

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

Credits 6.0 Study time 180 h Contact hrs 60.0 h

Course offerings and teaching methods in academic year 2018-2019

A (semester 2)	English	seminar: practical PC room classes	20.0 h
		lecture	30.0 h

Lecturers in academic year 2018-2019

Vandepoele, Klaas	WE09	lecturer-in-charge
Van de Peer, Yves	WE09	co-lecturer

Offered in the following programmes in 2018-2019

	crdts	offering
Brugprogramma Master of Science in Bioinformatics (main subject Engineering)	6	A
Master of Science in Bioinformatics (main subject Bioscience Engineering)	6	A
Master of Science in Bioinformatics (main subject Engineering)	6	A
Master of Science in Bioinformatics (main subject Systems Biology)	6	A
Exchange Programme in Bioinformatics (master's level)	6	A

Teaching languages

English

Keywords

Advanced sequence analysis, structural annotation, comparative genomics

Position of the course

This is an advanced course master of bioinformatics which focuses on sequence data as the main resource to make inferences. The course starts with outlining the principles of modern sequence analysis and subsequently gives an overview of the most important genome analysis methods. In the practical sessions the students will test and apply to tools and analysis pipeline to a dataset. During part of the course students will read a paper in small interdisciplinary groups. They need to understand the goal of the analysis presented in the paper and understand the method developed to solve the stated problem. This will require insights in both the biology and the statistics/mathematics of the tool and members of the same group with different background can assist each other to understand the paper. Students of each group will present their paper to the other members of the course (microteaching).

Contents

1. Structural genomics: annotation
 - a. Gene/ splice site predictions
 - b. Genome browsers
 - c. Genome wide alignment methods
2. Comparative genomics:
 - a. Orthology/paralogy methods for orthology identification:
 - Protein clustering
 - Tree construction en Tree reconciliation
3. Genome evolution
 - a. Detecting duplications, dating duplications
 - b. Modeling duplications
 - c. Local alignments
4. Exercises (students learn to apply basic annotation flows and implement own flows for a small dedicated problem)

Initial competences

identical to those of the Master in Bioinformatics

Final competences

- 1 Overview of the most important computational methods for sequence/genome analysis.
- 2 Recognize analysis techniques underlying bioinformatics tools.
- 3 Being able to independently read and analyse a genomics paper that combines biological results with advanced data-analysis.
- 4 Being able to apply the most important computational methods (understanding their background and understanding why they are being used).
- 5 Critical reading of state of the art literature.
- 6 Understanding bioinformatics as a fastly evolving discipline.
- 7 Functioning as member if a team in a multidisciplinary environment.
- 8 Communication in an interdisciplinary context.

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

Group work, lecture, seminar: practical PC room classes

Extra information on the teaching methods

Students have to read and understand a recent research article, and present its content to colleagues. This implies analyzing, synthesizing skills and the ability to position the content of the article in the broader research context.

Learning materials and price

Minerva/ slides, course notes

References

research articles

Course content-related study coaching

- Practica supervised by assistants.
- Additional information via Minerva.

Evaluation methods

end-of-term evaluation and continuous assessment

Examination methods in case of periodic evaluation during the first examination period

Written examination with open questions

Examination methods in case of periodic evaluation during the second examination period

Written examination, open book examination

Examination methods in case of permanent evaluation

Assignment, peer assessment

Possibilities of retake in case of permanent evaluation

examination during the second examination period is possible in modified form

Extra information on the examination methods

- Periodic evaluation: written examen
- Permanent evaluation: assessment of the microteaching, peer evaluation

Calculation of the examination mark

- 70% periodic evaluation
- 30% niet-periodic evaluation (30% evaluation by peers, 70% by teachers)