Bioinformatics

Academic Year: (2023 / 2024)   **Review date: 16-04-2018**

Department assigned to the subject: Bioengineering Department

Coordinating teacher: JORCANO NOVAL, JOSE LUIS

Type: Compulsory ECTS Credits : 6.0

Year : 4 Semester : 1

REQUIREMENTS (SUBJECTS THAT ARE ASSUMED TO BE KNOWN)

It is strongly advised to have completed Mathematics, Programming, Fundamentals of Biology and 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 covered include computational approaches and techniques for searching sequence, structural and expression databases and its relationship with disease databases, alignment and comparison of sequences by using dynamic programming, gene structure prediction, search for restriction sites, secondary structure prediction, generation of recombinant vectors in silico, obtaining the protein sequence encoded, folding and protein structure prediction, prediction of functional and protein-binding domains, protein interactions prediction, evaluating the pathogenicity of disease variants, molecular evolution and phylogenetic sequences analysis. Different examples will be reviewed in different areas and students make use of computational biology tools for analysis.

LEARNING ACTIVITIES AND METHODOLOGY

The teaching methodology will include:
-Lectures, which will present the skills that students should acquire. To facilitate its development students will receive class notes and baseline texts that facilitates follow lessons and develop further work.
-Classes of problems, in which the problems will be developed and discussed with the students.
-Practices in computer lab.

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. The shares allocated are defined in the following terms.

% end-of-term-examination: 60 (minimum mark required is equal to 4)
% of continuous assessment (assigments, laboratory, practicals...): 40

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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