



POLITÉCNICA

INTERNATIONAL  
CAMPUS OF  
EXCELLENCE

COORDINATION PROCESS OF  
LEARNING ACTIVITIES  
PR/CL/001



E.T.S. de Ingenieros  
Informáticos

# ANX-PR/CL/001-01

## LEARNING GUIDE

### SUBJECT

**203000027 - Computational Approaches In Evolutionary Biology**

### DEGREE PROGRAMME

20BC - Master Universitario En Biología Computacional

### ACADEMIC YEAR & SEMESTER

2022/23 - Semester 1

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## 1. Description

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### 1.1. Subject details

<b>Name of the subject</b>	203000027 - Computational Approaches In Evolutionary Biology
<b>No of credits</b>	3 ECTS
<b>Type</b>	Optional
<b>Academic year of the programme</b>	First year
<b>Semester of tuition</b>	Semester 1
<b>Tuition period</b>	September-January
<b>Tuition languages</b>	English
<b>Degree programme</b>	20BC - Master Universitario en Biología Computacional
<b>Centre</b>	20 - E.T.S. De Ingenieria Agronomica, Alimentaria Y De Biosistemas
<b>Academic year</b>	2022-23

## 2. Faculty

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### 2.1. Faculty members with subject teaching role

<b>Name and surname</b>	<b>Office/Room</b>	<b>Email</b>	<b>Tutoring hours *</b>
Jesus Israel Pagan Muñoz (Subject coordinator)	231	jesusisrael.pagan@upm.es	Tu - 12:00 - 13:00

\* The tutoring schedule is indicative and subject to possible changes. Please check tutoring times with the faculty member in charge.

### 3. Prior knowledge recommended to take the subject

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#### 3.1. Recommended (passed) subjects

The subject - recommended (passed), are not defined.

#### 3.2. Other recommended learning outcomes

- Basic Concepts of Population Genetics
- Basic Statistics

### 4. Skills and learning outcomes \*

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#### 4.1. Skills to be learned

CE02 - Utilizar sistemas operativos, programas y herramientas de uso común en biología computacional, así como, manejar plataformas de cómputo de altas prestaciones, lenguajes de programación y análisis bioinformáticos

CE03 - Analizar e interpretar bioinformáticamente los datos que se derivan de las tecnologías ómicas, y proponer soluciones bioinformáticas en relación a dichos datos.

CE05 - Utilizar herramientas de biología computacional para el análisis genómico, incluida la genómica comparativa y biología evolutiva.

CE10 - Conocimiento de las técnicas de representación del conocimiento reutilizables y modelos de razonamiento en entornos centralizados y distribuidos a utilizar en la resolución de problemas que impliquen conducta inteligente.

CG03 - Que los estudiantes sepan aplicar los conocimientos adquiridos y su capacidad de resolución de problemas en entornos nuevos o poco conocidos dentro de contextos más amplios (o multidisciplinares) relacionados con el área de la Biología Computacional.

CG05 - Que los estudiantes sean capaces de integrar conocimientos en el área de la Biología Computacional, de formular conclusiones, hipótesis o líneas de trabajo a partir de la información disponible, y de formarse una opinión fundamentada sobre las responsabilidades sociales y éticas vinculadas a la aplicación de sus conocimientos.

CT02 - Capacidad para aplicar el método científico para la resolución de problemas de forma efectiva y creativa.

## 4.2. Learning outcomes

RA18 - Conocer los supuestos teóricos y la base bioestadística en la que se apoyan los diferentes métodos de análisis computacional de la evolución de los organismos

RA19 - Adquirir los conocimientos necesarios para el uso e interpretación de paquetes informáticos enfocados al estudio de la evolución de los organismos.

RA16 - Aprender los conceptos básicos en Biología Evolutiva

RA17 - Conocer cuáles son las aproximaciones más utilizadas para el estudio de la evolución de los organismos

\* The Learning Guides should reflect the Skills and Learning Outcomes in the same way as indicated in the Degree Verification Memory. For this reason, they have not been translated into English and appear in Spanish.

## 5. Brief description of the subject and syllabus

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### 5.1. Brief description of the subject

The course combines a solid formation in theoretical aspects on the mechanisms and forces determining the evolution of living organisms, with a strong practical component developed to familiarize students with computational tools frequently used in evolutionary studies. In particular, students will learn which are the most important mechanisms of generating genetic diversity in natural populations, what forces determine the genetic variants that become fixed in the population, and which are the processes influencing the relative abundance of these variants. At the same time, the student will learn how to use bioinformatics tools commonly utilized to analyze how organisms evolve, including phylogenetic and population genetics approaches.

## 5.2. Syllabus

1. Mechanisms of evolution: mutation
  - 1.1. Workshop: Measurements of population genetic diversity
2. Natural selection
  - 2.1. Workshop: Selection coefficients and heritability
3. Evolution in finite populations: genetic drift
  - 3.1. Workshop: Population demography
4. Genetic variability in natural populations
  - 4.1. Workshop: Fixation indexes and genetic structure of natural populations
5. Sex and recombination
  - 5.1. Workshop: Procedures for identifying recombination and modular evolution
6. Coevolution
  - 6.1. Workshop: Analyses of coevolution and codivergence
7. Long-term evolution and macroevolution
  - 7.1. Workshop: Speciation

## 6. Schedule

### 6.1. Subject schedule\*

Week	Classroom activities	Laboratory activities	Distant / On-line	Assessment activities
1	<b>Mechanisms of evolution: mutation</b> Duration: 02:00			
2	<b>Measurements of population genetic diversity</b> Duration: 02:00			
3	<b>Natural selection</b> Duration: 02:00			
4	<b>Selection coefficients and heritability</b> Duration: 02:00			<b>Problems: Estimation of selection coefficients through the use of fitness measures</b>  Continuous assessment Not Presential Duration: 03:00
5	<b>Evolution in finite populations: genetic drift</b> Duration: 02:00			
6	<b>Population demography</b> Duration: 02:00			
7	<b>Genetic variability in natural populations</b> Duration: 02:00			
8	<b>Fixation indexes and genetic structure of natural populations</b> Duration: 02:00			<b>Practical work: The students will be provided with a nucleotide sequence alignment derived from individuals from a given population of the same organism. They will have to estimate mutation rates and the genetic structure of the population.</b>  Continuous assessment Not Presential Duration: 03:00
9	<b>Sex and recombination</b> Duration: 02:00			

10	<b>Procedures for identifying recombination and modular evolution</b> Duration: 02:00			
11	<b>Coevolution</b> Duration: 02:00			
12	<b>Analyses of coevolution and codivergence</b> Duration: 02:00			<p><b>Practical work:</b> The students are provided with an alignment with nucleotide sequence from the genome of two species, and they have to infer whether the the two species have coevolved.</p> <p>Continuous assessment Not Presential Duration: 03:00</p>
13	<b>Long-term evolution and macroevolution</b> Duration: 02:00			
14	<b>Speciation</b> Duration: 02:00			
15				<p><b>Practical work:</b> The students are provided with an alignment with nucleotide sequence from the genome of various related species, and they have to analyze whether these species followed a simpatric or an allopatric mode of speciation.</p> <p>Continuous assessment Presential Duration: 02:00</p>
16				<p><b>The students will be provided with genetic and phenotypic data for certain organisms and they will have to aswer five questions about the evolutionary dynamics of the population.</b></p> <p>Final examination Not Presential Duration: 05:00</p>
17				

Depending on the programme study plan, total values will be calculated according to the ECTS credit unit as 26/27 hours of student face-to-face contact and independent study time.

\* The schedule is based on an a priori planning of the subject; it might be modified during the academic year, especially considering the COVID19 evolution.



## 7. Activities and assessment criteria

### 7.1. Assessment activities

#### 7.1.1. Assessment

Week	Description	Modality	Type	Duration	Weight	Minimum grade	Evaluated skills
4	Problems: Estimation of selection coefficients through the use of fitness measures		No Presential	03:00	25%	5 / 10	CE05 CG03 CE10 CE02 CE03 CT02
8	Practical work: The students will be provided with a nucleotide sequence alignment derived from individuals from a given population of the same organism. They will have to estimate mutation rates and the genetic structure of the population.		No Presential	03:00	25%	5 / 10	CG05 CE05 CG03 CE10 CE02 CE03 CT02
12	Practical work: The students are provided with an alignment with nucleotide sequence from the genome of two species, and they have to infer whether the two species have coevolved.		No Presential	03:00	25%	5 / 10	CG05 CE05 CG03 CE10 CE02 CE03 CT02
15	Practical work: The students are provided with an alignment with nucleotide sequence from the genome of various related species, and they have to analyze whether these species followed a sympatric or an allopatric mode of speciation.		Face-to-face	02:00	25%	5 / 10	CG05 CE05 CG03 CE10 CE02 CE03 CT02

#### 7.1.2. Global examination

Week	Description	Modality	Type	Duration	Weight	Minimum grade	Evaluated skills
16	The students will be provided with genetic and phenotypic data for certain organisms and they will have to answer five questions about the evolutionary dynamics of the population.		No Presential	05:00	100%	5 / 10	CE05 CG03 CE10 CE02 CE03 CT02 CG05

### 7.1.3. Referred (re-sit) examination

Description	Modality	Type	Duration	Weight	Minimum grade	Evaluated skills
The students will be provided with genetic and phenotypic data for certain organisms and they will have to answer five questions about the evolutionary dynamics of the population.		Face-to-face	05:00	100%	5 / 10	CG05 CE05 CG03 CE10 CE02 CE03 CT02

## 7.2. Assessment criteria

Continuous evaluation: The practical and theoretical aspects of the course will be evaluated through a series of individual works consisting in a number of questions that each student will have to address and present in the form of a manuscript. The final grade will depend not only on the answers given to these questions, but also on the ability of the students to explain the rationale for the approach chosen to obtain these answers.

Final Evaluation: The practical and theoretical aspects of the course will be evaluated through a single individual work consisting in a series of questions covering all aspects of the course that the students will have to address and present in the form of a manuscript. The final grade will depend not only on the answers given to these questions, but also on the ability of the students to explain the rationale for the approach chosen to obtain these answers.

The results will follow the scheme established by the UPM in 2012 as A: Excellent, B: Advanced, C: Satisfactory, D: Not satisfactory.

## 8. Teaching resources

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### 8.1. Teaching resources for the subject

Name	Type	Notes
Nei, M. (1987) Molecular Evolutionary Genetics. Columbia University Press, New York	Bibliography	
Hartl, D.L., Clark, A.G. (2007) Principles of population genetics, fourth ed. Sinauer, Sunderland.	Bibliography	
Lemey, P., Salemi, M., Vandamme, A.-M. (2009) The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing. Cambridge University Press, Cambridge.	Bibliography	

## 9. Other information

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### 9.1. Other information about the subject

Part of the course syllabus is related to the ODS 12: Life in terrestrial ecosystems. For instance, the students will learn how to measure the genetic diversity in natural populations of any organisms. Together with the number of species, the genetic diversity of these species are the two major components of ecosystem biodiversity. Understanding how to calculate biodiversity components is central to preserve it in terrestrial ecosystems.