UNIVERSITY OF SKÖVDE

TRANSLATION FROM SWEDISH

COURSE SYLLABUS

Bioinformatics Analysis with R A1N

7.5 credits

Course code: BI731A
Version number: 15
Valid from: 1 January 2027
Ratified by: Curriculum Committee for Bioscience
Date of ratification: 28 May 2026

1. General information about the course

The course is provided by the University of Skövde and is named Bioinformatics Analysis with R A1N (Bioinformatisk analys med R A1N). It comprises 7.5 credits and is a second-cycle course. The level of progression is A1N.

The course is a part of the main field of study in Bioinformatics. It can also be a part of the main field of study in Systems Biology. The disciplinary domain of the course is Natural Sciences.

2. Entry requirements

The course has the following entry requirements: a total of at least 90 passed credits in one or some of the subjects of Biology, Medicine or Computer Science. Of these 90 credits, at least 15 credits must be on the level of progression G2F (or the equivalent).

An additional requirement is proof of skills in English equivalent of studies at upper secondary level in Sweden, known as the Swedish course English 6 or English level 2. This is normally demonstrated by means of an internationally recognized language test, e.g. IELTS or TOEFL or the equivalent.

3. Course content

The course introduces R as a tool for bioinformatics analysis of different types of omics data. The basics of the programming language R is covered with an aim to be able to solve specific questions, by reading and analyzing data, as well as visualize the results. Basic data types, functions and structure in R are described. An incremental way of working with data is emphasized, i.e. data from one type of analysis is used as input for the next step. Sources of error from different experiments and their effect on the data analysis are discussed. The course contains computer labs with excercises in R.

4. Objectives

After completed course the student should be able to:

- in an advanced way use R to read, organize and visualize data,
- in an advanced way describe different types of gene expression data,
- perform appropriate quality controls of gene expression data and interpret the results,
- in depth describe the concept of normalization and practically perform normalization of gene expression data and interpret results,
- independently perform advanced statistical analysis of gene expression data,
- independently perform data mining such as classification and clustering on gene expression data, and
- practically use public databases for downloading gene expression datasets.

5. Examination

The course is graded A (Excellent), B (Very good), C (Good), D (Satisfactory), E (Sufficient) or F (Fail).

A final grade of the course is only issued when all the examination parts have been passed and is determined by a weighted average of the grades for the three examination parts. The average value is rounded to the nearest integer (half rounded up) and translated into a final grade of the course.

The examinations of the course consist of the following modes of assessment:

- **Written assignment**
  4 credits, grades: A/B/C/D/E/F
- **On-campus supervised written examination**
  2 credits, grades: A/B/C/D/E/F
- **Seminar assignment**
  1.5 credits, grades: A/B/C/D/E/F

Students with a permanent disability who have been approved for directed educational support may be offered adapted modes of assessment.

6. Types of instruction and language of instruction

The teaching is comprised of lectures, exercises and laboratory sessions.

The teaching is conducted in English.

7. Course literature and other educational materials

Scientific articles and online materials. They are available on the course site of the learning platform.

8. Student influence

Student influence in the course is ensured by means of course evaluation. The students are informed about the results of the evaluation and potential measures that have been taken or are planned, based on the course evaluation.

9. Additional information

The content of the course corresponds completely or partially with the following course(s) and cannot be included in the required credits of a degree qualification:

- BI719A - Gene Expression Analysis Using R, Advanced level 7.5 credits
- SY740A - Gene Expression Analysis and Derivation of Networks using R A1F 7.5 credits

Further information about the course, as well as national and local governing documents for higher education, is available on the website of the University of Skövde.