

Course Specifications

From the academic year 2017-2018 up to and including the

Comparative Genomics (C002700)

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

Credits	3.0	Study time	80 h	Contact hrs	25.0 h
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Course offerings and teaching methods in academic year 2018-2019

A (semester 2)	English	seminar: practical PC room classes	10.0 h
		lecture	15.0 h

Lecturers in academic year 2018-2019

Vandepoele, Klaas	WE09	lecturer-in-charge
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Offered in the following programmes in 2018-2019

	crdts	offering
Master of Science in Biochemistry and Biotechnology	3	A
Exchange programme in Biochemistry and Biotechnology (master's level)	3	A

Teaching languages

English

Keywords

Genomes, Evolution, Sequence analysis, Homology

Position of the course

This course shows how basic bioinformatics techniques can be applied to solve complex biological questions regarding genome structure, gene regulation and evolution. This course gives an overview of some data resources publicly available for different eukaryotic species and demonstrates the application of different methods (e.g. sequence analysis, phylogenetic tree construction) to analyze the structure and evolution of genomes in more detail.

This course also includes an introduction to comparative gene expression analysis.

This course contributes to the following program competences: Ma.WE.BB.1.2, Ma.WE.BB.1.3, Ma.WE.BB.2.5, Ma.WE.BB.2.6

Contents

- (Genome-wide) Sequence retrieval and resources for comparative genomics
- Homology, orthology & paralogy detection (BLAST, Multiple Sequence Alignments, protein clustering, phylogeny)
- Non-coding sequence evolution (local/global pairwise/multiple alignment tools, Conserved Noncoding Sequences, TFBS identification)
- Genome organization, evolution (colinearity, synteny) and phylogenetic dating of duplication events
- Comparative gene expression analysis
- Case studies

Initial competences

Basic knowledge genetics & molecular biology (genomes, genes, proteins, DNA, RNA, promoter). You successfully followed a course Introduction to Bioinformatics.

Final competences

- 1 Application of basic comparative genomics techniques to retrieve and manipulate genomic sequence data.
- 2 Extracting computational research protocols from scientific publications.
- 3 Developing basic computational pipelines to answer specific biological questions regarding gene/genome structure and evolution.

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

Lecture, seminar: practical PC room classes

Learning materials and price

The slides used during the courses are available in electronic form for the students. In addition, URLs together with relevant scientific publications (review papers) will be provided.

Cost: 0 EUR

References

Course content-related study coaching

In addition to the lectures the student can ask questions or additional information (e-mail or personal appointment).

Evaluation methods

end-of-term evaluation

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

Examination methods in case of permanent evaluation

Possibilities of retake in case of permanent evaluation

not applicable

Extra information on the examination methods

Attendance practical sessions obliged.

Calculation of the examination mark

Written exam, oral discussion. Attendance to the practical sessions obliged.