

Academic Year: ( 2022 / 2023 )

Review date: 19-05-2022

Department assigned to the subject: Bioengineering Department

Coordinating teacher: QUILEZ LOPEZ, CRISTINA

Type: Compulsory ECTS Credits : 6.0

Year : 4 Semester : 1

#### REQUIREMENTS (SUBJECTS THAT ARE ASSUMED TO BE KNOWN)

It is strongly advised to have knowledge in programming, fundamentals of molecular and cellular Biology and/or Biochemistry.

#### OBJECTIVES

The student will acquire the ability to apply different computational techniques to solve complex problems typical of biology and medicine. Such problems are characterized by involving the analysis of large quantities of information (data base searching, comparative analysis of sequences of DNA, RNA, microRNA and protein, domain searching, evaluation of the pathogenicity of variants, evolutionary conservation, phylogeny .. ), so that in practice only they are approachable through intensive computing techniques, in which the student is formed.

#### DESCRIPTION OF CONTENTS: PROGRAMME

Topics to be addressed include approaches and computational techniques for the search of the genetic structure, sequence alignment through the use of dynamic programming, prediction of the folding and structure of proteins, interactions of proteins and drugs. Different examples will be studied in the different areas and students will make use of computational biology tools for their analysis. As part of the subject, the relationship between computational biology and biotechnology will be studied.

Topics covered include:

1. Computational approaches and techniques for searching sequence, structural and expression databases and its relationship with disease databases.
2. Alignment and comparison of sequences by using dynamic programming.
3. Gene structure prediction
4. Obtaining the protein sequence encoded
5. Folding and protein structure prediction
6. Prediction of functional and protein-binding domains
7. Molecular evolution and phylogenetic sequences analysis.
8. Linkage analysis, physical maps and identification of the disease-causing gene.
9. Genome structure analysis, repetitive sequence searching and microRNAs.
10. Evaluation of the pathogenicity of disease variants.
11. Search for restriction sites and generation of recombinant vectors in silico

Different examples will be reviewed in different areas and students make use of computational biology tools for analysis.

#### LEARNING ACTIVITIES AND METHODOLOGY

The teaching will be on site and it will include:

Lectures, which will present the skills that students should acquire and the bioinformatic tools to be used. To facilitate its development students will receive class notes and baseline texts that facilitates follow lessons and develop further work. Resolution of representative exercises will be included.

-Practices in computer lab for the resolution of exercises by means of bioinformatic tools.

-In-person classes for doubts resolution, tutorials and carrying out of the continuous evaluation exams and projects.

## ASSESSMENT SYSTEM

The evaluation system includes continuous assessment of student work (class participation and 2 skills assessment tests and theoretical and practical knowledge), and final evaluation through a final (theoretical and practical exam) that comprehensively assess the knowledge and skills acquired throughout the course. There can be an additional research project proposed by the teachers to have an additional mark. The shares allocated are defined in the following terms.

% end-of-term-examination: 60 (minimum mark required is equal to 4)

% of continuous assessment (assignments, laboratory, practicals...): 40

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**% of continuous assessment (assignments, laboratory, practicals...):** 40

## BASIC BIBLIOGRAPHY

- - Lesk, A.M. Introduction to Bioinformatics, Oxford University Press, Third Edition

- - Mount, DW Bioinformatics, Sequence and Genome Analysis, Cold Spring Harbor Laboratory Press, Second Edition