



## DEPARTMENT OF BIOLOGICAL AND ENVIRONMENTAL SCIENCES

### Target capture for Illumina sequencing, 2 credits

Target capture for Illumina sequencing, 2 högskolepoäng

*Third-cycle level / Forskarnivå*

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### Confirmation

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

#### *Responsible Department*

Department of Biological and Environmental Sciences, Faculty of Science

### Entry requirements

Admitted to third cycle education, basic understanding of command-line interactions.

### Learning outcomes

- Probe design from transcriptomic data or DNA sequences (theory)
- Laboratory procedure (theory)
- Data cleaning and processing (practical)
- De novo and reference-based assembly techniques (practical)
- Allele phasing, SNP extraction (practical)
- Phylogenetic application of target capture data (practical)

#### *Knowledge and understanding*

You will learn the complete process from designing a Next generation sequencing (NGS) target capture project, the most essential steps in the lab, and the bioinformatic processing of the produced data. The course is aimed to equip students with the necessary knowledge to design and carry out their own target capture project, and make sensible and informed decisions along the way.

#### *Competence and skills*

During this course you will learn hands-on bioinformatic tools that you will need for processing your target capture data. You will learn individual tools as well as more generalized bioinformatic pipeline solutions.

### *Judgement and approach*

The large volume of available approaches, lab techniques, sequencing platforms, and bioinformatic tools, requires researchers to possess the full background knowledge covered in this course, to properly plan and carry out a successful target capture project. After this course you will be aware of the critical junctions within such a project and will be equipped with the background to choose the most suitable approach for your project.

## **Course content**

The Target capture for Illumina sequencing workshop will cover state-of-the-art methodology for generating DNA sequence data from multiple loci and individuals for phylogenomics and population genomics analyses. It will cover all steps from the design of RNA probes, to library preparation, and will have a strong focus on data processing. The course will provide comprehensive understanding of the process from start to end, including possible pitfalls, optimisation, and demonstration of the use of software for different assembly, mapping, and phasing steps.

## **Types of instruction**

The course will consist of lectures covering the theoretical aspects of target capture. There will be a focus on hands-on processing of target capture data, during which all course teachers will be present and available for help, questions, and discussions.

### *Language of instruction*

The course is given in English.

## **Grades**

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

The grading scale comprises Fail (U), and Pass (G)

## **Types of assessment**

You will be assessed based on your capability of solving a bioinformatic exercise involving NGS data, similar to exercises covered during the course.

## **Course evaluation**

The course evaluation is carried out together with the PhD students at the end of the course, and is followed by an individual, anonymous survey. The results and possible changes in the course will be shared with the students who participated in the evaluation and to those who are

beginning the course.