



BB2255 Applied Gene Technology 7.5 credits

Tillämpad genteknologi

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 BB2255 valid from Autumn 2019

Grading scale

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

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

Language of instruction

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

Intended learning outcomes

Following completion and passing the course you should be able to:

- Describe, illustrate and relate different techniques in the fields of genomics and transcriptomics
- Critically evaluate, select and apply the most appropriate technique(s) in different biological and medical studies.
- Discuss and suggest strategies to tackle and solve challenging problems in various research studies.
- Construct and create biologically relevant studies by employing one or more of the discussed tools.
- Explain the theory of state-of-the-art tools/algorithms for processing data from high-throughput molecular biology experiments in genomics and transcriptomics
- Choose and use appropriate methods and tools for processing data from high-throughput molecular biology experiments in genomics and transcriptomics.

Course contents

The course will focus on describing, applying and relating state of the art technologies and high throughput data analysis.

Disposition

The course includes a short introduction to conventional strategies for whole genome sequencing followed by description of different high throughput methods for typing of genetic variations, advanced techniques and platforms for DNA sequencing including whole genome sequencing, RNA-seq, single cell and single molecule transcript and protein (DNA-assisted) profiling.

The course also consists of a series of lectures and computer-based laboratory exercises including genome assembly, mapping of reads to reference genome, analysis of RNA-seq and ChIP-seq data.

In addition, the course involves a literature workshop of selected articles, which will be performed in groups. Each group presents one article 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 fields of genome sequencing, massively parallel genotyping and single cell profiling. The project requires teamwork and planning, and participation in planning and execution of plans as well as presence on the workshop days is compulsory.

Course literature

Distributed handouts and articles

Examination

- PRO1 - Literature Seminar, 1.0 credits, grading scale: P, F
- PRO2 - Computer-based Laboratory exercises, 2.5 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.