Faculty of Science

BINP26, Bioinformatics: DNA sequencing informatics I, 7.5 credits

Bioinformatik: DNA-sekvenseringsinformatik I, 7,5 högskolepoäng

Second Cycle / Avancerad nivå

Details of approval

The syllabus was approved by Study programmes board, Faculty of Science on 2014-03-17 to be valid from 2014-03-17, autumn semester 2014.

General Information

The course is a compulsory second-cycle course for a degree of Master of Science in Bioinformatics. The course is also offered as a single subject course. The language of instruction is English.

Language of instruction: English

Main field of studies	*Depth of study relative to the degree requirements*
Bioinformatics	A1F, Second cycle, has second-cycle course/s as entry requirements

Learning outcomes

The general aim of the course is that the students should obtain basic skills within the bioinformatic field which is increasingly requested within academia and industry.

Knowledge and understanding
On completion of the course the student shall be able to:

- demonstrate basic bioinformatic skills within genome, transcriptome, and amplicon sequencing

Competence and skills
On completion of the course the student shall be able to:

- master programming with respect to sequence analysis
- master Linux-based operating systems including command shells

Judgement and approach
On completion of the course the student shall be able to:

- critically evaluate results from bioinformatic analyses

Course content

Sequencing by means of new methods, such as next generation sequencing, generates large data sets. The course focuses on the application of bioinformatic methods and technologies to analyse these data. The course includes assembly of genome, transcriptome, and amplicon data, and a first analysis of the results in the form of gene prediction (for genomes), expression analysis (for transcriptomes) and abundance calculation and taxon classification (for amplicons). Genes and transcripts are annotated at a basic level.

The students will carry out several command shell exercises and programming assignments in Perl. A part of the course deals with an individual project assignment that is solved by means of programming where the student can concentrate on one or several topics mentioned above.

Course design

The teaching is mainly carried out as hands on exercises, where the students work with assignments using computers. Each subject starts with a lecture about the current area of interest. In the course, a one week project is included, where the student works independently with a bioinformatic assignment. The work is presented in the form of a written project report and an oral presentation.

Assessment

Examination consists of compulsory exercises, a written project report, and a written examination.

For students who have not passed the regular examination, an additional examination in close connection to this is offered.

Subcourses that are part of this course can be found in an appendix at the end of this document.

Grades

Marking scale: Fail, Pass, Pass with distinction.
To pass the entire course, approved compulsory exercises, approved examination, and approved project are required.

The final grade is decided through a weighing of the results of the examination, the implementation of the project, and shown understanding of and knowledge on the exercises.

Entry requirements

For admission to the course, English 6/B and knowledge corresponding to BINP11 Bioinformatics and Sequence Analysis 7.5 credits, BINP13 Programming in Perl 7.5 credits, and BINP15 Bioinformatics: Data Processing and Analysis 15 credits, are required.

Further information

The course may not be included in a degree together with BINP14 Large Scale Analysis of Entire Genomes 7.5 credits.

Subcourses in BINP26, Bioinformatics: DNA sequencing informatics I

Applies from V14

1401   DNA sequencing informatics, 7,5 hp
       Grading scale: Fail, Pass, Pass with distinction