide how to adapt an examination for students with documented disability. The examiner may apply another examination format when re-examining individual students. If the course is discontinued, students may request to be examined during the following two academic years.

Ethical approach

- All members of a group are responsible for the group's work.
- In any assessment, every student shall honestly disclose any help received and sources used.
- In an oral assessment, every student shall be able to present and answer questions about the entire assignment and solution.