DEPARTMENT OF MARINE SCIENCES

UNIVERSITY OF GOTHENBURG

NMAR302   An introduction to bioinformatic tools for population genomic data analysis, 2.5 credits

Introduktion till bioinformatiska verktyg för populationsgenomisk dataanalys , 2,5 högskolepoäng

Third-cycle level / Forskarnivå

Confirmation

This syllabus was confirmed by the Department of Marine Sciences on 2020-05-05, and is valid from Autumn semester 2020.

Responsible Department
Department of Marine Sciences, Faculty of Science

Entry requirements

Admitted to third cycle education

Learning outcomes

See subheadings below.

Knowledge and understanding

a. Demonstrate advanced knowledge of experimental strategies, applications and bioinformatic tools for population genomics.

b. Demonstrate advanced knowledge of the potential of genomics approaches to answer ecosystem-wide questions, in particular for biodiversity monitoring.

Competence and skills

a. Ability to use basic commands in the Unix command line environmen (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

b. Ability to use different software tools to analyse sequence data from restriction-site digested

DNA (data cleaning steps, clustering of reads, mapping to reference genomes, extracting and filtering genotype data.

c. Ability to use population genomics software tools to assemble and a genome/transcriptome, and perform gene alignment/mapping, differential gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests, population structure, and demographic analysis.

Judgement and approach

Formulate one's own research questions, identify data and tools needed to answer these questions and critically evaluate and analyse the results.

Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one's own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of whole genome / exome / restriction site digested (RAD) DNA for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises using a remote server. The course introduces bioinformatics software for analysis of RAD-data, and downstream population genetic analysis of genotype data. The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, alignment/mapping, differential gene expression, functional enrichment tests, SNP genotyping, PCA, population structure analysis, outlier tests, and demographic analysis based on allele frequency spectra (AFS). The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

Types of instruction

Instruction is given through a combination of lectures introducing topics, followed by hands-on data analysis exercises. In addition, the final part of the course consists of group work in dataanalysis, followed by oral presentations.

Language of instruction
The course is given in English.

Grades

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

Types of assessment

Assessment will be done through observation of the outcome of the hands-on exercises. In addition, the final day of the course contains an exercise where participants will apply newly learnt skills to a given dataset, followed by group presentations of results.

Course evaluation

The course evaluation will be carried out through an online questionnaire.