Microbial Genomics (C002719)

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

Credits 3.0 **Study time** 80 h

Course offerings and teaching methods in academic year 2024-2025

| A (semester 2) | English | Gent | seminar |
| | | | lecture |

Lecturers in academic year 2024-2025

| De Tender, Caroline | WE10 | lecturer-in-charge |

Offered in the following programmes in 2024-2025	**crdts**	**offering**
Master of Science in Teaching in Science and Technology(main subject Biochemistry and Biotechnology)	3	A
Master of Science in Bioinformatics(main subject Systems Biology)	3	A
Master of Science in Biochemistry and Biotechnology	3	A
Exchange programme in Biochemistry and Biotechnology (master's level)	3	A

Teaching languages

English

Keywords

Assembly of genome sequences, gene finding, function annotation, genome statistics, comparative genome analyses, metagenomics

Position of the course

The course is scheduled in the major/minor Microbial Biotechnology and builds on the basis provided by the courses of General Microbiology (2nd bachelor) and General Microbiology: diversity of prokaryotes, fungi and yeasts (3rd bachelor). The objective is to familiarize the students, both in theory and practice, with data from genome sequencing and the subsequent genome annotation and comparative genome analysis of 1 organism versus multiple organisms.
This course contributes to the following program competences: Ma.WE.BB.1.2, Ma. WE.BB.1.3, Ma.WE.BB.2.2, Ma.WE.BB.2.4, Ma.WE.BB.2.6, Ma.WE.BB.2.7, Ma.WE.BB. 2.8, Ma.WE.BB.3.2, Ma.WE.BB.3.3, Ma.WE.BB.3.4, Ma.WE.BB.3.5, Ma.WE.BB.4.1, Ma.WE.BB.4.2, Ma.WE.BB.4.3, Ma.WE.BB.6.1, Ma.WE.BB.6.2

Contents

In recent years, high-throughput sequencing has greatly impacted Life Science research in general and microbiological research in particular. It is now possible to sequence a whole bacterial genome in one day, and new methodologies will again significantly shorten this analysis time. As a result, the bottleneck of sequence-associated research has now been shifted to data analysis. What do you need to do after the sequencing of a whole genome? How do you gather data on the metabolic functions of the sequenced microorganism? And how can you compare this information with other microbial genomes? These are the real questions microbiologists are currently considering in their experimental design and research. The purpose of this course is to equip students with the tools to conduct real-world analysis of bacterial genome sequences, including hands-on experience on sequencing read assembly, genome annotation and comparative genome analysis. In addition, we will see the first principles of metagenome sequencing: studying multiple organisms. We will compare the data analyseis of 1 genome versus multiple genomes.
A specific assignment based on genome data gathered from on-going research

projects at UGent or elsewhere will be given to each group consisting of two to three students. Knowledge from the lectures needs to be put into practice. The results need to be summarized and discussed in a scientific report and a presentation.

Initial competences

Bachelor BB. Basic knowledge microbiology, biochemistry, molecular biology, bioinformatics (biological databases, BLAST, FASTA, sequence alignment, construction phylogenetic trees).

Final competences

1 Understanding of the methodology of whole genome sequencing, assembly, annotation and analysis.
2 Knowledge of relevant research tools and awareness of the associated problems, drawbacks and limitations.
3 The student knows the difference between bacterial genome sequencing and metagenomics.
4 The student can produce a count table when receiving microbial sequencing data.

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

Extra information on the teaching methods

The course comprises a series of lectures on microbial genomics and high-throughput sequencing data analysis, complemented by a group project. The aim is to familiarize students with genome, assembly, annotation and associated data-analysis. The lectures provide the necessary theoretical background. The results of the project will form the basis of a report and presentation to peers.

Study material

Type: Slides

Name: Slides course microbial genomics
Indicative price: Free or paid by faculty
Optional: no
Available on Ufora : Yes
Online Available : Yes

References

Course content-related study coaching

The lectures provide all necessary theory and context for the paper. Short demonstrations are integrated in the lectures. Questions can be addressed during lectures or individually. The lecturer is also available via email or Ufora or after appointment to address individual questions or problems.

Assessment moments

continuous assessment

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

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

Examination methods in case of permanent assessment

Assignment

Possibilities of retake in case of permanent assessment

examination during the second examination period is possible in modified form

Extra information on the examination methods

Mid-term presentation and final scientific paper based on specific assignment.
The student (in groups of two to max. four) will receive a specific assignment at the

start of the course, which will be presented in a written scientific paper and evaluated by the lecturer. The project will be evaluated at least once during the course (mid-term presentation)and once after the course is finished (paper). Progress of individual students over the duration of the course will be monitored and taken into account. Possibility of oral defense of scientific paper when necessary.

Oral examination during the second examination period.

Calculation of the examination mark

Not applicable