VNIVERSITAT ĐĎ VALÈNCIA

COURSE DATA

Data Subject

Code	33142
Name	Bioinformatics
Cycle	Grade
ECTS Credits	4.5
Academic year	2022 - 2023

Study (s)

Degree	Center	Acad. year	Period
1109 - Degree in Biochemistry and Biomedical Sciences	Faculty of Biological Sciences	4	Second term

Subject-matter

Degree	Subject-matter	Character
1109 - Degree in Biochemistry and Biomedical Sciences	14 - Materia de asignaturas optativas	Optional

Coordination

Name	Department
SILVA MORENO, FRANCISCO J.	194 - Genetics

SUMMARY

Bioinformatics was originally defined as an interdisciplinary field that included the fields of biology, computer science, mathematics and statistics and aimed to analyze biological sequence data, content and structure of genomes, and the prediction and function of proteins. With the advent of the era of genomics, bioinformatics has expanded its field of study to the analysis of multiple biological data, including those derived from humans and therefore has great importance in current biomedical research.

The contents of this subject have been adapted to the other subjects taught in the curriculum of the Degree in Biochemistry and Biomedical Sciences so that they include practical activities related to the theory contents acquired in compulsory and optional subjects such as Genomics and Molecular and biochemical evolution. The knowledge and skills acquired in this course should be considered as an introduction to bioinformatics, as this is a broad subject both in relation to their applications and the tools used.

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PREVIOUS KNOWLEDGE

Relationship to other subjects of the same degree

There are no specified enrollment restrictions with other subjects of the curriculum.

Other requirements

This course will practice, among other issues, molecular evolution and phylogenetics, whose theory is deeply treated in the subject Molecular and biochemical evolution. It is advisable to take both subjects to have a more integrated theoretical / practical view.

OUTCOMES

1101 - Degree in Biochemistry and Biomedical Sciences

- Know how to use the different bibliographic sources and biological databases and be able to use bioinformatic tools.
- Conocer los métodos que permiten manejar grandes cantidades de datos derivados de las técnicas ómicas.
- Conocer los mecanismos evolutivos a escala molecular.
- Saber utilizar los principales métodos bioinformáticos.
- Acceder a las principales bases de datos biológicos y recuperar y emplear la información contenida en ellas.
- Aplicar correctamente los métodos de inferencia filogenética e interpretar los resultados.

LEARNING OUTCOMES

1. Obtaining and interpreting phylogenetic trees
2. Performing multiple sequence alignments
3. Performing searches in biological databases
4. Gene prediction
5. Finding conserved domains and motifs in proteins

DESCRIPTION OF CONTENTS

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1. Molecular databases, sequence alignment and molecular phylogenetics

Elemental analysis of sequences. Extraction of information from molecular and genomic databases. Searches for sequence similarity. Alignment of nucleotide and amino acid sequences. Sequence alignment and similarity search algorithms. The evolutionary change in the sequences and their estimation. Phylogenetic reconstruction. Nucleotide replacement rates and patterns. Phylogenetic reconstruction programs.

2. Annotation of bacterial and eukaryotic genomes

The BLAST algorithm. Methods to identify CDS, non-coding RNA genes and pseudogenes in prokaryotic genomes. Methods for annotating genes in eukaryotic genomes.

3. Basic and translational genomics. Transcriptomic

Basic introduction to using the command line in Linux and mass analysis of sequences. Genome sequencing methods and strategies. Translational genomics in biomedicine. Transcriptomic. RNA sequencing in prokaryotes and eukaryotes.

WORKLOAD

ACTIVITY	Hours	% To be attended
Computer classroom practice	26,00	100
Theory classes	16,00	100
Tutorials	3,00	100
Development of group work	12,00	0
Study and independent work	31,50	0
Preparing lectures	12,00	0
Preparation of practical classes and problem	12,00	0
TOTAL	**112,50**	

TEACHING METHODOLOGY

The subject will be structured in presential and nonpresential work:

Presential work

A)   One hour theory lessons following the masterly speech system.

B)   Practical lessons in informatics room where problems and exercises will be discuss that serve to illustrate the main points addressed in the theory lessons.

C)   Tutoring. Group tutoring sessions will serve to discuss results obtained by the different working groups organized in the practical sessions.

D)   Exam.

Nonpresential work

A)   Practical exercises and bioinformatics problems to be solved by groups of students. Results as well as the different approaches used by the different groups will be discussed in the tutoring sessions.

B)   Study contents and preparation of lessons in advance. Students will be told in advance the chapters of recommended books where they can reach the contents that will be taught in coming classes.

EVALUATION

The assessment of student learning in first call was made by assessing the following sections:

1) Exam. An examination of knowledge and interpretation of results after the application of bioinformatics tools. This test will provide up to 7 points.

2) Practical work. The resolution of a practical exercise. This section will be worth up to 3 points.

The second call works with the same rules as the first. The exam will be worth up to 7 points, in addition to the marks obtained in solving the exercises carried out druring the course (up to 3 points).

The minimum grade to pass the course is 5 in a 0 to 10 scale.

The minimum mark in the exam needed to pass the course is 4 in a 0 to 10 scale.

REFERENCES

Basic

-   Pevsner J. (2015) Bioinformatics and Functional Genomics, 3rd Edition Wiley-Blackwell.

    Pevsner J. (2009) Bioinformatics and Functional Genomics, 2nd Edition Wiley-Blackwell.

Additional

- Nei, M. and Kumar, S. (2000). Molecular Evolution and Phylogenetics. Oxford University Press.

- W-H. Li. (1997). Molecular Evolution.

- Mount, D. (2004). Bioinformatics: Sequence and Genome Analysis, Second Edition. Cold Spring Harbor Press.

- T.K. Attwood y D. J. Parry-Smith (2002). Introducción a la Bioinformática. Prentice Hall.