

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
Hours	4 weekly
Lecture	2 weekly
Exercises	2 weekly
Number of positions	

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>