

BASIC DETAILS:

Subject:	FILOGENÉTICA		
Id.:	33706		
Programme:	DOBLE GRADO EN FARMACIA Y BIOINFORMÁTICA. PLAN 2019		
Module:	CIENCIAS DE LA VIDA		
Subject type:	OBLIGATORIA		
Year:	3	Teaching period:	Primer Cuatrimestre
Credits:	6	Total hours:	150
Classroom activities:	62	Individual study:	88
Main teaching language:	Inglés	Secondary teaching language:	Castellano
Lecturer:	RANERA BELTRAN, BEATRIZ (T)	Email:	branera@usj.es

PRESENTATION:

The main goal of this subject is providing the tools to analyze molecular sequences in order to establish evolutionary relationships between each other by the creation of trees.

Historical background will be provided and how the discovers in biotechnology have provided new theories in the phylogenetics field. The process of tree building by detecting the difference between a given set of biological sequence will be analyzed. Substitution methods of evolution will be explored by using mathematical concepts.

Tree building algorithms based on distances or probabilistics approaches will be analyzed to determine which performs the best outcome. Already developed tools, as well as, R packages of functions and in-house python algorithms will be used for phylogenetics tree building.

Validation of trees will be also determined and the computational limitations due to genomic complexity will be analyzed.

PROFESSIONAL COMPETENCES ACQUIRED IN THE SUBJECT:

General programme competences	G03	Cooperate to achieve common results through teamwork in a context of integration, collaboration and empowerment of critical discussion.
	G04	Reason critically based on information, data and lines of action and their application on relevant issues of a social, scientific or ethical nature.
	G05	Communicate professional topics in Spanish and / or English both orally and in writing.
	G07	Choose between different complex models of knowledge to solve problems.
	G08	Recognise the role of the scientific method in the generation of knowledge and its applicability to a professional environment.
	G10	Apply creativity, independence of thought, self-criticism and autonomy in the professional practice.
Specific programme competences	E12	Apply the principles and techniques of protein computational modelling to predict their biological function, their activity or new therapeutic targets (Structural Bioinformatics, Computational Toxicology).
	E13	Apply omics technologies for the extraction of statistically significant information and for the creation of relational databases of biodata that can be updated and publicly accessible to the scientific community.
	E15	Infer the evolutionary history of genes and proteins through the creation and interpretation of phylogenetic trees.
	E16	Plan linkage and association studies for medical and environmental purposes.
	E17	Induce complex relationships between samples by applying statistical and classification techniques.
	E18	Apply statistical and computational methods to solve problems in the fields of molecular biology, genomics, medical research and population genetics.
	E19	Explain the main biochemical reactions by applying the principles of chemical kinetics and thermodynamics.
	E20	Relate the overall functioning of the organism with the basic mechanisms at the cellular and molecular level.
	E21	Apply computational and data processing techniques for the integration of physical, chemical

and biological concepts and data for the description and/ or prediction of the activity of a substance in a given context.

PRE-REQUISITES:

Basic statistics, probabilistic, genomics and alignment theory are needed to understand the underlying knowledge of phylogenetics. Programming skills in R and Python are mandatory to understand the provided code.

SUBJECT PROGRAMME:

Observations:

The order of the units might vary depending on the learning pace of the students. The content of the units can be modified to adapt it to all the students.

It is highly recommended to the student to study, revise and practise the learnt algorithms before starting with the next.

Unexpected events might change the subject, as resources availability, academic calendar or group capacity, for these reasons cannot be considered definitely closed.

Subject contents:

1 - Introduction to Phylogenetics
1.1 - Introduction and terminology
1.2 - Speciation. Tree topologies.
1.3 - Theories
1.4 - Applications
2 - Phylogenetics Analysis
2.1 - Types of trees
2.2 - Molecular markers
2.3 - Multiple sequence alignment
2.4 - Model evolution of nucleotides
2.5 - Model evolution of amino acids
2.6 - Model selection
2.7 - Tree building method
2.8 - Assessing tree reliability
2.9 - Available softwares
3 - Building algorithms based on distances. Neighbour joining.
4 - Building algorithms based on distances. Unweighted pair group method with arithmetic mean.
5 - Building algorithms based on distances. Maximum parsimony.
6 - Building algorithms based on probabilistic approaches. Maximum likelihood.
7 - Building algorithms based on probabilistic approaches. Bayesian inference.
8 - Assessing tree reliability.
9 - Genome complexity and phylogenetics analysis.

Subject planning could be modified due unforeseen circumstances (group performance, availability of resources, changes to academic calendar etc.) and should not, therefore, be considered to be definitive.

TEACHING AND LEARNING METHODOLOGIES AND ACTIVITIES:

Teaching and learning methodologies and activities applied:

This subject is based on active participation, for which different teaching and learning methodologies will be applied: master classes, problem-based learning and case-study learning.

Student work load:

Teaching mode	Teaching methods	Estimated hours
Classroom activities	Master classes	20
	Other theory activities	2
	Practical exercises	20
	Practical work, exercises, problem-solving etc.	20
Individual study	Tutorials	6
	Individual study	40
	Individual coursework preparation	10
	Project work	15
	Research work	10
	Recommended reading	7
Total hours:		150

ASSESSMENT SCHEME:

Calculation of final mark:

Written tests:	20 %
Individual coursework:	20 %
Final exam:	50 %
Case-study:	10 %
TOTAL	100 %

*Las observaciones específicas sobre el sistema de evaluación serán comunicadas por escrito a los alumnos al inicio de la materia.

BIBLIOGRAPHY AND DOCUMENTATION:

Basic bibliography:

PEVSNER, Jonathan. Bioinformatics and functional genomics. Oxford: John Wiley and Sons, 2015.
DURBIN, Richard. Biological sequence analysis. Cambridge: Cambridge University Press, 1998
BLEIDORN, Christoph. Phylogenomics An Introduction. Gewerberstrasse: Springer. 2017

Recommended bibliography:

ROCHA Miguel. Bioinformatics Algorithms Design and Implementation in Python. London: Academic Press 2018
XIONG, Jin. Essential Bioinformatics. Cambridge: Cambridge University Press, 2006

Recommended websites:

Bioconductor <https://www.bioconductor.org/>