



LUND
UNIVERSITY

Faculty of Science

BINP29, Bioinformatics: DNA Sequencing Informatics II, 7.5 credits

Bioinformatik: DNA-sekvenseringsinformatik II, 7,5 högskolepoäng
Second Cycle / Avancerad nivå

Details of approval

The syllabus is an old version, approved by Study programmes board, Faculty of Science on 2017-06-30 and was valid from 2017-06-30, spring semester 2018.

General Information

The course is a compulsory course for a degree of Master of Science (120 credits) in Bioinformatics.

Main field of studies

Bioinformatics

Depth of study relative to the degree requirements

A1F, Second cycle, has second-cycle course/s as entry requirements

Learning outcomes

The general aim of the course is that the students should acquire advanced skills in the bioinformatics field connected to biological questions.

Knowledge and understanding

On completion of the course the student shall be able to:

- in depth account for genome-, transcriptome-, and amplicon sequencing from a bioinformatics perspective
- describe large-scale bioinformatics analyses, including classification of genetic variants, phylogenetic analysis, and advanced sequence annotation

Competence and skills

On completion of the course the student shall be able to:

- process data from high-throughput DNA-sequencing
- use algorithms and programmes based on biological understanding
- write own programmes for sequence analysis
- build simple databases and visualise the results on internet
- carry out large-scale bioinformatics analyses

Judgement and approach

On completion of the course the student shall be able to:

- critically review and evaluate bioinformatics databases and programmes, as well as large-scale bioinformatics analyses

Course content

After assembling of data, generated by new sequencing methods such as "next generation sequencing", the results must be linked to the underlying biological questions. It implies that the subsequent analysis will require different bioinformatics methods. The course gives example of a large number of bioinformatics applications to answer different issues e.g. classification of genetic variants ("variant calling"), phylogenetic analysis, and advanced sequence annotation. Emphasis is on large-scale analyses.

The student also learns how to combine data from different analyses and performs several programming assignments in Python.

The course includes an individual project assignment that is solved by means of programming. The student hereby gets the opportunity to specialise in one or more of the above-mentioned areas.

Course design

The teaching is mainly based on teacher-supervised compulsory exercises where the students work with assignments using computers. Each subject starts with a lecture about the current area of interest. The course includes a one week compulsory project work, where the student works with a bioinformatics assignment independently. The work is presented in the form of a written project report and an oral presentation.

Assessment

Examination takes place in the form of a written examination as well as compulsory parts. For students who have not passed the regular examination, an additional examination in close connection to this is offered.

In consultation with the Disability Support Services, the examination may deviate from the regular form of examination in order to provide a permanently disabled student with a form of examination equal to that of a student without a disability. After having consulted the university's section for educational support, the examiner can make a decision about an alternative examination format for such student.

The examiner, in consultation with Disability Support Services, may deviate from the regular form of examination in order to provide a permanently disabled student with a form of examination equivalent to that of a student without a disability.

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 joining of the results of the examination (40%), the execution of the project (20%) as well as shown understanding and knowledge on the exercises (40%).

Entry requirements

For admission to the course, knowledge corresponding to BINP11 Bioinformatics and Sequence Analysis 7.5 credits, BINP16 Programming in Python 7.5 credits, BIOS13 Modelling of Biological Systems 7.5 credits, BIOS14 Processing and Analysis of Biological Data 7.5 credits, as well as BINP28 DNA Sequence Informatics I 7.5 credits, is required. Proficiency in English corresponding to English B/English 6 from Swedish upper secondary school.

Further information

The course may not be included in a degree together with BINP27 Bioinformatics: DNA Sequencing Informatics II 7.5 credits.

Subcourses in BINP29, Bioinformatics: DNA Sequencing Informatics II

Applies from V18

1701 DNA Sequencing Informatics, 7,5 hp
Grading scale: Fail, Pass, Pass with distinction