Course syllabus

Bioinformatik
Bioinformatics

KBKN10, 7,5 credits, A (Second Cycle)

Valid for: 2023/24
Faculty: Faculty of Engineering, LTH
Decided by: PLED B/K
Date of Decision: 2023-04-18

General Information

Main field: Biotechnology.
Elective for: B4-mb, MBIO1
Language of instruction: The course will be given in English on demand

Aim

The course aims at giving a theoretical knowledge in bioinformatics and its potentials. The aim is also to give practical experience in searching bioinformatics databases and to use bioinformatics software.

Learning outcomes

Knowledge and understanding
For a passing grade the student must

- be able to describe and to value information in the most widespread bioinformatics databases.
- be able to formulate a database search for example with the help of qualifiers and Boolean arguments.
- be able to describe, to formulate and to value results from sequence alignment.
- be able to describe, to explain and to set up hypothesis about protein structures with the help of models and simulations.

Competences and skills
For a passing grade the student must

- be able to choose and to use bioinformatics databases and their search software.
- be able to evaluate results of sequence comparisons or analysis.

- be able to use programs for structure modelling.
- be able to use technical terms both written and spoken form.

Judgement and approach
For a passing grade the student must

- have the basic knowledge to be able to find bioinformatic information and to be able to use the basic bioinformatics tools.

Contents

The course comprises knowledge about bioinformatics databases, as well as software that searches such databases. Additionally, the course comprises basic knowledge about software and algorithms that can predict nucleotide or amino acid sequence's biochemical or molecular biology properties and functions. Conceptions such as FASTA format, BLAST, archival & curated database, accession number, cross reference, data base field, Boolean qualifiers, In silico, alignment, algorithm, cluster, phylogenetic analysis, phenetic & cladistics approaches, bootstrapping, gap penalties, substitution matrices, homology modelling, threading and Ab Initio modelling are explained. An overview about systems biology and synthetic biology are given.

Examples on practical exercises are: database searching (both search using words and searching for sequences matching a known sequence) as well as interpretation of search results, phylogenetic evaluation of the probability that a dentist has infected his patients with HIV, theoretical development of a PCR method that could determine the gender of a human DNA sample, and exercises in protein modelling.

The course includes a poster presentation of a bioinformatics related topic.

Examination details

Grading scale: TH - (U,3,4,5) - (Fail, Three, Four, Five)
Assessment: Problem orientated individually written home exam. Degree is given on the home exam result. Report from computer exercises.

The examiner, in consultation with Disability Support Services, may deviate from the regular form of examination in order to provide a permanently disabled student with a form of examination equivalent to that of a student without a disability.

Admission

Assumed prior knowledge: KBKF01/KBK041 Gene Technology
The number of participants is limited to: No
The course overlaps following course/s: KBK075

Reading list

- Arthur M. Lesk : Introduction to Bioinformatics, 4th ed. Oxford University Press, 2014, ISBN: 9780199651566.
- Compendium: Exercises for Bioinformatics.

Contact and other information

Course coordinator: Forskare Johan Svensson-Bonde, Johan.Bonde@tbiokem.lth.se
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