CORE FACILITIES

SC00037   Bioinformatics 1, 2 credits

Bioinformatik 1, 2 högskolepoäng

Third-cycle level / Forskarnivå

Confirmation

This syllabus was confirmed by the --decisionmakingAuthority-- on --date--, and is valid from --semester--.

Responsible Department

Core Facilities, Sahlgrenska Academy

Entry requirements

The course is open for PhD students accepted by a Swedish or international university, in need to process and manage biological data.

In order to apply for the course, you should have:

- A background in genetics, cell biology, biomedicine, biochemistry, bioinformatics or similar.

Learning outcomes

After completing the course, the student is expected to be able to:

Knowledge and understanding

- Understand the usefulness of computer skills when analyzing genomics data.
- Be familiar with the most common databases and bioinformatics software and their functions.
- Give an overview of the various bioinformatic tools used in sequence analysis.
- Compare groups with different phenotypes in terms of protein expression.
- Identify significant differences and suggest how these differences could affect biological functions.

Competence and skills

- Search information in different databases.

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- Utilize relevant theory knowledge in sequence analysis in your own research project.
- Perform statistical analyzes for differences in protein expression between groups.

Judgement and approach

- Understand the purpose of the techniques introduced in the course and be able to choose appropriate methods to apply to their own research.
- Evaluate and interpret the significance of your own and others' scientific results.

Course content

The course includes a combination of lectures and practical sessions and covers:

- Use of molecular biological databases available from NCBI, UCSC and ENSEMBL.
- Work on web-based platforms for data-intensive biomedical research.
- Sequence analysis methods in theory and practice, to understand the function, structure and evolution of sequence data.
- Analysis of protein expression, in order to identify differences between different groups.
- Downstream analysis such as pathway analysis, clustering and gene ontology to analyze how changes in protein expression can affect biological processes in the cell.

Types of instruction

The course includes a combination of lectures, practical sessions and home assignments

Language of instruction
The course is given in English.

Grades

The grade Pass (G) or Fail (U) is given in this course.

To receive a passing grade, the student must complete all practical exercises with approved results.

Types of assessment

Assessment will be done through the practical sessions; these are design to test the understanding of the different applications, so completion of all of them is mandatory for a passing grade. Active participation during group sessions and attendance for at least 80% is also mandatory.

Student has the right to change examiner after having failed twice on the same examination, unless special reasons speak against it. (HF 6 Chapter 22 §). Such a request is made to the institution and must be in writing.

Course evaluation

The course evaluation will be done through a written questionnaire, available at the virtual learning environment, where students are asked to describe their opinions on the various stages

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of the course for future development.

The results of and possible changes to the course will be shared with students who participated in the course and students who are starting the course next term.

Other information

Computer access with administration rights as well as internet access is required since all communication concerning the course and relevant documents, such as lectures, exercises and literature, will be posted at the virtual learning environment.

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