BIOINFORMATICS

CU characterization:

CU name:
Name

Scientific area acronym:
Bioinformatics

Duration:
Semiannual

Working hours:
78

Contact hours:
28

ECTS:
3

Observations:
Mandatory CU

Teacher in charge and respective teaching load in the CU:
Ricardo Parreira - 27 hours

Other teachers and respective teaching load in the CU:
N/A

Intended learning outcomes (knowledge, skills and competences to be developed by the students):
After this unit, students should be able to:

1. Recognition of the potential use of bioinformatics in the field of biomedical sciences.

2. Application of the acquired knowledge to the resolution of complex problems, including: construction of nucleotide sequence contigs and identification of coding sequences, use of publicly accessible databases and search for homologous sequences using various algorithms or functional analysis of a protein sequence.

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Intended learning outcomes (knowledge, skills and competences to be developed by the students): (continuation)

3. Acquisition of basic skills in the field of molecular phylogeny and phylogenetic inference, and their application to the construction and interpretation of phylogenetic trees and the exploratory analysis of unknown sequences.
4. Demonstration of capacity for a critical presentation of data arising from two proposed research projects (evaluation).

Syllabus:

Introduction to bioinformatics. Reference searches using public databases. Presentation of the GenBank, EMBL, UniProtKB, SwissProt, PDB, InterPro and Pfam databases. Sequence formats and sequence annotation. Concepts of homology, positional homology, and similarity. Types of nucleotide substitutions. Nucleotide and protein sequence alignments and their use: multiple vs local, pairwise vs global. Construction of multiple sequence alignments using progressive (Clustal) and interative algorithms (MAFFT, Muscle). Phylogenetic trees, evolutionary models, and corrected genetic distance matrixes. Phylogenetic reconstruction (neighbor-joining and maximum likelihood). Assessment of tree topology stability. Analysis of mosaics. Composition (G+C), structure of RNA molecules and proteins, physical DNA mapping, gene research. Use of different tools in order to identify, characterize, analyze the possible function of proteins.

Teaching methodologies (including assessment):

In most classes, a theory/practical teaching approach will be used. Theoretical concepts will be taught using expository methods, based on Powerpoints. All classes will include the use of computers for the resolution of exercises or the access to public databases.

The assessment of knowledge will be essentially based on the presentation (in group) of a report in the format of a scientific article, and it is expected that students will be able to communicate their conclusions in a clear, critical and scientifically correct way. Most tutorial classes will guide students in preparing their assessment. This (writing) will include two components: analysis of a nucleotide sequence and the reconstruction of phylogenies based on analysis of previously provided nucleotide sequence alignments. The participation/interest shown in the class will also be evaluated.

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References for consultation / mandatory existence:

- Claverie, J.-M., Notredame, C. (2007). Bioinformatics for Dummies. 2nd Edition. Wiley Publishing Group.
- Lesk, A. (2008). Introduction to Bioinformatics. 3rd Edition. Oxford Press.
- Salemi, M. Vandamme, A.-M. (ed). (2003). The Phylogenetic Handbook. Cambridge University Press.
- Higgs, P.G. Attwood, T.K. (2005). Bioinformatics and Molecular Evolution. Blackwell Science, Ltd.
- Gibson, D.G., Glass, J.I, Lartigue, C, et al. (2010). Creation of a bacterial cell controlled by a chemically synthesized genome. Science, 329 (5987): 52-56.