



## CORE FACILITIES

### SC00038 Bioinformatics II, 2 credits

Bioinformatik II, 2 högskolepoäng

*Third-cycle level / Forskarnivå*

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### Confirmation

This syllabus was confirmed by the Council for PhD Education at Sahlgrenska Academy on 2020-10-22, and is valid from Spring semester 2021.

#### *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.
- You must have passed Bioinformatics 1

### Learning outcomes

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

#### *Knowledge and understanding*

- Knowledge of the importance of evaluating and filtering sequence data for quality.
- Understand how DNA sequence from exome can be used to eg find mutations that cause disease.
- Learn how RNA data can be used to understand more about how processes in the cell are affected by different conditions.
- Understand the difference in information that can be obtained with "total RNA" and "single cell RNA".

### ***Competence and skills***

- Evaluate quality of sequencing data.
- Analyze DNA from exome sequencing and identify genetic variants.
- Compare gene expression based on RNA sequencing data, both for so-called total RNA and single cell RNA data.

### ***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 programs to analyze the quality of DNA and RNA sequence data.
- Mapping DNA and RNA sequence data against a reference genome.
- Identify genetic variants in relation to a reference.
- Compare gene expression for groups of different phenotype using RNA sequence data.
- Analyze difference in gene expression, between different cell types using single cell data.
- Clustering and genontology to analyze how changes in RNA 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 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 (CANVAS).