VNIVERSITAT (D VALÈNCIA

COURSE DATA

Data Subject

Code	43459
Name	Bioinformatics
Cycle	Master's degree
ECTS Credits	3.0
Academic year	2023 - 2024

Study (s)

Degree	Center	Acad. year	Period
2210 - M.D. in Research in Molecular, Cellular and Genetics Biology	Faculty of Biological Sciences	1	First term
3102 - Biomedicine and Biotechnology	Doctoral School	0	First term
3173 - Biomedicina y Biotecnología	Doctoral School	0	First term

Subject-matter

Degree	Subject-matter	Character
2210 - M.D. in Research in Molecular, Cellular and Genetics Biology	4 - Bioinformatics	Obligatory
3102 - Biomedicine and Biotechnology	1 - Complementos de Formación	Optional
3173 - Biomedicina y Biotecnología	1 - Complementary Training	Optional

Coordination

Name	Department
SILVA MORENO, FRANCISCO J.	194 - Genetics

SUMMARY

The course is essentially practical and theoretical knowledge will be conducted simultaneously with the practical in the computer room.

Bioinformatics was originally defined as an interdisciplinary field that included the fields of biology, computer science, mathematics and statistics and who provide analysis of biological sequence data, content and structure of genomes, and prediction and function proteins. With the advent of the era of genomic, bioinformatics has extended its field of study to the analysis of many biological data, including those derived from humans and therefore currently has a great importance in biomedical research.

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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

Students should have basic knowledge of molecular sequence analysis.

OUTCOMES

2210 - M.D. in Research in Molecular, Cellular and Genetics Biology

- Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.

- Ser capaz de buscar en la red información sobre secuencias de ácidos nucleicos y proteínas y adquirir la capacidad de manejar software relacionado con el análisis de secuencias.

- Ser capaz de procesar y extraer información a partir de los datos proporcionados por un servicio de secuenciación y convertir dicha información a un formato que permita su análisis con diferentes programas de análisis de secuencias.

LEARNING OUTCOMES

The student, for passing this subject, must show:

1. Be able to handle a sequence assembly program from the initial stages of preparation of the reads until the end of assembly and mutation analysis.

2. Be able to work at a basic level with sequences derived from NGS systems in an assembly program and to know the sequence assembly algorithms.

3. Being able to annotate genomes of prokaryotes and eukaryotes

DESCRIPTION OF CONTENTS

1. Using the Staden program package

1. Introduction to Staden package.
2. Using Pregap4 program.
3. Using Gap4 program.
4. Advanced Streaming Assembly.
5. Analysis of mutations.
6. Analysis ESTs.

2. Databases and genome annotation

7. Databases
8. The computer program BLAST

3. Genome annotation and genome browsers

9. Annotation of bacterial genomes
10. Genome browsers
11. Annotation of eukaryotic genomes

4. NGS Technologies

12. Assembly of sequences derived from NGS technologies

WORKLOAD

ACTIVITY	Hours	% To be attended
Computer classroom practice	26,00	100
Other activities	4,00	100
Development of group work	15,00	0
Study and independent work	15,00	0
Preparation of practical classes and problem	15,00	0
TOTAL	**75,00**	

TEACHING METHODOLOGY

A) Class sessions in the computer lab with a theoretical introduction followed by practice and problem solving exercises.

B) Tutoring

C) Exam

D) Exercises and bioinformatics problems solved outside of class time.

E) Study the contents and preparation of classes.

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EVALUATION

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

1) An exam in the computer lab that may comprise both knowledge questions on theory and exercises that can be solved using the programs studied in the course. This test will earn up to 7 points and will be made after the end of classes.

2) Continuous Assessment based on class work and in solving exercises and bioinformatics problems. This section will be worth up to 3 points.

In the second call, the student will have two options: 1) an exam where you can collect up to 10 points and 2) if the student has obtained a note for the continuous evaluation on the first call, these points will be added to those of the test, which will be worth up to 7 points.

REFERENCES

Basic

- Bioinformatics and Functional Genomics, por Jonathan Pevsner (2009) publicado por Wiley_Blackwell. Segunda edición. Una introducción a la bioinformática y la genómica fácil de seguir y de entender los conceptos. Incluye muchos ejercicios prácticos y direcciones web.