GHENT
UNIVERSITY

Course Specifications

Valid in the academic year 2024-2025

Genome Analysis (I002616)

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

Credits 5.0 **Study time 150 h**

Course offerings in academic year 2024-2025

A (semester 2)	English	Gent

Lecturers in academic year 2024-2025

De Meyer, Tim	LA26	lecturer-in-charge
Coussement, Louis	LA26	co-lecturer

Offered in the following programmes in 2024-2025	**crdts**	**offering**
Master of Science in Bioscience Engineering: Cell and Gene Biotechnology	5	A
Exchange Programme in Bioscience Engineering: Cell and Gene Biotechnology (master's level)	5	A

Teaching languages

English

Keywords

Genome analysis, high-throughput data analysis, omics, next-generation sequencing, microarrays, RNA-seq

Position of the course

Many recent methods in molecular biology generate huge amounts of data. This course aims at familiarizing students with these data, how to process and statistically analyze them using state-of-the-art methods, and where/how to find or deposit this type of data. Ethical implications, including scientific integrity and sustainability, are discussed. We'll particularly focus on transcriptomics data for in depth analysis (both in theory and practical sessions), yet we'll also touch upon several other omics techniques, data types and analytical considerations.

Contents

The following methods and concepts will be discussed and illustrated for common omics data, such as microarrays, RNA-seq, ChIP-seq, bisulfite sequencing, single-cell methods, ...

- Omics data repositories and databases, ethical considerations/sustainability
- Multiple hypothesis testing: family-wise error rate / false discovery rate
- Data preprocessing for omics data: alignment (conceptual), background correction, summarization, data normalization, quality control
- Relevant data formats, bv. FASTQ, GTF/GFF, SAM/BAM, ...
- Moderated statistical methods for hypothesis testing
- Gene set analysis / pathway analysis
- Evolution of omics technologies and their (dis)advantages for specific applications
- Capita selecta (may vary from year to year): bulk-seggregant analysis, GWAS, data integration and visualization, genotyping

The course focuses on conceptual insight in concrete problems and solutions and their application rather than the statistical/mathematical/software implementation.

Initial competences

Genetics and molecular biology, solid knowledge of basic data analytical methods (e.g. ANOVA, regression, GLM, PCA)

Final competences

1 able to find relevant omics datasets
2 able to solve common research questions with appropriate data-analytical methods, using the R and Bioconductor software environment
3 have basic insight in several important methods for preprocessing and analysis of omics datasets
4 have insight in different omics technologies and their (dis)advantages, also from an ethical point of view
5 report scientifically on omics data analysis
6 work in a team in a constructive and responsible manner

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, Seminar, Lecture

Study material

Type: Syllabus

Name: Notes practical sessions
Indicative price: Free or paid by faculty
Optional: no
Language : English
Number of Pages : 200
Oldest Usable Edition : 2024
Available on Ufora : Yes
Online Available : No
Available in the Library : No
Available through Student Association : No

Type: Slides

Name: Slides genome analysis
Indicative price: Free or paid by faculty
Optional: no
Language : English
Number of Slides : 500
Available on Ufora : Yes
Online Available : No
Available in the Library : No
Available through Student Association : No

References

Course content-related study coaching

During the practical sessions students are coached by one or more assistants. Q&A sessions are organized to solve practical problems with the assignment. For non-assignment related questions, students may communicate with the lecturer/assistant by E-mail, which may lead to an appointment if required.

Assessment moments

end-of-term and continuous assessment

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

Written assessment open-book

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

Written assessment open-book

Examination methods in case of permanent assessment

Oral assessment, Peer and/or self assessment, Assignment

Possibilities of retake in case of permanent assessment

examination during the second examination period is possible

Extra information on the examination methods

The final examination consists of a written examination (open book). Most of the questions aim to assess the insight of the student in omics data-analysis and how this results in conclusions. The assignment relates to a real life problem and students may work together in groups. The result of the assignment will be reported by means of a written report and a presentation, upon which both results and used methods will be further discussed ("oral examination"). Depending on the group size, peer-evaluation may be used. This may lead to a score modification of at most two points for the assignment, unless a student did clearly insufficiently contribute (should be reported by fellow group members during semester), in which case a more severe penalty is possible.

Calculation of the examination mark

The total mark is a weighted average of:
- Assignment (10/20)
- Open book examination (10/20)