High throughput sequencing of non-model organisms

ECTS Credits: 5
Level of course: PhD level
Type of course: Elective
PhD in Aquatic Biosciences
Duration: Ten days summer course 27 May - 5 June, 2015
Study start: 27 May, 2015
Year of study: 2015
Study place: Bodø
Faculty responsible: Faculty of Biosciences and Aquaculture
Language of instruction: English
Course responsible person: Truls Moum
E-mail address: tmo@uin.no

Costs: Tuition fee 2 500 NOK. Students not affiliated with UiN need to arrange for lodging (contact Truls Moum for options). Students will have the option to analyze own samples during the course, at the expense of some of the materials used (contact Truls Moum for further information). Other course materials and sundry expenses will be covered.

Course evaluation:

Course contents:

- Introduction to next-generation sequencing
- Practical module and bioinformatics: Prepare and run fragment library on the Ion Torrent PGM, mapping and query of PGM data
- Basic computational resources and skills needed for HTS
- Sampling representative genomic sequence data from non-model species; Reduced Representation Libraries (RRL) and Restriction site Associated DNA (RAD) sequencing; enriching specific genomic targets for resequencing
- RNA-Seq, transcriptomics of non-model species, non-coding RNAs
- miRNAs and small RNAs of non-model species
- Advances in *de novo* genome assembly
- Population genomics of non-model species
- Participants' presentations of own projects

Learning outcomes:

On successful completion of the course the student should have the following learning outcomes

Knowledge
The student should:
- have a general understanding of the power and limitations of high-throughput sequencing technologies
- understand the specific strengths and weaknesses of alternative high-throughput sequencing technologies
- understand the principles of *de novo* genome and transcriptome assembly
- understand how to assess transcript prevalence from RNA-seq data

Skills
The student should:
- be able to prepare a genomic library and perform a sequencing run at the PGM platform
- be able to make use of basic computational resources
- know how to transfer large data sets between computers

- be able to execute scripts and run extended analyses
- be able to map short-read sequence data to sequenced genomes and query the mapping for variation

General competence
The student should:
- be able to address biological questions in non-model species using short sequence reads
- be able to choose the most suitable sequencing technologies and analytical tools to be used to address the problem at hand
- be able to convey essential topics, exchange experiences, and keep updated within the field of high-throughput sequencing

Especially recommended elective courses:

Offered as a free-standing course:

The course is offered to PhD students at UiN and PhD students unaffiliated with UiN.

Prerequisites:

All PhD students at Faculty of Biosciences and Aquaculture, UiN, and PhD students unaffiliated with UiN are eligible. An application is required by 30 April 2015. We can accommodate a maximum of 10 students.

Recommended previous knowledge:

Basic computer skills and some knowledge of molecular biology and genomics.

Mode of delivery:

Face-to-face teaching.

Learning activities and teaching methods:

Lectures, lab exercises, individual presentations, and feedback.

Assessment methods and criteria:

Individual oral presentation and written assignment based on a given study that applies high throughput sequencing. The candidate is required to demonstrate a clear understanding of, and discuss, the methods, principles and limitations of the relevant study assigned by the course responsible. Pass/not pass.

Work placement:

Campus UiN.

Recommended or required reading:

Updated literature list to be handed out after admission to the course