CB2040 Applied gene technology and large-scale data analysis 7.5 credits

Tillämpad genteknologi och storskalig dataanalys

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

If the course is discontinued, students may request to be examined during the following two academic years

Establishment

Course syllabus for CB2040 valid from Autumn 2022

Grading scale

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

Education cycle

Second cycle

Main field of study

Molecular Life Science

Specific prerequisites

A bachelor's degree, corresponding to at least 180 ECTS. Courses corresponding to at least 20 ECTS in life science subjects and 10 ECTS in mathematics (or related).

Language of instruction

The language of instruction is specified in the course offering information in the course catalogue.

Intended learning outcomes

On completion of the course, the students should be able to:

- Describe, illustrate and apply different techniques in the fields of genomics and transcriptomics
- Describe, illustrate and apply different techniques used for high-throughput molecular biology studies
- Report orally and in writing within the subject
- Review and give constructive feedback on the reports within the subject
- Explain the theory of state-of-the-art tools/algorithms for processing data from high-throughput molecular biology experiments
- Choose and use appropriate methods and tools for processing data from high-throughput molecular biology experiments

Course contents

The course aims to give detailed insight into the techniques and trends in the fields of genomics and transcriptomics, DNA-assisted proteomics and high throughput data analysis in genomics and transcriptomics. The focus of the course will thus be on describing, applying and relating state-of-the-art technologies and high throughput data analysis. This will build up the necessary foundations for further understanding of association studies, forensics, population genetics, diagnostics, medicine and drug development.

The course will describe conventional strategies for whole genome sequencing, high throughput methods for typing of genetic variations, advanced techniques and platforms for DNA sequencing including whole genome sequencing, RNA-seq, and single cell and spatially resolved transcript profiling.

The course also consists of a series of lectures, and computer-based laboratory exercises, aimed at understanding and analyzing data from genome sequencing, RNA-seq, single cell RNA-seq and spatial transcriptomics.

The course further includes an ethics seminar where the students are allowed to critically study and discuss a number of applications of gene technology in society and in research.

In addition, the students are involved in a literature project, which will be performed in groups. Each group presents scientific articles and will oppose other groups' articles. This project aims to teach critical reading, interpretation and comparison of the most advanced techniques and platforms in the field of high-throughput molecular biology. The project requires teamwork and planning, as well as participation in the groups' common work. Presence when the project is presented is compulsory.

Examination

- LAB1 - Computer assignment, 2.5 credits, grading scale: P, F
- PRO1 - Literature seminar, 1.0 credits, grading scale: P, F
- TEN1 - Written exam, 4.0 credits, grading scale: A, B, C, D, E, FX, 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.

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.