Course guide
2703128 - PCG - Phylogenomics and Comparative Genomics

Last modified: 30/01/2026

Unit in charge:	Barcelona School of Informatics
Teaching unit:	1004 - UB - (ENG)Universitat de Barcelona.

Degree:	BACHELOR'S DEGREE IN BIOINFORMATICS (Syllabus 2024). (Compulsory subject).

Academic year: 2025   **ECTS Credits:** 6.0   **Languages:** English

LECTURER

Coordinating lecturer: JESÚS LOZANO FERNÁNDEZ

Others:

LEARNING RESULTS

Knowledges:
K1. Recognise the fundamental principles of biology, from the cellular to the organismic scale, and how they relate to current knowledge in bioinformatics, data analysis and machine learning, achieving an interdisciplinary vision with an emphasis on biomedical applications.
K2. Identify statistical and computational methods and mathematical models that can be used to solve problems in molecular biology, genomics, medical research and population genetics.
K3. Identify the mathematical foundations, computational theories, algorithmic schemes and principles of information organisation relevant to modelling biological systems and efficiently solving bioinformatics problems through the design of computational tools.
K7. Analyse sources of valid and reliable scientific information to determine the state of the art of a bioinformatics problem and how to tackle it.

Skills:
S1. Integrate omic and clinical data to better understand and analyse biological phenomena.
S2. Computationally analyse DNA, RNA and protein sequences, including comparative genomic analysis, using computation, mathematics and statistics as the basic tools of bioinformatics.
S3. Solve problems in molecular biology, genomics, medical research and population genetics by applying statistical and computational methods and mathematical models.
S5. Communicate information, ideas, problems and solutions from bioinformatics and computational biology to a general audience.
S7. Implement programming methods and data analysis based on the development of working hypotheses within the area of study.
S8. Make and defend reasoned decisions when solving problems in biology and, in appropriate fields, the health sciences, computer science and experimental sciences.

Competences:
C2. Recognise the complexity of the economic and social phenomena typical of a welfare society and relate welfare to globalisation, sustainability and climate change in order to use techniques, technology and principles of economics and sustainability in a balanced and compatible way.
C3. Communicate orally and in writing with others in English about learning outcomes, thought processes and decision making.
C4. Work as part of a multidisciplinary team, whether as a team member or in a leadership role, to contribute to the development of projects (including business and research projects) with pragmatism, a sense of responsibility and ethical principles, undertaking commitments with due regard to the resources available.

TEACHING METHODOLOGY

Lectures will be mainly of expository type. There will be also practical sessions using a wide range of phylogenetics and comparative genomics softwares, a small research project developed in group, and a group seminar covering a recent comparative genomics publication.

LEARNING OBJECTIVES OF THE SUBJECT

1.Inferring phylogenies using genome-scale data
2.Acquisition of the specific knowledge of statistical inference and modelling in phylogenetics
3.Use comparative genomics tools for solving biological problems

STUDY LOAD

Type	Hours	Percentage
Hours large group	30,0	20.00
Hours small group	30,0	20.00
Self study	90,0	60.00

Total learning time: 150 h

CONTENTS

Genes and their functions

Description:
Origin of genes, duplication, losses and evolution. Gene structure and expression. Relationships between sequence, structure, and function and their evolution. Homology based functional inference. Protein domains and domain shuffling.

Phylogenetic analyses

Description:
Conceptual framework. Parsimony. Maximum Likelihood. Bayesian. Nodal support. Species and gene family tree reconstruction. Inference of gene duplication and other evolutionary events.

Comparative sequence analyses

Description:
Homology, Paralogy and Orthology. Methods for predicting orthology and paralogy: clustering-based and phylogeny-based. Gene families. Gene duplication, neo- and sub-functionalization. Gene family expansions and contractions. Adaptation and genome evolution.

Phylogenomics

Description:
Genome-wide phylogenetic analysis (phylome). Species tree reconstruction. Gene tree vs species tree. Non-vertical processes of evolution, horizontal gene transfer. Whole genome duplication. Timetrees and ancestral-state reconstruction

Modelling molecular substitutions

Description:
Model selection. Topological evaluation and incongruence. Inference in practice

Genome comparisons

Description:
Genome alignments and detection of conserved regions. Recent availability of chromosome-scale genomes and annotations thanks to global efforts (EBP, ERGA, CBP,...). Conserved motif discovery. Genome re-arrangements. Synteny analysis. Prediction of function from conserved gene order. Presence absence patterns. Convergent evolution. Gene tree comparison. Co-evolution between genes.

Gene expression and functional analyses

Description:
Genomics-based methods to assess gene expression. genome-wide functional annotation. Long-non-coding RNAs. Efforts in model and non-model species. Diversity of life and the tree of life. Variation of genome size and organization. Extreme genome expansions and reductions.

ACTIVITIES

Theoretical expository lectures

Specific objectives:
1, 2, 3

Full-or-part-time: 56h
Theory classes: 26h
Self study: 30h

Practical sessions

Specific objectives:
1, 2, 3

Full-or-part-time: 76h
Practical classes: 26h
Self study: 50h

Seminars on recent studies

Specific objectives:
1, 2, 3

Full-or-part-time: 14h
Practical classes: 4h
Self study: 10h

Mid-term exam

Full-or-part-time: 2h
Theory classes: 2h

Final exam

Full-or-part-time: 2h
Theory classes: 2h

GRADING SYSTEM

Laboratory practices and seminars are mandatory. The course assessment is as follows:

60% consists of a 2 partial theoretico-practical exams taken at mid term (20%) and final term (40%).
15% corresponds to regular individual practical assignments
15% corresponds to a research project done in teams
10% corresponds to a seminar presentation in teams

Recuperation Information
Only the students that after the evaluation have a grade equal or greater than 3,5 can perform the re-evaluation exam. The re-evaluation exam will substitute the theoretico-practical part (60%).

BIBLIOGRAPHY

Basic:
- Lindell Bromham. Reading the story in DNA : a beginner's guide to molecular evolution. Oxford ; New York : Oxford University Press, 2008, 2008. ISBN 9780199290918.
- Casey W. Dunn. Phylogenetic Biology. 2024.
- Celine Scornavacca, Frédéric Delsuc, Nicolas Galtier. Phylogenetics in the Genomic Era. Authors open access book, 2021. ISBN 2780-0539.
- Bergman, Nicholas H. Comparative genomics. Humana, cop. 2007. ISBN 9781934115374.
- Yang, Ziheng. Molecular evolution : a statistical approach. First edition. Oxford University Press, 2014. ISBN 0199602603.