## BIO403    Advanced Bioinformatics, 15 credits

Avancerad bioinformatik, 15 högskolepoäng

*Second Cycle*

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### Confirmation

This course syllabus was confirmed by Faculty of Science on 2012-05-24 and was last revised on 2017-09-21 by Department of Chemistry and Molecular Biology to be valid from 2017-09-22, autumn semester of 2017.

*Field of education:* Science 100%
*Department:* Department of Chemistry and Molecular Biology

### Position in the educational system

This is a course in biology at an advanced level that is designed to provide advanced knowledge in Bioinformatics. The course is included in the master's program in Genomics and Systems Biology or as a part of a Master's degree in Molecular Biology or Biology. The course is also offered as a separate course.

| *Main field of studies* | *Specialization* |
|---|---|
| Biology | A1N, Second cycle, has only first-cycle course/s as entry requirements |
| Molecular Biology | A1N, Second cycle, has only first-cycle course/s as entry requirements |

### Entry requirements

Passed courses in Cell Biology, BIO900,15 hec, Molecular Genetics, BIO905, 15 hec, Biological Form and Function, BIO910, 15 hec,  Ecology and Evolution, BIO915, 15 hec, and Biodiversity and Systematics, BIO920, 15 hec, and completion of Chemistry, 30 hec or equivalent courses.

English proficiency is required to the level of English 6/English Course B from Swedish Upper Secondary School, or be certified by an international recognized test, for example TOEFL, IELTS. In additon a passed advanced course in Biology is required,

Bioinformatics and Functional Genomics (e.g. BIO210) is recommended or an equivalent course.

**Learning outcomes**

After completeing the course students will be able to:

*Knowledge and understanding*
- Evaluate the results from different types of sequence-based analyses such as relations of homology based on primary sequence, domain comparisons, profile- or secundary structure analyses.
- Study changes in gene expression via sequencing of RNA/cDNA.
- Create hypotheses concerning gene function from different types of sequence analyses for parts and/or the full protein or RNA.
- Have an understanding for how to interpret different types of sequencing data from metagenomic projects.

*Competence and skills*
- Show an ability to independantly seek, read, understand and critically evaluate scientific literature and research information.
- Show an ability to present, explain and discuss contemporary topics, research results and questions about sequence-based information.
- Show an ability to independantly and creatively identify and formulate questions, and to plan and with adequate methods perform advanced tasks within limited time-frames.
- Visualize data using standard tools and present data in the usual scientific report formats.
- Identify gene structures using prediction of exon-intron boundaries in newly sequenced genomes.
- Perform assembly of genomes using state-of-the-art sofrware tools.
- Perform different types of sequence analyses for parts and/or full protein or RNA sequences.

*Judgement and approach*
- Criticially evaluate and judge the quality of scientific literature and research information.
- Have a wider understanding of ethical aspects of how genomics and systems biology influence our society, our health included, and have an ability to discuss these issues from different perspectives.

**Course content**

The course will provide the students with knowledge about methods and algorithms used in anlyses of sequence information regarding DNA, RNA and proteins. An important part is gaining an understanding of the types of sequence information available and the analyses made possible by using standard programs and programming languages.

The course also provides training in assembly of next generation sequencing (NGS) data produced by the latest technology. An important part is comparative genomic analyses, incorporating methods of gene identification och annotation of novel genomes. Understanding protein structure and function is another important part.

The course is divided into lectures, group exercises, seminars and projects performed individually or in small groups, as well as practicals. Projects are performed in collaboration with research groups. Furthermore the course has parts to give a deeper understanding of the  ethical aspects of genome-wide methods.

**Form of teaching**

See above.

Compulsory parts are case studies, individual project works, laborations and problem based group studies.

*Language of instruction:* English

**Assessment**

The student's knowledge is assessed during the course. The course ends with an written exam.

Missed compulsory sessions can be made up during the course if possible but otherwise the next time the course runs.

A student who has failed a test twice has the right to change examiner, if it is possible. A written application should be sent to the Department.

In cases where a course has been discontinued or major changes have been made a student should be guaranteed at least three examination occasions (including the ordinary examination occasion) during a time of at least one year from the last time the course was given.

**Grades**

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The grading scale comprises: Pass with Distinction (VG), Pass (G) and Fail (U).

**Course evaluation**

A written evaluation is done at the end of the course. The results of the evaluation will be communicated to the students and will function as a guide for the development of the course.