Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

Syllabus

BK0002.1 Genome analysis, 15.0 credits

Genomanalys

Version 1 in Slukurs. Corresponds to version 1 in Ladok

Syllabus approved

12 November 2020

The version applies to students admitted from autumn 2021

The version is not a module version

Subjects

Bioinformatic/Biology

Education cycle

Second cycle

Modules

Title	Code	Credits
Laboratory project	0102	5.0
Computer exercises	0103	2.0
Home exam	0104	8.0

Advanced study in the main field

Second cycle, only first-cycle courses as entry requirements (A1N)

Grading scale

5:Pass with Distinction, 4:Pass with Credit, 3:Pass, U:Fail
The requirements for attaining different grades are described in the course assessment criteria which are contained in a supplement to the course syllabus. Current information on assessment criteria shall be made available at the start of the course.

Language

English

Prior knowledge

- 180 credits at first cycle level, of which
- 60 credits biology, animal science, equine science, veterinary nursing or veterinary medicine

or

- 60 credits agricultural sciences (of which at least 30 credits animal and dairy science/zoology)

and

- English 6

Objectives

The course intends to provide advanced knowledge of methods for studies of eukaryotic genomes, including their organization and evolution. There is a focus on animal genomics, but methodological and theoretical aspects of the course are applicable on many different organisms.

On completion of the course, the student should be able to:

- in detail describe structure, diversity and evolution of eukaryotic genomes and genes,
- in detail describe various types of genetic variation,
- in detail explain state of the art and large-scale methods to analyze genetic variation (eg. whole genome sequencing), and gene expression analysis (eg. RNA-seq),
- apply and critically process basic molecular phylogenetic / -genomic and evolutionary analysis,
- in detail describe the different types of RNA in the transcriptome and their function,
- describe principles for transcriptional regulation,
- describe and plan different approaches for functional analysis of genes and genomes,
- summarize genetic recombination and its applications within genome analysis,
- summarize and evaluate the principles of whole genome mapping and comparative genomics to identify genes and loci underlying mendelian and quantitative inherited diseases as well as important phenotypic traits,
- explain epigenetic and epigenomic markers and methods for the analysis of these,
- explain the concept of genome editing and transgenic animals,
- compile data and apply basic statistics relevant to genome analysis,

- use and evaluate molecular genetic laboratory methods and basic bioinformatics methods.

Content

The course is based on lectures, exercises, discussions and laboratory sessions. The contents build largely on animal genome research. Both laboratory and theoretical teaching is for the most part directly applicable also within eg. human or plant genetics. The course is based on current state-of-the-art methodology and research.

Computer exercises and group discussions will cover:
- molecular evolution and phylogenetics/-genomics,
- genetic variation, sequence analysis and primer design,
- gene mapping and genomewide association analysis,
- QTL analysis,
- whole genome sequencing,
- epigenetics/-genomics,
- copy-number variation analysis

The aim of the computer exercises is to give the students useful tools for basic genetic and genomic analyses. Therefore the computer exercises use free and open source software that the student can download to their own laptop. Apart from in the written and the oral examination, compulsory components occur within eg. exercises, group assignments and laboratory sessions.

In the course the following general skills are trained: oral and written communication, problem solving and critical thinking.

Formats and requirements for examination

Passed written and oral examination. Passed participation in compulsory course modules.

- If the student fails a test, the examiner may give the student a supplementary assignment, provided this is possible and there is reason to do so.
- If the student has been granted special educational support because of a disability, the examiner has the right to offer the student an adapted test, or provide an alternative assessment.
- If changes are made to this course syllabus, or if the course is closed, SLU shall decide on transitional rules for examination of students admitted under this syllabus but who have not yet passed the course.
- For the examination of a degree project (independent project), the examiner may also allow the student to add supplemental information after the deadline.

For more information on this, please refer to the regulations for education at Bachelor's and Master's level.

Additional information

The course presupposes good prior knowledge of basic genetic mechanisms (genome structure and the genetic code, DNA replication, transcription), RNA processing, translation, regulation of gene expression, general genetics and population genetics, corresponding to 7.5 credits.

- The right to take part in teaching and/or supervision only applies to the course date to which the student has been admitted and registered on.
- If there are special reasons, the student may take part in course components that require compulsory attendance at a later date. For more information on this, please refer to the regulations for education at Bachelor's and Master's level.

Responsible department

Department of Animal Breeding and Genetics

Supplementary Information

Finalized by: Programnämnden för utbildning inom veterinärmedicin och husdjur (PN - VH)
Biology Area: Genetics
Replacement course: BI1218, HV0122, HV0164, HV0187