

Share



Email destinataire :

Vous devez renseigner un email valide

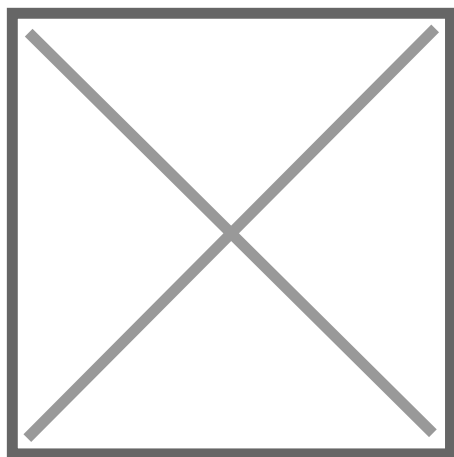
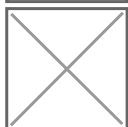
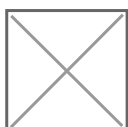
Envoyer

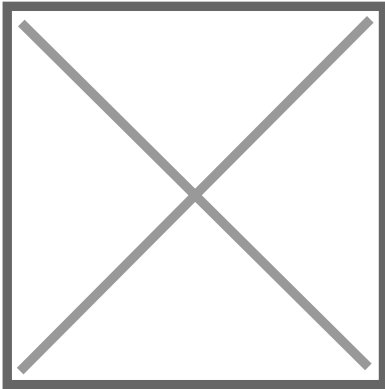
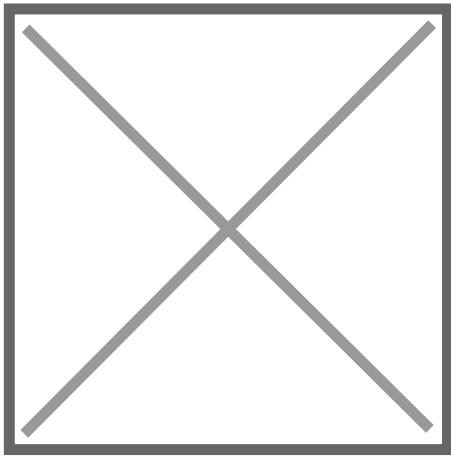
Une erreur est survenue. Merci de réessayer ultérieurement

Le mail de partage a bien été envoyé.

Add to Compare

M1 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 M1 GENIOMHE-AI program runs from September to March. A mandatory two-month internship will take place from April onwards in an academic research laboratory or a company.

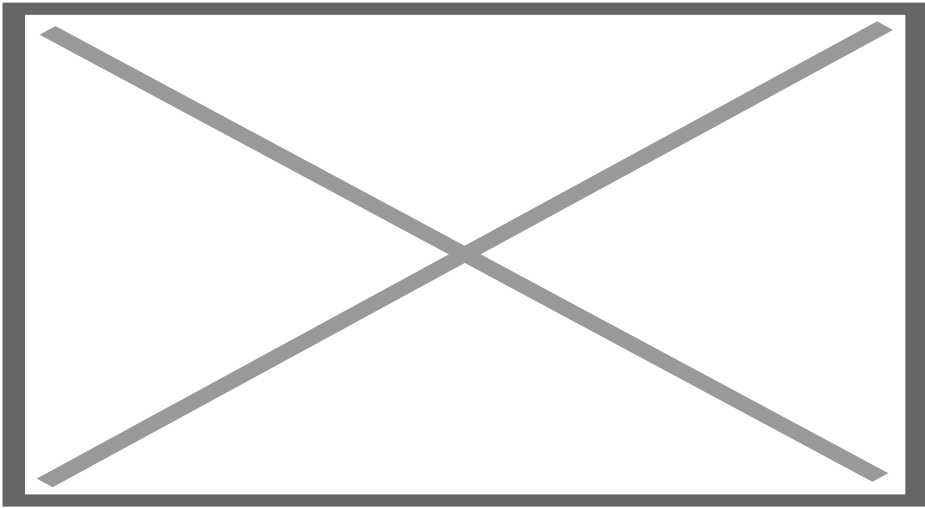
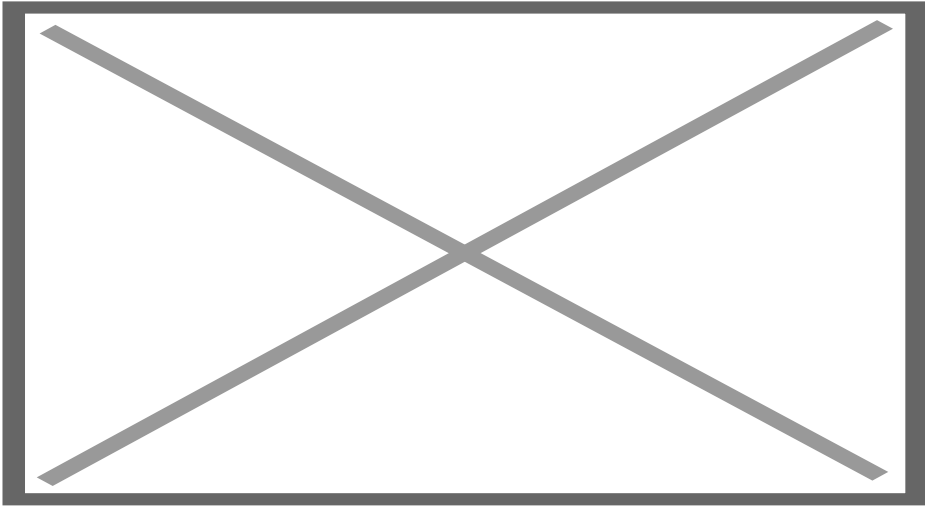
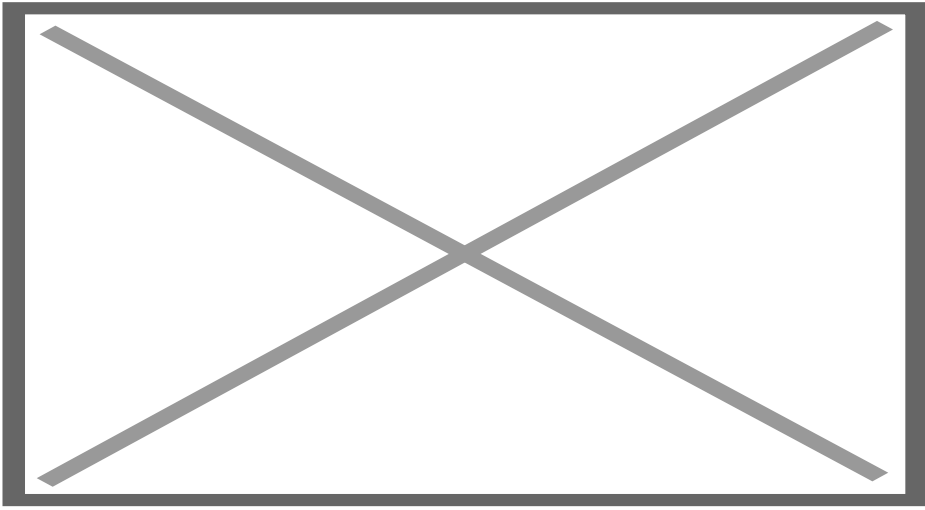
By the end of the M1, students will have acquired skills in genomics and human genetics, genomic data analysis, bioinformatics tools and phylogenetics, databases, machine learning and data mining, deep learning, imperative and object-oriented programming, biological systems modeling, and multivariate statistics.

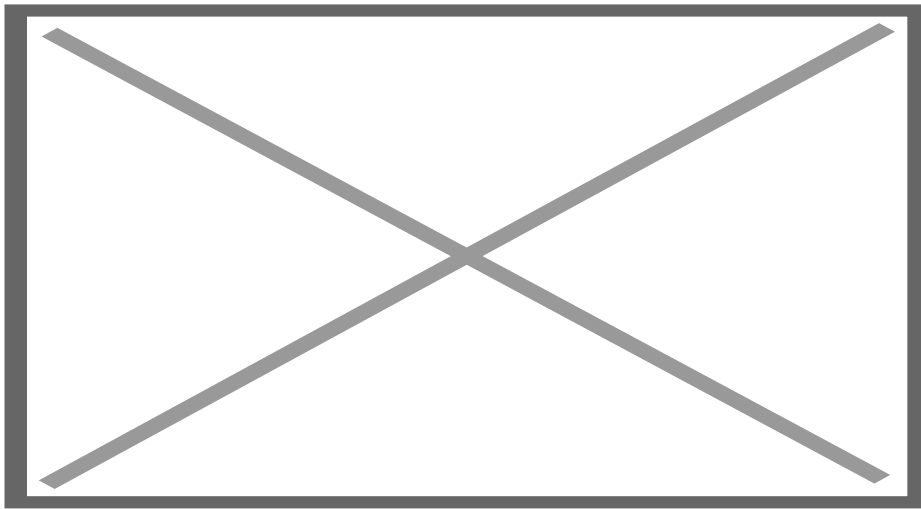
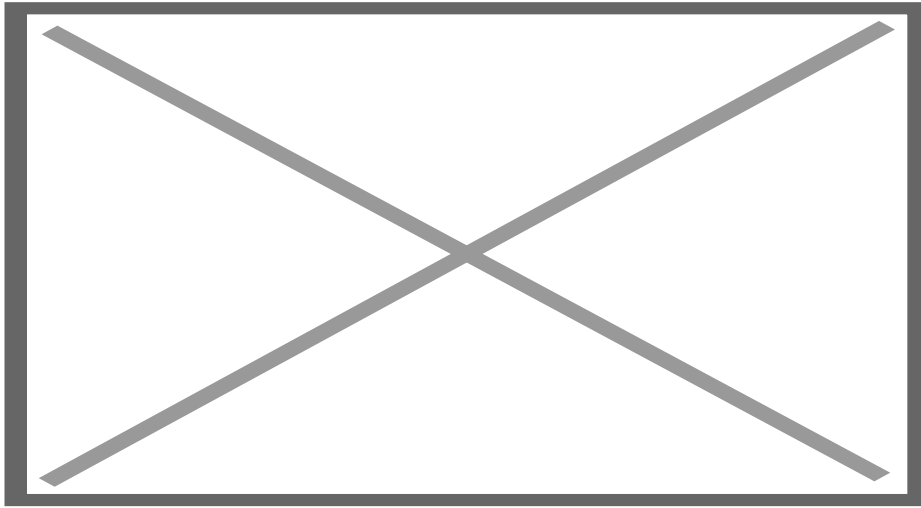
Students will also be introduced to FAIR principles and will have projects to complete.

Two opening modules will also be mandatory : a module on sustainable development and a module to be chosen from a list.

[Télécharger la fiche détaillée](#)

[Apply Now](#)





■ ■

Information

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

Présentation

Skills

Master the fundamental concepts of genomics, algorithms and programming, artificial intelligence, and statistics.

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

Further Study Opportunities

**Data Scientist, Data Analyst, Ingénieur·e en Machine Learning dans des secteurs innovants (tech, finance, santé, énergie, etc.) ;
2nd year Master's
Master of Bioinformatics**

Calendar

Start of programme (indicative date)

01/09/2026

End of programme (indicative date)

31/08/2027

Admission

Admission Route

Computer Science

Life Sciences

Life and Earth Sciences

Capacity

Available Places

25

Target Audience and Entry Requirements

- Students who have acquired knowledge and skills in both Biology and Informatics during their course (for example: Joint honours in Life Sciences-Informatics, Paris-Saclay undergraduate degree in selective Life Sciences-Info, Life Sciences undergraduate degree in Bioinformatics, undergraduate computing degree in Bioinformatics, Engineering school, etc.) . * Students who have completed a course in Biology but have an interest in Informatics and have acquired complementary knowledge and skills in this field.

Période(s) de candidature

Inception Platform

From 15/01/2026 to 25/04/2026

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.

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

Methods for Genomics 1

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
Bioinformatic tools	3	Semestre 1	9	13.5					

Bioinformatic tools

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Theory and practice concerning sequence data, databases and sequence formats, alignments with exact algorithms (dynamic programming) and practice of BLAST on standard databases online. Basical knowledge on evolution principles and population genetics. Unix/Linux concepts and utility filters.

Programme/contents

The course outline:

- Main courses:

- reminder about exact alignment algorithms and alignment scores,
- reminders of basic evolutionary principles,
- construction of scoring matrices (substitution matrices),
- BLAST algorithm, modification of parameters, statistical principles and local usage
- protocols to determine homologies

- Directed work:

- calculation of alignment scores and comparisons, alignment calculations using dynamic programming,
- interpretation of blast results (local and online)
- establishment of a bioinformatics protocol for the determination of protein families and subfamilies

Learning objectives

The objectives of this course are:

- to understand deeply the advantages and limits

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
Structural Genomics	3	Semestre 1	9	13.5					

Structural Genomics

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

General concepts in genetics and molecular biology usually covered during a Bachelor's degree in Biology or related sciences.

Programme/contents

- Characteristics of eucaryote genome : limits / advantages regarding sequencing, assembly and annotation
- Sequencing technologies
- Dynamic and evolution of eucaryote genome ; comparative genomics
- Introduction to assembly algorithms for 2nd and 3rd generation sequencing data.
- Key metrics for assessing genome assembly quality
- Overview of scaffolding approaches to obtain chromosome level and T2T quality genome
- Introduction to structural and functional annotation of genomes.
- Practical case study in the form of a project to annotate a genomic region.

Learning objectives

This course provides an in-depth exploration of the structure, organization, and evolution of genomes. Structural genomics focuses on describing the physical and functional organization of genetic material. Students will learn about genome architecture, sequencing technologies, genome assembly, annotation, and comparative genomics.

The course combines theoretical concepts with practical exercises in bioinformatics, using modern databases and tools to analyze genomic structures.

Overall organisation

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
Genome sequencing	3	Semestre 1	9	13.5					

Genome sequencing

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

This course covers genome resequencing studies, from data generation to result interpretation. It explores genomic variation within populations to determine gene functions, decipher pathogenic mechanisms and reconstruct disease history, as well as identify therapeutic opportunities.

Learning objectives:

- Describe the principles of data generation using high-throughput sequencing technologies.
- Explain the steps of data quality control and preprocessing, and their relevance.
- Understand the principles behind the identification of different types of genetic variants.
- Select appropriate variant filtering parameters according to the research question.
- Interpret and critically evaluate the results of publications in functional genomics.
- List the main applications of genome sequencing data in health and precision medicine.
- Understand how to identify altered signaling pathways, biological processes, and biomarkers from gene lists using functional annotation tools.
- Specify the advantages of single-cell approaches for studying tissue complexity or sample polyclonality.

Learning objectives

This course provides knowledge on analyzing genome sequencing data using the most recent deep-sequencing technologies and their numerous applications to specific biological questions. It will also train students to extract relevant data from scientific articles, identify their limitations, and synthesize them in a journal club format.

Overall organisation

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
Genetics of complex pathologies	3	Semestre 1	9	13.5					

Genetics of complex pathologies

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Fundamentals of formal genetics.

Programme/contents

1. Introduction
 - a. Types of human diseases and factors involved
 - b. Issues raised by multifactorial diseases
2. Data production methods
3. Data quality control
 - a. Missing data
 - b. Hardy-Weinberg model
 - c. Principal component analysis
 - d. Other
4. Search for causal genetic variants
 - a. Association analyses on family data (Transmission Disequilibrium Test)
 - b. Association analyses on population data (case-control studies)
 - c. Pan-genomic association studies
5. Generalizations
 - a. Association analysis for rare variants
 - b. Search for interactions

Learning objectives

- Identify the genetic analysis methods to be used for a given problem
- Describe methods for producing genetic data on a large scale
- Be familiar with various examples of complex pathologies
- Select the appropriate statistical tools
- Perform adequate data quality checks
- Conduct a genetic association study
- Know how to interpret the results of a genetic association study

Methods for Genomics 2

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
Prokaryotic genomics	3	Semestre 2	9	13.5					c

Prokaryotic genomics

ECTS : 3

Semester: Semestre 2

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

- ? Basic knowledge of molecular biology, microbial genetics, and genomics
- ? Familiarity with sequence formats (FASTA, GFF, GenBank)
- ? Awareness of databases such as NCBI, UniProt, and KEGG

Programme/contents

1. Introduction to Prokaryotic Genomes
 2. Genome Annotation
 3. Comparative Genomics
- Concepts: orthology, synteny, gene conservation, rearrangements
4. Pangenomics and Pangenome Graphs
 5. Metabolic Reconstruction and Comparative Metabolism analysis
 6. Integrative Project: Comparative Genomics, Pangenome, and/or Metabolic Reconstruction

Learning objectives

By the end of this course, students will be able to:

1. Describe the structure, organization, and variability of prokaryotic genomes
2. Perform genome annotation using reference pipelines and databases.
3. Compare genomes across species to identify orthologous and unique genes.
4. Reconstruct and analyze metabolic pathways from annotated genomes.
5. Build, interpret, and visualize pangenomes using comparative genomics tools.
6. Understand how genome diversity relates to functional and ecological adaptation

Overall organisation

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
Methods for Phylogeny	3	Semestre 2	9	13.5					

Methods for Phylogeny

ECTS : 3

Semester: Semestre 2

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

The following topics will be covered:

- the concept of evolution, homology, orthology and paralogy,
- Phylogenetic representation (networks, trees, roots, dendrograms, topology, branch lengths)
- Phylogenetic inference methods (distances, parsimony, the principle of maximum likelihood, ...)
- Measures of the robustness of phylogenies (bootstrap, topology comparison, multigene corroboration, gene and species trees)

Applications to the phylogeny of some major taxonomic groups and to gene families.

Learning objectives

This course will present the fundamental concepts in molecular evolution and phylogeny. Practical sessions and tutorials will allow students to become familiar with modern tools for reconstructing phylogenetic trees for species and/or genes.

Overall organisation

This teaching unit is organized in the form of main courses (9h) and practical work (13,5h) in the computer room. Students will be evaluated through several small exams in class and a final exam.

Skills

C1.1. Formuler des problématiques et des hypothèses de travail permettant la conception et la réalisation d'un projet dans son domaine d'expertise et /ou à l'interface de plusieurs domaines en biologie.

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di le c
NGS data processing methodology	2	Annualisé			17				

NGS data processing methodology

ECTS : 2

Semester: Annualisé

Detail

Practical study : 17

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Theory concerning NGS data analysis and statistical methods for association analyses.

Programme/contents

The course outline:

- Perform all bioinformatics steps of sequence data processing (alignment, local realignment, variant identification, variant visualization with IGV)
- Define and apply adequate quality control filters at each step of data processing
- Perform and interpret descriptive statistics at each step of data processing
- Choose and apply filters for the identified variants according to the problem considered (frequency, predicted effect, ...)
- Use the appropriate statistical tools to search for genetic variants associated with a complex disease.
- Interpret the statistical results obtained
- Synthesize the results obtained during the different stages (bioinformatics and statistics).

Learning objectives

The objective of this practical teaching is to manipulate Next Generation Sequencing DNA sequence data in order to identify genetic variants (SNV, indels) associated with a complex disease.

Overall organisation

This teaching unit is organized in the form of practical work in the computer room. 2/3 will focus on the bioinformatics processing of data, 1/3 on statistical analysis. Students will be

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
Refresher course in Shell, Python, algorithmics	1	Annualisé		40					

Refresher course in Shell, Python, algorithmics

ECTS : 1

Semester: Annualisé

Detail

Directed study: 40

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basic knowledge of scientific computing: computer operation, file hierarchy, and installation of simple software.

Basic knowledge of molecular biology and bioinformatics (sequences, FASTA/FASTQ files, etc.).

Prior experience with a programming language (even superficial, e.g., R, C, or Python).

Motivation to strengthen skills in algorithms and programming.

Programme/contents

This course is structured in two parts:
Algorithmics and Programming.

A. Algorithmics:

This part will be organized as lectures/tutorials where students will write algorithms in pseudocode for searching and updating in various data structures: arrays, matrices, lists, queues, stacks, trees, and graphs.

B. Programming:

1 – Introduction and UNIX/Bash Review (6–7 hours)

Objectives: to master basic navigation and operations under Linux, and to automate small tasks.

Contents:

- Introduction to the UNIX/Linux shell and environment
- Essential commands: navigation (cd, ls, pwd), file management (cp, mv, rm), reading (cat, less, head, tail)
- Redirections, pipes, and filters (>, |, grep, sort)

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
Object Oriented Programming for Machine Learning	3	Semestre 1	9	13.5					c

Object Oriented Programming for Machine Learning

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Python

Algorithms

Programme/contents

- Introduction to software design and development methods
- Machine learning frameworks and the design of libraries
- POO principles
- Classes in UML
- Class, object, methods, attributes, etc.
- Abstraction, Inheritance, Mixins, Interfaces
- Dunder methods
- Class decorators

Learning objectives

This course introduces students to object-oriented programming principles through software modeling activities using UML and extensive Python programming. Throughout the course, students will have the opportunity to study concrete use cases from machine learning frameworks and libraries. This will provide an opportunity to become familiar with the design philosophy of these frameworks. As a final project, students will have the opportunity to work on the modeling, design, and implementation of a machine learning library from scratch, with many features similar to those in the scikit-learn library.

By following this course, the students will be able to:

- Express software specifications in UML
- Implement specifications in Python

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	directed study/practical class
Multivariate statistics for genomics.	3	Semestre 1	9	13.5					

Multivariate statistics for genomics.

ECTS : 3

Semester: Semestre 1

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

- Basic knowledge of R
- Knowledge of univariate and bivariate inferential statistics (estimation, testing, p-values and interpretation of results)

Programme/contents

- Linear regression
- Logistic regression
- Poisson regression
- Variable selection and validation of models.

Learning objectives

Based on a problem and associated data, be able to recognise a suitable model, write it, implement it with R, and analyse all the results.

Overall organisation

- 9h lectures and 13.5h practicals
- Evaluations :
- * Practicals (35% of the final grade)
- * Final exam (65% of the final grade)

Special teaching arrangements

Lectures and practicals with computers. Use of R software.

Skills

C1.2. Concevoir une démarche expérimentale.

C3.2. Argumenter les choix méthodologiques et les interprétations d'une étude.

Bibliography

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
Machine learning and data mining	3	Annualisé	9	13.5					c

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
----------	------	----------	---------	----------------	-----------------	------------------------	-------------------------	--------------------------------	----

Machine learning and data mining

ECTS : 3

Semester: Annualisé

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

- Introduction to machine learning and data mining
- The clustering problem
- K-means algorithm
- Hierarchical clustering
- Spectral clustering
- Tree-based learning methods (Decision trees)
- Ensemble methods (Boosting, Bagging)

Learning objectives

This course provides an introduction to machine learning and data mining techniques. Students will learn to analyze datasets, discover structure with clustering algorithms, and build powerful and interpretable predictive models with decision trees and ensemble methods. Emphasis is placed on practicals related to multi-omics tabular datasets and applications in precision medicine. Students will have the opportunity to apply their acquired skills in cutting-edge machine learning challenges.

By following this course, students will be able to:

- Understand the underlying mathematical foundations of machine learning and data mining approaches
- Design, train, and evaluate machine learning and data mining pipelines on real-world tabular datasets
- Use popular frameworks like scikit-learn to build and deploy such pipelines
- Engage in cutting-edge real-world machine learning challenges, with a particular focus on applications in precision medicine

Skills

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	di
Sequence algorithmics	3	Annualisé	9	13.5					c

Sequence algorithmics

ECTS : 3

Semester: Annualisé

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

Basics of algorithms, data structures

Programme/contents

Review of algorithmic complexity calculation

Pattern matching

- Naive algorithm for exact pattern matching

- Suffix automata

Repetition matching

- Naive algorithm: matrix usage

- Suffix trees

Dynamic programming

- Longest common subsequence matching

- Pattern matching with k-errors

- Sequence alignment

Learning objectives

This course will cover algorithmic methods for sequence analysis. It will focus on pattern matching, and sequence alignment.

Overall organisation

EE 100% 1ere et 2eme session

Skills

Skills:

Master the theoretical and practical foundations of algorithmic methods used for sequence analysis.

Additional skills:

- Formalization of the concept of a biological sequence and its analysis

- Theoretical foundations of algorithms

Type of assessment

Evaluation Continue non Intégrale

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis
Modeling of biological systems	3	Semestre 2	9	13.5					co



Modeling of biological systems

ECTS : 3

Semester: Semestre 2

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Type of assessment

Evaluation Continue non Intégrale

[Advanced databases](#)

3 Annualisé 9 13.5

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis
----------	------	----------	---------	----------------	-----------------	------------------------	-------------------------	--------------------------------	-----

■

Advanced databases

ECTS : 3

Semester: Annualisé

Detail

Lecture: 9

Directed study: 13.5

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

SQL language and entity-relationship modeling, practical experience with a relational database management system. Unix/Linux concepts and utility filters.

Programme/contents

The course outline:

* Main courses:

- UML,
- translation of an object-oriented data representation model into a relational model
- ontologies in biology

* Directed work:

- conception in UML of different biological problems, mainly in genomics
- translation of the created object-oriented data representation models into a relational model and implementation for PostgreSQL
- practice of Gene Ontology database and data and the underlying data representation formalism

Learning objectives

The objective of this course is to present object-oriented data representation languages with a view to creating models for problems in biology and implementing them under a relational database management system. Ontologies in biology will also be presented, as well as different data representation languages.

Overall organisation

This teaching unit is organized in the form of main courses (9h) and practical work (13,5h) in the computer room. Students will be evaluated through several small exams in class and a final

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis
Frameworks for Deep Learning	2	Semestre 2		17					co

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis	lea	co
■											

Frameworks for Deep Learning

ECTS : 2

Semester: Semestre 2

Detail

Directed study: 17

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

- Introduction to deep learning frameworks
- Design patterns
- Meta-programming in Python
- Software testing and continuous integration

Learning objectives

This course introduces students to the widely used deep learning frameworks such as PyTorch, Keras, and TensorFlow, from an architectural perspective.

Students will have the opportunity to discover these complex frameworks through a concrete programming project: modeling, designing, and implementing a deep learning framework from scratch, including its fundamental components such as the computation graph and differentiation engine.

This will enable students to understand the underlying design principles of these software libraries and to develop their own libraries that adhere to these standards.

By following this course, the students will be able to:

- become familiar with deep learning frameworks such as PyTorch, Keras, and TensorFlow
- understand the software design principles of these frameworks
- use design patterns to improve software design
- build a deep learning framework from scratch, including its computation graph and differentiation engine
- apply software design principles in future projects

Overall organisation

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis
Deep learning	2	Annualisé	9	9					co

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis
----------	------	----------	---------	----------------	-----------------	------------------------	-------------------------	--------------------------------	-----

Deep learning

ECTS : 2

Semester: Annualisé

Detail

Lecture: 9

Directed study: 9

Language(s) of instruction

Anglais

Remote teaching

non

Programme/contents

- Introduction to deep learning for precision medicine: Motivation
- Perceptron and multilayer perceptron
- Gradient descent and the backpropagation algorithm
- Computation graph and automatic differentiation (autograd) engine
- Optimization (Adam, RMSprop, etc.)
- Regularization techniques
- Convolutional neural networks (CNN) for (medical) image processing (e.g., CT-scans, etc.)
- Recurrent neural networks (RNN) for (medical) time series (e.g., EEG signals, etc.)

Learning objectives

Deep learning is at the heart of the recent advances in artificial intelligence. Beyond computer vision and natural language processing, deep learning has made significant advances in precision medicine, enabling breakthroughs such as early disease onset prediction, personalized treatment plans, and drug prescription.

This course introduces the foundations of deep learning, from the classic perceptron to modern architectures. It will cover the design, training, and rigorous evaluation of deep learning architectures for various types of data, such as images and time series. Emphasis is placed on practicals related to deep learning for precision medicine applications. Students will participate in cutting-edge AI challenges related to precision medicine using deep learning models.

In parallel, students will follow the course “Frameworks for Deep Learning,” where they will have the opportunity to model, design, and

Professionalization

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis lea co
FAIR project management	1	Semestre 1	3	6					

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	discovery/learning
----------	------	----------	---------	----------------	-----------------	------------------------	-------------------------	--------------------------------	--------------------

FAIR project management

ECTS : 1

Semester: Semestre 1

Detail

Lecture: 3

Directed study: 6

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

- ? Basic knowledge of data management and scientific data formats
- ? Fundamental concepts in bioinformatics and computational biology
- ? Introductory skills in data analysis and scripting (Python/R/Shell)
- ? Awareness of ethical and legal issues in research data handling

Programme/contents

- ? Introduction to Open Science
- The six pillars of openness: Open Access, Open Data, Open Source, Open Peer Review, Open Education, Citizen Science
- ? FAIR Principles
- Overview of FAIR: origins, rationale, and implications
- ? Tools and Infrastructures for FAIR and Open Bioinformatic : Repositories, Code sharing and reproducibility
- ? Data privacy and protection : Intellectual property and open licenses, Balancing openness with confidentiality in biomedical research

Learning objectives

By the end of this course, students will be able to:

- ? Understand the foundations and challenges of Open Science in the context of life sciences and bioinformatics.
- ? Apply the FAIR principles (Findable, Accessible, Interoperable, Reusable) to biological data and code.
- ? Identify infrastructures, repositories, and tools supporting data sharing and reproducible research.
- ? Address ethical, legal, and technical aspects

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dis- lea- co
Project	2	Semestre 2			9				

Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	dissemination/learning outcomes
■									

Project

ECTS : 2

Semester: Semestre 2

Detail

Practical study : 9

Language(s) of instruction

Anglais

Remote teaching

non

Prerequisites

- ? Basic knowledge of data management and scientific data formats
- ? Fundamental concepts in bioinformatics and computational biology
- ? Introductory skills in data analysis and scripting (Python/R/Shell)
- ? Awareness of ethical and legal issues in research data handling

Programme/contents

Each student (or pair) will:

1. Select a dataset or analysis from a previous course module.
2. Describe and document the dataset:
Add structured metadata (sample origin, methods, software, version, author).
Identify suitable file formats.
3. Create a reproducible analysis workflow: Clearly record parameters and software versions.
4. Publish and share:
 - Host code and documentation on GitHub or GitLab.
 - Deposit dataset or notebook and assign a DOI.
 - Apply open licenses.

Learning objectives

By the end of this course, students will be able to:

- ? Apply the FAIR principles (Findable, Accessible, Interoperable, Reusable) to biological data and code.
- ? Use of open-source tools for reproducibility and data sharing
- ? Developed a critical assessment of data openness and reusability

Opening units

Opening units									
Subjects	ECTS	Semester	Lecture	directed study	practical class	Lecture/directed study	Lecture/practical class	directed study/practical class	discovery learning
UE libre Catalogue S1	2.5	Semestre 1							

UE libre Catalogue S1

ECTS : 2.5

Semester: Semestre 1

Language(s) of instruction

Français

Remote teaching

non

Type of assessment

Evaluation Terminale

Sustainable development and ethics 2

Semestre 1

Sustainable development and ethics

ECTS : 2

Semester: Semestre 1

Language(s) of instruction

Anglais

Remote teaching

oui

Overall organisation

This module will consist of taking 2 MOOCs:

- A MOOC on the environmental impacts of digital technology, particularly AI practices.
- A MOOC on societal impact of practices in ecological and ethical terms.

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 course
----------	------	----------	---------	----------------	-----------------	------------------------	-------------------------	--------------------------------	--------------------------

[Internship](#) 10 Semestre
2



Internship

ECTS : 10

Semester: Semestre 2

Language(s) of instruction

Anglais

Remote teaching

non

Overall organisation

Two-month internship in a research
laboratory.

Type of assessment

Evaluation Terminale

Teaching Location(s)

EVRY

Contact

- **Valérie CHAUDRU**

MCF

<http://www.universite-paris-saclay.fr/formation/master/bio-informatique/m1-genomics-informatics-mathematics-and-artificial-intelligence-health-and-environment-geniomhe-ai>