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

Course number and name	
Number	20504411
Name	Protein Structure and Engineering
Semester	S1 [(September-January)], 4rd Year

Credits and contact hours	
ECTS Credits	5
Contact hours	60

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Specific course information

Description of course content

The course presents an up-to-date overview of the state and nature of *in silico* studies methodological complement to experimental studies (*in vitro* and *in vivo*). The course covers protein structure as a foundation for developing hypotheses about function and biological interactions, computer-aided rational design of experiments, and the construction of structural and functional models of protein-protein and protein-ligand systems. The methodology employed in the course is entirely computational. So by the end of the course, students will be able to utilize multiple computational resources (databases and web servers, as well as generic and specific software related to protein structure and function) that will serve as a valuable complement to the experimental training they have received in various subjects within the Biotechnology Degree program.

List of topics to be covered

1. Molecular Structure and Intermolecular Interactions
   1.1. Molecular Geometry and Molecular Surfaces
   1.2. Electron Density and Molecular Structure
   1.3. Vibration, Torsion, and Conformation
   1.4. Symmetry Elements and Operations
   1.5. Intermolecular Interactions
   1.6. Amino Acids: Types and Properties

- 1.7. Amino Acid Scales in Proteins
- 2. Protein Structure
  - 2.1. Peptide Plane, Dihedrals, and Rotamers
  - 2.2. Secondary Structure
  - 2.3. Identification and Prediction of Secondary Structure
  - 2.4. Tertiary Structure, Protein Architecture, and Topology
  - 2.5. Structural Classification
  - 2.6. Quaternary Structure, Symmetry, and Protein-Protein Interfaces
- 3. Experimental Determination of Protein Structures
  - 3.1. X-ray Crystallography
  - 3.2. NMR Spectroscopy
  - 3.3. Cryo-Electron Microscopy
  - 3.4. Protein Data Bank
- 4. Protein Structure Analysis
  - 4.1. PDB Files
  - 4.2. Protein Surfaces
  - 4.3. Protein Electrostatics
  - 4.4. Structure Comparison
- 5. Structure and Function Prediction
  - 5.1. Folding and Structure Generation
  - 5.2. Protein Energy Calculations
  - 5.3. Structure Optimization
  - 5.4. Protein Structure Prediction
  - 5.5. Protein Function Prediction
- 6. Protein Design and Engineering: Proteins Without a Unique Structure
  - 6.1. Computational Protein Design and Engineering
  - 6.2. In Silico Mutations
  - 6.3. Scaffold Protein Engineering
  - 6.4. Analysis of Protein Design and Engineering Applications
  - 6.5. Intrinsically Disordered Proteins

Prerequisites or co-requisites

- Structural Biochemistry

Course category in the program

Mandatory	

Specific for course objectives

Specific learning outcomes

RA237 – To observe the structural effects of changes in proteins *in silico*
RA238 – To know the main methods for experimentally obtainment of protein structures

RA235 – To use appropriate software for analyzing the structure and function of biomolecules
RA236 – To analyze the structural bases of molecular interactions in protein-ligand and protein-protein systems
RA239 – To know the main methods for computationally modeling protein structures

Further reading and supplementary materials

Bibliography

- Branden C, Tooze J, 1999, Introduction to Protein Structure (2nd ed.), Garland Publishing
- Gu J, Bourne PE, 2009, Structural Bioinformatics, Wiley-Blackwell
- Lesk, A., 2016, Introduction to Protein Science. Architecture,Function, and Genomics, 3rd Edition, Oxford University Press
- Nussinov R, Schreiber G, 2009, Computational Protein-Protein Interactions, CRC Press
- Park SJ, Cochran JR, 2010, Protein Engineering and Design, CRC Press
- Petsko A, Ringe D, 2004, Protein Structure and Function. Primers in Biology, New Science Press
- Rhodes, Gale, 2006, Crystallography Made Crystal Clear. A Guide for Users of Macromolecular Models, 3rd. Edition, Academic Press-Elsevier
- 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
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Supplementary materials

Web Resources:
- SwissModel (http://swissmodel.expasy.org). Homology modeling
- PDB (http://www.pdb.org) Data base of experimental protein structure
- Chimera 1.15 (http://www.cgl.ucsf.edu/chimera/index.html). Software used in practical lectures
- PDBSum (http://www.ebi.ac.uk/pdbsum). Compendium of structural information on proteins
- ProFunc (https://www.ebi.ac.uk/thornton-srv/databases/profunc/). Prediction of protein function base don its structure and sequence
- PSIPRED (http://bioinf.cs.ucl.ac.uk/psipred/) Prediction of secondary structure
- JPred (http://www.compbio.dundee.ac.uk/jpred/) Prediction of secondary structure
- CUPSAT (http://cupsat.tu-bs.de/) Prediction of mutation effects on structural stability of proteins

Teaching methodology

Students will be able to download the six PowerPoint presentations from the course's Moodle page, containing virtually all of the lecture materials for the six topics included in the syllabus. A variety of materials will also be available on Moodle to be used throughout the course: protein structure files, program output that will be analyzed in class, and guide documents prepared by the professor, as well as videos with animations of protein structures and molecular interactions.
Before December, a guide for completing the final computer assignment will be uploaded to Moodle, with explicit details of the proposed tasks.

Evaluation Criteria

Progressive assessment. The progressive assessment consists of a first partial exam covering topics 1-3. Those who score at least 5 out of 10 on this partial exam will take the second progressive assessment test in January, covering only the second part of the course corresponding to topics 4-6. Those who score below 5 will be assessed in the second progressive assessment test on the complete course. Both tests will include a section of short questions on specific issues and a section for developing concepts and models based on the theoretical content presented in the lectures and the computer methods used in practical classes. These progressive assessment tests will constitute 90% of the final grade.

Therefore, the final grade of the course under the progressive assessment system will be calculated as: 0.90*(average grade of the two partial exams) + 0.10*(grade of the computer assignment). Each test will be graded out of a total of 10 points. Students may voluntarily choose not to complete the computer assignment, thus forgoing the 10% of the final grade, in which case the maximum grade for the course will be 9.

Final Assessment
Those who have not passed the course through the progressive assessment tests will have to take a single comprehensive assessment test in the form of a final written exam. This exam will cover the entire syllabus (topics 1-6) but will not include the content covered in the computer traineeship conducted under the progressive assessment system. To pass the course through this comprehensive exam, 100% of the grade will be based on this final exam, which must be at least 5 out of 10.