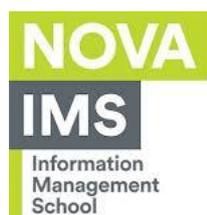# MSc in Computational Biology and Bioinformatics

## NOVA University of Lisbon

# Educational Structure

## 1st Semester

### *COMMON CORE DISCIPLINES*

| Code | Name | ECTS |
|------|------|------|
| | Advanced Programming for Biology | 6 |
| | Algorithms and Data Structures for Bioinformatics | 6 |
| | Statistics for Biology | 6 |
| | Fundamentals of Computational Biology | 6 |
| | Electives A | 6 |

| Electives A | | |
|------|------|------|
| Code | Name | ECTS |
| | Perspectives in Computational Biology | 3 |
| 8518 | Multivariate Statistics | 6 |
| 12107 | Cell Death and Lesion | 3 |
| | Nanomedicine | 3 |
| 10380 | Entrepreneurship | 3 |
| 11186 | Drug Discovery, Design and Development | 3 |

## 2nd Semester

### *MULTI-OMICS FOR LIFE AND HEALTH SCIENCES*

| Code | Name | ECTS |
|------|------|------|
| | Artificial Intelligence Techniques for Biology | 3 |
| | Applied Computational Multi-Omics | 6 |
| | Gene Expression Modulation | 6 |
| | Advanced Evolutionary Genomics | 3 |
| | Advanced Proteomics and Metabolomics | 3 |
| | Electives B | 9 |

| | Electives B | |
|------|------|------|
| Code | Name | ECTS |
| | Project in Multi-Omics | 6 |
| 12080 | Bayesian Methods | 6 |
| 11188 | Molecular Immunology | 3 |
| 10777 | Human Genetics and Oncobiology | 6 |
| 11853 | Molecular Biomedicine | 3 |
| 12106 | Neurobiology and Disease | 3 |
| 7637 | Structural Biochemistry | 6 |
| | Systems Biology | 6 |
| | Biomolecular Simulation | 6 |
| | Computational intelligence for Optimization in Bioinformatics | 3 |
| | Database Development and Applications in Biology | 3 |
| | Visualization and Data Analytics | 6 |
| | Molecular Epidemiology | 3 |
| | Research Methods in Health | 3 |
| | Systems and Precision Medicine | 3 |

## 2nd Semester

# 2nd Semester

## *BIOSYSTEMS SIMULATION FOR LIFE AND HEALTH SCIENCES*

| Code | Name | ECTS |
|------|------|------|
| | Artificial Intelligence Techniques for Biology | 3 |
| | Systems Biology | 6 |
| | Biomolecular Simulation | 6 |
| | Computational Intelligence for Optimization in Bioinformatics | 3 |
| | Database Development and Application in Biology | 3 |
| | Electives B | 9 |

| | Electives B | |
|------|------|------|
| Code | Name | ECTS |
| | Project in Simulation | 6 |
| 12080 | Bayesian Methods | 6 |
| 11188 | Molecular Immunology | 3 |
| 10777 | Human Genetics and Oncobiology | 6 |
| 11853 | Molecular Biomedicine | 3 |
| 12106 | Neurobiology and Disease | 3 |
| 7637 | Structural Biochemistry | 6 |
| | Applied Computational Multi-Omics | 6 |
| | Gene Expression Modulation | 6 |
| | Advanced Evolutionary Genomics | 3 |
| | Advanced Proteomics and Metabolomics | 3 |
| | Visualization and Data Analytics | 6 |
| | Molecular Epidemiology | 3 |
| | Research Methods in Health | 3 |
| | Systems and Precision Medicine | 3 |

# Advanced Programming for Biology

Responsible Lecturer: *Carla Ferreira*
Other Lecturers: *Carmen Morgado*
ECTS: **6**

**Objectives**

Knowledge: The meaning of programming constructs for the Python language fragment covered in the course; How to build a small application using the methodology defined in this course; Know the components and basic tools of a software development environment and their role. Selection of basic building blocks for algorithms in computational biology and bioinformatics.

Know-how: Develop well-organized, small-sized, programs, following a set of standards; Project and write correctly simple algorithms; Read, explain,and mentally simulate functionality of Pyhton code fragments; Correctly use, to the expected level, of programming tools, as well as interpret their results; Develop as a team, a software development mini-project, using the skills acquired in this course.

Soft-Skills: Develop disciplined work and deadline meeting skills; Develop a concern with rigour and systematic execution of work plans, following previously defined methods; Develop teamwork skills.

**Syllabus**

1. Introduction to programming languages;
2. Python basics;
3. Variables and data types;
4. Code readability;
5. Programming methodologies;
6. Control structures;
7. Repetition structures;
8. Functions and modules;
9. Strings;
10. Reading and writing data in persistent storage;
11. Basic data structures: arrays, lists, dictionaries, tuples;
12. Basic algorithms: sorting and dichotomic search, dictionaries traversals;
13. Programming structure and design;
14: Libraries for data handling and visualization.
15. Selection of fundamental scientific algorithms relevant for the area of the program (biology).

# Algorithms and Data Structures for Bioinformatics

Responsible Lecturer: *Pedro Barahona*
Other Lecturers: *Ludwig Krippahl*
ECTS: **6**

**Objectives**

This curricular unit will provide the student with the skills to:

Understand:

- The core problems of bioinformatics as the study of information flow in biological systems.

- The most used algorithms, their use and limitations, for important bioinformatics problems: sequence comparison and alignment, phylogeny, structure prediction and docking.

Be able to:

- Select appropriate solutions for core problems in bioinformatics.

- Reason about bioinformatics problems, decomposing them in their basic elements

- Chain existing programs to solve problems requiring several processing steps

- Critically evaluate the results obtained.

Know:

- Most used software and servers for core bioinformatics problems

- How to write scripts to chain different processing steps

- How to assess the quality of results.

**Syllabus**

1. Dynamic programming for local and global alignment
2. Substitution matrices
3. Sequence search algorithms
4. Hierarchical and Iterative multiple sequence alignments
5. Phylogenetics: distance, parsimony and likelihood methods; bootstrapping
6. Supervised learning algorithms for pattern recognition and prediction in biological sequences
6. Unsupervised learning algorithms for clustering and modelling of biological sequences
8. Genome assembly and analysis algorithms
9. Introduction of structural biology

# Statistics for Biology

Responsible Lecturer: ***Regina Bispo***
ECTS: **6**

**Objectives**

In this curricular unit we intend to explore some of the main methods of statistical modeling covering theory, applications and software. These methods will allow the student to deal with different type of variables (for example, continuous, counts, and presence/absence) and deal with observations indexed in time and/or space, and thus go beyond the standard statistical modelling techniques. Frequently used multivariate statistical methods are also presented.

It is intended that at the end of the course the student had acquired skills and abilities that allowed him to (1) use the generalized linear models as a basic statistical modeling tool, (2) recognize the most appropriate statistical approach according to type and behavior (3) incorporate non-independence cases between observations and (4) consider multivariate analysis. It is also expected that students will learn to use R software as a basic tool for statistical modeling.

**Syllabus**

1. Introduction to R and RStudio. Programming language and object types. Operators and indexing. Built-in functions and user functions. Graphics. Dataframes.
2. Basic concepts of Statistics. Basic sampling and experimental design techniques. Exploratory data analysis. Statistical inference. Parameter estimation and hypothesis testing.
3. Linear Models (LM) and Generalized Linear Models (GLM)
3.1. Continuous models (classical linear regression, ANOVA, ANCOVA, gamma regression and survival models)
3.2 Discrete models (logistic regression, Poisson regression and negative binomial regression).
3.3 Generalized linear mixed models (GLMM). Fixed vs. random effects (non-independent or grouped data).
4. Introduction to Multivariate Statistics
4.1 MANOVA
4.2 Principal Component Analysis
4.3 Cluster Analysis

# Fundamentals of Computational Biology

Responsible Lecturer: **José Paulo Sampaio**
Other Lecturers: **Ana R. Grosso,
Patrícia Brito, Ana Abecasis, Rune Matthiesen,
Cláudio M. Soares, Diana Lousa, Manuel N. Melo,
Isabel Rocha**
ECTS: **6**

## Objectives

This course will provide the students with a detailed introduction to the main areas of Computational Biology, with more enpghasis on topics related with Genomics and Evolution. It is expected that the students will obtain an informed perspective of Computational Biology and its diverse applications and will be in a good position to choose their preferred branch and elective courses in the second semester. Some of the topics covered in FCB will be expanded in more advanced branch-mandatory or elective courses.

- • Acquire basic knowledge on genomics and NGS data processing (high throughput sequencing)
- • To learn fundamental concepts of Evolutionary Biology
- • To get well acquainted with the various aspects of Computational Biology and how they can contribute to clarify problems in Biology

## Syllabus

1. Genomics
1.1. High-throughput sequencing technologies and applications
1.2. High-throughput sequencing pre-processing and data alignment.
1.3. Genome assembly and annotation.
1.4. Multi-Omics Resources
2. Molecular Evolution and Phylogenomics
2.1. Introduction to genomics.
2.2. Phylogenetic signal and models of sequence evolution.
2.3. Algorithms of phylogenetic inference.
3. Proteomics and Metabolomics
3.1. Technologies and applications
3.2. Describe analysis pipelines
3.3. Show databases.
4. Structural Bioinformatics
4.1 Introduction to structural bioinformatics
4.2 Protein structure prediction
4.3 Modeling biomolecular interactions
5. Molecular Dynamics Simulations of Biomolecules
5.1 Introduction to molecular mechanics/molecular dynamics methods
5.2 Molecular dynamics simulations using atomistic models
5.3 Molecular dynamics simulations using coarse grain models
6. Systems Biology
6.1 Introduction to systems biology
6.2 Metabolic models
6.3 Metabolic engineering

# Artificial Intelligence Techniques for Biology

Responsible Lecturer: *Pedro Barahona*
Other Lecturers: *João Leite, Ludwig Krippahl*
ECTS: **3**

**Objectives**

This curricular unit aims to provide the student with the skills to:

Understand:

- The role of ontologies and symbolic reasoning in biology.
- Fundamental concepts of machine learning
- Elementary notions of neural networks and deep learning.

Be able to:

- Select and apply correctly the methods and models addressed to biology problems
- Critically evaluate the results obtained.
- Use modern libraries of automatic learning and deep learning.

Know:

- Applications of supervised learning and neural networks to biology
- Modern AI tools used in biology.

**Syllabus**

1. Introduction to symbolic AI: knowledge representation and ontologies
2. Semantic web and applications to biology
3. Fundamentals of machine learning: supervised, unsupervised, overfitting and model selection
4. Regression and classification models with artificial neural networks
5. Introduction to deep learning

# Applied Computational Multi-Omics

Responsible Lecturer: *João M. Almeida*
Other Lecturers: *Ana R. Grosso,*
*Pedro Costa*
ECTS: **6**

**Objectives**

1. Understand state-of-the-art approaches applied to the study of the genome, transcriptome and transcriptional regulatory factors using high-throughput sequencing data.

2. Acquire hands-on in-depth knowledge concerning the application of computational approaches to analyse and integrate Multi-Omics data.

3. Understand the importance of the integration of Multi-Omics data in solving relevant questions in the Life and Health sciences.

**Syllabus**

Lectures:

1. Determination of Single Nucleotide Variants and Functional Impact

2. Determination of Structural Variants.

3. Biomedical Applications: study of diseases with a genetic component, Population Structure, Genome-wide Association Studies (GWAS), Survival Analysis.

4. Chromatin Immunoprecipation Sequencing (ChIP-seq) data analysis.

5. Motif discovery from ChIP-seq data.

6. Transcriptome sequencing (RNA-seq) data analysis.

7. Characterization of the Transcriptome profiles.

8. Identification of significant transcriptome alterations.

9. Integration of Multi-Omics data.

10. Functional Annotation and Analysis.

Lab Sessions

Introduction to high-throughput sequencing data files and formats. Computational "hands-on" sessions to comprehensively analyse high-throughput sequencing data, from pre-processing raw data to integration of multi-omics and clinical data.

# Gene Expression Modulation

<div align="right">

Responsible Lecturer: *Paula Gonçalves*
Other Lecturers: *Ana R. Grosso*
ECTS: **6**

</div>

**Objectives**

At the end of this course the student will have acquired the knowledge, skills and competences that allow him/her to:

-Understand the basic mechanisms of Gene Expression

-Be able to recognize the major differences in the regulation of gene expression in eukaryotes and prokaryotes

-To know the molecular protagonists that take part in the initiation of transcription in both types of cells

-Understand the role of chromatin in the regulation of gene expression

-Be familiar with the most important mechanisms of post-transcriptional regulation

-Be familiar with the main experimental techniques for the study of regulation of gene expression in particular high-troughput.

**Syllabus**

Topics covered include:

1) Basic mechanisms of gene expression: major differences between eukaryotes and prokaryotes

2) RNA polymerases and promoters in prokaryotes

3) Regulation of transcription in prokaryotes: activation, repression and attenuation

4) Mechanisms of gene expression regulation in eukaryotes

5) Expressed Quantitative Trait Loci (eQTLs)

6) Mechanisms of post-transcriptional regulation

7) Influence of chromatin structure and modifications on the regulation of gene expression

8) Regulatory RNAs

In the practical sessions students are expected to prepare individual essays under supervision on a topic related to regulation of gene expression, using appropriate databases such as Ensembl, GTEX and miRanda.

# Advanced Evolutionary Genomics

Responsible Lecturer: *José P. Sampaio*
Other Lecturers: *Patricia Brito, Ana Abecasis,*
*Ana R. Grosso, Ricardo Parreira*
ECTS: **3**

**Objectives**

This course will provide the students with advance knowledge in the field of Evolutionary Genomics growing from the basic concepts and methodologies that were acquired during the first semester. The students will be introduced to the theoretical foundations of the mechanisms of molecular evolution and how these processes affect the evolution of genes and genomes. The students will be also exposed to recent methodological developments in the field as well as applications of Evolutionary Genomics in the study of natural diversity and in biomedical research. It is intended that the students acquire a critical thinking in evolutionary genomics, that they can recognize signals of the evolutionary process in genomes, and understand the most relevant methodologies of analysis.

**Syllabus**

1. Mechanisms of molecular evolution
2. Evolution of genome structure in Eucaryotes and Prokaryotes
3. Phylogenetic inference from genome-scale data
4. Applied population genomics to phylogeography and speciation
5. Evolution in infectious diseases from large-scale population structure to transmission studies and within-host evolution.
5.1. Comparative analysis of microbial genomes and pangenomes
5.2. Virus evolution and molecular epidemiology
6. Metagenomics in the analysis of Human microbiota in health and in disease
7. Evolution in cancer: clonal evolution and inference of intratumor diversity

# Advanced Proteomics and Metabolomics

Responsible Lecturer: *Rune Matthiesen*
Other Lecturers: *Isabel Abreu,*
*Luis G. Gonçalves, Ana S. Carvalho*
ECTS: **3**

**Objectives**

The overall goal of the course is to familiarize the student to the broad application of proteomics and metabolomics and the software tools used in this area of research. The student will understand how the technologies work and can be applied, in particular he/she will be familiar with spectroscopy and spectrometric methods used. Furthermore, the student will understand how the underlining algorithms used in the data analysis work and will be able to use state of the art tools.

The student will acquire the following specific competences:

1. Know the broad number of applications of proteomics and metabolomics in biomedicine and agricultural research

2. Know the spectrometric and spectroscopic methods used in this field, the instruments used and the type of data generated

3. Be able to use and develop critical thinking and reasoning on computational methods used in this area

4. Understand how the choice of algorithms influences the final results.

**Syllabus**

The curricular unit will run over one semester (14 weeks) with 2 hours of either practical or theoretical lessons per week. The theoretical lectures will be followed up with homework questions and the practical sessions will include small programing challenges. The final evaluation will be based on written exam.

The following topics will be covered:

- Basics of mass spectrometry-based proteomics, sample preparation and instrumentation
- Introduction to applications of MS-based proteomics
- Spectra processing algorithms
- Database dependent search
- FDR filtering algorithms
- Protein inference
- De novo sequencing algorithms
- Post translational modifications
- Quantitative proteomics and experimental design
- Proteomics data standards
- Interaction proteomics
- Introduction to applications of metabolomics
- Analytical methods for metabolomics: experimental design and data analysis
- Integration of proteomics and metabolomics data

# Systems Biology

Responsible Lecturer: *Isabel Rocha*
Other Lecturers: *Rui Oliveira, Rafael Costa*
ECTS: **6**

**Objectives**

-To provide the theoretical basis for modelling biological systems, namely the ones that involve metabolic and regulatory processes;
- To identify and describe the methodologies for the mathematical representation of complex cellular processes;
- To implement and simulate, using programming languages, mathematical models of metabolic processes;
- To enumerate and explain the main analytical methodologies for the quantification of the transcriptome, proteome, fluxome and the metabolome;
- To apply tools for the analysis of genome-scale data and to design strategies for the integration of these data with cellular models;
- To apply models and data integration methodologies to solve different problems in the fields of synthetic biology, metabolic engineering, functional genomics and drug discovery.

**Syllabus**

- Mathematical modelling of biological systems: dynamic and stoichiometric models. Simulations using differential equations and metabolic flux analysis. Metabolic Control Analysis. Graph theoretical representation. Stochastic modelling.
- Metabolic, regulatory and signal transduction models – Model reconstruction
- Analytical methods for the quantification and characterization of the transcriptome, metabolome, fluxome and metabolome: RNA-seq, DNA microarrays, Mass spectrometry chromatography-mass spectrometry.
- Integration of omics data with cellular models
- Utilization of models and omics data to problems in sytnthetic biology, metabolic engineering, functional genomics and drug targeting.

# Biomolecular Simulation

Responsible Lecturer: *Cláudio M. Soares, António M. Baptista*
Other Lecturers: *João Aires de Sousa, Manuel Melo,*
*Diana Lousa, Sara Campos, Pedro Matias,*
*Ricardo Louro, Margarida Archer*
ECTS: **6**

**Objectives**

This curricular unit aims at giving a general overview of the major areas of Biomolecular Simulation / Structural Bioinformatics, providing the students with knowledge on the fundamentals as well as on practical applications to biosciences. The knowledge and skills acquired in this curricular unit will allow the students to have a general understanding of the scientific literature in the area, to use general software tools to tackling scientific problems involving structural bioinformatics, and, by (individually) deepening their knowledge on selected areas, to start supervised research projects in these areas of work to study real-life problems in biosciences.

**Syllabus**

The topics in this curricular unit are very varied, reflecting the diverse methodologies present in the field. The topics below aim at covering the majority of the field with different depths of coverage.

1) Introduction to structural biology, experimental techniques for structural determination and databases of structural data.
2) Representation and visualisation of molecular structures.
3) Statistical mechanics in biomolecular modelling.
4) Molecular mechanics/dynamics.
5) Molecular docking.
6) Protein structure prediction.
7) Quantitative Structure-Activity Relationships (QSAR).
8) Introduction to drug discovery using structural bioinformatics methods.

# Computational Intelligence for Optimization in Bioinformatics

Responsible Lecturer: *Leonardo Vanneschi*

ECTS: **3**

**Objectives**

This course introduces students to the basic concept of optimization and to a set of heuristic methods for solving, or approximating, optimization problems. A special focus will be given to the modelling phase of problems in Bioinformatics or Computational Biology, where students will be invited to tackle real-life optimization problems, formalize them and solve them, choosing from time to time the most appropriate solution. At the same time, this discipline should help students to strengthen some bases of programming languages and familiarizing with some of the most well-known computational environments.

**Syllabus**

- Motivations of the course - Optimization Problems
- Fitness Landscapes
- Hill Climbing
- Simulated Annealing
- Tabu Search
- Genetic Algorithms
- Advanced Evolutionary Algorithms methods
- Particle Swarm Optimization

# Database Development and Application in Biology

Responsible Lecturer: *Jorge Neves*
ECTS: **3**

**Objectives**

Introduce the fundamental concepts inherent to relational databases namely data modeling - conceptual, logical and physical; normalization; interrogation optimization; data integrity and transaction management, aiming to support the development of transactional systems. This curricular unit places great emphasis on a theoretical structuring of knowledge combined with the provision of extensive practical experience based on the use of Relational Database Management Systems (RDBMS) and data modeling tools. In practical cases, particular emphasis will be placed on data modeling, information extraction, and business rule-making in functional contexts within Bioinformatics. This course should provide students with the skills of structuring information as well as using the SQL language for querying databases and programming business rules.

**Syllabus**
- Introduction to database design
- Introduction to SQL.
- Entity-Relationship Model
- Relational Model. Transformation Conceptual - Logical - Physical.
- Normalization. Functional dependency and other fundamental concepts.
- Normal Forms (1, 2 and 3). Boyce-Codd Normal Form (BCNF).
- SQL Language. DDL and DML Statements.
- Advanced SQL.
- Views and Indices.
- Restrictions, Triggers and Transactions.

# Perspectives in Computational Biology

Responsible Lecturer: *Diana Lousa, Cláudio M. Soares*
Other Lecturers: *Isabel Rocha, Ana Abecasis,*
*Ana Rita Grosso, Rune Matthiesen,*
*Leonardo Vanneschi, Patrícia Abrantes*
ECTS: **3**

**Objectives**

This curricular unit aims to complement the knowledge that will acquired by the students in other curricular units, by showing them how this knowledge is applied in practice by specialists in different fields, working either in academia or in industry. This will help the students to have a clear notion of how the knowledge obtained throughout the Master program may be applied in practice. By the end of this curricular unit the student will have acquired knowledge, abilities and competences that enable her/him to:

- Understand the role of computational biology and bioinformatics in the context of modern biology, as well as the scientific and technological impact of this field
- Know the latest developments and state of the art applications of the different branches of computational biology
- Be able to read, interpret and discuss scientific papers in this field
- Be able to elaborate a written work on a topic in this

**Syllabus**

The topics of this curricular unit are very diverse, reflecting the large number of areas and methodologies present in this field. These topics will be discussed in the context of their applications, both in academia and in industry.

An overview of the different branches in this field and their recent developments and applications will be given, through seminars presented by experts in the topics and through the analysis and discussion of scientific papers.

Additionally, students will elaborate a written work on one of these topics. The following topics will be discussed:

1) Applications of computational evolutionary biology
2) Applications of computational multi-omics
3) Applications of computational proteomics
4) Applications of systems biology
5) Applications of biomolecular simulation and chemoinformatics
6) Applications of artificial intelligence in biology

# Multivariate Statistics

Responsible Lecturer: *Regina Bispo*

ECTS: **6**

**Objectives**

It is expected to familiarize the student with inference techniques for multivariate mean values and covariance matrices, as well as multivariate linear models in Gaussian populations, dimensionality reduction methods, discrimination and data classification. In particular, we intend to address the methods of canonical analysis, principal component analysis, factorial analysis, discriminant analysis and cluster analysis.

I is also expected that the student use properly the concepts and techniques learned in the R environment to solve the most diverse real-life problems.

**Syllabus**

1 – Brief review of basic notions in Linear Algebra. Multivariate descriptive statistics

2 – The Multivariate Normal distribution. Maximum likelihood estimators and their distributions. The Wishart distribution

3 – Inference on mean vectors

3.1 – One sample tests

3.2 – Two sample tests – paired and independent samples

3.3 – Tests based on more than two samples

4 – Multivariate Regression and Canonical Analysis

5 – Principal Component Analysis and Factorial Analysis

6 – Discriminant Analysis and Classification

7 – Cluster analysis

# Cell Death and Lesion

Responsible Lecturer: *Margarida Castro Caldas*
Other Lecturers: *Paula Videira, Alexandra Fernandes*
ECTS: **3**

## Objectives

It is expected that at the end of this course students will have achieved the following general competences: i) understanding the concept of oxidative stress; ii) to understand, through practical cases, the concept of cellular injury and the mechanisms activated in the endogenous response to the injury; iii) enumerate and distinguish different types and cell death, relating the inductors and mechanisms involved; iv) to identify the deregulation of the mechanisms involved in cell death as being the basis of several diseases; v) to use the acquired concepts and to understand strategies and therapeutic targets to modulate cell death in the different diseases; vi) acquisition of research skills of recent literature on subjects taught, in order to expose and critically discuss scientific works in the area; Vii) to acquire laboratory skills and contact with methodologies currently used in the evaluation of different injury and cell death parameters.

## Syllabus

Theoretical classes
1. Oxidative stress: inducers, mechanisms involved and adaptation of cells and tissues
2. Cell death in homeostasis and deregulation of cell death in pathological processes
3. Role of autophagy in the regulation of cell death.
4. Modulation of cell death. Development of drugs and research of therapeutic targets.
Practical classes:
1. Evaluation of oxidative stress
1.1. Griess reaction
1.2. Evaluation of ROS: staining with DCF-DA dye
2. Evaluation of cell death (apoptosis/necrosis)
2.1. Evaluation of nuclear morphology with Hoechst staining
2.2. Evaluation of lactate desidrogenase activity (LDH assay)

# Nanomedicine

Responsible Lecturer: *Pedro V. Baptista*

ECTS: **3**

**Objectives**

The main learning objective is directed towards raising awareness and provide general knowledge on Nanomedicine and its innovation driven impact in biomedicine.

Specific goals: to develop critical thinking and reasoning on nanoscale events and their impact on medical aplications, such as (but not limited to) diagnostics, research in biomedicine (tools adn novel approaches), therapeutics (drug delivery, nanoformulations, molecular actuators), tissue regeneration and precision medicine.

**Syllabus**

1. Nanotechnology and biologic systems
a. Scale effects and properties of nanomateriais
b. Characterization of nanomaterials in a biology context
c. Nanosystem-cell/nanosystems-organism interaction
d. Pharmacology of nanodrugs
2. Nanoparticles in biomedicine
a. Metal NPs, polymers, lipidic, VLPs
b. Nanovectors for drug delivery/gene therapy
c. Controlled release mechanisms in nanodrugs
d. Imaging via nanoplatforms
e. Nanodiagnostics
3. Multifunctional NPs for therapeutics
a. Molecular Targeting
b. EPR
c. Multimodal: PTT, PAT, PDT, etc and applications thereof
d. Nanoteheranostics
4. DNA nanotechnology– self assembly and origami
5. Lab-on-chip/organ-on-chip
6. Nanotoxicology in humans
7. Clinical translation and regulatory issues

# Entrepreneurship

Responsible Lecturer: *António Grilo*
ECTS: **3**

**Objectives**

This course is intended to motivate students for entrepreneurship and the need for technological innovation. It covers a list of topics and tools that are important for new venture creation as well as for the development of creative initiatives within existing enterprises. Students are expected to develop an entrepreneurship culture, including the following skills:

1) To identify ideas and opportunities to launch new projects;

2) To get knowledge on how to deal with technical and organizational issues required to launch entrepreneurial projects;

3) To understand the project implementation challenges, namely venture capital and teamwork management, and find the right tools to implement it;

4) To show and explain ideas and to convince stakeholders.

**Syllabus**

Strategy for entrepreneurship. Ideation and processes for the creation of new ideas. Industrial property rights and protection: patents and technical formalities. Managing an entrepreneurial project: planning; communication and motivation; leadership and teamwork. Marketing and innovation for the development of new products and businesses. Business plan and entrepreneurial finance. System of Incentives for young entrepreneurs. Managing growth and intrapreneurship.

# Drug Discovery, Design and Development

Responsible Lecturer: *Maria Rita Lima*
ECTS: **3**

**Objectives**

The objective of this curricular unit (CU) is to contribute to the formation of future researchers or pharmaceutical industry professionals, equipped to understand and act upon the several stages of the creation of an active principle, its transformation into a drug and its introduction to the market as an efficient and safe medicine.

At the end of this CU the student must grasp and be able to articulate the following topics:

1. Processes of identification and discovery of new active principles;
2. Methodologies for the design and optimization of the active principles relative to their therapeutic target;
3. Methods to optimize administration, distribution and delivery of the active principle in vivo;
4. Stages and requirements of the process of bringing a drug to the market.

**Syllabus**

Drugs and drug targets: Introduction

Drug targets

- Proteins as drug targets
- Enzymes as drug targets
- Receptors as drug targets
- Nucleic Acids as drug targets
- Other molecular drug targets: lipids, carbohydrates, etc...

Drug discovery, Design and Development

- Finding a lead compound
- Develop a bioassay

Design of the Lead compound

optimize interactions with the Target: (SAR; pharmacophore)

-optimizing the drug

-optimizing access to the target

-drug targeting

-prodrugs

Problems of Formulation and Drug Delivery

- methods to prepare water soluble compounds
- solubilizing drugs in organic solventes, micelles or coloidal dispersions
- solubilization with cyclodextrins

Bringing Drugs to the Market

Selected Topics (e.g. antibacterials, anti-cancer drugs) and Case Studies.

# Project in Multi-Omics

Responsible Lecturer: *Paula Gonçalves*
ECTS: **3**

**Objectives**

At the end of this curricular unit the student will have acquired the knowledge, skills and competences in the area of multiomics applications( experimental or computational) that allow him/her to:

- Improve for laboratory work skills

- Conduct autonomously the various stages of the scientific process, including information gathering, scientific writing, and presentation and discussion of results

-Interact productively with the host research team.

**Syllabus**

Conducting computational or laboratory research work (or a combination of both), writing, oral presentation and discussion of a report. Laboratory or computational work is expected to take about 84 hours, with approximately the same time set aside for literature research work and preparation of oral and written communications.

**Project in Multi-Omics**

# Bayesian Methods

Responsible Lecturer: *Miguel Fonseca*
ECTS: **6**

**Objectives**

The huge increase of computational capabilities and the expertise of Bayesian models on the analysis of very complex data structures, as the ones that come up in areas as Artificial Intelligence, justify the relevance of this CU.

Its main objective is to introduce the Bayesian statistics approach. By the end of this CU, a student must understand the principles that rules Bayesian inference, know how to incorporate, in various problems, the existing prior knowledge and its corresponding uncertainty in a probability distribution, know how to update the prior distribution with data to estimate analytically or numerically (through intensive programming methods as MCMC, Markov Chain Monte Carlo) the resulting posterior probability and predictive distributions, know how to use hierarchical modelling to represent and analyze complex systems, how to make model selection and prediction, using the software R-project and OpenBUGS (run in R).

**Syllabus**

This CU begins by introducing, in point 1 of the syllabus, the Bayesian paradigm. Point 2 is dedicated to the quantification of uncertainty of the existing information before data collection, in the formulation of the prior distribution. Points 3, 4 and 5 study the necessary ingredients for the estimation objective of the posterior, predictive and marginal distributions, either in an analytic way, if possible, or using intensive programming methods of MCMC (Markov Chain Monte Carlo), which permits to apply in an efficient way the Bayesian methods in complex models. Point 6 refers to the objective of quality assessment and model selection though the study of adequate methodologies, and point 7 details hierarchical models, more adequate for modelling data with complex structures. Software R and OpenBUGS (are used for running the applications of the Bayesian methodologies learnt, in a more relevant way if MCMC methods are needed.

# Molecular Immunology

Responsible Lecturer: *Paula Videira*

ECTS: **3**

**Objectives**

During this Unit the students should be able to:

• Acquire knowledge about the constitution and function of the Immune System.

• Acquire basic knowledge about the mechanisms of immune response, in the different steps of the immune response.

• Learning the molecular basis and mechanisms of antigen recognition and leukocyte activation

• Identify the role of immune dysfunction in autoimmune diseases and immunodeficiencies.

• Develop skills on the applicability of methodologies / technologies used in the study of Immunology in different areas, such as, basic research, diagnosis and new therapies.

• Understand the dynamics of knowledge contained in a rapidly developing science that integrates in all other biomedical sciences.

**Syllabus**

Elements and mechanisms of innate immune response

Elements and Mechanisms of adaptive immune response

Bases of the diversity of antigen recognition

Tumour and infection immunology

Hipersensivities, autoimmunity and immunodeficiencies

Immunotherapies

# Human Genetics and Oncobiology

Responsible Lecturer: *Alexandra Fernandes*

ECTS: **6**

**Objectives**

Students should learn the basic concepts of heredity - Mendelian, chromosomal and multifactorial in order to understand the developments of the Medical Genetic field in the post-genomic era. It is also an aim that the students learn the molecular and cellular bases of cancer and its development and of therapy in cancer.

**Syllabus**

Human karyotype. Chromosomal abnormalities. Types of cell division: mitosis and meiose. Mechanisms of change in the genome. Mutations and polymorphisms. Classification of mutations. Functional Classification of mutations. Mendelian patterns of inheritance. Complexity in Mendelian Heredity. Multifactorial character: Non-Mendelian Inheritance: complex (or multifactorial). Determination of a multifactorial disease or character. Population genetics. Linkage disequilibrium.

Cancer Biology. Normal and Tumor Cell; Metastasis. Angiogenesis in the tumor process. Apoptosis and Cancer. Oncogenes and tumor suppressor genes. Chemical and physical agents and biological agents as carcinogens. Diagnosis and therapy in cancer.

# Molecular Biomedicine

Responsible Lecturer: *Pedro V. Baptista*
Other Lecturers: *Alexandra Fernandes*
ECTS: **3**

**Objectives**

The main objective is to provide students with an overview of the use of molecular technologies in medicine and the relevance of Biomedicine in research.

Specifically, to investigate application of molecular structures in biomedicine: diagnostics and therapeutics; biomedical applications; smart design; nanotechnology for biomedicine.

Arguing and discussion skills based on critical evaluation of molecular biomedicine studies and applications.

Team work skills and scientific discussion

**Syllabus**

1. Molecular mechanisms in cell control
2. Molecular actuators
3. Smart design of molecular structures
4. Biosensing applications
5. Molecular therapeutics
6. Therapeutic nucleic acids: gene silencing and dose compensation
7. in vitro models
8. in vivo models
9. Drug discovery, development and validation
10. Bionanotechnology and Bionanomachines
11. Regenerative systems
12. Translation, ethical and societal impact, regulation.

# Neurobiology and Disease

Responsible Lecturer: *Margarida Braga*
ECTS: **3**

**Objectives**

The fundamental objective of this course is the acquisition of solid knowledge regarding the cellular and molecular processes involved in the onset and progression of various neurodegenerative diseases.

It is intended the student acquires research skills of recent literature on subjects taught and can make a critical exposition and discussion of scientific works, as well as outline a scientific mini-project.

**Syllabus**

1. Brief historical perspective on the knowledge of the neural function. Methods for studying the neural function: ACT, MRI,. FMRI, SPECT, PET. Association lesion/function and activation/function. Paradigmatic cases.

2. Neurodegenerative diseases: general principles and models. Definition of therapeutic target in neurodegenerative diseases.

3. Neuroinflammation.

4. Etiology and neuropathology of Parkinson's disease.

5. Etiology and neuropathology of Alzheimer's disease

6. Etiology and neuropathology of multiple sclerosis

7. Etiology and neuropathology of amyotrophic lateral sclerosis

# Structural Biochemistry

Responsible Lecturer: *Maria João Romão*
ECTS: **6**

**Objectives**

The aim of this UC is to provide the necessary background and know-how for the determination and analysis of the 3D structures of proteins and nucleic acids using X-ray Crystallography, Cryo-EM and NMR.

With this CU, the student should be able to use on-line computational tools as well as programs for data processing, visualization and molecular representation.

For the structural analysis, the student should be able to:

-In X-ray crystallography: obtain and characterize protein crystals; measure and process diffraction data; use programs for structure solution, validation and structure analysis.

-In Cryo-EM: learn about the main methodologies, advantages and limitations.

-In NMR: spectra processing; methodologies for solving protein structures in solution; analysis and validation;

different approaches for studying protein-ligand interaction; other applications of NMR.

-Analysis of case studies.

**Syllabus**

1 – Introduction to Structural Biochemistry

2 – Introduction to X-ray crystallography; protein crystals, symmetry and space groups; Diffraction and the Bragg´s law; Reciprocal space and the Ewald sphere; The "phase problem" and methods to solve it (MIR/SIR, MAD/SAD and MR); Building a structural model; Refinement methods and convergence; Validation criteria.

3 – Introduction to Nuclear Magnetic Resonance/overview of basic principles; Obtaining structural information;

Determination of protein structures; Protein dynamics by NMR. Interaction of proteins with ligands/small molecules/RNAs. Complementary techniques for imaging.

4 –Cryo-Electron Microscopy (Cryo-EM): Image reconstruction and Electron Crystallography.

5 – Interpretation of structural results - Validation Criteria; Quality of the model and accuracy of the 3D structure; Structural data bases; Comparison of structures solved by X-ray, NMR and Cryo-EM.

6 – Analysis of case studies.

# Visualization and Data Analytics

Responsible Lecturer: *João C. Pires*

ECTS: **6**

**Objectives**

Knowledge

•What is Interactive Data Visualization (IDV); The role of interaction in IDV.

• VID's role in Exploratory Data Analysis (DA) and the design of machine learning models.

• The concept of Visual Variable.

• Visualization and data analysis techniques for multivariate data, spatial data and time dependent data.

• The main general components of Analytical Data Visualization (ADV) systems.

• Methodologies for comparison and evaluation of ADV techniques and systems.

Do

• Choose the visual variables and visualization techniques most appropriate to a data set and objectives.

• Use a IDV system to explore and view one or more datasets.

• Design and implement a ADV solution for a data class and for a set of exploration objectives.

• Experimental bench to evaluate a IDV technique.

Soft-Skills

• Understand the multidisciplinary nature of this area and understand its relationship with other areas of knowledge and engineering.

• Explore the experimental nature of ADV system design.


**Syllabus**

Introduction to Data Visualization

- What Is Visualization?

- Relationship between Visualization and Other Fields.

- The Visualization Process.

- The role of Interactive DV in the Advanced Data Analytics

- Data Foundations.

- Human Perception and Information Processing.

- Semiology of Graphical Symbols.

- The Visual Variables.

Visualization Techniques for:

- Spatial Data

- Geospatial Data

- Time-Oriented Data

- Multivariate Data

-Trees, Graphs, and Networks

Interaction Concepts and Techniques

- Interaction Operators, Operands and Spaces

- Components of Visual Analytics Systems

- Designing Effective Visualizations

- Comparing and Evaluating Visualization Techniques-

Analytical Data Visualization Systems

- The role of IDV in exploratory Data Analysis

- The role of IDV in Explanatory Data Models

- Modern Analytical Data Visualization Systems

Research Directions in Analytical Data Visualization

# Project in Simulation

Responsible Lecturer: *Manuel Melo*
Other Lecturers: *Isabel Rocha*
ECTS: **6**

**Objectives**

The goal of this curricular unit is to expose the student to work in research on simulation and modeling of biosystems through an individual research project. At the end of the unit the student will have experienced, at an advanced and personal level, one of the several fields of research for which this branch is directed. They will then be in a privileged position to decide on subsequent academic steps — namely, the choice and planning of the dissertation project.

This unit further aims to teach or reinforce several scientific skills, both general and specific to the Master's:

1) Critical planning and description of research work;

2) Efficient review of literature specific to a field of research;

3) Adaptation and deployment of computational methodologies learned during the Master's — both on modelling/simulation as well as on analysis and visualization of results; and

4) Efficient communication of the developed research to peers.

**Syllabus**

Students will be offered a range of scientific questions and respective host labs — validated by the coordination of the unit. Work will be carried out under the supervision of specialists. Alternatively, students will be allowed to propose their own question and host lab — equally subject to validation by the unit's coordination.

Project topics will focus on:

1) Systems biology;

2) Biomolecular simulation and chemioinformatics; or

3) Artificial intelligence in biology.

and will cover both method application as well as analysis and visualization of results. Students will spend about 84h performing computational work, and are expected to spend the same amount of time for literature research work and preparation of oral and written communications

Besides the scientific aspects specific to the field and project, the following general skills will be taught/reinforced:

1) Planning and execution of scientific research;

2) Review of scientific literature; and

3) Science communication.

# Molecular Epidemiology

Responsible Lecturer: **Sofia Seabra** and **Ana Abecasis**
Other Lecturers: **Marta Pingarilho, Carla Sousa, Patrícia Abrantes, Isabel Couto, Fátima Nogueira, Victor Pimentel, Isabel Maurício, Ricardo Parreira, Ana Ceia Hasse, Miguel Viveiros**
ECTS: **3**

**Objectives**

This curricular unit aims to provide notions of molecular epidemiology, with a focus on infectious diseases and antimicrobial resistance. Topics to be developed include methods for identifying pathogens and biomarkers, epidemiological surveillance, pathogen transmission dynamics, phenotype/genotype association analysis, spatial and dispersal analysis.

At the end of this course unit, students should be able to:

- Understand how molecular epidemiology can contribute to epidemiological studies.

- Identify the main bioinformatics tools used in molecular epidemiology.

- Identify the most appropriate analysis approaches for concrete problems in molecular epidemiology.

- Apply the knowledge acquired in the analysis of molecular epidemiology data to a particular study.

- Interpret, analyze and critically present published works on molecular epidemiology.

**Syllabus**

1. Basic notions of epidemiology applied to molecular epidemiology.
2. Genotyping and identification of biomarkers in bacteria, parasites and viruses.
3. Epidemiological surveillance, epidemic intelligence and detection of outbreaks of emerging infectious diseases.
4. Dynamics of transmission of pathogenic agents.
5. Association between genetic characteristics of pathogenic agents and their transmissibility and pathogenicity.
6. Spatial analysis and dispersion of pathogens.
7. Molecular epidemiology of antimicrobial resistance.

# Research Methods in Health

Responsible Lecturer: **Ana Abecasis**
ECTS: **3**

**Objectives**

By the end of this Curricular Unit, students should be able to:

— Identify the stages involved in the planning and execution of a health research project.

— Formulate research questions and testable hypotheses in health.

— Plan a study to test proposed hypotheses, define objectives, study design, target population, sampling methods, sample size, and the most appropriate data collection methods.

— Identify the most relevant ethical issues to consider in the planning and implementation of the study.

— Recognize and apply the principles underlying the design and selection of samples.

**Syllabus:**

1. Fundamental principles of research in health, types of research, and criteria for choosing research topics.
2. Research process and principles for research planning.
3. Study design: scientific rigor, analytical project structure, control, and quality assurance.
4. Work plan and key stages of health research.
5. Definition of research questions and formulation of hypotheses; null and alternative hypotheses.
6. Sampling: target population, sample, sampling unit, desirable sample characteristics, sources of error, sampling methods.
7. Ethical issues: ethical reflections and most important ethical principles, ethical conduct standards.
8. Questionnaire design.
9. Methods and techniques of data collection, experimental and observational studies, analytical and descriptive studies.

# Systems and Precision Medicine

Responsible Lecturer: *António Jacinto*
Other Lecturers: *Isabel Rocha*
*Invited Speakers*
ECTS: **3**

## Objectives

Systems and precision medicine are interdisciplinary fields characterized by using advanced multi-omics technologies and complex data analysis to research on human biology and mechanisms of disease, and to assess disease risks, diagnosis, prognosis, and treatment options. The students will learn about: 1) fundamental concepts and available tools in medical systems biology and precision medicine approaches; 2) integration of computational and systems approaches to address unmet medical needs and scientific questions in biomedicine; 3) emerging technologies with potential high impact in precision medicine. The students will also be exposed to real life applications in the format of research seminars and paper presentations and discussions.

## Syllabus

1) Introduction to systems and precision medicine;
2) Research with humans, ethics and data protection;
3) Biomarkers for diagnostics, prognostics and therapeutic decision;
4) High-resolution and single-cell technologies in precision medicine;
5) Experimental and big data analysis workflows;
6) Multiscale computational modelling of disease;
7) Systems approaches for drug discovery and repurposing;
8) Emerging applications in systems and precision medicine.