Course Guide
42584 Basics of bioinformatics and genomics

COURSE DATA

DATA SUBJECT

Code: 42584
Name: Basics of bioinformatics and genomics
Cycle: Master's Degree
ECTS Credits: 6
Academic year: 2026-27

STUDY (S)

Degree	Center	Acad. year	Period
2116 - Master's Degree in Bioinformatics	Escola Tècnica Superior d'Enginyeria	1	Second quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
2116 - Master's Degree in Bioinformatics	Basics of bioinformatics and genomics	COMPULSORY

COORDINATION

ARNAU LLOMBART VICENTE

SUMMARY

This course is designed for basic bioinformatics, understood as a general purpose methodologies for the analysis of sequences and genomes. It will give an overview of the available databases and their corresponding interfaces most commonly used. Be reviewed freeware most common basic operations sequence analysis and alignment, similarity search, identification of different types of domains such as regulatory motifs and functional domains in proteins. We will study the most commonly used genomic environments (ENSEMBL and UCSC) and their ability to extract information about genes, transcription, variation, function, conservation, etc.., And the possibilities to compare genomes and genomic resolve complex issues.

PREVIOUS KNOWLEDGE

RELATIONSHIP TO OTHER SUBJECTS OF THE SAME DEGREE

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

OTHER REQUIREMENTS

None

COMPETENCES / LEARNING OUTCOMES

2116 - Master's Degree in Bioinformatics

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

Be able to access to information tools in other areas of knowledge and use them properly.

Desarrollar la iniciativa personal y ser capaces de realizar una toma rápida y eficaz de decisiones en su labor profesional y/o investigadora.

Dominar los conceptos básicos de bioinformática que incluyen el conocimiento de las bases de datos más comunes así como los programas básicos de alineamiento, búsqueda por similitud y búsqueda de motivos y dominios en secuencias biológicas.

Students should apply acquired knowledge to solve problems in unfamiliar contexts within their field of study, including multidisciplinary scenarios.

Students should be able to integrate knowledge and address the complexity of making informed judgments based on incomplete or limited information, including reflections on the social and ethical responsibilities associated with the application of their knowledge and judgments.

Students should communicate conclusions and underlying knowledge clearly and unambiguously to both specialized and non-specialized audiences.

Students should demonstrate self-directed learning skills for continued academic growth.

Students should possess and understand foundational knowledge that enables original thinking and research in the field.

To be able to assess the need to complete the scientific, historical, language, informatics, literature, ethics, social and human background in general, attending conferences, courses or doing complementary activities, self-assessing the contribution of these activities towards a comprehensive development.

Trabajar en equipo con eficiencia en su labor profesional y/o investigadora y con personas de diferente procedencia.

Usar entornos genómicos con todas sus posibilidades de explotación de la información sobre genes, variantes, funciones, etc así como sus capacidades de comparación entre especies.

DESCRIPTION OF CONTENTS

1. Databases of sequences, proteins, genomes and other biomedical data

Will access and describe the major bioinformatics databases that exist in the scientific community.

2. Sequence alignment

A sequence alignment in bioinformatics is a way to represent and compare two or more sequences, which may indicate functional relationships or evolutionary relationships among genes or proteins consulted. Analyze key alignment algorithms and examine the results.
We will study one of the processes performed in bioinformatics, similarity search of a sequence with the sequences contained in databases.

3. Visualization of omic data

The most common methods and tools for visualizing omic data using networks and different types of graphical representations will be studied.

4. Identification of motifs and domains of proteins and genes

An important aspect in the further sequence analysis of alignment is the functional similarity between different sequences. The functionality and purpose of certain proteins is often determined by the operation and existence of small patterns in composition. We will study these concepts.

5. Visualization environments genomes (EMBL, UCSC)

We study the main tools for visualization of genomes.

WORKLOAD

PRESENCIAL ACTIVITIES

Activity	Hours
Theory	21,00
Laboratory	9,00
Total hours	**30,00**

NON PRESENCIAL ACTIVITIES

Activity	Hours
Attendance at other activities	0,00
Individual or group project	27,00
Independent study and work	63,00
Preparation of lessons	5,00
Preparation for assessment activities	15,00
Resolution of case studies	18,00
Total hours	**128,00**

TEACHING METHODOLOGY

MD1 - Task training of the teaching-learning environment interaction in the classroom through expository sessions. Previous assignments include preparation (information search, reading texts supplied by teachers), teaching sessions themselves and the later work of deepening.

MD2 - Learning through problem solving and case studies, through which it is acquiring skills on different aspects of materials and subjects.

MD3 - Hands-on lab. Include preparation, implementation of practices to monitor and teacher support, independent work online and reporting practices.

MD4 - Cross-disciplinary skills. Include attendance at courses, conferences or round tables organized by the CEC of the Master and / or conduct of a bibliographic work on issues that contribute to the integral. It produces a report of activities.

EVALUATION

In both sessions:

SE1: Continuous assessment, 5% of the grade.

SE2: Assessment of activities will be 30% of the grade.

SE3: Assessment of reports, 65% of the grade.

Continuous assessment will only be taken into account in the first session.

REFERENCES

- Referencia b1: GENETICA. J.A. GRIFFITHS, MCGRAW-HILL / INTERAMERICANA DE ESPAÑA, S. A., 2008. ISBN 9788448160913

- Referencia b2: Molecular Biology of the Gene, 6/E. James D. Watson, et. alt. ISBN: 9780805395921. Publisher: Benjamin Cummings. 2008

- Referencia c1: Genética Humana. Fundamentos y aplicaciones en Medicina. Alberto Juan Solari. Panamericana, 2011. Edición: 4ª