Universidad
de Navarra

Computational Biology (F.Ciencias)
Teaching guide 2025-26

INTRODUCTION

Course description: This course will introduce students to some **computational methods and online tools** that will enable them to search databases, analyze nucleotide and protein sequences, and **extract biological knowledge** from bioinformatic resources.

Students should **bring a laptop** computer or a large tablet where they can navigate comfortably to explore online bioinformatic tools and carry out in-class exercises. The online platform **Wooclap** will be used as an interactive tool for active learning during classes.

- **Degree**: Biochemistry and double degree Chemistry/Biochemistry
- **Module in the Degree Program**: Quantitative instrumental methods and systems molecular biology
- **ECTS**: 6 ECTS
- **Year**: 4th (BQ), 6th (Q-BQ)
- **Semester:** 2º semester
- **Type of course**: Compulsory
- **Instructor**: Dr. Sergio Roa Gómez *(Department of Biochemistry and Genetics)*
- **Language**: English
- **Pre-requisites:** students should have passed '*Informática básica' (2nd year)* and '*Human Molecular Genetics' (3rd year)*

- **Schedule/Classroom**: see corresponding BQ calendar or Q-BQ calendar for more details

> **Lectures** in A12 Room (Bibliotecas) will be on *Tuesdays (1h, 17:00h-18:00h)* and *Wednesdays (2h, 15:00-17:00h)* from January to March.

> **Practical computer Labs** in 0C04 Room (Hexágono) will consist on 4 sessions (3h each, for a total of 12h per student), organized by randomized groups:

- *Group 1:* P1 (17-March, 08:00h), P2 (20-March, 08:00h), P3 (24-March, 10:00h), P4 (25-March, 10:00h)
- *Group 2:* P1 (17-March, 11:00h), P2 (20-March, 11:00h), P3 (26-March, 10:00h), P4 (27-March, 10:00h)

GOALS

Knowledge

- Ability to describe the structure and features of the main databases for nucleic and protein sequences.
- Good understanding of the variables required to correctly design PCR primers.
- Understanding of the various algorithms for global, local and multiple sequence alignment, and of the more common scoring matrices.
- The basis for Gene Ontologies and understanding the basis of functional enrichment analysis.

Skills

- Ability to perform and interpret advanced searches in the main nucleotide and protein databases.
- Design correctly PCR primers.
- Correct use of programs to perform global, local and multiple sequence alignments.
- Correct use and interpretation of BLAST in its various flavours (blastn, blastp, blastx y tblastx).
- Correct use of tools to identify open reading frames and to perform common sequence manipulation tasks.
- Correct use of tools to perform functional enrichment analysis in genomic experiments.

LEARNING OUTCOMES

- Students will be familiar with sequence databases and will be able to query them.
- Students will use sequence manipulation tools to perform basic tasks.
- Students will correctly identify functionally interesting genes in genomic experiments

LEARNING OUTCOMES (Competencies)

Basic Competencies

- **CB2:** Apply their knowledge to their work in a professional manner and develop skills to elaborate and defend argumentation in ther field of study.
- **CB3:** Students show the ability to collect and interpret relevant data (usually within their field of study) in order to make judgements based on the consideration of wider social, scientific and ethical issues.
- **CB5:** Develop skills that will allow them to independently pursue future studies.

General Competencies

- **CG1:** Planning and time management skills to organize their own learning process, updating knowledge about scientific innovations and being able to analyze future trends.
- **CG2:** Integrative thinking and tackling problems from diffrent perspectives. Critical thinking. Providing solutions to scientific problems.

Specific Competencies

- **CE3:** Apply Maths, Statistics and Informatics to obtain, analyze and interpret data, and to develop models of biochemical systems and processes.
- **CE5:** Understand, analyze, discuss, write and present scientific arguments in Spanish and in English as a reference language in the scientific sphere.
- **CE12:** Have a deeper understanding of issues related to Biomedical Science that will complement the knowledge.
- **CE13:** Apply knowledge, concepts and theories of molecular Biosciences and Biomedicina to practical problems.

PROGRAM

Theoretical program

MODULE 1: *NAVIGATING INFORMATION ABOUT NUCLEOTIDE AND PROTEIN SEQUENCES*

. TASK 1: OBTAINING A NUCLEOTIDE SEQUENCE

- Introduction to Computational Biology
- Sequencing, accuracy during base calling, and the FASTQ/FASTA formats
- Sequence submission and data retrieval. GenBank, EMBL-Bank, and DDBJ
- Sequence formats and structure of a GenBank record

. TASK 2: OBTAINING INFORMATION ABOUT A PROTEINS AND PROTEIN DOMAINS

- Primary and secondary protein databases
- UniProtKB, Pfam and InterPro as Protein domain databases
- Motif representation: patterns, PWMs and sequence logos
- Redundancy. RefSeq and NCBI Gene

MODULE 2: *FUNCTIONAL GENETIC INFORMATION AND SEQUENCE ALIGNMENTS*

. TASK 3: EXPLORING GENE EXPRESSION AND FUNCTION

- Baseline expression of a gene
- Differential gene expression and GO/KEGG enrichment

. TASK 4: PERFORMING A CORRECT SEQUENCE ALIGNMENT

- Homology, identity and similarity
- Scoring statistics for alignments
- Global and local sequence alignment

. TASK 5: CREATING PHYLOGENETIC TREES

- Multiple sequence alignment
- Character-based and distance-based methods for building phylogenetic trees
- Clustal-Omega and the Newick format

MODULE 3: *BLAST AND THE HEURISTIC SEARCH OF GENETIC INFORMATION*

. TASK 6: USING BLAST TO SEARCH DATABASES

- Introduction to the BLAST family of programs
- Using BLAST and specialized BLAST to search databases

. TASK 7: DATA VISUALIZATION IN GENOME BROWSERS

- UCSC Genome Browser
- Ensembl Genome Browser
- NCBI Genome Data Viewer

. TASK 8: PCR primer design

- Introduction to primer design for PCR applications
- Using primer-BLAST and in silico PCR tools

Practical program

. COMPUTER LAB 1: Hands-on exercise (3h)

. COMPUTER LAB 2: Hands-on exercise (3h)

. COMPUTER LAB 3: Hands-on exercise (3h)

. COMPUTER LAB 4: Hands-on exercise (3h)

EDUCATIONAL ACTIVITIES

1. Presential classes. *29 Hours (1.16 ECTS)*

- Methodology: Seminars and interactive exercises designed to promote learning, discussion and demonstration of practical application of skills and principles. **STUDENTS ARE EXPECTED TO BRING A LAPTOP**.
- Skills and specific goals: basic knowledge of the tools that will be used throughout the course. They can see different ways to solve a problem, so they develop critical skills and learn to discuss results.

2. Practical computer labs. *12 hours (0.48 ECTS)*

- Methodology: students must work following the tutorials provided, which will then be solved step-by-step in practical sessions.
- Skills and specific goals: students learn to use bioinformatic tools to solve problems, working in group.
- These practical sessions are mandatory.

3. Study of materials and work in groups for the elaboration of 'brief reports' as deliverables to be assessed after each Module of the program. *55 hours (2.2 ECTS)*

- Methodology: students must study the materials provided in class as lectures and during team-based learning activities, delivering one 'brief report' in groups at the end of each module.
- Skills and specific goals: students learn the background information working individually and in group.

4. Preparation for the final exam. *50 hours (2.0 ECTS)*

- Methodology: students go over the contents and exercises of the course either individually or in groups, reviewing the concepts, correcting mistakes and improving their skills.
- Skills and specific goals: students reinforce their knowledge.

5. Final Exam. *4 hours (0.16 ECTS)*

- Methodology: **written multiple-choice test** *(1h)* and **practical exercise** *(3h)* about the contents of the course.
- Skills and specific goals: students must apply their knowledge to solve questions and practical problems.

ASSESSMENT

ORDINARY CALL

CUMULATIVE EVALUATION ***(20% of final score):*** During the course, active learning will include:

- ***Group Deliverables:*** (scoring 2 / 10 points) students will be required to work in groups and submit 3 brief reports related to each of the 3 modules of the course.
    - ***Report score (1.5 points total):*** The professor will assign a score worth 0.5 points per report, based on quality, completeness, and relevance.
    - ***Peer evaluation system (0.5 points total):*** after each report submission, students will complete an anonymous peer review using a structured rubric, where each group member will be rated by their peers from 1 to 5 based on contribution, effort, quality, collaboration, and communication. The peer scores will be averaged across the 3 modules to determine a peer adjustment factor.
    - ***Final report score per student (2 points total):*** Each student's final score for the group deliverables will be the sum of the instructor-assigned score (up to 1.5 points) and a peer adjustment (up to 0.5 points). Students who receive an average peer rating of 4.5 or higher will earn the full 0.5 points, those with average ratings between 3.0 and 4.4 will receive a proportional deduction (typically between 0.3 and 0.4 points), and those rated below 3.0 may face a further deduction (generally between 0.1 and 0.2 points, or subject to case-by-case review). This system is designed to recognize high-performing, collaborative students while encouraging accountability within the group.
- **In-class individual and group discussions:** (not directly assessed) multiple exercises and team-based learning activities are programmed during the course, which will be important for self-progress assessment.

FINAL EXAM ***(80% of final score):*** The final exam at the end of the course will have two parts:

- **Final test:** (scoring 2 / 10 points) written multiple-choice exam (1h) covering concepts, principles and knowledge acquired during the course.
- **Practical exercise:** (scoring 6 / 10 points) resolution of a computational biology exercise (3h) will be assessed in the computer room.

EXTRAORDINARY CALL

For students who do not pass the course in May, the **June** evaluation will adhere to the same criteria. There is also an option to revise and combine the three brief reports into a single, comprehensive project based on a new assignment.

SPECIAL ASSESSMENT

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.

OFFICE HOURS

Dr Sergio Roa Gómez (sroa@unav.es)

- Office 3321. Edificio de Investigación. Planta 3
- Schedule an appointment in advance via email.

BIBLIOGRAPHY AND RESOURCES

We will use the textbook **Bioinformatics for beginners**, **Chapters 4 to 8.** (Find it in the Library)

- Students will be provided with **preparatory materials** before each class or at the start of each Task. These materials may be text, visual or other, and set to prepare them for in-class and off-class active learning activities.
- We will use Wooclap as an intereactive electronic platform to be used through student's smart-phones or laptops.