



## 1. INTRODUCTION

**Optional** course in the Degree in Biochemistry (4th year).

**Genomics** is the integrative study of the structure, function, content, evolution, origin and variation of genomes. One of its main goals is to characterize all genes in an organism analyzing their functional organization in an integrative manner. The practice of genomics requires the use of computational tools, so a good knowledge of bioinformatics is essential.

In this course we will analyze the results of an RNA-seq experiment, from data acquisition to functional analysis of differentially expressed genes, using R/Bioconductor and other tools. **Students must have a good knowledge of R/RStudio** and the basic functions for manipulation of dataframes.

**Students** who want to take this course **must pass a test on R/RStudio** before they are allowed to register.

This course carries **3 ECTS** (75 h) and it is taught in **english** during the second semester. In 2024, lectures (practical sessions with **personal laptop mandatory**) will run from Jan 9th to March 1st (Tuesdays 15.00-16.00 and Fridays 16:00-18:00) in **ROOM 12**.

## 2. COMPETENCES

### Conocimientos

El alumno debe:

1. Conocer las técnicas y aproximaciones experimentales que han llevado al conocimiento de las secuencias de distintos genomas.
2. Comprender la base científica de los métodos informáticos empleados para analizar secuencias de genomas y funciones de genes
3. Conocer la estructura, organización y función de los genomas en la escala evolutiva

### Competencias y habilidades

El alumno debe ser capaz de:

1. Describir los términos genoma, transcriptoma y epigenoma.
2. Conocer la terminología y herramientas propias de la materia.
3. Utilizar programas informáticos y bases de datos que permiten el análisis de la información contenida en el genoma.
4. Interpretar los resultados del análisis genómico a distintos niveles.
5. Comprender artículos científicos publicados en el ámbito de la Genómica.
6. Resolver problemas prácticos relacionados con la materia y aplicar el razonamiento crítico.
7. Aplicar el conocimiento adquirido en este ámbito en la resolución de cuestiones con criterio científico y ético.
8. Integrar en la Genómica los conocimientos de otras materias afines.
9. Demostrar espíritu crítico y capacidad de síntesis.



**Competencias del Módulo IX del Grado en Bioquímica (Optatividad)**

CB2	Que los estudiantes sepan aplicar sus conocimientos a su trabajo o vocación de una forma profesional y posean las competencias que suelen demostrarse por medio de la elaboración y defensa de argumentos y la resolución de problemas dentro de su área de estudio
CB3	Que los estudiantes tengan la capacidad de reunir e interpretar datos relevantes (normalmente dentro de su área de estudio) para emitir juicios que incluyan una reflexión sobre temas relevantes de índole social, científica o ética
CB4	Que los estudiantes puedan transmitir información, ideas, problemas y soluciones a un público tanto especializado como no especializado
CG2	Pensar de forma integrada y abordar los problemas desde diferentes perspectivas. Tener razonamiento crítico. Aportar soluciones a problemas en el ámbito científico
CG4	Fomentar el sentido de responsabilidad hacia la vida con sentido ético. Buscar información, evaluarla, así como analizar, sintetizar, resumir, comunicar, citar y presentar trabajos
CG5	Comunicar de forma escrita y oral sobre temas de biomedicina molecular, con un estilo y lenguaje adecuado a la situación y al interlocutor
CE12	Profundizar en aspectos relacionados con las Ciencias Biomédicas que complementen la formación
CE13	Aplicar los conocimientos, conceptos y teorías de las Biociencias moleculares y de la Biomedicina a la práctica



### 3. PROGRAM

1. General overview of RNA-seq experiments: reads, mapping, counting, differential expression, functional analysis.
2. Pre-processing FASTQ files. Mapping reads and generating BAM files. Create the counts matrix.
3. Preparing the counts matrix object. Filtering and normalization using edgeR. Multidimensional scaling with Glimma.
4. Finding differentially expressed genes. Heatmaps and volcano plots.
5. GSEA and Over Representation Analysis (ORA) using ClusterProfiler.
6. Making biological sense of results: other databases and resources.

### 4. EDUCATIONAL ACTIVITIES

#### 1. Lectures. 24 Hours (1 ECTS)

- Methodology: interactive lectures in a Team-Based Learning environment. Students will work through the exercises for each class.
- Skills and specific goals: understanding the core concepts of the course. Students must apply their knowledge to solve questions and practical problems, using bioinformatic tools and working in groups.

#### 2. Homework. 14 Hours (0.5 ECTS)

- Methodology: students practice the concepts and workflows learned in class, reading the necessary documentation to understand the concepts.
- Skills and specific goals: Working alone or in teams, they improve their comprehension of concepts and they practice programming skills developing their own pipelines.

#### 3. Practical exercise. 36 Hours (1.5 ECTS)

- Methodology: students must carry out a team-based project to solve a problem using the resources learned throughout the course, and write a final report following the format of a scientific paper.
- Skills and specific goals: Working in group, improving the comprehension of concepts and developing analytic abilities. Scientific writing.

### 5. ASSESSMENT

The final mark of the course will be the result of a final practical project carried out by each team, in which they submit a brief scientific report (**4000 words máx.**) on their findings after the analysis of an RNAseq experiment. This project should reflect about **36 hours of personal work per student**.

Those who fail the course will have to re-submit the practical project in June.

Students with special educational needs: Exceptions will be allowed in Methodology and Evaluation in order to facilitate the achievement of the skills and the goals of this Course.



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## 6. BIBLIOGRAPHY AND RESOURCES

This course is taught in a **Team-Based Learning (TBL)** format. Students will be provided with all materials required for each session.

We will work through the **User's Guide** pdf available at the web page for the Bioconductor package edgeR (<https://bioconductor.org/packages/release/bioc/html/edgeR.html>) and the tutorials available at the ClusterProfiler web page (<https://bioconductor.org/packages/release/bioc/vignettes/clusterProfiler/inst/doc/clusterProfiler.html>).

## 7. OFFICE HOURS

Please make an appointment with Dr. Novo by email: [fnovo@unav.es](mailto:fnovo@unav.es)

Department of Biochemistry and Genetics

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