

## Bioinformatics (I002610)

**Course size** *(nominal values; actual values may depend on programme)*

**Credits 5.0**

**Study time 150 h**

**Course offerings in academic year 2025-2026**

A (semester 1)

English

Gent

**Lecturers in academic year 2025-2026**

Van Criekinge, Wim

LA26

lecturer-in-charge

**Offered in the following programmes in 2025-2026**

[Master of Science in Bioscience Engineering: Cell and Gene Biotechnology](#)

**crdts**

5

**offering**

A

[Exchange Programme in Bioscience Engineering: Cell and Gene Biotechnology \(master's level\)](#)

5

A

**Teaching languages**

English

**Keywords**

Algorithms for sequence analysis, gene structure and function prediction, phylogenetics, hidden Markov models, biological databases

**Position of the course**

This course on bio-informatics focuses on the algorithmic and computational aspects of biological datamanagement and -exploitation. It complements the students mathematical and computational background and lays the foundation for the bio-informatician.

**Contents**

The contents of bio-informatics courses at foreign universities is extremely variable. Considering the background of the bio-engineer student, the following elements are essential for this course:

1. Databases: types, querying, design, internet-aspects, existing biological databases
2. Computational molecular biology:
  - 2.1. String and sequence algorithms: similarity of sequences, (multiple) alignments, sequence assembly
  - 2.2. Tree algorithms: phylogenetic trees, parsimony, consensus trees
  - 2.3. Graph algorithms: interval graphs, physical mapping
3. Probability and statistics: hidden Markov models, clustering
4. Biological applications: gene discovery, structure prediction, function prediction

These elements will be combined in a consistent manner, with a balance between the mathematical, computational aspects and their biological relevance.

The exercises will familiarize the student with the algorithms with the help of pen and paper and by own implementation (e.g. in Perl). The exercises will also show how to use and evaluate some of the many available bio-informatics tools on the internet.

**Initial competences**

Mathematics and computer science courses on Bachelor level.

**Final competences**

- 1 Clear understanding of what Bioinformatics is
- 2 A working knowledge of biological databases
- 3 Knowledge in algorithms used in sequence manipulations (alignment, assembly and pattern recognition)
- 4 Understanding of protein modeling and phylogeny
- 5 Understanding in how bioinformatics can be applied in white, green, blue and red biotechnology

**Conditions for credit contract**

Access to this course unit via a credit contract is determined after successful competences assessment

**Conditions for exam contract**

This course unit cannot be taken via an exam contract

**Teaching methods**

Seminar, Lecture, Independent work

**Extra information on the teaching methods**

Theory: oral lectures

Exercises: computer and paper exercises

**Study material**

None

**References**

On-line forum (<http://www.bioinformatics.be>)

**Course content-related study coaching**

On-line forum (<http://www.bioinformatics.be>)

**Assessment moments**

end-of-term assessment

**Examination methods in case of periodic assessment during the first examination period**

Oral assessment

**Examination methods in case of periodic assessment during the second examination period**

Oral assessment

**Examination methods in case of permanent assessment****Possibilities of retake in case of permanent assessment**

not applicable

**Extra information on the examination methods**

Theory: period aligned evaluation (50%)

Exercises: period aligned evaluation (50%)

Theory: oral (closed book) examination

Exercises: written/computer (open book) examination

**Calculation of the examination mark**

Theory: period aligned evaluation (50%)

Exercises: period aligned evaluation (50%)

Students who eschew period aligned and/or non-period aligned evaluations for this course unit may be failed by the examiner.