



LUND
UNIVERSITY

Faculty of Science

BINP17, Bioinformatics: Bioinformatics and Sequence Analysis, 7.5 credits

Bioinformatik: Bioinformatik och sekvensanalys, 7,5 högskolepoäng
Second Cycle / Avancerad nivå

Details of approval

The syllabus was approved by Study programmes board, Faculty of Science on 2023-06-08 to be valid from 2023-06-08, autumn semester 2024.

General Information

The course is a compulsory second-cycle course for a degree of Master in Bioinformatics and for a degree of master in Applied Computational Science with specialization in Biology. The course is an elective second-cycle course for a degree of Master in Biology or Molecular Biology.

Language of instruction: English

Main field of studies

Depth of study relative to the degree requirements

Biology

A1N, Second cycle, has only first-cycle course/s as entry requirements

Bioinformatics

A1N, Second cycle, has only first-cycle course/s as entry requirements

Molecular Biology

A1N, Second cycle, has only first-cycle course/s as entry requirements

Applied Computational Science with specialization in Biology

A1N, Second cycle, has only first-cycle course/s as entry requirements

Learning outcomes

The primary aim of the course is that the students shall acquire deeper understanding of, and skills in, basic concepts and tools for comparative sequence analysis, including various types of primary and secondary sequence databases.

Knowledge and understanding

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

- describe the extent and potential of the biological sequence information accumulated in public databases from molecular biology and genomic studies
- explain basic concepts and algorithms used in sequence-based projects
- describe common bioinformatics methods and resources, including sequence databases, pairwise and multiple sequence alignment, sequence database searches, amino acid substitution matrices, secondary structure, RNA and polypeptide prediction, and models for protein classification
- describe modern sequencing technologies and their areas of use
- describe similarities and differences between the genomes from different organisms and be able to tailor the bioinformatics analyses accordingly

Competence and skills

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

- solve biological problems with bioinformatics tools
- work reproducibly and know how to use version control systems
- use various biological databases, programs and other bioinformatics tools to translate the data into knowledge relevant for molecular studies of DNA, RNA and proteins as well as the cellular processes they are part of
- examine different genomes to identify homologues and reconstruct phylogenetic trees
- present the results from bioinformatic analyses both orally and in writing

Judgement and approach

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

- critically evaluate results from bioinformatic analyses
- assess his/her own bioinformatic knowledge and take responsibility for acquiring the skills required to solve simple bioinformatic tasks

Course content

The course covers:

- sequence databases and database searches
- pairwise and multiple sequence alignment
- protein structure bioinformatics
- the algorithms behind the bioinformatics methods, for example dynamic programming, neural networks and hidden Markov models
- phylogenetic reconstruction
- genomics of prokaryotes and eukaryotes
- reproducibility

Course design

The teaching consists of lectures, computer exercises, seminars, group exercises and project work. Some of these components include written assignments.

Participation in computer exercises, seminars, group exercises and project work and associated elements, is compulsory.

Assessment

The assessment is based on the written examination at the end of the course, written assignments during the course and through compulsory components. For students who do not pass the written examination during the course, an additional examination in close connection to this is offered.

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 written examination, approved written assignments and approved exercises, are required.

For a grade of Pass on the whole course, the student must have passed the written examination, the written assignments and compulsory components. The final grade is determined by the written examination.

The grading scale for Written examination is Fail, Pass and Pass with distinction, while the grading scale for Exercises and Assignments is Fail and Pass.

Entry requirements

For admission to the course, the student must have knowledge corresponding to the entry requirements for the Master's program in Bioinformatics, or a bachelor's degree 120 credits including at least 60 credits biology or molecular biology. English 6.

Further information

The course may not be included in a degree together with BINP11 Bioinformatics: Bioinformatics and Sequence Analysis, 7,5 credits.

The course is given by the Department of Biology, Lund University.

Subcourses in BINP17, Bioinformatics: Bioinformatics and Sequence Analysis

Applies from H24

- 2401 Exercises and Assignments, 3,5 hp
Grading scale: Fail, Pass
- 2402 Written examination, 4,0 hp
Grading scale: Fail, Pass, Pass with distinction