| ETS Ingeniería Agronómica, Alimentaria y de Biosistemas | |
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| **Program** | 20BT– Degree in Biotechnology |

| **Course number and name** | |
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| **Number** | 20504424 |
| **Name** | Computational Structural Biology |
| **Semester** | S2 [(February-June)], 4rd Year |

| **Credits and contact hours** | |
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| **ECTS Credits** | 5 |
| **Contact hours** | 60 |



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| **Coordinator's name** | María Garrido Arandia | maria.garrido@upm.es |
| **Professors´ name** | Krzysztof Teodor Wabnik | k.wabnik@upm.es |



| **Specific course information** |
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| **Description of course content** |
| This course is part of the Computational Biotechnology pathway in the final semester of the Biotechnology Degree. It presents advanced content of computational itinerary based on the Structure and Protein Engineering course, a mandatory course taught in the previous semester of the same 4th year.<br>The course provides an updated presentation of the theory and fundamental methods along with the corresponding software for studying structures, properties, and interactions in biomolecular systems, with a particular focus on docking methods and molecular dynamics. At various points in the syllabus, students will also have to develop their own programs or scripts for specific tasks that will arise. Given the low number of students typically enrolled in the Computational Biotechnology pathway, the course is designed to be fully interactive. Each student will be assigned a molecular system to which they will apply the different computational methods and resources they learn. This way, each student individually and personally develops the study and research activities related to the course content. |
| **List of topics to be covered** |
| 1. Proteins<br>1.1. Large Structures<br>1.2. Application to Structural Data Analysis<br>1.3. Normal Mode Analysis<br>1.4. Protein-Protein Interfaces<br>1.5. Solvation Models |

2. Small Molecule Modeling
  2.1. Computer Construction of Small Molecules
  2.2. Molecular Mechanics (MM)
  2.3. Electrostatic Potential (PB) for Small Molecules
  2.4. Small Molecule Databases
  2.5. MM Parameters and Topologies: Practical Application of CHARMM
  2.6. Optimization in Water: VMD/NAMD-autoIMD
  2.7. Building Peptide Structures on a Computer
  2.8. Modeling Nucleic Acid Structures
3. Docking
  3.1. Introduction to Docking
  3.2. Protein-Ligand Docking
  3.3. Protein-Protein Docking
4. Molecular Dynamics (MD)
  4.1. Introduction to MD
  4.2. Statistical Mechanics Notes
  4.3. Equations of Motion
  4.4. Initial Conditions, Equilibrium
  4.5. Solvation
  4.6. Nonbonding Interactions
  4.7. Controlling Constant T and P. Langevin Dynamics
  4.8. Coarse-Grained MD
  4.9. QM/MM Simulations
  4.10. A Brief History of DM Calculations. Supercomputing
  4.11. DM Calculations: Minimization-Balancing-Simulation Cycle
  4.12. Properties Calculated in DM Simulations
  4.13. Practice in DM Calculations
  4.14. Trajectory Analysis
  4.15. Visualization and Animation

**Prerequisites or co-requisites**

- Protein Structure and Engineering

**Course category in the program**

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| **Elective** | |

**Specific for course objectives**

**Specific learning outcomes**

RA235 - Know and use appropriate software for analyzing the structure and function of biomolecules
RA239 - Know the main methods for computationally modeling protein structures
RA86 - Know the structure and function of the main types of biomolecules and their relevance in biotechnology

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| RA236 - Know the structural bases of molecular interactions in protein-ligand and protein-protein systems |

## Further reading and supplementary materials

### Bibliography


- Burkowski FJ, 2015, Computational and Visualization Techiques for Structural Bioinformatics Using Chimera, CRC Press, Taylor&Francis
- Gu J, Bourne PE, 2009, Structural Bioinformatics, Wiley-Blackwell
- Jensen F, 2007, Introduction to Computational Chemistry, 2nd Edition, Wiley
- Martín-Santamaría, S (Ed), 2018, Computational Tools for Chemical Biology, Royal Society of Chemistry, London, UK
- Schlick T, 2010, Molecular Modeling and Simulation: An Interdisciplinary Guide, 2nd Edition, Springer
- Schwede T, Peitsch M, 2008, Computational Structural Biology. Methods and Applications, World Scientific Publishing Co.
- Tramontano A, 2006, Protein Structure Prediction, Wiley-VCH
- Uversky VN, 2014, Intrinsically Disordered Proteins (Springer Briefs in Molecular Science / Protein Folding and Structure), Springer


### Supplementary materials

**Web Resources:**

- APBS (http://sourceforge.net/projects/apbs/)
- AutoDock Vina (http://vina.scripps.edu/)
- Chimera 1.15 (http://www.cgl.ucsf.edu/chimera/index.html). Software used in practical lectures
- NAMD (http://www.ks.uiuc.edu/Research/namd/)
- PyMOL (http://sourcefoge.net/projects/pymol/)
- VMD (http://www.ks.uiuc.edu/Research/vmd/)
- Free Maestro (https://www.schrodinger.com/academic-licensing)
- ChemSketch (https://www.acdlabs.com/resources/free-chemistry-softwareapps/chemsketch

## Teaching methodology

The teaching activities are an indistinguishable blend of "theory and practice." Students will use their laptops to implement the entire computational methodology. At the beginning of the course, the professor will indicate the set of programs (all "open source," free for academic users) to be installed. At the same time, students must use various computer tools such as editing, scientific graphics, programming environment (mainly Python) and mathematical analysis

As indicated in the "Course Description," the central approach is that each student will develop, throughout the course, a personalized analysis and research project on a biomolecular system, which they will develop and submit to computational study using the various methodologies and models that will be presented.
At the end of the course, each student will submit this individual research project with the results and analysis of their biomolecular system.

## Evaluation Criteria

**Progressive assessment.** Consist of the delivery of the results and analysis that each student will present in the form of an **individual research work** at the end of the course. This personalized work will consist of the application of the contents of the subject to different problems of a biomolecular system that the student will build throughout the course from a different protein that the teacher will have assigned to each student.
Altogether, the tasks assigned to each student involve the use and application of the computational methods and tools that constitute the syllabus, and that are managed in class by the students on their personal computers. Due to the advanced nature of the subject, these classes are developed uniformly without distinction between theoretical or practical activities. Some of these tasks also imply that the student must develop their own computational solutions for specific properties of their molecular system (in particular, related to data formats and types of structural information).
Carrying out individual research work is **mandatory** to pass the subject through progressive evaluation tests and **represents 100% of the final grade.**

**Final Assessment**
Those who have not passed the subject through the progressive evaluation tests will have to take **a single global evaluation test** in the form of a final written exam that will cover the complete syllabus (topics 1-4) and represent 100% of the final grade.