

BIO-463

**Genomics and bioinformatics**

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Cursus	Sem.	Type
Computational and Quantitative Biology		Opt.
Life Sciences Engineering	MA2, MA4	Obl.
Minor in life sciences engineering	E	Opt.
Statistics	MA2, MA4	Opt.
Systems Engineering minor	E	Opt.

Language of teaching	English
Credits	4
Session	Summer
Semester	Spring
Exam	During the semester
Workload	120h
Weeks	14
<b>Hours</b>	<b>4 weekly</b>
Courses	2 weekly
Exercises	2 weekly
<b>Number of positions</b>	

**Summary**

This course covers various data analysis approaches associated with applications of DNA sequencing technologies, from genome sequencing to quantifying gene evolution, gene expression, transcription factor binding and chromosome conformation.

**Content**

- Genome sequencing and assembly
- Genome annotation, gene prediction
- Hidden Markov Models
- Comparative genomics
- Phylogenetic trees
- Molecular evolution
- Population genetics
- Transcription
- Gene expression profiling
- Gene regulation
- Chromosome conformation

**Learning Prerequisites****Recommended courses**

Molecular biology, genetics, linear algebra, ordinary differential equations, basic statistics, computer programming

**Important concepts to start the course**

DNA and RNA, replication, transcription and translation.

**Learning Outcomes**

By the end of the course, the student must be able to:

- Choose a method or algorithm to analyse different kinds of genomic data
- Design an analysis strategy to interpret complex, heterogenous genomic data

- Assess / Evaluate a publication based on genomic data
- Perform genomic analyses in R

### Transversal skills

- Access and evaluate appropriate sources of information.
- Summarize an article or a technical report.
- Communicate effectively with professionals from other disciplines.
- Use both general and domain specific IT resources and tools

### Teaching methods

2 hours lectures (introducing theoretical concepts) followed by 2 hours practical exercises (to apply the theory and perform hands-on bioinformatic analysis of genomic data).

Most exercises involve computational questions, and the recommended programming language is R.

Lecture notes, slides, exercises and solutions are provided on Moodle.

### Expected student activities

Following the lectures, completing exercises, performing data analyses and implementing the relevant algorithms.

### Assessment methods

The evaluation is based on 2 graded problem classes (each contributing 25% of the final grade), and a mini-project that involves analyzing data from a recent publication (contributing 50% of the final grade).

### Supervision

Office hours	No
Assistants	Yes
Forum	Yes

### Resources

#### Bibliography

- Bioinformatics: sequence and genome analysis, David W. Mount
- Bioinformatics and functional genomics, Jonathan Pevsner
- Biological sequence analysis: probabilistic models of proteins and nucleic acids, Richard Durbin, Sean R. Eddy, Anders Krogh & Graeme Mitchison
- Computational molecular evolution, Ziheng Yang
- Physical Biology of the Cell, Rob Phillips, Jané Kondev, Julie Theriot & Hernan Garcia

#### Ressources en bibliothèque

- [Physical Biology of the Cell, Rob Phillips](#)
- [Bioinformatics: sequence and genome analysis, David W. Mount](#)
- [Computational molecular evolution, Ziheng Yang](#)
- [Biological sequence analysis: probabilistic models of proteins and nucleic acids, Richard Durbin](#)
- [Bioinformatics and functional genomics, Jonathan Pevsner](#)

#### Références suggérées par la bibliothèque

- [Molecular evolution : a statistical approach / Yang](#)

**Moodle Link**

- <https://go.epfl.ch/BIO-463>