

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

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| Code | 42584 |
| Name | Basics of bioinformatics and genomics |
| Cycle | Master's degree |
| ECTS Credits | 6.0 |
| Academic year | 2024 - 2025 |

Study (s)

| Degree | Center | Acad. Period | year |
|--|-----------------------|---------------------|-------------|
| 2116 - Master's Degree in Bioinformatics | School of Engineering | 1 | Second term |

Subject-matter

| Degree | Subject-matter | Character |
|--|---|------------------|
| 2116 - Master's Degree in Bioinformatics | 1 - Basics of bioinformatics and genomics | Obligatory |

Coordination

| Name | Department |
|-------------------------|------------------------|
| ARNAU LLOMBART, VICENTE | 240 - Computer Science |

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 (RD 1393/2007) // LEARNING OUTCOMES (RD 822/2021)

2116 - Master's Degree in Bioinformatics

- 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.
- Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.
- Students should possess and understand foundational knowledge that enables original thinking and research in the field.
- Be able to access to information tools in other areas of knowledge and use them properly.
- 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.
- Desarrollar la iniciativa personal y ser capaces de realizar una toma rápida y eficaz de decisiones en su labor profesional y/o investigadora.
- Trabajar en equipo con eficiencia en su labor profesional y/o investigadora y con personas de diferente procedencia.
- 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.
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- 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.

LEARNING OUTCOMES (RD 1393/2007) // NO CONTENT (RD 822/2021)

Master the basics of bioinformatics including knowledge of databases more useful and its management. Knowing the basic programs of alignment, similarity search and search for motifs and domains of interest in biological sequences. Understand the algorithms and the basic techniques of search and data classification, localization motifs and biological sequence analysis in general. Using a genomic environment with all its possibilities of use of information on genes, variants, functions, etc. as well as their ability to compare species.

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

| ACTIVITY | Hours | % To be attended |
|--|---------------|------------------|
| Theory classes | 30,00 | 100 |
| Development of group work | 10,00 | 0 |
| Development of individual work | 20,00 | 0 |
| Study and independent work | 30,00 | 0 |
| Readings supplementary material | 20,00 | 0 |
| Preparation of evaluation activities | 10,00 | 0 |
| Preparing lectures | 5,00 | 0 |
| Preparation of practical classes and problem | 15,00 | 0 |
| Resolution of case studies | 10,00 | 0 |
| TOTAL | 150,00 | |

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

SE1 Continuous assessment: minimum 5 and maximum 15.



SE2 Activities: minimum 10 and maximum 50.

SE3 Laboratory: minimum 25 and maximum 75.

REFERENCES

Basic

- 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

Additional

- Referencia c1: Genética Humana. Fundamentos y aplicaciones en Medicina. Alberto Juan Solari EAN: 9789500602693. Edición: 4ª