

Omics (I003075)

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

Credits 6.0

Study time 180 h

Course offerings in academic year 2027-2028

A (semester 2)

English

Gent

Lecturers in academic year 2027-2028

De Meyer, Tim

LA26

lecturer-in-charge

Coussement, Louis

LA26

co-lecturer

Van Herreweghen, Florence

LA25

staff member

Offered in the following programmes in 2027-2028

[Master of Science in Bioscience Engineering: Cell and Gene Biotechnology](#)

crdts 6

offering A

[Exchange Programme in Bioscience Engineering: Cell and Gene Biotechnology \(master's level\)](#)

6

A

Teaching languages

English

Keywords

Genome analysis, high-throughput data analysis, omics, next-generation sequencing, microarrays, RNA-seq, amplicon sequencing, shotgun sequencing, quantitative microbial profiling

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. The primary focus will be on transcriptomics data, providing an in-depth analysis through both theoretical and practical sessions. There will also be significant emphasis on 16S rRNA gene amplicon sequencing, covering both its theoretical aspects and practical applications. Additionally, we will touch upon various other omics techniques, exploring different data types and discussing important analytical considerations.

Contents

Part 0: Introduction

- Aims, overview and context of the course, including ethical considerations (sustainability, transparency, privacy) and important databases/resources and data repositories.

Part 1: Microarrays

- Experimental technology and types, with focus on gene expression microarrays. Data preprocessing concepts, covering quality control concepts (including MA-plot), background correction, data summary and normalization. Statistical data analysis by means of moderated tests (limma). Also other widely used microarrays will be discussed, including SNP-arrays and Infinium HumanMethylation microarrays.
- Generic/refresher lecture on p-values, p-value distribution under the null hypothesis, and error control by means of Family-Wise Error Rate (FWER) vs. False Discovery Rate (FDR).

Part 2: Next generation (NGS) and single-molecule sequencing (SMS)

- NGS Technology: brief overview of experimental technologies. Data

preprocessing (RNA-seq and related data): FASTQ file format, alignment methods (e.g. BWA, STAR, pseudo-alignment using KALISTO, relying on Expectation-Maximization) and BAM file format, quality control (including trimming and impact overclustering), and data summary (GTF and alternatives).

- Statistical NGS analysis (for RNA-seq and related data): data distribution, overdispersion (Poisson vs. Negative Binomial), Maximum Likelihood Estimation (MLE)/Generalized Linear Models (GLM), trended moderation methods like DESeq, EdgeR, and limma-voom.
- Gene set analysis: conceptual differences between methods and specific implementations for both microarray and NGS data, such as GSEA, GOSec, and their implementation in limma.
- NGS-based enrichment sequencing (ChIP-seq, Cut&Tag, ATAC-seq) and related methods (Hi-C): brief overview of experimental methods, preprocessing & data analysis techniques, data output formats and manipulation
- SMS: brief overview of experimental technology and state-of-the-art applications
- NGS and SMS based (epi-)genotyping, structural variation detection: experimental methods and data-analytical approaches based on specific data characteristics (including GATK, model-based approaches by means of Empirical Bayes), GWAS
- Single-cell and spatial transcriptomics.

Part 3: Microbial community analysis

- (i) 16S rRNA gene amplicon sequencing: DADA2 pipeline
- (ii) NGS in combination with flow cytometry to perform quantitative microbial profiling (QMP)
- (iii) shotgun metagenomic sequencing (case study).

Initial competences

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

Final competences

- 1 Retrieve relevant omics datasets for a specific research question
- 2 Assess and compare different omics technologies and their (dis)advantages, also from an ethical point of view
- 3 Assess and compare important methods for preprocessing and analysis of omics data
- 4 Solve common omics research questions with the appropriate data-analytical methods using the R and Bioconductor software environment
- 5 Report scientifically on omics data and its analysis

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

Lectures: theory

Seminars: computer exercises

Study material

Type: Syllabus

Name: Notes exercises

Indicative price: Free or paid by faculty

Optional: no

Available on Ufora : Yes

Additional information: All study material can be freely downloaded from Ufora

Type: Slides

Name: Annotated slides

Indicative price: Free or paid by faculty

Optional: no

Available on Ufora : Yes

Additional information: All study material can be freely downloaded from Ufora

Type: Other

Name: Scientific papers

Indicative price: Free or paid by faculty

Optional: no

Available on Ufora : Yes

Additional information: All study material can be freely downloaded from Ufora

References

Course content-related study coaching

During the practical sessions in the PC classes, the students are coached by assistants. Practical questions will be solved by a combination of Q&A sessions, a Ufora FAQ overview and a Ufora discussion board. Remaining issues can be addressed through E-mail with the lecturer/teaching assistant, 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

Written assessment open-book

Possibilities of retake in case of permanent assessment

examination during the second examination period is possible

Extra information on the examination methods

PE: Theory: written assessment, open book exam

NPE: PC practical exam, open book

Calculation of the examination mark

The total mark is a weighted average of:

- Theory: open book examination (weight 14/20)
- Exercises: computer examination (weight 6/20)

When a student obtains less than 8/20 for at least one component, they can no longer pass the course unit as a whole. If the total score does turn out to be a mark of ten or more out of twenty, this is reduced to the highest fail mark (9/20). Students who eschew one or more parts of the assessment can no longer obtain a pass mark for the course unit. Should the final mark be higher than 10/20, it will be reduced to the highest non-tolerable mark (i.e. 7/20).