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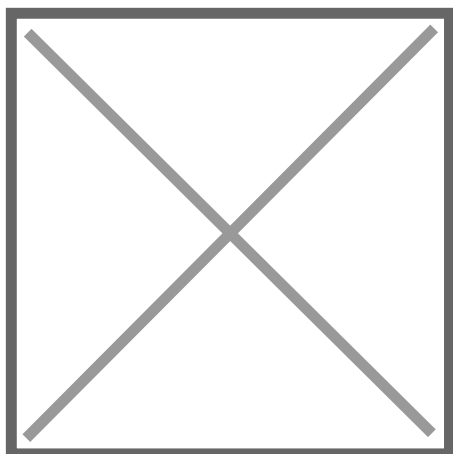
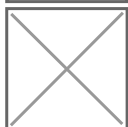
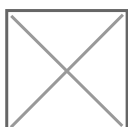
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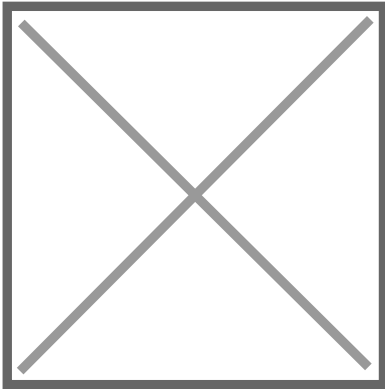
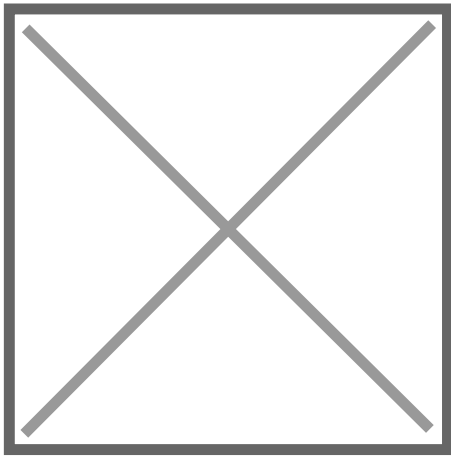
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Add to Compare

M2 Genomics Informatics Mathematics and Artificial Intelligence for Health and Environment (GENIOMHE)





Master's degree

Specialisation Bioinformatics / Computational Biology

Enrolment type

Full-time academic programmes Life-long learning

Language(s) of instruction

English

The GENIOMHE-AI Master's degree trains specialists in research and development in the field of Bioinformatics for **genomics** and **precision medicine**. This program allows students to master **algorithmics**, various **programming** languages ??and techniques, as well as advanced techniques in **data science**, **artificial intelligence**, **statistics**, and databases for analyzing massive data.

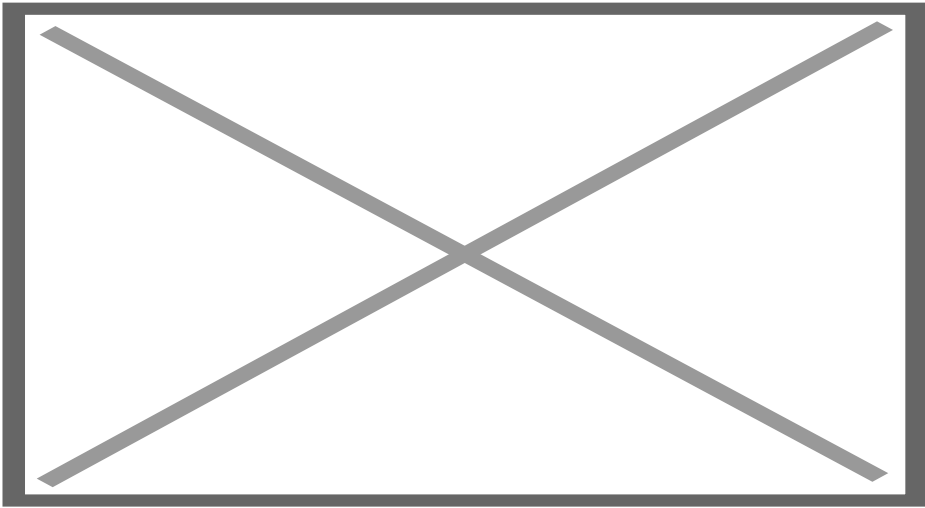
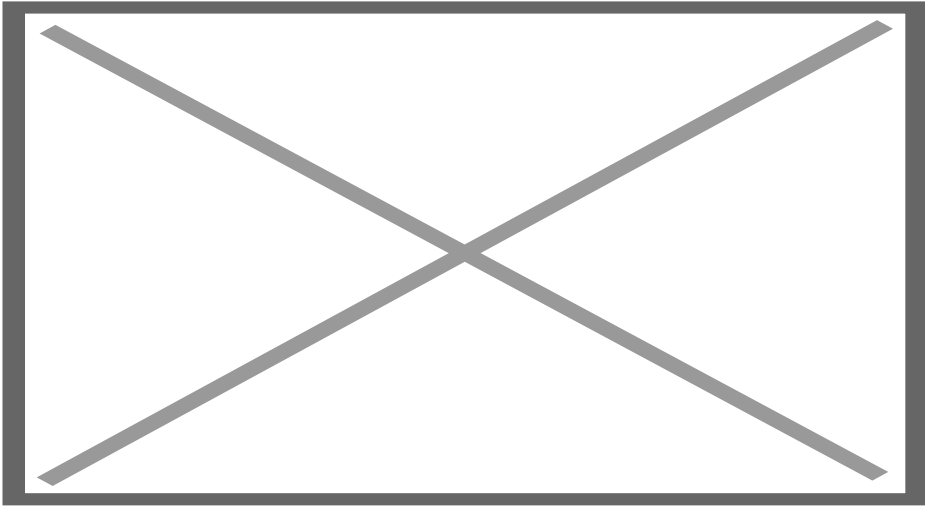
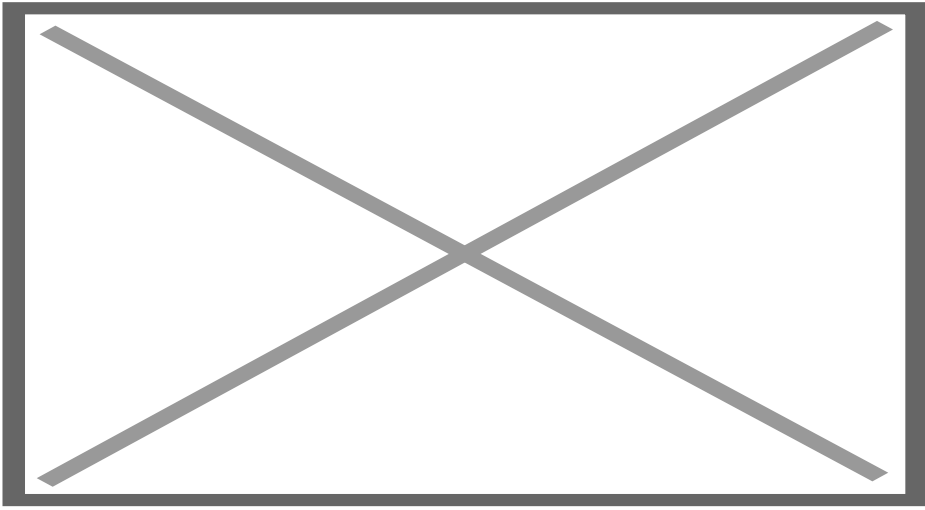
The GENIOMHE-AI Master's degree program consists of a set of teaching units organized into several blocks: Advanced Genomics, Computer Science for Big Data, Data Science and Artificial Intelligence for Precision Medicine, and Computational Systems and Structural Biology. Optional teaching units will also be offered, such as an introduction to entrepreneurship.

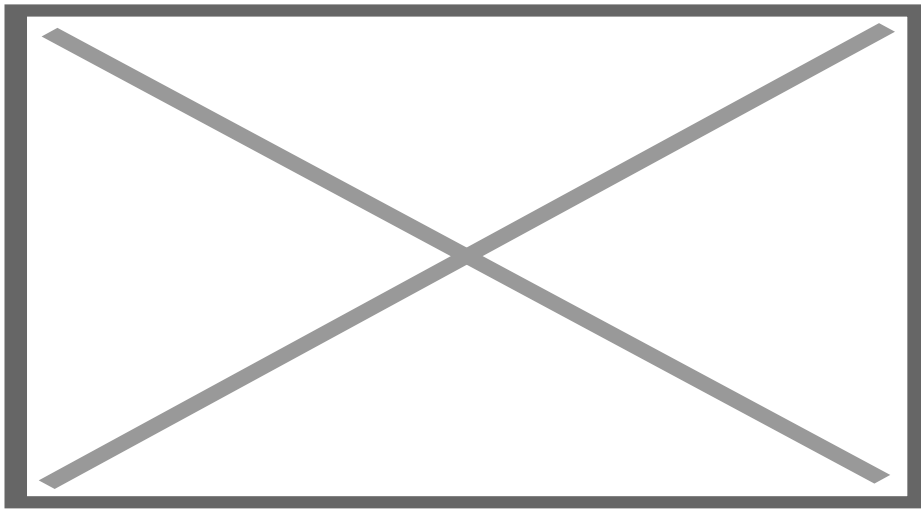
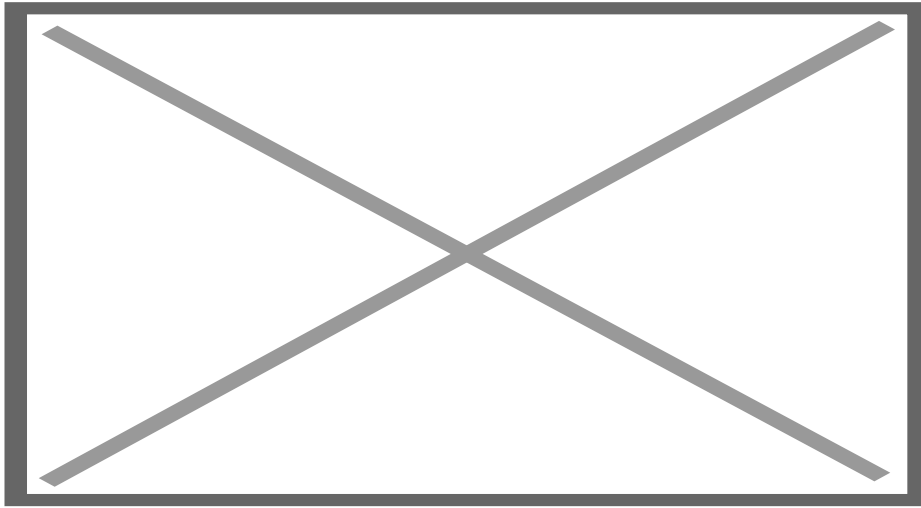
Students will have various projects to carry out, within each of the teaching units and through cross-disciplinary work. They will also have the opportunity to attend keynote lectures.

The second semester of the academic year (starting in January) is devoted to a 5-6 month internship in an academic research laboratory or a company.

[Télécharger la fiche détaillée](#)

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Information

- [Overview](#)
- [Application requirements](#)
- [Schedule](#)

Présentation

Skills

Develop and use advanced techniques in computer science, data science and artificial intelligence for the analysis of massive genomic data, particularly in the context of precision medicine.

Objectives

This master's degree is a multidisciplinary training program that allows students to: understand the complex and diverse challenges of biology in order to meet current research and innovation needs in academic research, the biotechnology industry, the pharmaceutical industry and health; meet the new challenges related to precision medicine made possible by the rapid and massive production of genomic data; meet the challenges of using artificial intelligence in the health fields; master biomedical data analysis and modeling techniques; be autonomous in managing application development projects in various programming languages, and propose innovative IT solutions.

Débouchés

Career prospects

After a Master's + PhD: researcher or lecturer

Data Scientist

Data Manager

Platform manager

Bioinformatics Engineer (Research and Development)

After a Master's degree: Data scientist

After a Master's degree: Artificial intelligence (AI) specialist

Research or Design Engineer

Lecturer (after a PhD)

Data scientist

Consultant

Further Study Opportunities

R&D researcher or data modelling and analysis expert in leading-edge companies or laboratories.

Data Scientist, Data Analyst, Ingénieur·e en Machine Learning dans des secteurs innovants (tech, finance, santé, énergie, etc.) ;

PhD

PhD in Bioinformatics

fields of statistical learning, artificial intelligence and advanced data analysis

Engineering, research and development

Students with a 2nd year Master's degree have the possibility to pursue doctoral research.

PhD

Poursuite en thèse en apprentissage statistique, mathématiques appliquées ou intelligence artificielle ;

PhD thesis

Calendar

Start of programme (indicative date)

07/09/2026

End of programme (indicative date)

31/08/2027

Admission

Capacity

Available Places

25

Target Audience and Entry Requirements

Students who have validated an M1 in bioinformatics (M1 GENIOMHE-AI or other) or a mono-disciplinary master's degree in computer science or biology with proven skills and real motivations for bioinformatics.

Période(s) de candidature

Inception Platform

From 15/01/2026 to 15/07/2026

Supporting documents

Compulsory supporting documents

Motivation letter.

All transcripts of the years / semesters validated since the high school diploma at the date of application.

Certificate of English level.

Selection sheet for continuation in M2 to download on this web page.

Curriculum Vitae.

Detailed description and hourly volume of courses taken since the beginning of the university program.

Additional supporting documents

VAP file (obligatory for all persons requesting a valuation of the assets to enter the diploma).

Supporting documents :

- Residence permit stating the country of residence of the first country
- Or receipt of request stating the country of first asylum
- Or document from the UNHCR granting refugee status
- Or receipt of refugee status request delivered in France
- Or residence permit stating the refugee status delivered in France
- Or document stating subsidiary protection in France or abroad
- Or document stating temporary protection in France or abroad.

Programme

Computational systems and structural biology

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	c
Computational Systems Biology and Network Medicine	2.5	Semestre 1	12	12					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	other
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Computational Systems Biology and Network Medicine

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 12

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

The prerequisites for the course are a solid background in molecular and cellular biology, and a confirmed grasp of computer programming. The students are also assumed to have basic knowledge of discrete mathematics.

Programme/contents

1. Introduction to Systems Biology and Network Medicine

2. Foundations

a. Topological analysis

i. Graphs: definition and fundamental algorithms

ii. Graph measures

iii. Case studies

iv. Random networks study

b. Discrete dynamics

i. Boolean networks

ii. Petri nets

3. Applications to systems biology & tools

a. Introduction

b. Types of biological networks

i. Types and functional roles

ii. Databases

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	class
Structural Bioinformatics and RNA world	2.5	Semestre 1	12	12					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	class
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Structural Bioinformatics and RNA world

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 12

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basics in molecular biology and in functional RNA

Basics in sequence algorithmic and machine learning.

Programme/contents

The course will cover the different bioinformatics approaches existing for RNA prediction

- RNA secondary structure prediction
- RNA complexes structure prediction
- RNA 3D structure prediction

- RNA 3D segmentation

- ncRNA prediction and classification

- Prediction of small ncRNAs (microRNA, piRNA, ...)

- Prediction of lncRNAs

Learning objectives

The goal of the course is to present the bioinformatics methods for the prediction of non-coding RNAs (ncRNAs), their classification and the prediction of their structures (2D and 3D), and the challenges that remain, particularly for identification at large scale.

Special teaching arrangements

A project will be proposed and evaluated, as well as a study of scientific publications.

Type of assessment

Evaluation Continue non Intégrale

Internship

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	distance learning
Internship	30	Semestre 2							
■									

Internship

ECTS : 30

Semester: Semestre 2

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

Internship of 5 to 6 months in an academic research laboratory or in an entreprise.

Type of assessment

Evaluation Terminale

Advanced AI and Data Sciences for Genomics and Precision Medicine

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	distance learning
Advanced Deep Learning	2.5	Semestre 1	12	12					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
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Advanced Deep Learning

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 12

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Python

Programming

Deep learning course of M1 GENIOMHE-AI or equivalent

Programme/contents

4. Programme/Plan/Contenus

- Introduction to deep learning for precision medicine: motivation, applications, and challenges
- Advanced recurrent architectures (Transformers) and large language models (LLMs)
- Advanced computer vision architectures (ViT)
- Generative adversarial networks (GAN)
- Overview of machine learning paradigms, including multi-task, self-supervised, federated, continual, and meta-learning in the context of precision medicine applications.

Learning objectives

This course explores further the recent developments of AI and deep learning.

Students will also have the opportunity to explore advanced model architectures such as transformers and diffusion models, which constitute the foundation of many state-of-the-art systems, including modern conversational agents like ChatGPT and scientific breakthroughs such as AlphaFold. The course will also cover advanced learning paradigms, including multi-task, continual, and meta-learning, and show how these

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Statistics and statistical learning	2.5	Semestre 1	12	12					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
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Statistics and statistical learning

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 12

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basic Knowledge in Probability, Descriptive Statistics, Sampling and Hypothesis Testing, R programming.

Programme/contents

This UE is composed of three parts which revolve around the quantitative analysis of gene expression : 1. A first part on the statistical methods for gene expression data analysis 2. A second part on Bayesian networks 3. A third part on information-based methods for experimental design and statistical learning.

Contenu :

- Microarray and RNA-seq technologies
- gene expression Data : large Data with high fluctuations
- statistical Methods for differential analysis of gene expression Data
- clustering and statistical Methods for coexpressed genes Identification
- statistical Methods for inference of gene regulatory network
- bayesian reasoning : Principles and difficulties
- definition and properties of The bayesian Networks
- exact and approximate inference
- designing and learning a network
- /* JC */
- bayesian classification
- information measures, entropy, application to experimental design
- information-based tree learning algorithms

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Reinforcement Learning	2	Semestre 1	9	9					



Reinforcement Learning

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 9

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

- Knowledge of Python
- Understanding of probability
- Basic notions of deep learning

Programme/contents

Session 1: Introduction to Reinforcement Learning

- What is RL?
 - Differences between RL, supervised learning, and unsupervised learning
 - Applications and use cases
- Basic terminology and notation
- Markov Decision Processes (MDPs)
 - Formal framework of RL
 - States, actions, rewards, and transition dynamics
 - Policy and value functions
- Dynamic programming concepts
- Policy evaluation and improvement
- Policy iteration
- Value iteration

Session 2: Tabular Methods

- Monte Carlo methods
- Monte Carlo prediction and control
- Exploration and initial visit
- Episodic tasks
 - Temporal difference (TD) learning
 - SARSA and Q-learning
- On-policy vs. off-policy learning
- Bootstrapping

Session 3: Function approximation

- Linear approximation
- Gradient descent methods

Project and Conferences

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dissemination
Transversal Project	2	Semestre 1		33					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	discovery learning
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Transversal Project

ECTS : 2

Semester: Semestre 1

Detail

Directed study: 33

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

The course outline for the available data assigned:

- identify the type of data / consider biological questions / choice of the right software to answer biological questions and/or necessary developments (if development is required, criteria for validating the method (quality controls) and estimation of the time needed for development)
- Descriptive statistics of the available data
- Analysis strategies / description of tasks to be performed
- Validation criteria / results / giving biological meaning to the results obtained / discussion (limitations, additional analyses with planned protocols, etc.)
- Reporting (strategies, scripts, available/processed data, results obtained/quality of analysis and reflection)

Learning objectives

An interdisciplinary project which will allow the students to understand the place of digital technologies in the processing and interpretation of generated data to address biological problems.

Special teaching arrangements

Students will be evaluated through reports (Mini preview, logbook), ability to communicate/work together and interact with the tutor, and oral presentation

Skills

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	discovery learning
Conferences	0.5	Semestre 1		9					
■									

Conferences

ECTS : 0.5

Semester: Semestre 1

Detail

Directed study: 9

Language(s) of instruction

Anglais

Remote teaching

non

Learning objectives

This module aims to consolidate the professional project of our students, giving them a broad view by offering conferences series, meetings and debates with professionals and researchers in the areas of bioinformatics and biotechnology.

Type of assessment

Evaluation Continue Intégrale

Advanced Computing for Big Data

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	discovery learning
Data Integration and Big Data	2	Semestre 1	9	9					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
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Data Integration and Big Data

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 9

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Programming language

Algorithmic

Databases

Programme/contents

Tutorial course 1 : Introduction to Big Data and Cloud Computing

Tutorial course 2: Introduction to NoSQL databases and data integration

Tutorial course 3: Introduction to Map Reduce and Spark

Directed work course 1: Docker containerization and MangoDB NoQL Database

Directed work course 2: Hadoop Map Reduce

Directed work course 3: Spark

Learning objectives

Understanding biological processes requires storing, accessing and processing many complex and more and more large scale datasets. These data are usually heterogeneous generated by humans, machines (imaging systems, sequencing systems, etc.) or by programs (simulations tools). In parallel, computer science has made significant progress in developing new methods, models and technologies to storing, integrating and processing big heterogeneous data in the Cloud Computing. It is of the benefit of modern biology to be able to use these concepts and tools to achieve its need in term of integration and processing of large amounts of heterogeneous data, with different formats and semantics, and manipulate them

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
<u>Advanced Programming</u>	2.5	Semestre 1	15	15					

Advanced Programming

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 15

Directed study: 15

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basics in programming

Programme/contents

The first part of the course will provide a solid foundation in fundamental C programming concepts, including data types, control structures, functions, and arrays. It progresses to more advanced topics such as pointers, dynamic memory management, structures, and linked lists, preparing students to design and implement efficient, low-level data structures.

The second part will focus how to design and build a scalable application to launch or use many external components at the same time to be efficient. This design must be flexible to accept, to grow up, with all new breakthrough in Health.

- We will see the Domain Driven Design and the software Hexagonal Architecture to design a scalable application. And all the automatization to build a robust and reactive application.
- Feedback and theory on the application of the agile framework for the construction, management and maintainability of a code developed in team and in the long term.

The third part will provide minimum theoretical foundations for developing algorithms in a context of massively distributed architectures. This will include the different types of parallel architectures (including GPU), the parallel programming models. Then will be shown aspects of concurrent programming and distributed programming, and programming with GPUs. The theory is then put into practice by implementing different parallel and distributed algorithms in C / C ++ using common tools such as POSIX threads, OpenMP and MPI.

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Advanced Algorithmic and Combinatorial Optimization	2.5	Semestre 1	12	12					
■									

Advanced Algorithmic and Combinatorial Optimization

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 12

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basic knowledge in graphs, computational complexity and algorithmics.

Programme/contents

Algorithmic techniques useful when dealing with NP-hard combinatorial optimization problems.

- approximation algorithms (vertex cover problem)
- integer programming
- randomized algorithms
- multicriteria optimization (Pareto front)
- metaheuristics (genetic algorithms, tabu search).

Type of assessment

Evaluation Continue non Intégrale

Advanced genomics

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Advanced Functional Genomics	2.5	Semestre 1	15	7.5					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
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Advanced Functional Genomics

ECTS : 2.5

Semester: Semestre 1

Detail

Lecture: 15

Directed study: 7.5

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

At the end of this course, the students will be able to

- Enumerate and differentiate large-scale sequencing technology driven-approaches, i.e. RNA-seq, ChIP-seq, Cut&tag, Cut&Run, Methyl-seq, WGBS, ATAC-seq, Hi-C

- Specify the distinct steps of the analysis workflows from raw data to pathway analysis (read mapping strategies, transcript assembly, data normalization, isoform-specific or differential gene expression analysis) for both quantitative and qualitative analysis of transcriptomic data

- Understand the limits of bulk RNAseq in regard to Single-cell approach

- Describe the principle of data production and analysis of ChIP-seq from peak calling to data visualization

- Explain the methods of data exploration: common tools of genes &/or samples classification and functional annotation

- Determine which technology to use among a broad spectrum of functional genomics methods to address specific biological questions

- Interpret results of the high-throughput data in a scientifically stringent manner

- Enumerate applications of these sequencing data in health and precision medicine

Learning objectives

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Metagenomics and Multiomics for microbiome studies	2	Semestre 1	9	12					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
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Metagenomics and Multiomics for microbiome studies

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 12

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Microbiology, Molecular biology, genetics, Bioinformatics, Biostatistics.

Programme/contents

Metagenomics, also known as ecogenomics, is founded on the genomic analysis of complex microbial communities directly extracted from diverse environments such as natural and polluted waters, marine ecosystems, and the digestive tract. This approach enables a comprehensive understanding of the composition and dynamics of microbial communities, as well as their interactions with each other and with their environments, without relying on traditional cultivation techniques.

Bioinformaticians will explore the various approaches used in metagenomic sequence analysis, including sequence alignment, assembly, taxonomic identification, phylogenetic reconstruction, and functional gene screening and annotation in environmental samples. By mining metagenomes for gene discovery, researchers can expand our understanding of microbial metabolism and diversity, identify novel enzymes, and investigate their evolutionary relationships. Finally, the industrial and biotechnological applications of metagenomics will also be discussed.

Learning objectives

The objectives of this UE are to provide the students an insight of complex microbial communities in terms of phylogeny and metabolic diversity using bioinformatics and statistical

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	d
Comparative Genomics	2	Semestre 1	9	9					

Comparative Genomics

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 9

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

The prerequisites are general concepts in structural genomics and evolution, and concepts covered in the first year of the Master's program (M1) regarding bioinformatics tools. Unix/Linux concepts and utility filters.

Programme/contents

The course outline:

- Basic evolutionary principles
- Scales of comparison
- Comparison of genomic data and characteristics
- Parameters Ks and Ka

Two main themes will be addressed as examples:

- Evolution of duplicated genes
- Evolution of transposable elements

Directed work:

- Critical analysis of bioinformatics articles and protocols
- Implementation of a bioinformatics protocol for determining duplicated genes in a plant genome
- Examples of studies on transposable elements (distribution analysis, elements in the vicinity of genes...).

Learning objectives

The course addresses the questions posed in comparative genomics and the different scales of study. The objectives are to determine which characteristics of the genomes are being compared and what data enables these comparisons. The

Optional/Opening Units

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class
Data Camp	2	Semestre 1	20		10			

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	practical class	directed study/practical class
■								

Data Camp

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 20

Practical study : 10

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Une bonne connaissance de python et de l'écosystème de calcul scientifique en python est requise (numpy, scipy, scikit-learn). Une connaissance des bases de l'apprentissage automatique et des algorithmes de classification est aussi nécessaires.

Programme/contents

Jour 1 : Préparation et manipulation des données

- * Introduction du workflow (VSCode, Python, git, GitHub, tests, ...)
- * Cours avancé sur Pandas
- * Exercices GitHub : NumPy et Pandas

Jour 2 : Pipelines de ML et évaluation de modèles

- * Scikit-learn avancé : ColumnTransformer et pipelines
- * Traitement parallèle avec joblib
- * Généralisation et validation croisée
- * Exercices sur scikit-learn
- * Introduction à Codalab et présentation des challenges

Jour 3 : Métriques et gestion des données déséquilibrées

- * Présentation des différentes métriques de ML
- * Problèmes liés aux métriques avec des données déséquilibrées
- * Approches d'apprentissage automatique pour traiter les jeux de données déséquilibrés
- * Travail sur les challenges de données

Jour 4 : Données complexes

- * Feature engineering et encodage avancé des variables catégorielles
- * Travail sur les challenges de données complexes

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class
Introduction to Entrepreneurship: Creat Your Deeptech Startup	2	Semestre 1						



Introduction to Entrepreneurship: Creat Your Deeptech Startup

ECTS : 2

Semester: Semestre 1

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

No prerequisites, but this course unit is designed for students potentially interested in entrepreneurship (without the prerequisite of having a business project) or who want to explore whether becoming an entrepreneur would be right for them.

Programme/contents

This course will cover the key elements of a deeptech entrepreneurial project, detailing each of the essential building blocks for creating a business:

- Introduction: myth and reality of entrepreneurship, the entrepreneur profile, specific characteristics of deeptech entrepreneurship

Presentation of Genopole and the Shaker business creation support program

- Proof of concept (POC)

- Market research

- Business plan

- Sources of funding

- Legal and administrative aspects

- HR, partner search, management

- Intellectual property

- Moving from research to commercialization: the connections?

- Marketing/communication

- Business development, partnerships with large

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class
Computational DNA nanotechnology	2	Semestre 1	18					

Computational DNA nanotechnology

ECTS : 2

Semester: Semestre 1

Detail

Lecture: 18

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

1. **basics of computer science (complexity, automata theory, langage theory)**
2. **basics of the biology of DNA**

Programme/contents

1. **Presentation of DNA self-assembly, theory and experiments.**
2. **Biomedical applications of DNA self-assembly : reading and discussion.**
3. **Supervised project on the design of a DNA origami.**

Learning objectives

1. **Understand the basic principles of DNA self-assembly and DNA computing.**
2. **Understand basic applications of DNA nanotechnology in biology and medicine.**
3. **Learn how to design basic DNA nanostructures.**

Overall organisation

This class starts by a brief presentation of the computational aspects of DNA self-assembly and the experimental technique of DNA origami. This presentation is followed by a reading session in which the students are encouraged to present their favorite aspects in detail to their peers. The class ends with a practical assignment in the DNA origami design software <https://www.ens-lyon.fr/ensnano/>, in which the students are encouraged to design a shape having a high probability of folding in a test tube.

Skills

Compétence 1.1

Formuler des problématiques et des hypothèses de

Teaching Location(s)

EVRY

Contact

- **Fariza TAHI**

PR

<http://www.universite-paris-saclay.fr/formation/master/bio-informatique/m2-genomics-informatics-mathematics-and-artificial-intelligence-health-and-environment-geniomhe-ai>