

**COURSE DATA****Data Subject**

Code	33190
Name	Bioinformatics
Cycle	Grade
ECTS Credits	4.5
Academic year	2022 - 2023

Study (s)

Degree	Center	Acad. year	Period
1102 - Degree in Biotechnology	Faculty of Biological Sciences	4	Second term

Subject-matter

Degree	Subject-matter	Character
1102 - Degree in Biotechnology	100 - Bioinformatics	Optional

Coordination

Name	Department
MARTINEZ TORRES, DAVID	194 - Genetics
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 designed so that for each theoretical lesson, related practical activities are planned to help settling the main concepts and ideas. 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.



PREVIOUS KNOWLEDGE

Relationship to other subjects of the same degree

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

Other requirements

OUTCOMES

1102 - Degree in Biotechnology

- Poseer y comprender los conocimientos en Biotecnología.
- The ability to apply this knowledge in the professional world.
- Capacidad de interpretar datos relevantes.
- Be able to convey ideas, problems and solutions in the field of biotechnology.
- Be able to use English to write reports and to interpret information from protocols, manuals and databases.
- Analizar a nivel molecular el resultado de la manipulación de un organismo.
- Ser capaz de abordar el análisis de la estructura de macromoléculas al objeto de modificarla con fines biotecnológicos.

LEARNING OUTCOMES

English version is not available

DESCRIPTION OF CONTENTS

1. Databases and molecular sequence alignment

Basic sequence analysis. Extracting information from molecular and genomics databases. Searches for sequence similarity. Alignment of nucleotide and amino acids. Sequence alignment algorithms and similarity search

2. Molecular phylogenetics

Molecular phylogenetics. Evolutionary change in sequences and its estimation. Phylogenetic reconstruction. Rates and patterns of nucleotide substitution. Phylogenetic reconstruction programs.

**3. Applications and tools for sequence analysis**

Editing and computer manipulation of sequences. Sequence analysis. ESTs. Gene prediction in eukaryotes and prokaryotes. Introduction to microarrays. Computer prediction of nucleic acid structures and proteins

WORKLOAD

ACTIVITY	Hours	% To be attended
Theory classes	28,00	100
Computer classroom practice	14,00	100
Tutorials	3,00	100
Development of individual 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.

NOTE:



The distribution of teaching sessions and the ratio between presential and nonpresential activities may be modified throughout the course if health conditions require it

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 8 points.
- 2) Practical work. The resolution of a practical exercise in groups of students. This section will be worth up to 2 points.

In the **second call**, an examination equivalent to the first will permit to obtain up to 10 points. If the student had a mark corresponding to the practical exercises from the first call, it will be added to the examination mark, which will then be worth up to 8 points. It is not possible to present the practical work in the second call.

For both calls:

The minimum grade to pass the course is 5.

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.

Una introducción a la bioinformática y la genómica fácil de seguir y de entender los conceptos. Incluye muchos ejercicios prácticos y direcciones web. La primera edición del año 2003 también puede usarse al ser similar en muchos capítulos.

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.