

## Computational Challenges in Bioinformatics (C003711)

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

**Credits 6.0**                      **Study time 180 h**

**Course offerings and teaching methods in academic year 2024-2025**

A (semester 2)	English	Gent	independent work seminar lecture
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**Lecturers in academic year 2024-2025**

Dawyndt, Peter	WE02	lecturer-in-charge
Fostier, Jan	TW05	co-lecturer

**Offered in the following programmes in 2024-2025**

	<b>crdts</b>	<b>offering</b>
<a href="#">Master of Science in Teaching in Science and Technology(main subject Mathematics)</a>	6	A
<a href="#">Bridging Programme Master of Science in Bioinformatics(main subject Engineering)</a>	6	A
<a href="#">Master of Science in Bioinformatics(main subject Engineering)</a>	6	A
<a href="#">Master of Science in Computer Science</a>	6	A
<a href="#">Master of Science in Computer Science Engineering</a>	6	A
<a href="#">Master of Science in Mathematics</a>	6	A
<a href="#">Exchange Programme in Bioinformatics (master's level)</a>	6	A
<a href="#">Exchange Programme in Computer Science (master's level)</a>	6	A
<a href="#">Exchange Programme in Mathematics (master's level)</a>	6	A

**Teaching languages**

English

**Keywords**

Performance, compute intensive applications, big data, hardware acceleration, data structures and algorithms, bioinformatics

**Position of the course**

The objective of this course is to focus on existing computational challenges in the field of bioinformatics and the techniques that are applied in scientific literature to deal with those challenges. Both compute intensive and data intensive ('big data') problems are considered. Even though the main focus of the course is on the software aspects, certain hardware acceleration techniques are covered. The goal of this course is aimed at students that are interested in software development in the field of bioinformatics.

**Contents**

- Sequence alignment
  - Needleman-Wunsch and Smith-Waterman algorithm, advanced variants
  - Multiple sequence alignment
  - Implementation aspects and hardware acceleration
- Gene prediction
  - Markov models
  - Viterbi algorithm
- String matching and applications
  - Data structures and algorithms for string matching: suffix trees, suffix arrays, Burrows-Wheeler transformation, FM index
  - Applications to read mapping

- Graph-based algorithms and applications
  - De Bruijn graphs
  - Application to genome assembly

### Initial competences

Advanced programming skills in Java, Python or C/C++, advanced knowledge of data structures and algorithms

### Final competences

- 1 To understand the commonly used data structures and algorithms that are commonly used in bioinformatics applications.
- 2 To understand the most important computationally intensive problems in bioinformatics and the existing solutions (or heuristics) to solve them.
- 3 Being able to estimate the runtime and memory footprint based on the computational complexity of the underlying algorithm and the size of the problem.
- 4 Being able to design advanced algorithms and software implementations based on standard data structures and algorithms.
- 5 To take into account the computational feasibility when critically assessing several algorithmic approaches.
- 6 To spend enough time on the design and the computational complexity evaluation prior to the actual implementation of software.
- 7 To understand the tradeoffs between performance, memory footprint and accuracy.

### 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

### Study material

Type: Slides

Name: Course slides

Indicative price: Free or paid by faculty

Optional: no

Language : English

### References

- "Biological Sequence Analysis", Richard Durbin, Cambridge University Press, 1998
- "Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology", Dan Gusfield, 2001
- "Bioinformatics Algorithms: Sequence Analysis, Genome Rearrangements, and Phylogenetic Reconstruction", Enno Ohlebusch, Oldenbusch-Verlag, 2013.

### Course content-related study coaching

- By e-mail or after appointment
- Additional information through Ufora

### Assessment moments

end-of-term and continuous assessment

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

Oral assessment, Written assessment

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

Oral assessment, Written assessment

### Examination methods in case of permanent assessment

Skills test, Assignment

### Possibilities of retake in case of permanent assessment

examination during the second examination period is not possible

**Extra information on the examination methods**

- Periodic evaluation: open-book examination (exercises), oral examination with written preparation
- Permanent evaluation: graded homework assignments (source code + report)

**Calculation of the examination mark**

For both examination periods, the final mark will be composed as follows: 25% homework assignments, 75% exam. For both examination periods, a minimum score of 50% is required for the examination part. If this condition is not fulfilled, the final mark for this course will be limited to 9/20.