

BASIC DETAILS:

Subject:	FILOGENÉTICA		
Id.:	33296		
Programme:	GRADUADO EN BIOINFORMÁTICA. PLAN 2019 (BOE 06/02/2019)		
Module:	CIENCIAS DE LA VIDA		
Subject type:	OBLIGATORIA		
Year:	3	Teaching period:	Primer Cuatrimestre
Credits:	6	Total hours:	150
Classroom activities:	64	Individual study:	86
Main teaching language:	Inglés	Secondary teaching language:	Castellano
Lecturer:		Email:	

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, python specific modules and specific software of phylogenetic analysis 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	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	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.
	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.
Learning outcomes	R01	Definir el concepto de filogenética.
	R02	Describir los principales términos asociados a la filogenética.
	R03	Explicar los mecanismos evolutivos requeridos para construir árboles filogenéticos.
	R04	Discriminar las diferentes metodologías de construcción de árboles filogenéticos.
	R05	Componer árboles filogenéticos a partir de datos morfológicos.

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:

Subject contents:

1 - Introduction to Phylogenetics
1.1 - Introduction and terminology
1.2 - Tree topologies and structures.
1.3 - Molecular Clock Hypothesis. Positive and Negative Selection. Neutral Theory.
1.4 - Applications
2 - Phylogenetics Analysis
2.1 - Types of trees
2.2 - DNA, Protein-Based Trees
2.3 - Phylogenetic Analysis. Molecular markers.
2.4 - Phylogenetic Analysis. Multiple Sequence Alignment.
2.5 - Phylogenetic Analysis. Models of Nucleotide Substitution.
2.6 - Phylogenetic Analysis. Models of Aminoacid Substitution.
2.7 - Phylogenetic Analysis. Tree building methods
2.8 - Phylogenetic Analysis. Assessing tree reliability
2.9 - Available softwares
3 - Building algorithms based on distances. Unweighted pair group method with arithmetic mean.
3.1 - Distance Methods
3.2 - UPGMA
3.3 - UPGMA in Python
3.4 - UPGMA in Mega
4 - Building algorithms based on distances. Neighbour Joining.
4.1 - Neighbour Joining
4.2 - Rooting a tree.
4.3 - NJ in Python
4.4 - NJ in R
4.5 - Selection of Evolution Model
4.6 - NJ in MEGA
5 - Building algorithms based on characters. Maximum parsimony.
5.1 - Character based methods.
5.2 - Maximum Parsimony.
5.3 - Tree Searching Methods
5.4 - MP in Python
5.5 - MP in R
5.6 - MP in MEGA
5.7 - Pros and Cons of MP
6 - Building algorithms based on probabilistic approaches. Maximum likelihood.
6.1 - Probabilistic Methods in Phylogeny
6.2 - Maximum Likelihood
6.3 - ML Procedures
6.4 - ML in R
6.5 - ML in MEGA
7 - Assessing tree reliability.
7.1 - Resampling strategies
7.2 - Bootstrapping
7.3 - Bootstrapping in MEGA
8 - Building algorithms based on probabilistic approaches. Bayesian inference.

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
	Other practical activities	2
Individual study	Tutorials	6
	Individual study	38
	Individual coursework preparation	10
	Project work	15
	Research work	10
	Recommended reading	7
Total hours:		150

ASSESSMENT SCHEME:

Calculation of final mark:

Individual coursework:	25	%
Final exam:	50	%
Case-study:	10	%
On line Test:	15	%
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:

BLEIDORN, Christoph. Phylogenomics An Introduction. Gewerberstrasse: Springer. 2017
DURBIN, Richard. Biological sequence analysis. Cambridge: Cambridge University Press, 1998
LEMEY, Philippe. The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing. Cambridge University Press, 2009.
PEVSNER, Jonathan. Bioinformatics and functiona genomics. Oxford: John Wiley and Sons, 2015.

Recommended bibliography:

ROCHA Miguel. Bioinformatics Algorithms Design and Implementation in Python. London: Academic Press 2018
XIONG, Jin. Essential Bioinformatics. Cambridge: Cambridge University Press, 2006
YANG, Ziheng, et al. Computational molecular evolution. Oxford: Oxford University Press, 2006.

Recommended websites:

Bioconductor	https://www.bioconductor.org/
BioPython	https://biopython.org/
MEGA Software	www.megasoftware.net/docs

* Guía Docente sujeta a modificaciones