INSTITUT NATIONAL DES SCIENCES APPLIQUÉES LYON

DPT BIOSCIENCES
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Bioinformatique

Omics 1: NGS, Applications and Analysis

IDENTIFICATION

CODE : BS-3-S2-EC-COOMIQ1
ECTS : 2.0

HOURS

Lectures :	8.0 h
Seminars :	16.0 h
Laboratory :	0.0 h
Project :	0.0 h
Teacher-student contact :	24.0 h
Personal work :	26.0 h
Total :	50.0 h

ASSESSMENT METHOD

1 final exam

TEACHING AIDS

Learning materials will be available on the Moodle page dedicated to this course.

TEACHING LANGUAGE

French

CONTACT

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AIMS

SKILLS
- Analyzing high throughput sequencing data (quality control, de novo genome assembly, detection of mutations, RNA-seq, ChIP-seq, 16S diversity study)

OBJECTIVES
At the end of this course, students will be able to work on high throughput sequencing data analysis projects.

The learning outcomes of this course module are :
- Know the main DNA sequencing methods
- Know the main types of sequencing projects and the methodology for analyzing the corresponding data.
- Know how to analyze high-throughput sequencing data with Galaxy

CONTENT

Theoretical part:
Introductory course to sequencing methods (Sanger, 454, Illumina, Ion Torrent, Pacbio, Nanopore), various sequencing projects and associated analytical methods (de novo assembly, re-sequencing/mapping, RNA-seq, 16S diversity studies)

Practical part:
Analysis of NGS data in Galaxy: i) Genome Assembly, ii) Detection of mutations, iii) RNA-seq, iv) ChIP-seq, v) 16S Diversity studies

BIBLIOGRAPHY

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PRE-REQUISITE

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