

COURSE UNIT DESCRIPTION

Study Cycle: Doctoral Program

Course Unit: Computational Biology and Bioinformatics

Scientific Area Abbreviation: CB-BCM

Course Unit Code: 5573038

Year: 1st

Duration: One semester

Academic Year: 2024–25

Remarks: Mandatory course unit

Total hours	Contact hours	Nr. Hours/week	ECTS
112	9 T ; 17 PL ; 8 S ; 4 OT	1.73	4

L - Lecture; **TP** - Theoretical and Practical; **Lab** - Laboratory Practice; **FC** - Field Work; **S** - Seminar; **I** - Internship; **Tut** - Tutorial Guidance; **O** - Other

Responsible Lecturer: Pedro Cravo – 9 hours

Other Lecturers: Ana Abecasis – 14 hours; Victor Pimentel – 4 hours; João Pinto – 4 hours; Isabel Maurício – 4 hours; Ricardo Parreira – 9 hours

Learning Objectives (LO)

This course aims to provide students with the knowledge, skills, and competencies to use bioinformatics tools and computational applications:

1. To study DNA sequences, genes of interest, and genomes
2. To analyze the properties, structure, and function of proteins
3. To infer phylogenetic and evolutionary relationships between molecules or organisms
4. To study genetic variation and structure in human populations and infectious agents

Course Content

This course unit is organized into four thematic blocks:

1. Sequence and Genome Analysis

- a) Concepts of genome and genomic analysis
- b) Genome databases
- c) Sequencing and sequence alignment
- d) Genetic mapping
- e) *In silico* mutation detection and genotyping methods

2. Protein Analysis

- a) Concepts of translation and protein structure
- b) Protein databases
- c) Protein structure prediction
- d) Protein function analysis
- e) Proteomics, transcriptomics, and metabolomics: concepts and applications

3. Phylogenetic Analysis

- a) Concepts of molecular evolution
- b) Phylogenetic reconstruction methods
- c) Testing evolutionary models
- d) Selective pressure testing
- e) Phylogeography

4. Computational Solutions for Population Genetics

- a) Concepts of population genetics
- b) Molecular markers for population studies
- c) Genotypic databases
- d) Bioinformatics tools for population genetic analysis

Teaching Methodologies

This course will employ the following methods:

1. Theoretical lectures (lecture-based method)
2. Theoretical-practical classes (lecture/demonstration method)
3. Practical classes (demonstration/active learning method)

Assessment

Student assessment will consist of a practical exam involving an exercise in which students must apply bioinformatics tools to solve a problem. Students will be graded on a scale of 0 to 20.

Course evaluation will be conducted using the standard IHMT student satisfaction survey.

Bibliography

- Claverie J-M, Notredame C. 2007. *Bioinformatics for Dummies*, 2nd Ed. Wiley Publishing. 436 pages.
- Lemey P, Salemi M, Vandamme A-M. 2009. *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*, 2nd Ed. Cambridge University Press. 750 pages.
- Hartl DL, Clark AG. 2007. *Principles of Population Genetics*, 4th Ed. Sinauer Associates.