



COMPUTER SCIENCE AND ENGINEERING

DIT741 Computational methods in bioinformatics, 7.5 credits

Beräkningsmetoder i bioinformatik, 7,5 högskolepoäng

Second Cycle

Confirmation

This course syllabus was confirmed by Department of Computer Science and Engineering on 2014-10-24 and was last revised on 2017-06-16 to be valid from 2017-08-20, autumn semester of 2017.

Field of education: Science 100%

Department: Computer Science and Engineering

Position in the educational system

The course is offered within the framework of several degree programmes. The course is also a single subject course at the University of Gothenburg.

The course can be part of the following programmes: 1) Computer Science, Master's Programme (N2COS), 2) Applied Data Science Master's Programme (N2ADS) and 3) Computer Science, Bachelor's Programme (N1COS)

Main field of studies

Computer Science

Computer Science-Algorithms and Logic

Specialization

A1F, Second cycle, has second-cycle course/s as entry requirements

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Entry requirements

To be eligible for the course the student should have successfully completed 90 hec of studies within the subject Computer Science or equivalent. Furthermore, the student should have successfully completed a course in Programming (DIT011 Object-oriented Software Development, DIT142 Functional programming or DIT950 Programming, Advanced Course or equivalent) and in Discrete Mathematics (MMGD10 Introductory Discrete Mathematics or equivalent). Applicants must prove knowledge of English:

English 6/English B or the equivalent level of an internationally recognized test, for example TOEFL, IELTS.

Learning outcomes

After completion of the course, the student is expected to be able to:

Knowledge and understanding

- describe bioinformatics problems and computational approaches to solving them.

Skills and abilities

- implement computational solutions to problems in bioinformatics.

Judgement and approach

- summarise problems and methods described in research articles
- critically discuss different methods that address the same task
- identify situations where methods can be applied across different application areas

Course content

This course demonstrates how computational methods that have possibly been presented in other computing courses can be applied to solve problems in an application area.

We look at problems related to the analysis of biological sequence data (sequence bioinformatics) and macromolecular structures (structural bioinformatics). Computing scientists need to be able to understand problems that originate in areas that may be unfamiliar to them, and to identify computational methods and approaches that can be used to solve them. Biological concepts needed to understand the problems will be introduced.

This is an advanced level course which uses research articles as the main reference materials. Reading research articles is valuable training for scientists and researchers. These demonstrate how to present ideas and methods, and how to critically evaluate them. Developing skill in reading research articles is useful preparation for future scientific investigations, and one's own scientific writing can improve through reading.

Computational methods and concepts featured in this course include: dynamic programming; heuristic algorithms; graph partitioning; image skeletonisation, smoothing and edge detection; clustering; sub-matrix matching; geometric hashing;

constraint logic programming; Monte Carlo optimisation; simulated annealing; self-avoiding walks.

Biological problems featured in this course include: sequence alignment; domain assignment; structure comparison; comparative modelling; protein folding; fold recognition; finding channels; molecular docking; protein design.

Form of teaching

The teaching of this course will consist of lectures and literature studies.

Language of instruction: English

Assessment

The course is examined by individual programming assignments, written assignments and oral presentations.

A student who has failed two examinations on the same material has the right to request a change of examiner. Such a request must be submitted to the Department in writing and shall be granted unless there are particular reasons not to do so.

In cases where a course has been discontinued or has undergone major changes, students must be guaranteed at least three examination opportunities (including the regular opportunity) based on the previous content of the course for a period of at least one year.

Grades

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

The grade G reflects fulfilment of the learning outcomes demonstrated by satisfactory completion of the assignments and oral presentation. Grade VG, requires a greater level of understanding, insight and reflection.

Course evaluation

The course is evaluated through meetings both during and after the course between teachers and student representatives. Further, an anonymous questionnaire is used to

ensure written information. The outcome of the evaluations serves to improve the course by indicating which parts could be added, improved, changed or removed. The results of and possible changes to the course will be shared with students who participated in the evaluation and students who are starting the course. The results of and possible changes to the course will be shared with students who participated in the evaluation and students who are starting the course.

Additional information

The course is a joint course together with Chalmers.

It is recommended to have taken an introductory course in data structures beforehand.

Familiarity with some basic chemistry concepts (including atoms and molecules, chemical bonding) is useful.