



**LUND**  
UNIVERSITY

Faculty of Science

## **BINP11, Bioinformatics: Bioinformatics and Sequence Analysis, 7.5 credits**

*Bioinformatik: Bioinformatik och sekvensanalys, 7,5 högskolepoäng*  
**Second Cycle / Avancerad nivå**

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### **Details of approval**

The syllabus was approved by Study programmes board, Faculty of Science on 2007-03-01 to be valid from 2007-07-01, autumn semester 2007.

### **General Information**

The course is a compulsory second-cycle course for a degree of Master in Bioinformatics or Biomedicine.

*Language of instruction:* English

*Main field of studies*

Bioinformatics

*Depth of study relative to the degree requirements*

A1N, Second cycle, has only first-cycle course/s as entry requirements

### **Learning outcomes**

On completion of the course the student shall be able to:

- understand the extent and potential of the biological sequence information that has been accumulated in public databases from molecular biological and genomic studies, and the basic concepts and algorithms to use this information
- use different biological databases, programmes and other bioinformatics tools to implement these data into knowledge relevant to molecular studies of DNA, RNA and proteins, and the cellular processes they are part of
- know how biological problems can be solved with bioinformatics tools and how the achieved results can be evaluated critically.

The primary aim of the course is that the students shall acquire deeper understanding of, and skills in, basic concepts and tools for comparative sequence analysis, including various types of primary and secondary sequence databases. Another aim is to facilitate the formation of networks among students from different Master's

programmes for future collaboration on issues that need to be processed using bioinformatics and statistics.

## Course content

The focus of the course is to give an overview of the most common methods used within applied bioinformatics. Areas that will be covered include: sequence databases, pairwise and multiple sequence alignment, searches in sequence databases, amino acid substitution matrices, secondary structure, prediction of RNA and polypeptides, and models for protein classification. The algorithms behind the bioinformatics methods are discussed. For example dynamic programming, neural networks, and hidden Markov models.

## Course design

The teaching consists of lectures, problem-solving and computer exercises with written assignments.

## Assessment

Examination takes place as written and computer-based examination at the end of the course. For students who have not passed the regular examination, an additional examination in close connection to this is offered.

*Subcourses that are part of this course can be found in an appendix at the end of this document.*

## Grades

Marking scale: Fail, Pass, Pass with distinction.

To pass the entire course, approved examination and approved written assignments are required

The final grade is decided through a weighing of the results of the examination and the written assignments.

## Entry requirements

For admission to the course, English 6/English B and entry requirements for the Master's programme in Bioinformatics, or knowledge corresponding to 120 credits in biomedicine or molecular biology, is required.

## Further information

The course may not be included in a degree together with BNF071.

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## Subcourses in BINP11, Bioinformatics: Bioinformatics and Sequence Analysis

Applies from H07

0701 Bioinformatics and Sequence Analysis, 7,5 hp  
Grading scale: Fail, Pass, Pass with distinction