



# Full Syllabus



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| <b>Course Title</b>   |   |
| Computational Structural Biology  |   |
| <b>Lecturer</b>   |   |
| Pr. Nir Ben Tal, Dr. Jérôme Tubiana   |   |
| <b>Semester</b>   |   |
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| <b>Course requirements</b>  |   |
| <ul style="list-style-type: none"> <li>• <b>Prerequisites for CS/engineering students:</b> Prior biological background is valuable but not necessary, as the main biological concepts will be introduced in class.</li> <li>• <b>Prerequisites for Life Science / Med students:</b> Prior knowledge of Python (e.g. an introductory Coursera course or course 0455-1819) is valuable as we will study Python codes in class. However, <b>programming is not necessary to complete the assignments.</b></li> </ul> |   |
| <b>Final grade components</b>   |   |
| Grade = 0.25 * home_exam_grade + 0.15 * homeworks + 0.6 * project_grade   |   |
| <b>Course schedule</b>  |   |
| <b>Class no.</b>  | <b>Subject and Requirements (assignments, reading materials, tasks, etc.)</b>   |
| Classes 1-2   | Introduction to Protein Structures; Forces and interactions.  |
| Classes 3-4   | Alignments of biological sequences (Pairwise & multiple alignments; Substitution Matrices; Dynamic Programming).  |
| Classes 5-6   | Homology Search (BLAST/MMSeqs; pHMMs; FoldSeek; paired MSAs).   |
| Class 7   | Prediction of Protein Structures #1: Homology modelling & Threading.  |
| Classes 8-9   | Alignments of Protein Structures (Kabsch algorithm; TM-Align; Sequence order-independent Alignments).   |
| Class 10  | Prediction of Protein Structures #2: Coevolution models (Direct Coupling Analysis)  |
| Class 11  | Prediction of Protein Functional Sites (ConSurf)  |
| Class 12  | Prediction of Protein-Ligand interactions (Small Molecule Docking).   |
| Class 13  | Prediction of Protein Motion (Normal Mode Analysis; Molecular Dynamics)   |
| Class 14  | RNA structure prediction and analysis.  |
| Class 15  | Prediction of Protein Structures #3: Deep Convolutional Neural Networks (AlphaFold1).   |
| Classes 16-17   | Computational Protein Design #1: Background; Fixed-backbone design with Rosetta; Inverse Folding Graph Neural Networks Generative Models (ProteinMPNN). |
| Classes 18-19   | Protein embeddings (Protein language models) & Protein Function Prediction (Gene Ontology terms).   |
| Classes 20-21   | Prediction of Protein Structures #4: AlphaFold2-3.  |



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| Class 22   | Computational Protein Design #2: Structure Generative Models (Diffusion Generative Models; Binder Design). |
| Classes 23-24  | Selected research topics   |
| <b>Required course reading</b>   |  |
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| <b>Optional course reading</b>   |  |
| <ul style="list-style-type: none"><li>• Introduction to Proteins: Structure, Function and Motion, Kessel and Ben Tal, 2018</li></ul>   |  |
| <b>Comments</b>  |  |
| <ul style="list-style-type: none"><li>• The course is taught in English.</li><li>• The course is open to Life Science, Computer Science, Engineering (bioengineering) and Medicine students.</li></ul> |  |