



Bioinformatics methods for next generation sequencing analysis

Course code:	MOL8008
Time:	September 19-23 2016,
Place:	Norwegian University of Science and Technology (NTNU), Trondheim, Norway
Lecturers:	Morten Beck Rye, Einar Ryeng ++
Credits:	7.5 ECTS
Registration:	by 19 th August, at norbis.no

Course description

The course will introduce bioinformatic approaches, tools and pipelines for computational analyses of Next Generation Sequencing (NGS) data. Focus will be on analysis methods for coding and non-coding RNA from RNA-seq, and transcription factors and epigenetic markers from ChIP-Seq. The course will cover strategies, methods and workflows used for analyses of such data, including mapping to reference genomes, feature extraction, and statistical analysis. In addition, the biological interpretation of output from such analyses will be presented as case studies from scientific journals.

Learning outcome

After completing the course the student should be able to:

1. Create and use an analysis pipeline for topics introduced
2. Understand the bioinformatics approaches used for different tasks in NGS
3. Have an overview of the type of biological questions that are typically assessed using NGS
4. Assist in the design and implementation of an experiment using NGS at their own facility

Learning methods and activities

There will be a one week intensive period of lecturing, followed by a period of self-study and project work. The students will then meet again for presentation of their project work. The exam will be on a pass/fail basis based on the evaluation of their project work.

Prerequisites

Masters degree in relevant programmes. Medical Doctors degree. Or medical students at The Student Research Programme. Candidates with other or lower degree will be assessed individually.

Recommended previous knowledge

Attending students should be familiar with basic high-level programming of scripting languages like Python, R and Matlab. Some basic knowledge in applied bioinformatics is recommended.

Learning outcome and competence

To acquire the tools and abilities to conduct genetic association analyses, including data quality control, analyses, interpretation of results, and post-processing/presentation of results

Compulsory assignments

- Presentation
- Attendance in lectures

Specific conditions

Exam registration requires that class registration is approved in the same semester, or that compulsory activities are approved in a previous semester.

Note:

NORBIS will cover travel- and accommodation expenses for PhD students affiliated to our school.