



# BB2490 Analysis of Data from High-throughput Molecular Biology Experiments 7.5 credits

Analys av data från storskaliga molekylärbiologiska experiment

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 BB2490 valid from Spring 2011

## Grading scale

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

## Education cycle

Second cycle

## Main field of study

Biotechnology

## Specific prerequisites

### **Admission requirements for independent students:**

A total of 20 university credits (hp) in biochemistry, microbiology and gene technology/molecular biology. 30 university credits (hp) chemistry, as well as 20 university credits (hp) in mathematics and computer science as well as bioinformatics 3,5 university credits (hp) and

statistics 3,5 university credits (hp) or corresponding. Documented proficiency in English corresponding to English B.

### **Admission requirements for programme students at KTH:**

## **Language of instruction**

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

## **Intended learning outcomes**

This is an advanced course in bioinformatics. After passing the course, the student should:

- be familiar with widely used high-throughput experimental techniques employed to investigate the DNA, RNA, and protein contents of a cell, tissue, or organism.
- be able to explain the theory behind advanced algorithms for processing data from high-throughput molecular biology experiments.
- know how to process DNA sequencing data to gain information about (i) genomic DNA sequence and its variation, (ii) chromatin structure and protein-DNA interaction, (iii) transcription of mRNA and ncRNA.
- know how to process data from proteomics assays, **e.g.** from mass spectrometry, in order to (i) identify peptides and proteins, (ii) identify post-translational protein modifications, (iii) quantify protein levels.
- be able to describe parametric and non-parametric statistical methods relevant for high-throughput molecular biology data.

## **Course contents**

This is an advanced course in bioinformatics. The course contains the fundamentals of bioinformatics analysis of large-scale data sets from genomics and proteomics experiments (in particular, DNA sequencing and mass spectrometry). The course is primarily aimed at students at the Biotechnology Master of Science in Engineering Degree program and the Medical Biotechnology Masters' program. The course consists of lectures and computer-based laboratory exercises.

## **Course literature**

Scientific articles and web resources as assigned during the course. Handouts from the lectures.

This list might be subject to change. Any changes will be announced on the course homepage at least four weeks prior to course start.

## **Examination**

- LAB1 - Laboratory work, 2.5 credits, grading scale: P, F
- TEN1 - Examination, 5.0 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.

- LAB1 – Laboratory work, 2.5 credits, grade scale: P, F
- TEN1 – Written examination, 5.0 credits, grade scale: A, B, C, D, E, FX, F

## Other requirements for final grade

Examination (TEN1; 5.0 credits, grade scale A-F), Laboratory course with written reports (LAB1; 2.5 credits, grade scale Pass/Fail)

## 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.