BB2441 Bioinformatics 7.5 credits

Bioinformatik

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 BB2441 valid from Autumn 2017

Grading scale

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

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

For degree programme students at KTH is required:

At least 150 credits from school year 1, 2 and 3 of which at least 100 credits from school year 1 and 2 as well as bachelor's thesis must be completed. The 150 credits should include completed courses equivalent to at least 20 credits in mathematics, numerical methods, data, of which at least 5 credits are constituted by numerical methods and data as well as at least 15 credits in total in biotechnology, biochemistry and/or molecular biology

For independent students is required:

In total 15 credits (credits) in biotechnology, biochemistry and/or molecular biology. In total 20 credits (credits) in mathematics, numerical methods and programming of which 5 credits (credits) are constituted by numerical methods and data as well as documented knowledge in English equivalent English B.

Language of instruction

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

Intended learning outcomes

After passing the course the student should be able to:

- account for the importance of bioinformatics in modern life science
- account for applications and limitations of bio-informatic methods
- explain basic bio-informatic methods
- use relevant bio-informatic tools to solve bio-informatic issues
- justify the choice of bio-informatic tools
- interpret the results of bio-informatic analyses
- use programming scripts to carry out basic bio-informatic operations
- use basic commands in Unix/Linux or the equivalent

Course contents

Bio-informatic theory and practice: Pairwise sequence alignment of protein and DNA/RNA-sequences, multiple sequence alignment, significance of alignment results, properties of protein- and DNA/RNA-sequences including sequence conservation, homology, phylogeny, gene expression and differential gene expression, clustering of vectors, introduction to public databases with relevance for the subject as well as extraction of relevant data from the same. Use of both command line operations for data analysis and file management (in Unix/Linux or the equivalent operating system) and available web-based tools for data analysis (e g Galaxy).

Programming: read-in from file, basic operations on imported data such as conditional execution, loops, and regular expression as well as printout of results to file.

Course literature

Scientific articles, web resources and lecture slides that are distributed during the course. Possible prescribed books are granted on the web page of the course no later than four weeks before start of the course.

Examination

- LAB1 - Computer exercises, 2.5 credits, grading scale: P, F
- TEN1 - Written exam, 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.

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.