

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

Code	42587
Name	Developmental bioinformatics
Cycle	Master's degree
ECTS Credits	6.0
Academic year	2021 - 2022

Study (s)

Degree	Center	Acad. year	Period
2116 - M.U. en Bioinformàtica 12-V.1	School of Engineering	1	Second term

Subject-matter

Degree	Subject-matter	Character
2116 - M.U. en Bioinformàtica 12-V.1	5 - Developmental bioinformatics	Obligatory

Coordination

Name	Department
GONZALEZ CANDELAS, FERNANDO	194 - Genetics
PALERO PASTOR, FERRAN	194 - Genetics

SUMMARY

Evolutionary Bioinformatics has the main objective of understanding the form and function of organisms considering their evolutionary history, the factors that have acted throughout their ancestors and that still exert their influence today, in order to determine the species distribution and abundance. To do this, Evolutionary Bioinformatics retrieves the genetic information and the footprints left on it by different processes, making extensive use of comparative analysis by reconstructing phylogenies and genealogies. The course covers the fundamental concepts of molecular evolution and evolutionary processes that act on genes and genomes, populations and species, and puts special emphasis on the knowledge and practical use of the main methods, algorithms and software of this area.



PREVIOUS KNOWLEDGE

Relationship to other subjects of the same degree

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

Other requirements

To have passed the basic subjects Evolution, Genetics and Biochemistry and Molecular Biology

OUTCOMES

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- 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.
- Aplicar las herramientas bioinformáticas necesarias para estudiar e interpretar la evolución de las macromoléculas biológicas o de los organismos que las portan.
- Abordar estudios de genómica comparada para descifrar la evolución de la organización, complejidad y la variabilidad de los genomas de los organismos, tanto en investigación básica como en el desarrollo de aplicaciones (Farmacogenómica, Nutrigenómica, etc.).



LEARNING OUTCOMES

- Understand the biological, mathematical and computational methods used in bioinformatics in order to make inferences about evolutionary processes at different levels.
- Applying different methods according to the requirements and conditions suitable for each problem.
- To advise on methods or implementations of them more suitable for troubleshooting.
- To design new strategies in solving problems within the subject area.

DESCRIPTION OF CONTENTS

1. Multiple alignment

Multiple alignments of sequences: based on primary sequence, secondary structure, alignment and phylogeny. Evaluation of alignments.

2. Sequence evolution

Evolutionary change in sequences. Rates and patterns of evolution in macromolecules.

3. Advanced phylogenetic reconstruction

Advanced phylogenetic reconstruction. Evaluation of the phylogenetic signal. Maximum likelihood. Heuristic search. Parameter optimization. Bayesian methods of phylogenetic reconstruction.

4. Recombination and gene conversion

Recombination, defined as exchange of genetic material, is a universal evolutionary force. Along with mutation, recombination generates new genetic combinations into genomes. Due to its importance in genomic evolution and its effect in evolutionary inferences many bioinformatic approaches have been developed to trace and characterize recombinant events. Concepts (linkage disequilibrium, mechanisms of recombination, recombination rate, homologous and non-homologous recombination), and some recombination detection tools (Simplot, RDP3) will be shown in this unit.

Especificación de contenidos de la unidad: Analysis of recombination and molecular gene conversion. Methods based on phylogenies: evaluating incongruence. Methods for reconstructing network evolution.



5. Selection at the molecular level

Analysis of selection at the molecular level. Selection in coding regions. Selection in non-coding regions. Selection and recombination.

6. Phylodynamics and phylogeography

Especificación de contenidos de la unidad Phylodynamics and phylogeography. Phylogenetic reconstruction dating nodes and / or terminal leaves. Relaxed clock methods. Demographic models and geographic models

7. Phylogenomics and horizontal gene transfer

Our capacity to reveal and weight the impact of different evolutionary processes on genome evolution depends on our ability to accurately reconstruct the evolutionary relationships of the taxa studied. This has been the aim of phylogenetics since the first reported phylogenetic trees. Now that thousands of genomes are being compared at very different divergence levels from populations to domains traditional phylogenetic analysis has to adapt to the change in the amount of available information that ultimately will allow to understand better genomic evolution. In this UT we will show how to take advantage of available genomic information to make evolutionary inferences using phylogenetic tools and how these tools can be used to reveal the genomic impact of evolutionary processes illustrated by the analyses of the horizontal gene transfer phenomenon in prokaryotes and eukaryotes.

Especificación de contenidos de la unidad Introduction to phylogenomics. Supermatrices. Supertrees. Evaluation and interpretation of phylogenetic incongruence. Application to the detection of horizontal gene transfer events.

8. Functional divergence and coevolution

Functional divergence among homologous genes enables the diversification and specialisation of organisms into different ecological niches. In this UT we will analyse the diverse existing models of gene duplication and divergence and will learn to analyse the evolutionary history of gene families. We will learn to distinguish between orthologs and paralogs by means of phylogenetic analyses, and will study the processes of functional divergence and concerted evolution in gene families. Besides, we will discuss how functional divergence can be affected by coevolution between different proteins. The rates and patterns of genic duplication will be analysed on the base of birth and death models and other approaches. We will also present cases of functional divergence after genomic duplications and of proteomic divergence. Finally, there will be practical exercises of gene family analysis in which several of the processes presented will be investigated.

Especificación de contenidos de la unidad: Functional divergence. Analysis of functional divergence in paralogous genes. Divergent evolution, concerted evolution and evolution by birth and death. Analysis of functional divergence of the proteome. Coevolution.

**WORKLOAD**

ACTIVITY	Hours	% To be attended
Theory classes	21,00	100
Laboratory practices	9,00	100
Development of individual work	10,00	0
Study and independent work	30,00	0
Readings supplementary material	10,00	0
Preparation of evaluation activities	10,00	0
Preparing lectures	15,00	0
Preparation of practical classes and problem	15,00	0
Resolution of case studies	30,00	0
TOTAL	150,00	

TEACHING METHODOLOGY

MD1 - Tasks within the teaching-learning environment interaction through expository sessions in the classroom. Previous assignments include preparation (information search, reading texts supplied by the teachers), teaching sessions and in-depth study.

MD2 - Learning through problem-solving and case studies, and acquiring skills on different aspects of the subject.

MD3 - Hands-on labs. Include preparation, implementation of practical exercises to monitor the student and get the teacher's support, independent online work and writing reports on the practical exercises.

MD4 - Cross-disciplinary skills. Include attendance at the lectures, conferences or round tables organized by the **CCA** of the Master and / or conduct a bibliographic study on issues that contribute to the integration of the subject. Writing up a report on the activities carried out during the course

EVALUATION

The evaluation shall consider the following sections and content:

1. Continuous assessment (10%), based on attendance to lectures for which attendance will be monitored through a sign-up sheet. As you miss more than 2 lectures without justification, your qualification will be reduced proportionally.

2. Laboratory (60%). Assessment of self-work performance and interpretation of the results of the 10 exercises from reports presented for each one of them.



3. Examination (20%). Short questionnaire on the main concepts seen in the course.

It must achieve a minimum score of 4 out of 10 in each of the sections that can be considered for the final grade, which will be obtained as a weighted average of the same.

REFERENCES

Basic

- Referencia b1: Lemey P, Salemi M, Vandamme AM, editors. The phylogenetic handbook. A practical approach to phylogenetic analysis and hypothesis testing. 2nd ed. Cambridge: Cambridge University Press; 2009.
- Referencia b2: Nielsen R, editor. Statistical Methods in Molecular Evolution. Springer-Verlag. 2005.
- Referencia b3: Yang, Z. Computational Molecular Evolution. Oxford: Oxford Univ. Press; 2006.
- Referencia b4:
Felsenstein J. Inferring Phylogenies. Sunderland: Sinauer Assoc. 2004.
- Referencia b5: Gascuel O, Steel MA, editors. Reconstructing Evolution: New Mathematical and Computational Advances. Oxford: Oxford University Press; 2007.
- Referencia b6: Gascuel O. Mathematics of Evolution and Phylogeny. Oxford: Oxford University Press; 2005.

Additional

- Referencia c1: Lynch M. The Origins of Genome Architecture. Sunderland: Sinauer Assoc., 2007.
- Referencia c2: Caetano-Anollés G. Evolutionary Genomics and Systems Biology. John Wiley & Sons; 2010.

ADDENDUM COVID-19

This addendum will only be activated if the health situation requires so and with the prior agreement of the Governing Council

English version is not available