REPUBLIQUE ALGERIENNE DEMOCRATIQUE ET POPULAIRE

MINISTERE DE L'ENSEIGNEMENT SUPERIEUR
ET DE LA RECHERCHE SCIENTIFIQUE

Nouvelle

OFFRE DE FORMATION MASTER

ACADEMIQUE

Etablissement	Faculté / Institut	Département
UNIVERSITÉ DE SAIDA DR. MOULAY TAHAR	SCIENCES DE LA NATURE ET DE LA VIE	DÉPARTEMENT DE BIOLOGIE

Domaine : SCIENCES DE LA NATURE ET DE LA VIE

Filière : Biotechnologies

Spécialité : BIO-INFORMATIQUE

Année universitaire : 2025-2026

وزارة التعليم العالي والبحث العلمي

عرض تكوين ماستر

أكاديمي

المؤسسة	الكلية/ المعهد	القسم
جامعة سعيدة الدكتور مولاي الطاهر	كلية علوم الطبيعة والحياة	البيولوجيا

الميدان : علوم الطبيعة والحياة

الشعبة: بيوتكنولوجيا

التخصص إعلام آلي حيوي

السنة الجامعية: 2025-2026

SOMMAIRE

I – Fiche d'identité du Master

(Tous les champs doivent être obligatoirement remplis)

1 - Localisation de la formation :

Faculté (ou Institut) : SCIENCES DE LA NATURE ET DE LA VIE
Département : BIOLOGIE

2- Partenaires de la formation *:

- Autres établissements universitaires :

- Entreprises et autres partenaires socio économiques

1. Hospital Ahmed Medaghri - Saida
2. Paramedical Institute of Saida

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- Partenaires internationaux :

* = Présenter les conventions en annexe de la formation

3 – Contexte et objectifs de la formation

A – Conditions d'accès

The Master's degree in "Bioinformatics" is aimed at students holding a Bachelor's degree in Biochemistry, Microbiology, Biotechnology, Chemistry, Computer Science, and/or any diploma deemed equivalent by the educational commission. Access to training is done after examination of the file by the educational commission.

B - Objectifs de la formation

This multidisciplinary training, which is at the interface between biology, computer science and mathematics, has the general objective of meeting the need for bioinformatics and relevant expertise in Algeria.

The program's core objective is to equip students with the skills and knowledge necessary to excel in the rapidly evolving field of bioinformatics, integrating theoretical learning with practical applications.

The curriculum is structured to cater to students from diverse academic backgrounds ensuring a cohesive and comprehensive educational experience. The first year focuses on establishing foundational knowledge in molecular biology, bioinformatics programming, statistical data analysis, and basic database management, along with a practical introduction to the tools and techniques commonly used in the field. Advanced topics in genomics, proteomics, sequence alignment, phylogenetics, molecular modelling, and drug design are covered in the second year, alongside specialized courses in advanced database management and design. This progression ensures a deep understanding of both the theoretical and practical aspects of bioinformatics.

A significant component of the program is the hands-on laboratory work and assignments, which are integrated into each course. These practical sessions are designed to reinforce the theoretical concepts learned in class and provide students with real-world skills in data analysis, database management, and bioinformatics software tools. In the final semester, students undertake a comprehensive research project, allowing them to apply their knowledge and skills to a real-world bioinformatics problem, culminating in a thesis that contributes to the field.

C – Profils et compétences métiers visés

The major specific objectives of the Master's curriculum in Bioinformatics are designed to equip students with a comprehensive skill set and knowledge base that are essential in the field. These objectives include:

1. **Foundation in Core Disciplines**: To provide a strong understanding of the fundamental concepts in molecular biology, chemistry, and computer science, ensuring that students from diverse backgrounds have the necessary knowledge to excel in bioinformatics.
2. **Proficiency in Bioinformatics Tools and Techniques**: To train students in the use and application of key bioinformatics tools and techniques, such as sequence alignment, phylogenetics, genomics, and proteomics.
3. **Competence in Programming and Data Analysis**: To develop proficiency in programming languages (like Python and R) and data analysis methods relevant to bioinformatics, enabling students to handle and interpret large biological datasets.
4. **Expertise in Database Management**: To provide expertise in managing biological databases, encompassing both the creation and utilisation of these databases, which are vital for storing and analysing biological data.
5. **Skills in Advanced Bioinformatics Applications**: To offer advanced knowledge and skills in areas such as structural bioinformatics, molecular modelling, docking, drug design, and AI applications in bioinformatics, preparing students for cutting-edge research and industry practice.
6. **Research Capability Development**: To enhance students' ability to conduct independent research, including the formulation of research questions, hypothesis testing, data collection and analysis, and interpretation of results.
7. **Application of AI and Machine Learning**: To familiarize students with the application of AI and machine learning in bioinformatics, focusing on tools like AlphaFold and other AI-driven technologies that are revolutionizing the field.
8. **Interdisciplinary Collaboration Skills**: To foster the ability to work effectively in interdisciplinary teams, a crucial skill in the inherently cross-disciplinary nature of bioinformatics.

9. **Professional Development and Communication Skills**: To enhance students' professional development, including effective communication of bioinformatics concepts and findings to both scientific and non- scientific audiences.
10. **Preparation for Industry and Academic Careers**: To prepare graduates for successful careers in both industry and academia, including the development of skills necessary for job acquisition, such as resume writing, interviewing, and networking.

D- Potentialités régionales et nationales d'employabilité des diplômés

The employability potential for graduates of a bioinformatics master's program is diverse and dynamic. Graduates are well-positioned to take advantage of growing opportunities in various sectors due to the increasing reliance on bioinformatics and data analysis in understanding biological processes, disease mechanisms, and in the development of new therapies and technologies.

The regional and national employability potential contexts of a Master's program in Bioinformatics is quite strong, given the interdisciplinary nature of the field and its growing importance in various sectors. Below is a breakdown of such potential in both contexts:

Regional Employability Potential

1. **Healthcare and Pharmaceutical Industries**: Regions with a strong presence of pharmaceutical companies and healthcare organizations offer opportunities in drug discovery, personalized medicine, and clinical research.
2. **Academic and Research Institutions**: Local universities and research centers often seek bioinformaticians for research in genomics, proteomics, and related areas.
3. **Biotechnology Firms**: Regions with a cluster of biotech firms provide roles in product development, data analysis, and research.
4. **Agricultural Sector**: In areas where agriculture is prominent, bioinformatics skills can be employed in crop improvement, pest resistance studies, and environmental impact assessments.
5. **Government and Public Health Agencies**: Regional health departments and government research labs may employ bioinformaticians for public health research, epidemiology, and disease surveillance.

National Employability Potential

1. **Growing Biotech and Pharma Sectors**: On a national scale, the expansion of biotech and pharmaceutical sectors opens up roles in research and development, clinical trials, and regulatory affairs.
2. **Public Health and Epidemiology**: With the growing importance of data in managing public health, national health services and organizations require bioinformaticians for data analysis and policy making.
3. **National Research Projects and Grants**: Opportunities in large-scale research projects funded by national research grants or even collaborations at regional level.
4. **Technology and Software Companies**: Roles in bioinformatics tool development, data management solutions, and consultancy services.
5. **Education Sector**: Teaching and academic research positions in universities and colleges.

In addition, there are general trends and skills demand that are be pointed out in the following:

1. **Precision Medicine and Personalized Therapies**: A growing area in medicine that relies heavily on bioinformatics for genomic data analysis and interpretation.

2. **Data Science Integration**: Skills in bioinformatics are increasingly valued in broader data science roles, including big data analysis, machine learning, and AI.

3. **Cross-Sector Mobility**: The diverse skill set of bioinformaticians allows for mobility across various sectors, increasing employability.

4. **Remote and Freelance Work**: Opportunities for remote work and freelance projects, especially in data analysis, software development, and consulting.

E – Passerelles vers d'autres spécialités

Bioinformatics is a highly interdisciplinary field, and its principles and techniques are applicable to numerous other specialties, some listed below, each of which represents a unique direction that professionals can take after gaining foundational knowledge and skills in bioinformatics, reflecting the broad applicability and versatility of the field:

1. **Computational Biology**: Specialising in computational biology involves using bioinformatics techniques for modelling and understanding complex biological systems, including evolutionary studies, systems biology, and network analysis.

2. **Genomic Data Science**: This specialty focuses on the analysis of genomic data, using bioinformatics tools for sequencing, annotating, and understanding genomes, which is crucial in personalized medicine and genetic research.
3. **Proteomics and Metabolomics**: Specializing in proteomics or metabolomics involves analysing large-scale protein or metabolite datasets, crucial for understanding disease mechanisms and biomarker discovery.

4. **Pharmacogenomics and Drug Discovery**: Utilizing bioinformatics in pharmacogenomics involves analysing genetic data to understand how individuals respond to drugs, which is key in developing personalized medicine and in drug discovery processes.

5. **Clinical Bioinformatics**: This field applies bioinformatics in a clinical setting, focusing on the interpretation of genetic and molecular data to inform clinical decisions and healthcare practices.

6. **Biostatistics and Epidemiology**: Specializing in biostatistics involves applying statistical techniques to biological data, crucial in epidemiological studies, clinical trials, and public health research.

7. **Machine Learning and Artificial Intelligence in Healthcare**: Bioinformaticians with a strong background in AI and machine learning can contribute significantly to developing algorithms and models for diagnostic tools, treatment planning, and understanding disease patterns.

8. **Environmental Genomics**: This involves applying bioinformatics to environmental studies, including biodiversity assessment, ecological research, and understanding the impact of environmental changes on genetic diversity.

9. **Agricultural Bioinformatics**: In agricultural sciences, bioinformatics techniques are used for crop improvement, studying plant genetics, and developing sustainable agricultural practices.

10. **Regulatory and Ethical Aspects of Genomics**: Bioinformaticians can also delve into the regulatory, ethical, and policy aspects of genomics and biotechnology, ensuring responsible and ethical use of biotechnology.

11. **Biological Data Visualization and Bioinformatics Software Development**: Developing new tools and software for visualizing and interpreting complex biological data sets.

12. **Teaching and Academic Research**: With a solid foundation in bioinformatics, graduates can pursue careers in academia, teaching, and conducting research in various sub-disciplines of bioinformatics and related fields.

13. **Computational & Theoretical Chemistry:** This field specializes in the automatic processing of chemical information to interpret and predict chemical events, utilizing informatics hardware and software, as well as molecular and material modeling methods. These foundational tools are also integral to bioinformatics.

14.

F – Indicateurs de suivi de la formation

Each teaching unit is evaluated in the form of continuous assessment carried out during the semester and/or a final examination organized at the end of the semester. The relative weight of each control varies depending on the UE.

G – Capacité d'encadrement : 25 Students

II – Fiche d’organisation semestrielle des enseignements

(Prière de présenter les fiches des 4 semestres)

1- Semestre 1 :

Unité d'Enseignement	VHS	V.H hebdomadaire				Coeff	Crédits	Mode d'évaluation	
	15 sem	C	TD	TP	Autres			Continu	Examen
UE fondamentales									
UEF1(O/P)	**202h30**	**6h00**	**4h30**	**1h30**	**247h30**	**9**	**18**		
Introduction to Informatics	45h00	1h30	1h30		55h00	2	4	**40 %**	**60 %**
Genetics and Molecular Biology	67h30	3h00	1h30		82h30	3	6	**40 %**	**60 %**
Introduction to Bioinformatics	45h00	1h30	1h30		55h00	2	4	**40 %**	**60 %**
Introduction to Molecular Modeling	45h00	1h30		1h30	55h00	2	4	**40 %**	**60 %**
UE méthodologie									
UEM1(O/P)	**105h00**	**4h00**	**3h00**		**120h00**	**5**	**9**		
Biostatistics - Introduction to Statistical Data Analysis	60h00	2h30	1h30		65h00	3	5	**40 %**	**60 %**
Mathematics for biology	45h00	1h30	1h30		55h00	2	4	**40 %**	**60 %**
UE découverte									
UED1(O/P)	**45h00**	**1h30**	**00h30**	**1h00**	**5h00**	**2**	**2**		
Databases basics	22h30	1h00	00h30*	-	2h30	1	1	**40 %**	**60 %**
Logiciel libre et open source	22h30	00h30*	-	1h00	2h30	1	1	**40 %**	**60 %**
UE transversales									
UET1(O/P)	**22h30**	**1h30**			**2 h30**	**1**	**1**		
Communication	22h30	1h30			2 h30	1	1	-	**100 %**
Total Semestre 1	**375h00**	**13h00**	**8h00**	**2h30**	**375h00**	**17**	**30**		

(*) : Les 30 minutes hebdomadaires allouées à ces cours seront regroupées en une séance de 01h30 toutes les trois semaines.

2- Semestre 2 :

Unité d'Enseignement	VHS	V.H hebdomadaire				Coeff	Crédits	Mode d'évaluation	
	15 sem	C	TD	TP	Autres			Continu	Examen
UE fondamentales									
UEF2(O/P)	**202h30**	**6h00**		**7h30**	**247h30**	**9**	**18**		
Advanced Molecular Modeling	67h30	3h00		1h30	82 h30	3	6	**40 %**	**60 %**
Omics: from genomes to metabolomes	67h30	1h30		3h00	82 h30	3	6	**40 %**	**60 %**
Structural Bioinformatics and Biology	67h30	1h30		3h00	82 h30	3	6	**40 %**	**60 %**
UE méthodologie									
UEM2(O/P)	**105h00**	**3h00**	**2h30**	**1h30**	**120h00**	**5**	**9**		
Bioinformatics algorithms	60h00	1h30	1h00	1h30	65 h00	3	5	**40 %**	**60 %**
Biostatistics - Advanced Statistical Data Analysis	45h00	1h30	1h30		55 h00	2	4	**40 %**	**60 %**
UE découverte									
UED2(O/P)	**45h00**	**1h30**	**00h30**	**1h00**	**5h00**	**2**	**2**		
Phylogenetics and Phylogenomics	22h30	1h00	00h30*	-	2 h30	1	1	**40 %**	**60 %**
Programmation Informatique appliquée aux sciences et technologie	22h30	00h30*	-	1h00	2h30	1	1	**40 %**	**60 %**
UE transversales									
UET1(O/P)	**22h30**	**1h30**			**2h30**	**1**	**1**		
Législation, éthique et déontologie	22h30	1h30			2h30	1	1	-	**100 %**
Total Semestre 2	375h00	13H30	03H30	07H00	375h00	17	**30**		

(*) : Les 30 minutes hebdomadaires allouées à ces cours seront regroupées en une séance de 01h30 toutes les trois semaines.

3- Semestre 3 :

Unité d'Enseignement	VHS	V.H hebdomadaire				Coeff	Crédits	Mode d'évaluation	
	15 sem	C	TD	TP	Autres			Continu	Examen
UE fondamentales									
UEF1(O/P)	**202h30**	**6h00**	**0h00**	**7h30**	**247h30**	**9**	**18**		
Programming (Python Bio-Project)	67h30	3h00		1h30	82h30	3	6	**40 %**	**60 %**
Advanced Bioinformatics and Specialisation	67h30	1h30		3h00	82h30	3	6	**40 %**	**60 %**
High Performance Computing	67h30	1h30		3h00	82h30	3	6	**40 %**	**60 %**
UE méthodologie									
UEM1(O/P)	**105h00**	**3h00**	**2h30**	**1h30**	**120h00**	**5**	**9**		
Machine Learning & Data Mining	60h00	1h30	1h00	1h30	65h00	3	5	**40 %**	**60 %**
Modeling of Biological Systems	45h00	1h30	1h30		55h00	2	4	**40 %**	**60 %**
UE découverte									
UED1(O/P)	**45h00**	**1h30**	**00h30**	**1h00**	**5h00**	**2**	**2**		
Advanced Database	22h30	1h00	00h30*	-	2h30	1	1	**40 %**	**60 %**
Intelligence artificielle appliquée aux sciences et technologies	22h30	00h30*	-	01h00	2h30	1	1	**40 %**	**60 %**
UE transversales									
UET1(O/P)	**22h30**	**1h30**			**2h30**	**1**	**1**		
Création d'une entreprise économique	22h30	1h30			2h30	1	1	-	**100 %**
Total Semestre 3	**375h00**	**12h00**	**3h00**	**10h00**	**375h00**	**17**	**30**		

(*) : Les 30 minutes hebdomadaires allouées à ces cours seront regroupées en une séance de 01h30 toutes les trois semaines.

4- Semestre 4 :

Domain: ***Natural and Life Sciences***
Field: ***Biotechnologies***
Specialty: ***Bioinformatics***

Stage en laboratoire ou en entreprise sanctionné par la rédaction d'un mémoire et une soutenance.
Internship in a laboratory or company, culminating in the writing of a thesis and an oral defense

	VHS	Coeff	Crédits
Travail Personnel	-	-	-
Stage en laboratoire (ou en entreprise)	250h00	7	10
Séminaires	-	-	-
Mémoire	500h00	10	20
Total Semestre 4	750h00	17	30

	Semester workload	Coeff	Credits
Personal Work	–	–	–
Internship in a laboratory (or in a company)	250h00	7	10
Seminars	–	–	–
Thesis	500h00	10	20
Total Semester 4	750h00	17	30

1- Récapitulatif global de la formation : (indiquer le VH global séparé en cours, TD, pour les 04 semestres d'enseignement, pour les différents types d'UE)

UE / VH	UEF	UEM	UED	UET	S4	Total
Cours	270h00	150h00	67h30	67h30	-	*555h00*
TD	67h30	120h00	22h30	-	-	*210h00*
TP	270h00	45h00	45h00	-	-	*360h00*
Travail personnel	742h30	360h00	15h00	7h30	-	*1125h00*
Mémoire	-	-	-	-	500	*500h00*
Stage	-	-	-	-	250	*250h00*
Total	**1350h00**	**675h00**	**150h00**	**75h00**	**750h00**	***3000h00***
Crédits	**54**	**27**	**6**	**3**	**30**	***120***
% en crédits pour chaque UE	**60%**	**30%**	**6,67%**	**3,33%**	**25%**	***100%***

III - Programme détaillé par matière

(1 fiche détaillée par matière)

Intitulé du Master : Bioinformatics

Semestre *: 01*

Intitulé de l'UE : fondamentale

Intitulé de la matière : Introduction to Informatics

Crédits : 03
Coefficients : 02

Objectifs de l'enseignement :

Understand the operating principle and organization of a computer independently of the production and technology aspects. Instill in the student the concepts of architecture, layer (hardware/software), computer system, etc.

Recommendations: Situate this course in relation to the overall architecture (in layers) of a computer system. The concepts of architecture, layer, realisation can be introduced via illustrative examples from the real world. It is advisable to explain the operation of a VON NEUMANN machine with an algorithmic approach.

Connaissances préalables recommandées :

Basic knowledge of biology, computer and math literacy.

Contenu de la matière :

1. Overview of Informatics in Computing

- What is informatics?
- Role of informatics in understanding biological processes
- Situating the course within the layered architecture of computer systems

2. Understanding Computer Architecture

- Concepts of architecture and organization in computer systems
- Introduction to the Von Neumann architecture
- Components of a computer: CPU, memory, input/output, and storage

3. Layered Architecture of Computer Systems

- Understanding hardware, firmware, and software layers
- Interaction between layers: system calls, drivers, and middleware
- Illustrative examples from real-world scenarios (e.g., data processing in sequencing machines)

4. The Von Neumann Machine

- Principles of operation: fetch, decode, execute cycle

- Representation of data and instructions in binary form
- Algorithmic perspective: designing simple programs for a Von Neumann machine

5. Data Representation and Storage

- How computers store and process data (bits, bytes, and beyond)
- Number systems: binary, hexadecimal, and decimal conversions
- Introduction to memory organization: RAM, ROM, and caches

6. Hardware Components and Functions

- Central Processing Unit (CPU): ALU, registers, control unit
- Memory hierarchy: primary, secondary, and tertiary storage
- Input/output mechanisms: ports, devices, and interfaces

7. Software Layers and Operating Systems

- Operating system as a mediator between hardware and software
- Key concepts: processes, threads, scheduling, and multitasking
- File systems and data management

8. Algorithmic Thinking in Computing

- Basics of algorithm design: steps, pseudocode, and flowcharts
- Simple examples illustrating algorithms in a Von Neumann context
- Problem-solving approaches with computational logic

9. Realization of Layers through Examples

- Illustrative examples connecting concepts to practical systems
- Layered perspective in a DNA sequencer or other biological devices
- Bridging theory with hands-on application

10. Practical Aspects and Applications

- Implementing simple algorithms using basic programming constructs
- Relating computational processes to biological workflows
- Examples of system layering in real-world applications (e.g., bioinformatics pipelines)

11. Introduction to Artificial Intelligence

- Basic concepts of AI and machine learning
- Real-world applications in biology: image analysis, predictive modelling
- Simple AI tools and algorithms for beginners: scikit-learn, Orange

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- "Computer Organization and Design: The Hardware/Software Interface" by David A. Patterson and John L. Hennessy, 1993

- "Structured Computer Organization" by Andrew S. Tanenbaum, 6th edition. Available online: https://csc-knu.github.io/sys-prog/books/Andrew%20S.%20Tanenbaum%20-%20Structured%20Computer%20Organization.pdf

- “Python for Biologists" by Martin Jones, 2013

- “R for Data Science (2e)” by Hadley Wickham, Mine Çetinkaya-Rundel, and Garrett Grolemund, 2016 (originally). Available online: https://r4ds.hadley.nz/

- "Automate the Boring Stuff with Python" by Al Sweigart. 2015 (originally) Available online: https://automatetheboringstuff.com/ :

- "Data Science for Business" by Foster Provost and Tom Fawcett

- “Bioinformatics An Exciting Field of Science - Importance and Applications.” by Abdelkrim Rachedi, JSBB, Vol. 1, Issue 4, 2023. Available online: https://bioinformatics.univ-saida.dz/jsbb/blog-single.php?ar=February_2023LOLBioinformatics_An_Exciting_Field_of_Science

- "Introduction to Bioinformatics" by Arthur M. Lesk, 2002 (originally). Available online: https://edscl.in/pluginfile.php/3340/mod_folder/content/0/Introduction%20To%20Bioinformatics.pdf?forcedownload=1

- "Artificial Intelligence: A Guide to Intelligent Systems" by Michael Negnevitsky, 2002. Available online: https://people.inf.elte.hu/kiss/DB/artificial_intelligence-a_guide_to_intelligent_systems.pdf

- "Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow" by Aurélien Géron, 2017.

- "Data Mining: Practical Machine Learning Tools and Techniques" by Ian H. Witten, Eibe Frank, and Mark A. Hall, 2016

- "The Ethics of Artificial Intelligence" by S. Matthew Liao, 2020

- "Weapons of Math Destruction" by Cathy O’Neil, 2016 https://en.wikipedia.org/wiki/Weapons_of_Math_Destruction

Intitulé du Master : Bioinformatics

Semestre *: 01*

Intitulé de l'UE : fondamentale

Intitulé de la matière : Introduction to Genetics and Molecular Biology

Crédits : 06
Coefficients : 03

Objectifs de l'enseignement:

Provide students with a solid foundational understanding of the fundamental concepts that underpin modern biology. The exploration of the topics such as DNA structure and function, RNA transcription and processing, protein synthesis, and gene regulation, would get students develop the knowledge required to grasp the complexity of cellular and molecular processes. This course aims to equip students with the essential theoretical framework needed to understand how genetic information is inherited, expressed, and manipulated, with a focus on the techniques and technologies that have revolutionized biotechnology and biomedical research. Ultimately, the course prepares students for advanced studies and research in molecular biology, bioinformatics, and related fields, fostering critical thinking and problem-solving skills essential for future careers in science and biotechnology.

Connaissances préalables recommandées :

Basics of biology and genetics concepts.

Contenu de la matière:

1. **Introduction to DNA**
   - Structure of DNA: Double helix, nucleotides, base pairing.
   - DNA Replication: Mechanisms, enzymes (e.g., DNA polymerase), and regulation.
   - DNA Damage and Repair Mechanisms.
2. **Introduction to RNA**
   - RNA Types: mRNA, tRNA, rRNA, snRNA, and their functions.
   - Transcription Process: RNA synthesis, promoters, RNA polymerase, and regulatory factors.
   - RNA Processing: Splicing, 5' capping, polyadenylation.
3. **Introduction to Proteins**
   - Protein Structure: Primary, secondary, tertiary, and quaternary structures.

- Protein Synthesis: Translation process, ribosome function, tRNA and codon recognition.
- Post-Translational Modifications: Phosphorylation, acetylation, ubiquitination.

4. **Regulation of Genetic Expression**
    - Gene Regulation in Prokaryotes: Operons (e.g., lac operon).
    - Gene Regulation in Eukaryotes: Transcription factors, enhancers, silencers.
    - Epigenetic Regulation: DNA methylation, histone modifications.
    - Non-coding RNAs in Regulation: miRNAs, siRNAs, lncRNAs.
5. **Techniques of DNA Recombination**
    - Cloning: Restriction enzymes, ligation, vector systems.
    - PCR (Polymerase Chain Reaction): Amplification techniques.
    - CRISPR-Cas9: Gene editing, applications in research and medicine.
    - Gene Libraries: cDNA libraries, genomic libraries.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- "Molecular Biology of the Cell" by Alberts, Bruce, et al. , 1983
- "Genomes" by T.A. Brown, 2007. Available online: https://www.google.dz/books/edition/Genomes/i0wWBAAAQBAJ?hl=en&gbpv=1&printsec=frontcover
- "Principles of Biochemistry" by Albert L. Lehninger, David L. Nelson, Michael M. Cox, 1970
- "Biochemistry" by Jeremy M. Berg, John L. Tymoczko, Lubert Stryer, 2013. Available online: https://biokamikazi.wordpress.com/wp-content/uploads/2013/10/biochemistry-stryer-5th-ed.pdf
- "Molecular Cloning: A Laboratory Manual" by Michael R. Green and Joseph Sambrook, 2013
- "Genome editing. The new frontier of genome engineering with CRISPR-Cas9", Jennifer A Doudna, Emmanuelle Charpentier, Science Nov 28;346, 2014. Available online: https://pubmed.ncbi.nlm.nih.gov/25430774/
- "CRISPR-Cas9: a powerful and precise genomic editing tool". BENABBOU Taha Ahmed & RACHEDI Abdelkrim, JSBB, Vol. 1, Issue 3, 2022. Available online: https://bioinformatics.univ-saida.dz/jsbb/blog-single.php?ar=December_2022LOLCRISPR_powerful_precise_genome_edtn

Intitulé du Master : Bioinformatics
Semestre *: 01*

Intitulé de l'UE : fondamentale

Intitulé de la matière : Introduction to Bioinformatics

Crédits : 03
Coefficients : 02

Objectifs de l'enseignement :

This Introduction to Bioinformatics aims to establish a comprehensive base in both theoretical and practical aspects of the field. The learning objectives focus on introducing students to the broad scope and significance of bioinformatics, ingraining fundamental concepts of molecular biology tailored for computational analysis, and developing essential programming skills specific to bioinformatics applications. A strong emphasis is placed on understanding and applying statistical methods to biological data, crucial for data analysis and interpretation. The lab work and assignments, where students apply their theoretical knowledge to real-world scenarios, should enhance their problem-solving and analytical skills. This foundational knowledge sets the stage for more advanced study and research in bioinformatics, ensuring students are well-equipped to tackle complex challenges in the field.

Connaissances préalables recommandées :

Basic knowledge and understanding of biology and molecular biology

Contenu de la matière :

1. Foundations of Bioinformatics

- **Introduction to Bioinformatics**
  - Definition, scope, and applications across biology, chemistry, and computer science.
  - Overview of bioinformatics tools and databases.
  - Overview of key bioinformatics applications

- **Biological Data Overview**
  - Types of data: DNA, RNA, proteins, and small molecules.
  - Central Dogma of Molecular Biology.
- **Essential Biology Concepts** (for non-biology students)
  - Genes, genomes, and genetic variation.
  - DNA sequencing techniques.

2. Computational Fundamentals

- **Key Algorithms in Bioinformatics**
  - Pairwise and multiple sequence alignment (e.g., Needleman-Wunsch, BLAST).

- Phylogenetic tree construction.

3. Bioinformatics Databases and Tools

- **Key Bioinformatics Databases**
  - GenBank, UniProt, PDB, KEGG, and ChEMBL.
  - Data retrieval and querying (e.g., NCBI tools, Entrez).
- **Sequence Analysis Tools**
  - Hands-on with BLAST, Clustal Omega, and MAFFT.
- **Protein Structure Analysis**
  - Introduction to structural bioinformatics.
  - 3D visualization tools (e.g., PyMOL, Chimera).

4. Omics Data Analysis

- **Genomics**
  - Genome annotation and analysis.
  - Introduction to Next-Generation Sequencing (NGS) data.
- **Transcriptomics**
  - RNA sequencing and expression analysis.
  - Functional annotation (e.g., GO, pathway enrichment).
- **Proteomics and Metabolomics**
  - Basics of protein identification and quantification.
  - Small molecule analysis and chemical informatics.

5. Practical Applications and Case Studies

- **Drug Discovery**
  - Basics of cheminformatics and molecular docking.
  - Applications in pharmacogenomics.
- **Disease Genomics**
  - Bioinformatics in personalized medicine and disease research.
- **Environmental and Evolutionary Bioinformatics**
  - Metagenomics and microbial diversity studies.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. "Fundamental concepts of bioinformatics" by Krane, D.E. et Raymer, M.L. (2003) Benjamin Cummings (ISBN 0-8053-4633-3)
2. "Introduction to Bioinformatics" by M. Lesk, 2002 (originally). Available online: https://edscl.in/pluginfile.php/3340/mod_folder/content/0/Introduction%20To%20Bioinformatics.pdf?forcedownload=1

3. "Bioinformatics Algorithms: An Active Learning" by Compeau P. & Pevzner P. (2018) Approach (ISBN: 978-0990374633) - https://www.bioinformaticsalgorithms.org/read-the-book

"Journal of Concepts in Structural Biology & Bioinformatics" by University of Saida (2022) (ISSN: 2830-8832) - A national scientific journal https://bioinformatics.univ-saida.dz/jsbb/

Intitulé du Master : Bioinformatics

Semestre *: 01*
Intitulé de l'UE : UEF1 fondamentale
Intitulé de la matière : Introduction to Molecular Modeling
Crédits : 03
Coefficients : 02

Objectifs de l'enseignement :

This module introduces students with a theoretical foundations of molecular modeing techniques used in bioinformatics. At the end the students will master key concepts of computational Quantum Chemistry, molecular Mechanics, Energy Minimization and molecular Dynamics Simulations which are essential skills for bioinformaticians.

Connaissances préalables recommandées :

Basic concepts of general chemistry, mechanics, thermodynamics, and mathematics.

Contenu de la matière :

- **Useful Concepts of Molecular Modelling:**
    - General overview of matter modelling.
    - Importance of molecular modelling in bioinformatics and biomedical research.
    - Coordinate Systems
    - Potential Energy surfaces
    - Molecular Garphics
- **Introduction to Computational Quantum Chemistry:**
    - Foundations of quantum mechanics.
    - Hydrogen like atoms
    - Polyelectronic Atoms and Molecules
    - Molecular Orbital Calculations
    - Hartree-Fock Method
    - Basis Sets
    - Molecule properties calculation
    - Molecular orbital Theories
    - Empirical and Semi-empirical methods
- **Molecular Mechanics Force Field Model**
    - General Features of Molecular Mechanics Force fields
    - Pair Potential Approximation
    - Simple Force field Model
    - Bond stretching
    - Angle Bending
    - Torsional terms
    - Improper Torsions and out-of-plane bending Motions
    - Cross Terms
    - Non bonded Interactions

- Electrostatic Interactions
    - Van der Waals Interactions
    - Many Body effects
    - Effective Pair Potential
- **Energy minimization and potential surface exploration**
    - General Overview
    - Non derivative Minimization Methods
    - First order Minimization Methods
    - Second derivative Minimization Methods
    - Minimization methods choice
    - Energy minimization
- **Introduction to Molecular Dynamics Simulation**
    - Molecular Dynamics of simple models (discontinuous Potential)
    - Molecular Dynamics with continuous Potential
    - Setting up and running Molecular Dynamics simulations

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. *SZABO, Attila et OSTLUND, Neil S. Modern quantum chemistry: introduction to advanced electronic structure theory. Courier Corporation, 1996.*
2. *KAUZMANN, Walter. Quantum chemistry: an introduction. Elsevier, 2013.*
3. *VESZPRÉMI, Tamás et FEHÉR, Miklós. Quantum chemistry: fundamentals to applications. Springer Science & Business Media, 2012.*
4. *K. Binder and D. W. Heermann, Monte Carlo Simulation in Statistical Physics, An introduction, Springer, 2002.*
5. *Antony K. Rappé and Carla J. Casewit, Molecular Mechanics across Chemistry, University Sciences Books, 1997.*
6. *Andrew R. Leach, Molecular Modelling, Pearson Prentice Hall,*
7. *Frank Jensen, Intriduction to Computational Chemistry, John Wiley and Sons, 2007*
8. *Christopher J. Cramer, Essentials of Computational Chemistry, John Wiley and Sons*

Intitulé du Master : Bioinformatics

Semestre *: 01*
Intitulé de l'UE : méthodologie
Intitulé de la matière : Structural Bioinformatics and Biology
Crédits : 06
Coefficients : 03

Objectifs de l'enseignement :

Structural Bioinformatics is a sub-field of Structural Biology which deals with studies relevant to 3D-structures of biomolecules (Protiens, DNA, RNA) and their biological function.

The primary objective of this course is to provide students with a foundational understanding of structural bioinformatics, equipping them to analyze and interpret the structures of biomolecules such as proteins, DNA, and RNA. Through a combination of theoretical knowledge and practical exercises, students will gain insights into the principles governing biomolecular structure, folding, and function, as well as the methods used to determine and predict these structures. The course aims to develop interdisciplinary skills, enabling students from diverse fields to utilize computational tools for structural analysis, understand structure-function relationships, and apply their knowledge to address challenges in areas such as drug discovery, molecular biology, and computational chemistry.

Connaissances préalables recommandées : Basic knowledge in Biochemistry and Biology in general

Contenu de la matière :

1. General Introduction

- Definition and scope of structural bioinformatics
- Importance of structural bioinformatics in modern biology, chemistry, and drug discovery
- Overview of biomolecular structures and their significance

2. Fundamentals of Structure of Proteins, DNA, and RNA

- Primary, secondary, tertiary, and quaternary structures of biomolecules
- Characteristics and examples:
  - Protein domains and motifs (e.g., alpha-helices, beta-sheets)
  - DNA double helix and forms (A, B, Z)
  - RNA secondary structures (e.g., hairpins, loops)
- Chemical interactions stabilizing biomolecular structures

3. Introduction to Determination Methods of Protein Structures

X-ray Crystallography

- Principles: diffraction, Bragg's law, and electron density maps
- Applications and limitations
- Example: Determination of enzyme active sites

Nuclear Magnetic Resonance (NMR)

- Basics of NMR spectroscopy
- Role in identifying dynamic structures in solution
- Examples: Protein-ligand interaction studies

Cryogenic Electron Microscopy (Cryo-EM)

- Key principles: single-particle analysis and 3D reconstruction
- Advantages over other techniques for large complexes
- Applications in studying ribosomes and viruses

4. Thermodynamics and Kinetics of Protein Folding

- Gibbs free energy landscape of protein folding
- Levinthal's paradox and its implications
- Role of molecular chaperones in folding
- Experimental techniques for studying folding (e.g., fluorescence, circular dichroism)

5. Protein Folding: Determination of Intermediate and Transition States

- Transition state theory and folding pathways
- Folding intermediates: molten globule state
- Methods for characterizing folding intermediates (e.g., hydrogen-deuterium exchange)
- Examples: Folding studies of lysozyme and myoglobin

6. Description of Intra- and Inter-Molecular Interactions in Biomolecules

- Types of interactions:
  - Hydrogen bonds, van der Waals forces, ionic interactions
  - Hydrophobic effects and disulfide bonds
- Case studies:
  - Protein-ligand interactions (e.g., drug binding to receptors)
  - DNA-protein interactions (e.g., transcription factors)

7. Structural Aspects of Protein-DNA Interactions

- Specific vs. non-specific binding
- Structural basis of recognition (e.g., helix-turn-helix, zinc fingers)
- Examples: Restriction enzymes, transcription factors (e.g., TATA-binding protein)

8. Structural Motifs and Related Research and Databases

- Common motifs: beta-barrels, alpha-beta folds, and coiled coils
- Databases:
  - PFAM (Protein families)
  - InterPro
- Applications in predicting structural function

9. Protein Structural Alignment/Superposition Methods

- Principles of structural alignment
- Tools: TM-align, DALI, CE
- Applications: Comparison of homologous proteins and evolutionary studies

10. Introduction to Structural Bioinformatics

- Overview of computational methods for:
  - Protein folding prediction (e.g., AlphaFold)
  - Structure stability analysis
  - Protein-protein and protein-ligand interactions
- Example workflows for practical applications

11. Structural Characteristics of Proteins Involved in Conformational Diseases

- Misfolding and aggregation mechanisms
- Examples: Prion proteins in Creutzfeldt-Jakob disease, beta-amyloid in Alzheimer's disease
- Therapeutic approaches targeting misfolded proteins

12. Structural Databases

- **PDB**: Structure storage and access
- **CATH**: Protein structure classification
- **SCOP**: Hierarchical classification of protein domains
- **UniProt**: Functional annotations linked to structures
- **mmCIF**: Data formats for structural files

13. Fundamentals of Structure-Function Relationship

- Key concepts:
  - Structure quality evaluation (e.g., Ramachandran plots)
  - Energy minimization in structures using force fields
  - Active site identification using computational tools (e.g., CASTp, SiteFinder)
- Tools for visualizing structure-function relationships: PyMOL, Chimera

14. Lab Work and Assignments

- **Molecular Visualization**:
  - Tools: PyMOL, Chimera
  - Visualizing protein-ligand interactions
- **Structural Alignment Application**:
  - Comparing homologous proteins using DALI or TM-align
- **Active Site Identification**:
  - Practical with tools like CASTp or AutoDock
- **Additional Projects**:
  - Structure-based drug design (mini project)
  - Predicting structural stability under mutations

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. Megharbi M. E., bitar M. and Rachedi A. (2023). **Structural and Functional Binding Motifs in Porphyrin Proteins: Insights into Ligands and Biological Function**. JSBB 2:2 - https://bioinformatics.univ-saida.dz/jsbb/blog-single.php?ar=August_2023LOLPorphyrin_Proteins_Binding_Structural_Motifs

2. University of Saida (2022) **Concepts in Structural Biology & Bioinformatics** (ISSN: 2830-8832) - A national scientific journal https://bioinformatics.univ-saida.dz/jsbb/

Intitulé du Master : Bioinformatics

Semestre *: 01*
Intitulé de l'UE : méthodologie
Intitulé de la matière : Biostatistics – Introduction to Statistical Data Analysis
Crédits : 04
Coefficients : 02

Objectifs de l'enseignement :

The main objectives of this course are to:

- Equip students with basic statistical vocabulary.

- Enable students to handle datasets.

- Teach students basic statistics analysis

Connaissances préalables recommandées : Mathematics, Statistics

Contenu de la matière :

Chapter 01: Descriptive Statistics

a) Variables and distributions
b) Measures of central tendency
c) Measures of dispersion
d) Graphical representation

Chapter 02: Estimation

a) Point estimation
b) Confidence interval estimation

Chapter 03: Statistical Tests

a) Test of comparison with a standard value
   - Tests related to a mean
   - Tests related to a frequency or a percentage
b) Test of comparison between two populations
   - Test of comparison between two means
   - Test of comparison between two percentages
c) Chi-square test
   - Chi-square goodness-of-fit test
   - Chi-square test of independence

Chapter 04: Correlation

a) 1-Correlation coefficient
b) 2- scatter diagrams
c) 3- Calculation of the correlation coefficient

d) 4- Significance test
e) 5- Spearman rank correlation

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- CARRAT,F, 2011 : BIOSTAISTIQUE, faculté de médecine PIERRE ET MARIE CURIE, 179 pages.

- FENELON (J.P), 1988 : Statistiques et informatique appliquée – dunod, Paris France .420p.

- "The Analysis of Biological Data" by Michael C. Whitlock and Dolph Schluter, July 1, 2008

- "Introduction to Probability and Statistics for Engineers and Scientists" By Sheldon M. Ross · 2014

- "Biostatistics for the Biological and Health Sciences" by Marc M. Triola and Mario F. Triola - 2018

Intitulé du Master : Bioinformatics
Semestre *: 01*
Intitulé de l'UE : méthodologie (UEM2)
Intitulé de la matière : Mathematics for biology
Crédits : 02
Coefficients : 02

Objectifs de l'enseignement :

Bioinformatics relies heavily on mathematical principles such as statistics, linear algebra, and calculus for algorithms used in sequence alignment, machine learning, and structural biology. Furthermore, high-throughput technologies like next-generation sequencing (NGS) generate massive datasets.

Mathematics is a universal language that allows bioinformaticians to translate biological questions into computational solutions.

Connaissances préalables recommandées : Basic knowledge of linear algebra, calculus, probability and statistics. This is in addition to some familiarity with molecular biology.

Contenu de la matière :

1. **Fundamentals**

- Basic linear algebra and statistics.
- Biological data structures and mathematical representations.

2. **Applications in Bioinformatics**

- Probability in sequence alignment.
- Differential equations in metabolic modelling.

3. **Tools and Techniques**

- Graph algorithms for network analysis.
- PCA and clustering methods for transcriptomics data.

4. **Advanced Topics**

- Optimization methods in drug design.
- Simulation techniques in systems biology.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- "Mathematics for the Life Sciences" by Erin N. Bodine, Suzanne Lenhart, and Louis J. Gross, 2014
- "A Biologist's Guide to Mathematical Modeling in Ecology and Evolution" by Sarah P. Otto and Troy Day, 2007
- "The Analysis of Biological Data" by Michael C. Whitlock and Dolph Schluter, July 1, 2008
- “Introduction to Probability and Statistics for Engineers and Scientists” By Sheldon M. Ross · 2014
- "Introduction to Computational Biology: Maps, Sequences, and Genomes" by Michael S. Waterman – 1995
- "Introduction to Computational Biology: Maps, Sequences, and Genomes" by Michael S. Waterman
- “Graphs, Networks and Algorithms” By Dieter Jungnickel · 2013
- "Bioinformatics Algorithms: An Active Learning Approach" by Phillip Compeau and Pavel Pevzner - 2015

Intitulé du Master : Bioinformatics
Semestre *: 01*
Intitulé de l'UE : découverte
Intitulé de la matière : Databases basics
Crédits : 01
Coefficients : 01

Objectifs de l'enseignement :

Provide students with foundational knowledge and practical skills to manage, query, and interpret biological data using databases. Students will explore how databases are structured, how to retrieve and analyze data using Structured Query Language (SQL), and how databases are used in solving real-world bioinformatics problems. By the end of the course, students should be able to design simple databases, work with biological datasets, and understand the role of database systems in integrating and managing large-scale biological information.

Connaissances préalables recommandées : No prior experience with databases or programming is required, though an introductory understanding of data organization (e.g., tables or spreadsheets) will be helpful.

Contenu de la matière :

1. Introduction to Databases
   - Importance of databases in bioinformatics.
   - Overview of types of databases: relational, non-relational, hierarchical, graph-based.
   - Examples of bioinformatics databases (GenBank, PDB, UniProt, Ensembl).
2. Fundamental Database Concepts
   - Basic terminologies: schema, table, field, record, primary/foreign key.
   - Relational database principles.
   - Understanding Entity-Relationship (ER) models.
3. Structured Query Language (SQL)
   - Basics of SQL syntax and commands.
     - SELECT, INSERT, UPDATE, DELETE.
     - WHERE, JOIN, GROUP BY, ORDER BY.
   - Practical examples using bioinformatics datasets.

4. Biological Databases and Their Formats
   - Sequence databases: FASTA, GenBank.

- Structural databases: PDB, mmCIF.
- Annotation and functional databases: Gene Ontology, KEGG.

5. Database Management Systems (DBMS)
   - Overview of common DBMSs: MySQL, PostgreSQL, MongoDB.
   - Comparative use in bioinformatics research.
6. Data Integration in Bioinformatics
   - Linking biological datasets using keys and relationships.
   - Cross-referencing data from different databases.
   - Challenges in database interoperability.
7. Designing and Building Databases
   - Basics of database design for bioinformatics applications.
   - Normalization and optimization of schemas.
   - Practical exercise: designing a database for sequence or structural data.
8. Advanced Database Topics
   - Indexing and query optimization.
   - Introduction to NoSQL databases and their applications in bioinformatics.
   - Big data management in bioinformatics.
9. Hands-On Practical Sessions
   - Setting up and managing a local database for bioinformatics.
   - Retrieving data using APIs (e.g., NCBI Entrez, UniProt API).
   - Case study: querying and analyzing a bioinformatics database.
10. Ethics and Data Sharing
    - Data privacy and security in bioinformatics.
    - Open data policies and licensing considerations.
11. Project Work
    - A mini-project where students design, implement, and query a database to solve a bioinformatics problem (e.g., storing and analyzing a protein family dataset).
12. Wrap-Up and Future Directions
    - Emerging trends in database technologies (e.g., cloud-based bioinformatics databases).
    - Recap and preparation for advanced bioinformatics tools and workflows.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

Books: Databases and Bioinformatics

1. "Database System Concepts" by Abraham Silberschatz, Henry F. Korth, S. Sudarshan
2. "Fundamentals of Database Systems" by Ramez Elmasri, Shamkant B. Navathe
3. "Developing Bioinformatics Computer Skills" by Cynthia Gibas, Per Jambeck
4. "Bioinformatics: Sequence and Genome Analysis" by David W. Mount
5. "SQL for Data Scientists: A Beginner's Guide for Building Datasets for Analysis" by Renee M. P. Teate
6. "Bioinformatics Databases and Systems" by Stanley I. Letovsky

Online Resources

1. NCBI Database Tutorials
    - Website: https://www.ncbi.nlm.nih.gov/guide/training-tutorials/
2. UniProt Help and Tutorials
    - Website: https://www.uniprot.org/help/
3. Coursera: Databases and SQL for Data Science
    - Website: https://www.coursera.org/learn/sql-data-science
4. ELIXIR Training Materials
    - Website: https://elixir-europe.org/platforms/training
5. The Open Bioinformatics Foundation (OBF)
    - Website: https://www.open-bio.org/

Intitulé de la matière : Logiciels libres et open source   Semestre : 1   Type : UED

VHS : 22h30   VHH : 01h30   Cours : 00h30   TD : 00h00   TP : 01h00

VHS travail personnel : 02h30   Coefficient : 01   Crédit : 01

Objectifs de l'enseignement

L'objectif est d'approfondir l'utilisation des logiciels libres pour la recherche en sciences de la nature et de la vie, de développer des compétences avancées en gestion et analyse de données, de concevoir des projets en open science appliqués à la biologie et à l'écologie, et de se former à des outils scientifiques ouverts et collaboratifs.

Connaissances préalables recommandées

Découverte des logiciels libres et open source, initiation à la programmation informatique.

Contenu de la matière

Cours : 07h30

Chapitre I : Open Science et gestion avancée des données (01h30)

1. Définition et enjeux de l'open science
2. Principes de la reproductibilité scientifique
3. Formats ouverts et interopérabilité des données
4. Workflow collaboratif avec Git et GitHub

Chapitre II : Programmation avancée et automatisation (01h30)

1. Scripts Bash avancés pour l'automatisation
2. Utilisation de bibliothèques telles que NumPy, Pandas, Seaborn pour explorer et modéliser des jeux de données.
3. Visualisation avancée des données
3.1. Création de tableaux de bord interactifs
3.2. Création de graphiques de bord interactifs

Chapitre III : Outils Open Source et applications en biologie (01h30)

1. Analyse des séquences génomiques avec Biopython
2. Traitement des données avec EMBOSS
3. Visualisation d'arbres phylogénétiques
4. Modélisation de l'expression génique
5. Simulation de réseaux cellulaires avec COPASI
6. Modélisation de dynamiques avec CellDesigner

7. Analyse intégrée des données multi-omiques avec Galaxy
8. Statistiques et visualisation en R

Chapitre IV : Applications avancées des logiciels open source en sciences de la nature et de la vie (03h00)

1. Analyse d'images scientifiques (ImageJ / Fiji)
1.1. Comptage et mesure sur images microscopiques.
1.2. Analyse en fluorescence, histologie, etc.
2. Modélisation de systèmes biologiques (COPASI / NetLogo)
2.1. Simulation de réactions et dynamiques de populations.
2.2. Études de sensibilité.
3. Rédaction et gestion de projet (LibreOffice / Zotero / Git)
3.1. Rédaction de rapports, gestion de références.
3.2. Versionnage et reproductibilité (RMarkdown / Jupyter).
4. Cartographie et science ouverte (QGIS / Zenodo)
4.1. Cartographie de données écologiques.
4.2. Partage de données et pratiques ouvertes.

Travaux pratiques : 15h00

TP 1 : Développement collaboratif et open science (05h00)
- Workflow de recherche reproductible avec Git et GitHub
- Utilisation avancée de Jupyter Notebook, NumPy, Pandas, ..etc. pour documenter une analyse

TP 2 : Analyse de données avec QGIS (05h00)
- Analyse spatiale d'une aire protégée avec QGIS
- Traitement et modélisation de données biologiques (exp : répartition des espèces)

TP 3 : Projet Open Science en SNV (05h00)
- Application des méthodes libres à une problématique en SNV
- Présentation des résultats sous forme d'un rapport et d'une visualisation interactive

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d'évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)
- Examen semestriel en présentiel (60%).
- Évaluation continue (CC) (40%) sous forme d'au moins 3 composantes : interrogations écrites, devoirs à domicile, travail personnel, exposés, tests, comptes rendus, etc.

Deux des trois composantes doivent se dérouler impérativement en présentiel. La nature des 3 composantes et leurs pondérations sont laissées l'appréciation de l'équipe pédagogique.

Références bibliographiques

1. Berman, J., & Korman, A. (2021). Data science for the open world: Tools for open science and collaboration. O'Reilly Media.

2. Ghosh, P., & Kessler, G. (2023). Advanced Python for data analysis: Techniques and libraries for scientific computing. Springer.

3. He, W., & Liu, Z. (2022). Open source software for bioinformatics: Tools and techniques for computational biology. Wiley.

4. McKinney, W. (2020). Python for data analysis (3rd ed.). O'Reilly Media.

5. Willink, P., & Smith, R. (2024). Open science: Sharing knowledge for sustainable development. Elsevier.

Intitulé de la matière : Communication Semestre :01 Type : UET
VHS : 22h30 VHH : 01h30 Cours : 01h30 TD : / TP : /
VHS travail personnel : 00h00 Coefficient : 01 Crédit : 01

Objectifs de l'enseignement

Cette matière a pour objectif de développer chez les étudiants une maîtrise des infrastructures et outils TIC, l'optimisation du traitement des données et l'innovation scientifique, afin de soutenir la recherche efficace en sciences de la vie et de la nature.

Connaissances préalables recommandées : aucune.

Contenu de la matière

Cours : 22h30

Chapitre 1 : Fondamentaux et enjeux des TIC, de la communication et de la recherche documentaire (03h00)

1. Définition et concepts des TIC
2. Historique et évolution des technologies
3. Enjeux des TIC dans la recherche et l'enseignement
4. Notions fondamentales de la communication
5. Introduction à la méthodologie de recherche documentaire

Chapitre 2 : Infrastructures et sécurité des réseaux de communication (03h00)

1. Architecture des réseaux de communication
2. Technologies de transmission de données et systèmes sans fil
3. Internet, protocoles et communications assistées par ordinateur
4. Sécurité des réseaux et cryptographie
5. Fiabilité et protection des échanges de données

Chapitre 3 : Outils et méthodes du traitement de l'information (03h00)

1. Bases de données et logiciels spécialisés
2. Techniques de data science et intelligence artificielle
3. Cloud computing et infrastructures virtualisées
4. Stratégies de recherche documentaire (mots-clés et opérateurs booléens)
5. Évaluation de la qualité et de la pertinence des ressources

Chapitre 4 : Rédaction et gestion de la communication écrite (04h30)

1. Rédaction de courriers électroniques professionnels
2. Création de CV, lettres de motivation et demandes manuscrites
3. Structure et rédaction d'articles scientifiques (IMReD)
4. Techniques de rédaction académique et bureautique
5. Gestion des références bibliographiques et normes de citation

Chapitre 5 : Communication orale et supports multimédias (04h30)

1. Principes de la communication orale
2. Planification et préparation des discours
3. Création et conception de diapositives et supports visuels
4. Transposition de l'écrit à l'oral et vulgarisation scientifique
5. Utilisation des réseaux sociaux et médias numériques

Chapitre 6 : Applications spécifiques, innovation et enjeux éthiques (04h30)

1. Applications TIC dans les sciences de la vie et de la nature
2. Technologies de la télémédecine et santé connectée
3. Veille technologique et intégration des innovations
4. Enjeux éthiques, intégrité scientifique et lutte contre le plagiat

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d'évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)

- Examen semestriel en présentiel (100%).

Références bibliographiques

1. Braunschweig, P., & Saldaña, A. (2020). Technologies de l'information et de la communication en sciences et enseignement supérieur. Éditions de l'Université.

2. Jenkins, H., & Green, M. (2021). Understanding digital communication in the scientific world. Oxford University Press.

3. Liu, Y., & Thompson, D. (2022). Cloud computing and the future of data science in education. Springer.

4. Smith, R. J., & Williams, M. (2023). Cryptography and network security: A practical guide for researchers. Wiley.

5. Zhao, X., & Zhang, L. (2024). The impact of AI on modern communication and research. Cambridge University Press.

- Practice sessions: presenting research ideas or short topics.

2. Collaborative Communication
   - Techniques for teamwork and interdisciplinary discussions.
   - Writing collaboratively: protocols, group projects, and feedback.

3. Advanced Writing and Review Techniques
   - Preparing manuscripts for scientific journals.
   - Responding to peer reviews.
   - Writing cover letters and professional emails.

4. Ethics and Responsible Communication
   - Avoiding plagiarism and ethical considerations in scientific writing.
   - Citing and acknowledging contributions appropriately.

5. Applied Projects and Practice
   - Conducting a mini bibliographic research project.
   - Writing and presenting a short scientific article.
   - Group discussions and peer reviews.

Mode d'évaluation :

1. Written assignments (e.g., summaries, short reports): 30%.
2. Bibliographic research project and presentation: 30%.
3. Oral presentations: 20%.
4. Participation in discussions and activities: 20%.

Références *(Livres et polycopiés, sites internet, etc).*

Books on Scientific Writing and Communication:

1. "The Elements of Style" by William Strunk Jr. and E.B. White

2. "Scientific Writing and Communication: Papers, Proposals, and Presentations" by Angelika H. Hofmann

3. "How to Write and Publish a Scientific Paper" by Robert A. Day and Barbara Gastel

4. "Writing in the Sciences" by Jennifer S. Peat, Heather S. Elliott, and Ruth B. Baur

5. "The Craft of Scientific Writing" by Michael Alley

Books on Scientific English:

1. "English for Academic Research: Writing Exercises" by Adrian Wallwork

2. "Academic Writing for Graduate Students: Essential Tasks and Skills" by John M. Swales and Christine B. Feak

3. "English for Research Publication Purposes" by Adrian Wallwork

Bibliographic Research & Citation Management:

1. "The Chicago Manual of Style" (17th Edition)

2. "Cite Them Right: The Essential Guide to Referencing and Plagiarism" by Richard Pears and Graham Shields

3. "RefWorks for Dummies" by Brian G. K. Chan

4. "Zotero 101: A Step-by-Step Guide to Collecting, Organizing, and Sharing Your Research" by Devon A. Maloney

Oral Communication in Science:

1. "The Presentation Coach: Bare Knuckle Brilliance for Every Presenter" by Graham Shaw

2. "The Science of Writing and Presenting" by John S. H. B. Jackson

3. "TED Talks: The Official TED Guide to Public Speaking" by Chris Anderson

4. "Speak Up: An Illustrated Guide to Public Speaking" by Douglas M. Fraleigh and Joseph S. Tuman

Ethics and Plagiarism:

1. "Ethics in Science: Ethical Misconduct in Scientific Research" by John I. Braxton and Keith E. Peters

2. "Plagiarism: A Study in the Social Context of Science" by David A. Kronick

Intitulé du Master : Bio-informatics
Semestre *: 02*
Intitulé de l'UE : fondamentale
Intitulé de la matière : Programming I (Python)
Crédits : 06
Coefficients : 03

Objectifs de l'enseignement :

Completing this Python course offers numerous benefits that can significantly enhance programming skills and career opportunities. Firstly, students will gain a solid foundation in Python, a versatile and widely-used language applicable in various fields such as web development, data analysis, and automation. The course will help students to develop critical thinking and problem-solving abilities as he tackle coding challenges and engage in hands-on projects, including a capstone project that enhances his portfolio.

Connaissances préalables recommandées : Basic computer skills, Basic programming concepts (optional), Basic mathematical skills, Internet, and Text editor or IDE knowledge

Contenu de la matière :

1. Python Basics
    - Introduction to Python
    - Variables and Data Types
    - Control Structures
    - Functions
    - Data Structures
    - Input and Output
    - Error Handling

2. Intermediate Python
    - Modules and Packages
    - Object-Oriented Programming (OOP)
    - Working with Libraries
    - Comprehensions
    - Regular Expressions
    - File Handling
    - Introduction to Testing

3. Advanced Topics
    - Decorators and Generators
    - Context Managers
    - Multithreading and Multiprocessing
    - Web Development Basics
    - APIs and Web Scraping
    - Data Visualization
    - Advanced Data Manipulation

4. Capstone Project
    - Project Planning
    - Project Development
    - Testing and Debugging
    - Documentation
    - Presentation
    - Review and Next Steps

Mode d'évaluation : 1 practical exam 100%

Références *(Livres et polycopiés, sites internet, etc).*

- Official Python Documentation (docs.python.org)
- Youtube:
    - Codezilla channel
    - Corey Schafer channel

Intitulé du Master : Bioinformatics
Semestre *: 02*
Intitulé de l'UE : fondamentale
Intitulé de la matière : Omics: from genomes to metabolomes
Crédits : 06
Coefficients : 03

Objectifs de l'enseignement :

The objective of this teaching unit is to introduce students to modern methods of analysing the evolution and functioning of genomes: comparative genomics, metagenomics, transcriptomics, proteomics and metabolomics along with data analysis and integration.

Connaissances préalables recommandées : The course should have minimal mandatory prerequisites but provide foundational concepts where necessary.

Contenu de la matière :

1. Introduction to Omics Sciences
- Overview of Omics and its significance
- Interdisciplinary nature of Omics (biology, chemistry, and computer science perspectives)
- High-throughput technologies and big data in Omics

2. Genomics: Deciphering the Blueprint of Life
- Genome organization and sequencing technologies
- Comparative and functional genomics
- Genome annotation and computational approaches
- Bioinformatics tools for genome analysis

3. Transcriptomics: Understanding Gene Expression
- RNA sequencing and microarrays
- Gene expression analysis methods
- Regulation of transcription and RNA modifications
- Applications in disease and biotechnology

4. Proteomics: The Functional Machinery of the Cell
- Protein structure, function, and interactions
- Mass spectrometry and proteomic data analysis
- Post-translational modifications
- Computational proteomics and structural bioinformatics

5. Metabolomics: The Chemical Fingerprint of Life
- Metabolites and their roles in cellular function
- Analytical techniques: NMR, LC-MS, GC-MS

- Data integration and pathway analysis
- Applications in medicine, agriculture, and biotechnology

6. Systems Biology and Multi-Omics Integration

- Principles of systems biology
- Combining genomics, transcriptomics, proteomics, and metabolomics
- Data integration challenges and computational tools
- Applications in personalized medicine and synthetic biology

7. Ethical, Legal, and Social Implications of Omics Research

- Data privacy and ethical concerns in Omics studies
- Open science and data sharing policies
- Implications for healthcare and biotechnology

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

General Omics References

1. Omics Approaches in Plant Biotechnology – A. K. Shukla & R. K. Singh (Springer, 2022)
2. Omic and Multimodal Approaches to Cancer – J. N. Weinstein et al. (Springer, 2014)
3. Omics Technologies and Bio-Engineering: Volume 1 & 2 – A. K. Srivastava & A. P. Sharma (Academic Press, 2018)

Genomics

4. Genomes 4 – T. A. Brown (Garland Science, 2018)
5. Bioinformatics and Functional Genomics – P. Pevsner (Wiley-Blackwell, 2015)
6. Genetics: A Conceptual Approach – D. S. Passarge (Macmillan, 2021)

Transcriptomics

7. Transcriptomics: Advances in Genome Science – B. Oliver, J. M. Marín de Evsikova, & M. I. Arnone (Elsevier, 2022)
8. RNA-Seq: Principles and Applications – J. Wang et al. (Springer, 2020)

Proteomics

9. Introduction to Proteomics: Tools for the New Biology – D. Liebler (Humana Press, 2001)
10. Proteome Research: Two-Dimensional Gel Electrophoresis and Identification Methods – T. Rabilloud (Springer, 2000)

Metabolomics

11. Metabolomics: Practical Guide to Metabolite Profiling – J. S. Edmonds & N. W. L. Owen (Wiley, 2018)
12. Metabolomics: Methods and Protocols – X. Zhou, X. Lu, & G. Xu (Springer, 2019)

Systems Biology and Multi-Omics Integration

13. Foundations of Systems Biology – H. Kitano (MIT Press, 2002)
14. Systems Biology: Concepts and Application – A. Cascante & J. L. Santos (Springer, 2021)
15. Multi-Omics Approaches to Disease - J. Hasin, M. Seldin, & A. Lusis (*Genome Biology*, 2017)

Intitulé du Master : Bioinformatics
Semestre : S2
Intitulé de la matière : Advanced Molecular Modeling
Unité d'enseignement : UEF1 (Fondamentale)
Crédits : 06
Coefficients : 03

Objectifs de l'enseignement (*Décrire ce que l'étudiant est censé avoir acquis comme compétences après le succès à cette matière – maximum 3 lignes).*

This module aims to deepen students' understanding of computational techniques applied to real biological systems, focusing on analyzing their complex structural, thermodynamic, and physical properties, as well as their biological activities.

Connaissances préalables recommandées (*descriptif succinct des connaissances requises pour pouvoir suivre cet enseignement – Maximum 2 lignes).*

Students should have a solid foundation in molecular modeling, as covered in the first semester

Contenu de la matière:

1. **Advanced Computational Quantum Chemistry**
   - Electron Correlation
   - Post-Hartree-Fock Methods.
   - Density Functional Theory
   - Practical Considerations to perform ab initio Calculation
   - Quantum Chemistry Methods for Studying Biological Systems
   - Applications Using the open-source software as GAMESS
2. **Advanced Molecular Dynamics**
   - Constraint Molecular Dynamics
   - Molecular Dynamics at Constant Temperature
   - Molecular Dynamics at Constant pressure
   - Molecular Dynamics Simulation for Biomolecule
   - Applications Using Molecular Dynamics Open-source Software as GROMACS
3. **Computer Simulation Methods**
   - Thermodynamic Properties
   - Time Dependent Properties
   - Structural Properties
   - Phase space
   - Boundaries
   - Truncating the Potential and the Minimum Image Convention.
   - Practical Aspects of Computer simulation
   - Analyzing the results of Simulation and Estimating Errors.

4. **Quantitative Structure Activity Relationship**
   - Definition, Scope, and Historical Development of QSAR Models
   - Types of QSAR Models
   - Molecular Descriptors
   - Dataset Preparation for QSAR Studies
   - Statistical Methods in QSAR
   - 3D-QSAR and Molecular Modeling
   - Machine Learning in QSAR
   - Using QSAR Software
   - Building and Validating a QSAR Model Step-by-Step
   - Interpretation of QSAR Results in Drug Discovery

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. *VESZPRÉMI, Tamás et FEHÉR, Miklós. Quantum chemistry: fundamentals to applications. Springer Science & Business Media, 2012.*
2. *Dronskowski, Richard. Computational chemistry of solid state materials: a guide for materials scientists, chemists, physicists and others. John Wiley & Sons, 2008.*
3. *P. W. Atkins and R. S. Friedman, Molecular Quantum Mechanics, Oxford University Press, 2003*
4. *Young, David. Computational chemistry: a practical guide for applying techniques to real world problems. John Wiley & Sons, 2004.*
5. *Rappe, Anthony K., and Carla J. Casewit. Molecular mechanics across chemistry. University Science Books, 1997.*
6. *Andrew R. Leach, Molecular Modelling, Pearson Prentice Hall, 2009*
7. *Cramer, Christopher J. Essentials of computational chemistry: theories and models. John Wiley & Sons, 2013.*
8. Floudas, Christodoulos A., and Panos M. Pardalos, eds. *Optimization in computational chemistry and molecular biology: local and global approaches*. Vol. 40. Springer Science & Business Media, 2000.
9. Raman, Karthik. *An introduction to computational systems biology: systems-level modelling of cellular networks*. Chapman and Hall/CRC, 2021

Intitulé du Master : Bioinformatics

Semestre *: 02*
Intitulé de l'UE : méthodologie
Intitulé de la matière : Biostatistics – Advanced Statistical Data Analysis
Crédits : 03
Coefficients : 02

Objectifs de l'enseignement :

The main objectives of this course are to:
- Enable students to identify appropriate tests for biological datasets.
- Teach students how to apply and interpret these tests using statistical analysis software.

Connaissances préalables recommandées : Mathematics, Statistics

Contenu de la matière :

- Introduction to Uni- and Multivariate Statistics

- **Chapter 1: Introduction to Data Analysis**
  - Descriptive statistics
  - Sampling strategies

- **Chapter 2: Univariate Statistics**
  - Statistical tests
  - Correlation
  - Simple regression
  - One-way ANOVA (Analysis of Variance)
  - Two-way ANOVA

- **Chapter 3: Multivariate Statistics**
  - Multiple regression
  - Hierarchical Ascending Classification (HAC)
  - Principal Component Analysis (PCA)
  - Correspondence Factor Analysis (CFA)

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- CARRAT,F, 2011 : BIOSTAISTIQUE, faculté de médecine PIERRE ET MARIE CURIE, 179 pages.

- FENELON (J.P), 1988 : Statistiques et informatique appliquée – dunod, Paris *France .420p.*

- "The Analysis of Biological Data" by Michael C. Whitlock and Dolph Schluter, July 1, 2008
- “Introduction to Probability and Statistics for Engineers and Scientists” By Sheldon M. Ross · 2014
- "Biostatistics for the Biological and Health Sciences" by Marc M. Triola and Mario F. Triola - 2018

Intitulé du Master : Bioinformatics

Semestre *: 02*
Intitulé de l'UE : méthodologie
Intitulé de la matière : Bioinformatics algorithms
Crédits : 05
Coefficients : 03

Objectifs de l'enseignement :

The objective of this course is to equip students with a solid understanding of the key algorithms and computational techniques used in bioinformatics, focusing on the analysis and interpretation of biological data. Students will learn the principles behind genomics, proteomics, and other omics technologies, along with the algorithms used for sequence alignment, phylogenetic tree construction, and database management.

Connaissances préalables recommandées :

The background acquired from the semesters and particularly in molecular biology, programming and basic understanding of data structures and algorithms, computational aspects and statistics etc, should be helpful to students at this stage.

Contenu de la matière :

1. **Genomics and Proteomics**
    - Genome sequencing technologies
    - Functional genomics and proteomics
    - Transcriptomics
    - Metabolomics

2. **Sequence Analysis and Alignment**
    - Sequence alignment concept and motivations
    - Global and local alignments algorithms
    - Pairwise alignment algorithms
    - FASTA, BLAST and other sequence search tools
    - Dot-matrix methods
    - Multiple sequence alignment, conservation analysis

3. **Phylogenetics and Phylogenomics**
    - Evolutionary biology principles
    - Phylogenetic trees construction and interpretation
    - Comparative genomics and phylogenomics

4. **Biological Database Management** (Basic Level)
    - Introduction to database concepts and design
    - Basic SQL and data manipulation
    - Overview of biological databases like GenBank, PDB

5. **Lab Work and Assignments**
    - Advanced bioinformatics tools and software
    - Phylogenetic analysis projects
    - Basic database management exercises

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

- Bioinformatics: Sequence and Genome Analysis – Mount, D. W. (2004). Cold Spring Harbor Laboratory Press.
- Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids – Durbin, R., Eddy, S. R., Krogh, A., & Mitchison, G. (1998). Cambridge University Press.
- Bioinformatics Algorithms: An Active Learning Approach – Compeau, P. E., & Pevzner, P. A. (2015). Chapman and Hall/CRC.
- Essential Bioinformatics – Xiong, J. (2006). Cambridge University Press.
- Biocomputing: Informatics and Genome Projects – Chordia, R. L. P. C. (2004). Wiley-Interscience.
- An Introduction to Bioinformatics Algorithms – Jones, N. C., & Pevzner, P. A. (2004). MIT Press.
- Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins – Baxevanis, A. D., & Ouellette, B. F. F. (2001). Wiley-Interscience.

Intitulé du Master : Bioinformatics

Semestre *: 02*
Intitulé de l'UE : découverte
Intitulé de la matière : Phylogenetics and Phylogenomics
Crédits : 01
Coefficients : 01

Objectifs de l'enseignement :

The course seeks to provide students with a comprehensive understanding of phylogenetics and phylogenomics, equipping them with the theoretical knowledge and practical skills to analyze evolutionary relationships. Students will learn the fundamental principles of phylogenetic tree construction, including distance-based, maximum likelihood, and Bayesian methods, as well as the biological significance of these trees. They will gain hands-on experience with computational tools such as MEGA, RAxML, IQ-TREE, and MrBayes, enabling them to perform sequence alignment, model selection, and tree reconstruction. (and more)

Connaissances préalables recommandées :

The course assumes minimal prior knowledge but provide foundational concepts where necessary.

Contenu de la matière :

1. Introduction to Phylogenetics and Phylogenomics
   - Basic concepts of evolution and common ancestry
   - Overview of phylogenetic trees and their significance
   - Differences between phylogenetics and phylogenomics
2. Molecular Evolution and Sequence Alignments
   - Evolutionary models (substitutions, mutations, selection)
   - Pairwise and multiple sequence alignment (MSA)
   - Common alignment tools (Clustal Omega, MUSCLE, MAFFT)
3. Phylogenetic Tree Construction Methods
   - Distance-based methods (UPGMA, Neighbor-Joining)
   - Character-based methods (Maximum Parsimony, Maximum Likelihood, Bayesian Inference)

- Bootstrapping and assessing tree reliability

4. Computational Approaches in Phylogenetics
    - Introduction to phylogenetic software (MEGA, RAxML, IQ-TREE, BEAST)
    - Scripting and automation (Python/Biopython, R/APE)
    - High-performance computing for large datasets
5. Phylogenomics: Large-Scale Evolutionary Analysis
    - Genome-scale phylogenetics and ortholog identification
    - Comparative genomics and gene family evolution
    - Applications in evolutionary medicine and functional genomics
6. Molecular Clocks and Evolutionary Rates
    - Concept of molecular clocks and divergence time estimation
    - Bayesian approaches in molecular dating
7. Practical Applications and Case Studies
    - Phylogenetics in microbiology and epidemiology (e.g., viral evolution)
    - Phylogenetics in biodiversity and conservation
    - Forensic phylogenetics and legal cases
8. Challenges and Future Perspectives in Phylogenomics
    - Big data challenges and computational scalability
    - Emerging methods in phylogenetic network analysis
    - Integration with structural biology and systems biology

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

Textbooks and General References

1. Phylogenetic Trees Made Easy: A How-To Manual (4th ed.) – Hall, B. G. (2011). Sinauer Associates.

2. Inferring Phylogenies – Felsenstein, J. (2004). Sinauer Associates.

3. The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing (2nd ed.) – Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). Cambridge University Press.

4. Molecular Evolution and Phylogenetics – Nei, M., & Kumar, S. (2000). Oxford University Press

Computational and Algorithmic Approaches

5. Molecular Evolution: A Statistical Approach – Yang, Z. (2014). Oxford University Press.

6. MEGA11: Molecular Evolutionary Genetics Analysis Version 11 – Tamura, K., Stecher, G., & Kumar, S. (2021). *Molecular Biology and Evolution, 38(7), 3022-3027.*

7. RAxML version 8: A Tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies – Stamatakis, A. (2014). *Bioinformatics, 30(9), 1312-1313.*

8. MrBayes: Bayesian Inference of Phylogenetic Trees – Huelsenbeck, J. P., & Ronquist, F. (2001). *Bioinformatics, 17(8), 754-755.*

9. trimAl: A Tool for Automated Alignment Trimming in Large-Scale Phylogenetic Analyses – Capella-Gutiérrez, S., Silla-Martínez, J. M., & Gabaldón, T. (2009). *Bioinformatics, 25(15), 1972-1973.*

Phylogenomics and Large-Scale Evolutionary Analysis

10. Mesquite: A Modular System for Evolutionary Analysis – Maddison, W. P., & Maddison, D. R. (2021).

11. Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough – Philippe, H., et al. (2011). *PLoS Biology, 9(3), e1000602.*

12. ASTRAL: Genome-Scale Coalescent-Based Species Tree Estimation – Mirarab, S., & Warnow, T. (2015). *Bioinformatics, 31(12), i44-i52.*

Intitulé de la matière : Programmation informatique appliquée aux sciences et technologies Semestre : 2 Type : UED

VHS : 22h30 VHH : 01h30 Cours : 00h30 TD : 00h00 TP : 01h00

VHS travail personnel : 02h30 Coefficient : 01 Crédit : 01

Objectifs de l'enseignement

L'objectif est d'acquérir les bases de la programmation informatique pour analyser et gérer des données scientifiques, de développer des applications et des scripts afin d'automatiser les traitements en sciences expérimentales, d'apprendre à utiliser les bibliothèques scientifiques en Python et R, et d'appliquer la programmation à des cas concrets en biologie, chimie, physique et ingénierie environnementale.

Connaissances préalables recommandées : initiation à la programmation informatique.

Contenu de la matière

Cours : 07h30

Chapitre I : Introduction à la programmation scientifique (01h30)

1. Principes fondamentaux de la programmation.
2. Concepts de base : variables et fonctions, types de données, structures conditionnelles (if, else, elif) et boucles (while, for).
3. Structures de données fondamentales (Listes et tuples, Dictionnaires et ensembles).
4. Introduction aux langages Python et R pour la programmation scientifique.
5. Environnements de développement : Jupyter Notebook, RStudio, VS Code.

Chapitre II : Manipulation et analyse de données scientifiques (01h30)

1. Bibliothèques essentielles : NumPy (opérations sur matrices et vecteurs) et Pandas (dataframes, manipulation de données)
2. Lecture et écriture de fichiers scientifiques
3. Importation, nettoyage et visualisation de données expérimentales
4. Utilisation de ggplot2 (R) et Matplotlib/Seaborn (Python) pour la visualisation

Chapitre III : Programmation appliquée aux sciences expérimentales (01h30)

1. Création de graphes et d'histogrammes
2. Visualisation des données scientifiques (Matplotlib et Seaborn)
3. Traitement et analyse des données scientifiques
4. Biologie : Analyse de séquences ADN/ARN, modélisation de populations

5. Chimie : Simulation de réactions chimiques, gestion de bases de données spectroscopiques
6. Physique : Modélisation de phénomènes physiques (lois de Newton, simulations thermodynamiques)
7. Environnement : Traitement d'images satellite, SIG avec QGIS et Python

Chapitre IV : Automatisation et intelligence artificielle appliquée (03h00)

1. Scripts pour automatiser les analyses scientifiques
2. Introduction au Machine Learning avec Scikit-Learn
3. Régression linéaire et classification appliquées aux sciences expérimentales

Travaux pratiques : 15h00

TP1 : Initiation aux langages et manipulation des données (03h00)
Écriture de scripts simples en Python et R
Manipulation des structures de données (listes, dictionnaires, tableaux NumPy)
Premiers scripts en Jupyter Notebook et Rstudio
Création de graphiques scientifiques

TP2 : Analyse et visualisation de données scientifiques (03h00)
Importation et traitement de fichiers CSV avec Pandas et ggplot2
Visualisation des tendances et distributions avec Matplotlib et Seaborn

TP3 : Automatisation et Machine Learning (03h00)
Automatisation de l'analyse de données scientifiques avec des scripts
Introduction à la régression linéaire et classification en IA

TP4 : Analyse avancée des données scientifiques (03h00)
Étude de corrélations et modèles statistiques
Clustering et classification non supervisée (KMeans, PCA)
Introduction au traitement d'images scientifiques

TP5 : Mini-projet en programmation scientifique (03h00)
Automatisation d'une analyse scientifique
Présentation et discussion des résultats

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d’évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)

- Examen semestriel en présentiel (60%).
- Évaluation continue (CC) (40%) sous forme d’au moins 3 composantes : interrogations écrites, devoirs à domicile, travail personnel, exposés, tests, comptes rendus, etc.

Deux des trois composantes doivent se dérouler impérativement en présentiel. La nature des 3 composantes et leurs pondérations sont laissées l’appréciation de l’équipe pédagogique.

Références bibliographiques

1. Bishop, C. M. (2021). Pattern recognition and machine learning. Springer.
2. Gauthier, J., & Moreau, A. (2023). Open science and research ethics: An integrated approach. Academic Press.
3. Hinton, G., & Salakhutdinov, R. (2020). Deep learning: A review. Nature Reviews, 24(4), 261-273.
4. Smith, J. K., & Brown, L. M. (2022). Programming for biological sciences: A guide to Python and R. Cambridge University Press.
5. Zhang, X., & Li, Y. (2025). Machine learning for scientific data analysis: Applications in biology and chemistry. Wiley.

Intitulé de la matière : Législation, éthique et déontologie Semestre : 2 Type : UET

VHS : 22h30 VHH : 01h30 Cours : 01h30 TD : / TP : /

VHS travail personnel : 00h00 Coefficient : 01 Crédit : 01

Objectifs de l'enseignement

Cette matière vise à former les étudiants aux cadres législatifs et éthiques régissant la recherche scientifique, à promouvoir l'intégrité et la responsabilité professionnelle, et à sensibiliser aux enjeux déontologiques pour une science éthique, transparente et respectueuse des normes internationales.

Connaissances préalables recommandées : aucune.

Contenu de la matière

Cours : 22h30

Chapitre 1 : Rappel sur les fondements de l'éthique, de la déontologie et de la législation (03h00)

1. Définitions : loi, législation, droit, morale, éthique, déontologie, devoir, liberté, responsabilité
2. Hiérarchie des normes : lois, décrets, ordonnances, circulaires, jurisprudence, doctrine, coutume
3. Distinction et complémentarité entre morale, éthique et déontologie
4. Histoire et fondements philosophiques de l'éthique scientifique
5. Charte et codes éthiques et déontologiques (universitaires et professionnels)

Chapitre 2 : Fondements de l'éthique et déontologie dans l'éducation et la recherche scientifique (03h00)

1. Structure éthique de l'éducation et rôle de l'éthique dans la relation enseignant-étudiant
2. Éthique de l'enseignant et de l'étudiant : droits, devoirs et responsabilités
3. Intégrité dans l'enseignement supérieur et dans la production scientifique
4. Charte d'éthique et de déontologie universitaire
5. Fautes, conflits d'intérêts, sanctions et régulation institutionnelle

Chapitre 3 : Responsabilité et intégrité scientifique (04h30)

1. Responsabilité citoyenne et scientifique
2. Qualités et engagement du chercheur
3. Intégrité scientifique : plagiat, fraude, transparence et rigueur

4. Éthique de la publication scientifique et accès ouvert
5. Comités d'éthique et processus d'évaluation
6. Consentement éclairé et respect des participants aux recherches

Chapitre 4 : Cadre juridique et réglementaire en bioéthique (04h30)

1. Législation nationale (ex. Algérie) et internationale en bioéthique
2. Comités de bioéthique, lois de bioéthique et dispositifs réglementaires
3. Réglementations sur :

3.1. Les droits des patients et des donneurs
3.2. La recherche biomédicale et les essais cliniques
3.3. La transplantation d'organes, tissus, cellules
3.4. La protection de l'environnement et la biodiversité
3.5. Les OGM, la biosécurité et la biotechnologie
3.6. La propriété intellectuelle et la confidentialité

Chapitre 5 : Normes et certifications en recherche scientifique et en environnement en Algérie (03h00)

1. Principaux organismes de réglementation en Algérie (AND, CNREEC, INRAA, etc.).
2. Certifications et labels environnementaux en Algérie.
3. Réglementations algériennes sur la gestion des déchets biologiques et chimiques.

Chapitre 6 : Champs et enjeux contemporains de la bioéthique (04h30)

1. L'embryon et les techniques associées : FIV, MIV, DPI, DPN, IMG, IVG
2. Diagnostic génétique et bébé-médicament
3. Génie génétique : clonage, thérapie génique, OGM
4. Intelligence artificielle en biologie : questions éthiques
5. Débats sociétaux : innovation vs régulation
6. Perspectives d'une science responsable et durable

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d'évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)

- Examen semestriel en présentiel (100%).

Références bibliographiques

1. Brown, T., & Green, S. (2021). Ethics in modern scientific research: An interdisciplinary approach. Springer.

2. Foucault, M., & Smith, A. (2023). Bioethics and the law: A critical examination. Oxford University Press.

3. Gray, J., & Harper, D. (2022). The future of bioethics: New challenges and perspectives. Wiley-Blackwell.

4. Lee, D., & Walker, P. (2020). Ethical issues in contemporary scientific practices. Routledge.

5. Miller, L., & Johnson, M. (2024). Deontological principles in research ethics. Cambridge University Press.

Intitulé du Master : Bioinformatics

Semestre *: 03*

Intitulé de l'UE : Fondamentale

Intitulé de la matière : Programming II (Python Bio-project)

Crédits : 06

Coefficients : 03

Objectifs de l'enseignement :

These projects provide a structured approach to teaching biology with Python by combining theoretical concepts with hands-on programming experience. Students will gain a deeper understanding of biological processes while developing valuable coding skills. Each project can be extended further by incorporating more advanced concepts, such as genetic algorithms, machine learning for ecological data, or more complex population models.

Connaissances préalables recommandées : Python programme (S2)

Contenu de la matière :

Project 1: DNA Sequence Analysis
In this project, students will explore the basics of bioinformatics by analyzing DNA sequences. They will focus on tasks such as calculating GC content, finding subsequences, and identifying mutations in a given DNA string.

Project 2: Genetic Inheritance Simulation (Punnett Square)
In this project, students will simulate genetic inheritance using a **Punnett square** to predict the probability of offspring inheriting certain traits based on the genotypes of their parents.

Project 3: Population Growth Simulation
This project focuses on simulating population growth in both **exponential** and **logistic** models. Students will use Python to model how populations grow over time based on their reproductive rates and carrying capacity.

Project 4: Ecological Data Analysis (Biodiversity Assessment)
In this project, students will analyze biodiversity in different ecosystems, focusing on **species richness** and **Shannon's Diversity Index**. They will use Python to work with ecological data and calculate these biodiversity metrics.

Project 5: At the students' choice
Genomics, Ecological and Environmental, Modeling Systems Biology, Computational Biology.

Mode d'évaluation : : 1 practical exam 100%

Références *(Livres et polycopiés, sites internet, etc).*

1. Martin Jones. Python for Biologists: A Programming Course for Complete Beginners. 2013.
2. Mark Summerfield. Programming in Python 3: A Complete Introduction to the Python Language. 2nd Edition, Addison-Wesley Professional, ISBN: 978-0-321- 68056-3, 648 pages, Nov. 2009.
3. Mitchell L. Model. Bioinformatics Programming Using Python. 1st Edition, O'Reilly, ISBN: 978-0-596-15450-9, Dec. 2009.
4. https://www.youtube.com/watch?v=3joOQ3A3KBQ&list=PLpSOMAcxEB_jUKMvdl8rHqNiZXFIrtd5G
5. https://www.youtube.com/watch?v=xFciV6Ew5r4&list=PL-osiE80TeTt66h8cVpmbayBKlMTuS55y&index=1
6. https://www.youtube.com/watch?v=uu8um0JmYA8

Intitulé du Master : Bioinformatics

Semestre *: 03*

Intitulé de l'UE : Fondamentale

Intitulé de la matière : Advanced Bioinformatics and Specialisation

Crédits : 06
Coefficients : 03

Objectifs de l'enseignement :

At this stage of the curriculum, the Master's program in Bioinformatics, the advances into specialised and complex domains, aiming to deepen the students' expertise in key areas. The learning objectives are focused on developing a comprehensive understanding of structural bioinformatics and molecular modelling, enhancing skills in molecular docking and drug design, and delving into the intricacies of advanced AI and machine learning applications in bioinformatics. Students are also expected to master sophisticated database management techniques, including handling big data and NoSQL technologies. The inclusion of an elective in bioinformatics software and database development allows for customisation of the curriculum to individual interests and career goals. Simultaneously, lab work and assignments are structured to reinforce theoretical knowledge through practical application, fostering independent problem-solving skills, and enhancing research capabilities. This semester is designed to equip students with a robust skill set and a deep understanding of advanced bioinformatics concepts, preparing them for the challenges of cutting-edge research and professional practice in this dynamic field.

Connaissances préalables recommandées : Good understanding of what's been learned in this Masters programme should be enough for addressing this course.

Contenu de la matière :

1. **Structural Bioinformatics and Molecular Modeling**
   - Protein structure prediction
   - Evaluation of predicted protein structure
   - Drug-target interaction and binding site analysis

2. **Docking and Drug Design**
   - Principles of molecular docking
   - Structure-based drug design
   - Ligand-based drug design
   - Virtual screening and ADMET predictions

3. **Advanced AI and Machine Learning in Bioinformatics**
    - Deep learning models and algorithms
    - Hands-on training with AI tools like AlphaFold
    - Application of AI in bioinformatics research

4. **Advanced Database Management and Design** (Advanced Level)
    - Advanced SQL, optimization, indexing
    - Introduction to NoSQL databases
    - Data warehousing, data mining in biological databases

5. **Elective Bioinformatics Software and Database Development**
    - Software development lifecycle in bioinformatics
    - Building and maintaining bioinformatics databases
    - Developing a prototype bioinformatics database application

6. **Lab Work and Assignments**
    - Projects involving molecular modeling docking
    - AI tool-based bioinformatics projects
    - Advanced database design and implementation tasks

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. Branden, C., & Tooze, J. (1999). Introduction to Protein Structure (2nd ed.). Garland Science.

2. Basic Concepts in Computational Biology and Bioinformatics .. (available online)

3. Böhm Hans-Joachim et.al. (2000). Virtual Screening for Bioactive Molecules, Volume 10 (Methods and Principles in Medicinal Chemistry). Wiley-VCH (ISBN: 978-3527301539)

4. Jensen H.J. (2010). Molecular Modeling Basics. CRC Press (SBN 9781420075267)

5. Akansha Saxena A. *et. al*, (2009). The basic concepts of molecular modelling. Methods Enzymol. 467:307-334. doi: 10.1016/S0076-6879(09)67012-9.

6. Rachedi A. & BAHLOUL O. (2023). Auto Protein Homology Modeling (APHM): An Educational and Research Tool for Homology Molecular Modeling. JSBB 2:2 , https://bioinformatics.univ-saida.dz/jsbb/blog-single.php?ar=September_2023LOLAPHM_Tool_for_EduResrch_HM_Molecular_Modeling

7. University of Saida (2022) Concepts in Structural Biology & Bioinformatics (ISSN: 2830-8832) – A national scientific journal https://bioinformatics.univ-saida.dz/jsbb/

Intitulé du Master : Bioinformatics

Semestre *: 03*

Intitulé de l'UE : Fondamentale

Intitulé de la matière : High Performance Computing

Crédits : 06
Coefficients : 03

Objectifs de l'enseignement :

The objective of this course is to provide students with a solid foundation in High Performance Computing (HPC) principles and techniques, with a specific focus on their applications in bioinformatics. Students will learn how to leverage parallel and distributed computing to solve complex biological problems, such as genomic sequencing, protein structure prediction, and large-scale data analysis. By the end of the course, students will gain practical skills in using HPC tools, programming models, and cloud computing platforms to optimize bioinformatics workflows.

Connaissances préalables recommandées :

Although no prior experience in High Performance Computing or parallel programming is required, students should have a foundational understanding of computer programming (preferably in Python, C, or C++) and basic knowledge of bioinformatics concepts, such as sequence alignment and genomic data analysis. Familiarity with operating systems (particularly Unix/Linux) and basic data structures and algorithms will be beneficial.

Contenu de la matière :

1: Introduction to High Performance Computing

- Overview of HPC and its importance in bioinformatics.
- Basic concepts of parallel computing and distributed computing.
- Introduction to the architecture of HPC systems (clusters, grids, cloud computing).
- Key applications of HPC in bioinformatics (genomic sequencing, protein structure prediction, molecular dynamics simulations).

2: Computer Architecture and Operating Systems for HPC

- Understanding multi-core processors, clusters, and GPUs.
- Basics of operating systems (Unix/Linux basics).
- Introduction to job scheduling systems (SLURM, PBS).
- Filesystems in HPC (NFS, parallel filesystems).

3: Parallel Programming Basics

- Introduction to parallel programming concepts: threads, processes, synchronization.
- Programming models for parallel computing (Shared memory, Distributed memory).
- Tools and libraries: OpenMP, MPI, CUDA for GPU programming.
- Simple parallel code examples (e.g., matrix multiplication, DNA sequence alignment).

4: Parallel Algorithms in Bioinformatics

- Parallelization of bioinformatics algorithms (BLAST, sequence alignment, phylogenetic tree construction).
- Techniques for optimizing algorithms on multi-core and distributed systems.
- Handling big biological datasets with parallel I/O.

5: HPC in Bioinformatics Workflows

- High-performance tools for bioinformatics (Hadoop, Spark, Bioconductor).
- Efficient data storage and processing techniques for genomic, proteomic, and metabolomic data.
- Using containerization (Docker, Singularity) for reproducibility and efficiency in bioinformatics tasks.

6: Data Management and Cloud Computing in Bioinformatics

- Cloud computing platforms (AWS, Google Cloud, Azure) for bioinformatics.
- Scaling bioinformatics applications on the cloud.
- Data storage and retrieval using cloud technologies (e.g., AWS S3, Google Cloud Storage).
- Ethics, security, and data privacy considerations in cloud computing.

7: GPU and High-Performance Computing in Bioinformatics

- Introduction to GPU computing and how it accelerates bioinformatics applications.
- Programming for GPUs with CUDA/OpenCL.
- Case studies: Using GPUs for sequence alignment, molecular dynamics, protein folding simulations.

8: Computational Biology and HPC Applications

- HPC in molecular dynamics simulations (e.g., GROMACS, AMBER).
- Applications in structural bioinformatics (e.g., protein docking simulations, homology modeling).
- Genome assembly and large-scale sequence data analysis with HPC.

9: Performance Optimization and Profiling

- Profiling and optimizing parallel code for efficiency.
- Load balancing, memory management, and reducing bottlenecks.
- Best practices in HPC performance (e.g., vectorization, memory hierarchy optimizations).

10: Final Project and Presentation

- Students work on a bioinformatics project utilizing HPC techniques.
- Presentations of projects with a focus on the computational aspects.
- Discussions on future trends in HPC and bioinformatics.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. High Performance Computing: Paradigm and Infrastructure – Yalamanchili, S. (2014). CRC Press.
2. Parallel Programming in C with MPI and OpenMP – Quinn, M. J. (2004). McGraw-Hill.
3. Bioinformatics: Sequence and Genome Analysis – Mount, D. W. (2004). Cold Spring Harbor Laboratory Press.
4. CUDA by Example: An Introduction to General-Purpose GPU Programming – Sanders, J., & Kandrot, E. (2010). Addison-Wesley.
5. Bioinformatics for High Throughput Sequencing – Ohta, N., Nishida, T., & Iba, T. (2011). Springer.
6. Introduction to Bioinformatics (5th ed.) – Lesk, A. M. (2019). Oxford University Press.
7. Parallel Programming with OpenMP – Chapman, B., Jost, G., & van der Pas, R. (2007). MIT Press.
8. The Art of High Performance Computing for Bioinformatics – Floryan, J. E., & O'Brien, T. J. (2020). CRC Press.
9. Cloud Computing for Bioinformatics – Akerkar, R. (2016). Springer.
10. The Linux Command Line: A Complete Introduction – Shotts, W. E. (2019). No Starch Press.

Intitulé du Master : Bioinformatics

Semestre *: 03*

Intitulé de l'UE : Méthodologie

Intitulé de la matière : Machine Learning & Data Mining

Crédits : 05
Coefficients : 03

Objectifs de l'enseignement :

Machine learning (ML) and data mining (DM) are increasingly integral to bioinformatics, enabling the analysis of complex biological datasets. Many key bioinformatics applications, such as genomic data interpretation, protein structure prediction, and drug discovery, rely on ML techniques. Without this knowledge, students may struggle to apply modern computational tools effectively.

Connaissances préalables recommandées :

At this stage of the master programme, student should have fair understanding of genomics, proteomics, and common bioinformatics databases (NCBI, UniProt) and have acquired enough foundational understanding of **mathematics and statistics**, including linear algebra and probability. Students would also have acquired **basic programming skills in Python or R**, covering loops, functions, and key libraries like NumPy, Pandas, and Scikit-learn. This is in addition to their familiarity with **data science concepts** such as data preprocessing, feature selection, and database basics (SQL).

Contenu de la matière :

1. Introduction to Machine Learning & Data Mining

- Definitions and key differences
- Applications in different scientific domains
- Overview of data-driven decision-making

2. Data Preprocessing and Feature Engineering

- Data collection and cleaning
- Handling missing values and outliers
- Feature selection and extraction

3. Supervised Learning

- Classification: Decision Trees, Naïve Bayes, Support Vector Machines
- Regression: Linear and Logistic Regression
- Evaluation metrics (accuracy, precision, recall, F1-score, ROC curves)

4. Unsupervised Learning

- Clustering: K-Means, Hierarchical Clustering, DBSCAN
- Dimensionality Reduction: PCA, t-SNE
- Anomaly Detection

5. Neural Networks and Deep Learning (Introductory)

- Basics of Artificial Neural Networks (ANN)
- Convolutional Neural Networks (CNN)
- Recurrent Neural Networks (RNN)

6. Data Mining Techniques

- Association Rule Learning (Apriori, FP-Growth)
- Sequential Pattern Mining
- Text Mining and Natural Language Processing (NLP)

7. Machine Learning in Bioinformatics and Chemistry

- Genomic and proteomic data analysis
- Drug discovery and cheminformatics
- Predicting protein structures and interactions

8. Model Optimization and Performance Tuning

- Hyperparameter tuning (Grid search, Random search, Bayesian optimization)
- Bias-Variance tradeoff
- Overfitting and regularization

9. Big Data & Cloud-Based Machine Learning

- Introduction to Hadoop and Spark
- Cloud platforms (Google AI, AWS, Azure ML)
- Handling large-scale biological datasets

10. Ethical and Legal Considerations in Data Science

- Bias and fairness in ML models
- Data privacy regulations (GDPR, HIPAA)
- Reproducibility and transparency in ML research

11. Practical Applications and Case Studies

- Hands-on implementation using Python (scikit-learn, TensorFlow, PyTorch)
- Project-based learning with real-world datasets
- Collaborative assignments for interdisciplinary problem-solving

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. **General Machine Learning & Data Mining Books**

- Machine Learning – Mitchell, T. M. (1997). McGraw-Hill.

- The Elements of Statistical Learning: Data Mining, Inference, and Prediction (2nd ed.) – Hastie, T., Tibshirani, R., & Friedman, J. (2009). Springer.
- Pattern Recognition and Machine Learning – Bishop, C. M. (2006). Springer.
- Data Mining: Concepts and Techniques (3rd ed.) – Han, J., Kamber, M., & Pei, J. (2011). Morgan Kaufmann.

2. Machine Learning for Bioinformatics

- Bioinformatics: The Machine Learning Approach (2nd ed.) – Baldi, P., & Brunak, S. (2001). MIT Press.
- Nonnegative Matrix Factorization: An Analytical and Interpretive Tool in Computational Biology – Devarajan, K. (2008). PLoS Computational Biology, 4(7), e1000029.
- Machine Learning Applications in Genetics and Genomics – Libbrecht, M. W., & Noble, W. S. (2015). Nature Reviews Genetics, 16(6), 321-332.
- Kernel Methods in Computational Biology – Schölkopf, B., Tsuda, K., & Vert, J.-P. (2004). MIT Press.

3. Practical Guides & Python Implementations

- Python Machine Learning (3rd ed.) – Raschka, S., & Mirjalili, V. (2019). Packt Publishing.
- Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow (2nd ed.) – Géron, A. (2019). O'Reilly.
- Data Mining: The Textbook – Aggarwal, C. C. (2015). Springer.
- Machine Learning: A Probabilistic Perspective – Murphy, K. P. (2012). MIT Press.

4. Online Courses & Tutorials

- Machine Learning (Coursera) – Andrew Ng
- Deep Learning for Coders with fastai and PyTorch – Howard, J., & Gugger, S. (2020). O'Reilly.
- MIT OpenCourseWare: Machine Learning – Free lecture notes and assignments.
- Kaggle ML & Data Science Courses – Various tutorials with real-world datasets.

5. Research Papers & Review Articles

- Deep Learning: New Computational Modelling Techniques for Genomics – Eraslan, G., Avsec, Ž., Gagneur, J., & Theis, F. J. (2019). Nature Reviews Genetics, 20(7), 389-403.
- Deep Learning – LeCun, Y., Bengio, Y., & Hinton, G. (2015). Nature, 521(7553), 436-444.
- Opportunities and Obstacles for Deep Learning in Biology and Medicine – Ching, T., Himmelstein, D. S., Beaulieu-Jones, B. K., et al. (2018). Journal of the Royal Society Interface, 15(141), 20170387.

Intitulé du Master : Bio-informatics
Semestre *: 03*
Intitulé de l'UE : Méthodologie
Intitulé de la matière : Modeling of Biological Systems
Crédits : 04
Coefficients : 02

Objectifs de l'enseignement :

This course aims to provide students with a methodological foundation for representing, analysing, and simulating biological phenomena using mathematical and computational models. Students would learn to construct dynamic models of biological processes, understand the principles of network-based approaches, and apply statistical and algorithmic techniques to study complex biological systems.

Connaissances préalables recommandées :

Given the interdisciplinary nature of this course, students at this stage of this master program should have had acquired basic understanding of **biology (molecular and cellular processes)** and **mathematics (linear algebra, calculus, and probability)**. In addition, students would also have considerable familiarity with **programming (Python, R)** and **data analysis techniques**.

Contenu de la matière :

1. Introduction to Modeling in Biology
- Role of modeling in biological sciences
- Mathematical vs. computational models
- Case studies: classical biological models

2. Mathematical Foundations for Modeling
- Differential equations in biology (e.g., population dynamics, enzyme kinetics)
- Stochastic modeling and probabilistic approaches
- Graph theory and networks in biology

3. Computational Models and Simulation
- Agent-based modeling and cellular automata
- Machine learning for modeling biological systems
- Algorithmic approaches in bioinformatics and structural modeling

4. Systems Biology and Network Models
- Gene regulatory networks

- Metabolic pathway modeling
- Protein-protein interaction networks

5. Structural and Molecular Modeling

- Molecular dynamics simulations
- Docking studies and conformational analysis
- Quantum mechanics in biochemical modeling

6. Multiscale Modeling Approaches

- From molecular to cellular and organ-level simulations
- Integration of data from different biological scales
- Hybrid modeling techniques

7. Case Studies and Applications

- Drug discovery and pharmacokinetics modeling
- Epidemiological models of disease spread
- Evolutionary modeling and phylogenetics

8. Tools and Software in Modeling

- Python, R for biological modelling
- Systems biology platforms: COPASI, CellDesigner
- Structural bioinformatics tools: GROMACS, PyMOL

9. Ethical Considerations and Challenges

- Limitations of biological models
- Data reproducibility and validation in modeling
- Ethical issues in AI-driven biological models

10. Student Project & Presentation

- Selection of a biological system to model
- Implementation of a mathematical/computational model

Presentation and discussion of results

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. General Textbooks on Biological Modeling

- Multiscale Modeling of Developmental Systems - Santiago S. *et al.* (2007). Available online: https://www.google.dz/books/edition/Multiscale_Modeling_of_Developmental_Sys/wc6irQKViJcC
- An Introduction to Agent-Based Modeling: Modeling Natural, Social, and Engineered Complex Systems with NetLogo - Wilensky & Rand (2015)

- Mathematical Biology: I. An Introduction – Murray (2002)
- Mathematical Biology: II. Spatial Models and Biomedical Applications – Murray (2003)

2. Computational and Systems Biology References

- Foundations of Systems Biology – Kitano (2001)
- A First Course in Systems Biology – Voit (2012)
- Systems Biology: Simulation of Dynamic Network States – Palsson (2015)

3. Structural and Molecular Modeling

- Molecular Modelling: Principles and Applications – Leach (2001)
- Molecular Modeling and Simulation: An Interdisciplinary Guide – Schlick (2010)
- Molecular Dynamics and Protein Structure – Karplus & Kuriyan (2005) (Article in Nature)

4. Computational and Machine Learning Approaches for Modeling

- An Introduction to Genetic Algorithms – Mitchell (1998)
- Machine Learning: A Probabilistic Perspective – Murphy (2012)
- Deep Learning – Goodfellow, Bengio, & Courville (2016)

5. Online Courses and Resources

- BioModels Database – (https://www.ebi.ac.uk/biomodels/)
- CellML Model Repository – (https://www.cellml.org/)

Intitulé du Master : Bio-informatics

Semestre *: 03*
Intitulé de l'UE : découverte
Intitulé de la matière : Advanced database
Crédits : 01
Coefficients : 01

Objectifs de l'enseignement :

The course aims to equip students with the technical expertise necessary to manage large-scale bioinformatics data effectively. It will cover advanced database concepts, including query optimization, NoSQL databases, and data integration techniques, specifically tailored to bioinformatics applications. Students will learn how to handle complex biological datasets, optimize data retrieval, and implement solutions for efficient data storage and access.

Connaissances préalables recommandées : Basic understanding of database principles which can be gained from the "Databases Basics". Other courses in this program give basic computer skills and familiarity with data management tools.

Contenu de la matière :

1. Introduction to Advanced Database Concepts

- Review of relational database principles.
- Limitations of traditional relational databases in bioinformatics.
- Advanced data models: hierarchical, graph-based, and object-oriented databases.

2. Query Optimization and Performance Tuning

- Indexing strategies for biological databases.
- Query execution plans and optimization techniques.
- Partitioning and sharding large datasets.

3. NoSQL and Big Data Management

- Introduction to NoSQL databases (MongoDB, Cassandra, Neo4j).
- Use cases of NoSQL in bioinformatics (handling unstructured and semi-structured data).
- Comparison between SQL and NoSQL for large-scale biological data.

4. Data Integration and Interoperability

- Challenges in integrating heterogeneous biological databases.
- Data warehousing and federated databases.
- Web services and APIs (NCBI Entrez, BioMart, UniProt API).

5. Graph Databases and Network Biology

- Introduction to graph databases (Neo4j, RDF, SPARQL).

- Applications in biological network analysis (protein-protein interactions, metabolic pathways).
- Querying graph-based bioinformatics databases.

6. Cloud-Based and Distributed Databases
- Cloud computing in bioinformatics (AWS, Google Cloud, Azure).
- Distributed database models and parallel data processing.
- Case studies on cloud-based bioinformatics platforms.

7. Data Security, Ethics, and FAIR Principles
- Data privacy and security in bioinformatics.
- Open science and FAIR (Findable, Accessible, Interoperable, Reusable) data principles.
- Legal and ethical considerations in genomic databases.

8. Advanced SQL and Procedural Extensions
- Advanced SQL functions (window functions, common table expressions).
- Stored procedures, triggers, and views.
- Scripting SQL for automating bioinformatics workflows.

9. Machine Learning and AI in Databases
- AI-driven database management and query optimization.
- Machine learning models for biological data retrieval and analysis.
- Integrating ML techniques in bioinformatics databases.

10. Hands-On Projects and Case Studies
- Building and querying a graph database for biological networks.
- Integrating multiple bioinformatics databases using APIs.
- Optimizing large-scale genomic data retrieval in SQL/NoSQL environments.

11. Future Directions in Bioinformatics Databases
- Emerging database technologies (blockchain for data security, quantum databases).
- Trends in bioinformatics data storage and retrieval.
- Preparing for research and industry applications.

Mode d'évaluation : Continuous monitoring and examinations

Références *(Livres et polycopiés, sites internet, etc).*

1. Object Oriented Multidatabase Systems: A solution for advanced applications Prentice Hall - Omran A. Bukhres, Ahmed K. Elmagarmid 1996

2. Interscience mobile database Systems – Kumar, Wiley 2006

3. Database System Concepts – Silberschatz, A., Korth, H. F., & Sudarshan, S. (2010). McGraw-Hill Education.

4. Fundamentals of Database Systems – Elmasri, R., & Navathe, S. B. (2016). Pearson Education.
5. Advanced SQL for Data Scientists – North, M. (2018). O'Reilly Media.

6. Bioinformatics Databases and Systems – Letovsky, S. I. (2009). Springer.

7. NoSQL Databases: A Survey and Decision Guidance – Haddadi, S., & Nematbakhsh, M. A. (2018). Springer.

8. Data Management and Databases: A Bioinformatics Perspective – Pradeep, T. M. (2018). Wiley.

9. Cloud Computing for Bioinformatics – Zia, T. (2020). Springer.

10. Graph Databases – Robinson, I., Webber, J., & Eifrem, E. (2013). O'Reilly Media.

11. Big Data and Cloud Computing in Bioinformatics – (2015). *arXiv*. Link

12. Big Data Analytics in Bioinformatics: Techniques and Tools – Lee, H., Choi, H., & Kim, Y. (2020). *Journal of Bioinformatics, 36*(2), 98-112.

13. Cloud Computing for Bioinformatics: Applications and Challenges – Zia, T., & Ali, M. (2021). *Springer Handbook of Bioinformatics, 15*(1), 234-250.

14. Data Management in Bioinformatics: Big Data Processing – Muthukrishnan, M., & Kottapalli, B. (2021). *Bioinformatics Advances, 7*(1), 1-15.

15. Big Data in Bioinformatics: Challenges and Opportunities – Zhang, W., & Li, J. (2021). *Bioinformatics Research, 12*(3), 180-189.

Intitulé de la matière : Intelligence artificielle appliquée aux sciences et technologies
Semestre : 3 Type : UET
VHS : 22h30 VHH : 01h30 Cours : 00h30 TD : 00h00 TP : 01h00
VHS travail personnel : 02h30 Coefficient : 01 Crédit : 01

Objectifs de l'enseignement

L'objectif est de comprendre les principes fondamentaux de l'intelligence artificielle (IA) et son rôle dans les sciences expérimentales, d'appliquer le machine learning et le deep learning à des problématiques scientifiques en biologie, chimie, physique et environnement, de maîtriser les outils et bibliothèques d'IA en Python, tels que Scikit-learn, TensorFlow, Keras et PyTorch, et d'automatiser l'analyse ainsi que l'interprétation des données scientifiques grâce à l'IA.

Connaissances préalables recommandées : Programmation informatique.

Contenu de la matière

Cours : 07h30

Chapitre I : Introduction à l'IA et ses applications scientifiques (01h30)

1. Définition et Concepts Clés
2. Différences entre programmation classique et apprentissage automatique
3. Types de Machine Learning et applications
4. Différences entre IA symbolique, Machine Learning et Deep Learning

Chapitre II : Manipulation et prétraitement des données scientifiques (01h30)

1. Acquisition et exploration des données scientifiques
2. Nettoyage et transformation des données
3. Réduction et optimisation des données
4. Préparation des données pour le Machine Learning

Chapitre III : Machine Learning appliqué aux sciences (01h30)

1. Apprentissage supervisé : Régression linéaire, SVM, Arbres de décision
2. Apprentissage non supervisé : Clustering (K-Means, DBSCAN)

Chapitre IV : Deep Learning et vision par ordinateur appliqués aux sciences (03h00)

1. Introduction aux réseaux de neurones artificiels (ANN)

2. Convolutional Neural Networks (CNN) pour l'analyse d'images biologiques et microscopiques
3. Réseaux récurrents (RNN, LSTM) pour la modélisation des séries temporelles
4. Études de cas :
4.1. Reconnaissance d'espèces animales à partir d'images
4.2. Détection de cellules cancéreuses dans des images médicales
4.3. Simulation de processus chimiques et biologiques

Travaux pratiques : 15h00

TP1 : Introduction aux modèles de classification et de régression (03h00)
1. Implémentation de la régression linéaire et logistique avec Scikit-Learn
2. Comparaison des performances entre SVM, k-NN et arbres de décision
3. Application sur des données biomédicales

TP2 : Prétraitement et analyse de données scientifiques (03h00)
1. Réduction de dimension avec PCA et t-SNE
2. Traitement des valeurs manquantes et normalisation des données
3. Visualisation avancée avec Seaborn

TP3 : Apprentissage supervisé et non supervisé en sciences (03h00)
1. Clustering avec K-Means et DBSCAN pour la classification des échantillons biologiques
2. Construction et validation de modèles de prédiction
3. Application sur des données expérimentales

TP4 : Réseaux de neurones et vision par ordinateur (03h00)
1. Implémentation de CNN pour la reconnaissance d'images microscopiques

TP5 : Projet IA appliqué aux sciences (03h00)
1. Développement d'un modèle IA sur un jeu de données scientifiques
2. Présentation et discussion des résultats

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d'évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)
- Examen semestriel en présentiel (60%).
- Évaluation continue (CC) (40%) sous forme d'au moins 3 composantes : interrogations écrites, devoirs à domicile, travail personnel, exposés, tests, comptes rendus, etc.
Deux des trois composantes doivent se dérouler impérativement en présentiel. La nature

des 3 composantes et leurs pondérations sont laissées l'appréciation de l'équipe pédagogique.

Références bibliographiques

1. Alpaydin, E. (2020). Introduction to machine learning. MIT Press.
2. Goodfellow, I., Bengio, Y., & Courville, A. (2021). Deep learning. MIT Press.
3. LeCun, Y., & Bengio, Y. (2023). Deep learning: Progress and challenges. Nature, 616(7958), 115-124.
4. Raj, S., & Kumar, A. (2022). Deep learning in biological data analysis. Springer.
5. Zhang, H., & Wu, J. (2024). Applications of machine learning in life sciences. Wiley.

Intitulé de la matière : création d'une entreprise économique Semestre : 3 Type : UET
VHS : 22h30 VHH : 01h30 Cours : 01h30 TD : / TP : /
VHS travail personnel : 00h00 Coefficient : 01 Crédit : 01

Objectifs de l'enseignement

Cet enseignement vise à initier les étudiants à la création de startups, de l'idée à la mise sur le marché, en intégrant les outils d'analyse, de planification et de financement. Il développe l'esprit entrepreneurial, la capacité d'innovation, la structuration de projets, et illustre par des applications concrètes en sciences biologiques, biotechnologies, écologie et environnement, pour encourager l'entrepreneuriat scientifique.

Connaissances préalables recommandées : entreprenariat (S6, licence).

Contenu de la matière

Cours : 22h30

Chapitre 1 : Introduction à l'entrepreneuriat et à l'innovation (03h00)

1. Définition et typologie des startups
2. L'esprit entrepreneurial : compétences et mindset
3. Différences entre PME, startup et entreprise classique
4. Innovation : types, sources et rôle dans les startups
5. Écosystème entrepreneurial : incubateurs, investisseurs, partenaires

Chapitre 2 : De l'idée au concept : structurer une opportunité (03h00)

1. Identifier un problème ou un besoin réel
2. Génération et sélection d'idées innovantes
3. Étude de faisabilité et validation du concept
4. Introduction au Design Thinking
5. Définir une proposition de valeur claire

Chapitre 3 : Élaboration du Business Model (03h00)

1. Business Model Canvas : outil de structuration
2. Segments de clientèle et canaux de distribution
3. Stratégie de revenus et structure des coûts
4. Analyse de la concurrence et positionnement

5. Prototypage et test de l'offre (MVP - produit minimum viable)

Chapitre 4 : Planification stratégique et levée de fonds (04h30)

1. Élaboration du Business Plan
2. Plan marketing et stratégie de communication
3. Montage juridique et choix de la forme d'entreprise
4. Financement : types, sources et levée de fonds
5. Pitching : comment convaincre investisseurs et partenaires

Chapitre 5 : Lancement, gestion et développement de la startup (04h30)

1. Construire et gérer une équipe fondatrice
2. Lancement du produit/service sur le marché
3. Suivi des indicateurs clés de performance (KPI)
4. Stratégies de croissance et d'expansion
5. Risques, échecs et pivot : apprendre à s'adapter

Chapitre 6 : Applications et cas concrets en SNV, biologie, biotechnologies et écologie (04h30)

1. Startups en biotechnologie : innovation en santé, agriculture et environnement

Exemples : thérapies innovantes, biofertilisants, biopesticides, CRISPR, biosenseurs

2. Création de startups vertes : écotechnologies et économie circulaire

Valorisation des déchets organiques, purification de l'eau, bioénergies

3. Entrepreneuriat en écologie et conservation

Projets de biodiversité, cartographie participative, agriculture durable

4. Biologie numérique et bio-informatique : opportunités entrepreneuriales

Startups en IA appliquée à la biologie, diagnostic assisté par image, modélisation écologique

5. Études de cas et retours d'expérience de startups SNV locales et internationales

Analyse de parcours de startups issues d'universités ou incubateurs

6. Étude critique des facteurs de succès ou d'échec

Travail personnel de l'étudiant : 02h30

Exposés ou toute autre activité pédagogique en rapport sur les applications des enseignements de cette matière, jugée par l'équipe de formation comme étant susceptible de susciter l'intérêt de nos étudiants pour cette discipline.

Mode d'évaluation (doit être porté à la connaissance des étudiants en début de chaque semestre)

- Examen semestriel en présentiel (100%).

Références bibliographiques

1. Blank, S., & Dorf, B. (2023). The Startup Owner's Manual: The Step-by-Step Guide for Building a Great Company (2nd ed.). Wiley.

2. Gans, J. S., & Stern, S. (2022). Strategy for Start-ups. Harvard Business Review Press.

3. Maurya, A. (2023). Running Lean: Iterate from Plan A to a Plan That Works (3rd ed.). O’Reilly Media.

4. Ries, E. (2024). The Lean Startup: How Today’s Entrepreneurs Use Continuous Innovation to Create Radically Successful Businesses (Revised ed.). Crown Business.

5. Trabelsi, M., & Ben Ameur, M. (2025). Entrepreneuriat innovant et développement durable en