MCB*6370
Protein Structural Biology and Bioinformatics
Course Outline Winter 2016
Department of Molecular and Cellular Biology

Instructors: **Drs. Steffen Graether & Matt Kimber**

Meetings: **Tuesdays 1:00 to 4:00 p.m.**
                   SCIE 3513

Web site: Log onto MCB*6370 on Courselink/Desire2Learn. Lecture notes and
                   assignments will be uploaded to D2L.

Course synopsis: This course will explore the relationship between protein sequence and three-dimensional structure. Students will gain experience with critical assessment of recent protein structure journal articles and the tools and methodology required for modeling, docking, and designing protein structure.

Objectives:
>   Mastery of PyMOL for analysing structures and generating figures
>   Understanding and applying homology modelling
>   Understanding of the process of scientific dissemination
>>   Writing proficiency
>>   Mastery of scientific manuscript formatting / style
>>   Multipanel figure generation
>   Critical analysis of contemporary primary literature
>   Mastery of oral presentation skills

Recommended background: The course is designed for students who have met the requirements for entry to the M.Sc. or Ph.D. programs of the Department of Molecular and Cellular Biology, having completed an honours (science) B.Sc. degree or the equivalent. It is expected that students have a good working knowledge of basic biochemistry, including a familiarity with the main concepts of protein structures.

Lectures: Course content will be presented primarily in the form of faculty lectures. A <u>tentative</u> schedule of topics follows:

Schedule

Week	Topics	Tutorials	Assignments
1	Review of the Course; writing, oral presentations	PyMOL tutorial advanced features superposition	
2	Review of Structure Fundamentals		Simple PyMOL picture
3	Sequences Sequence alignments BLAST and other sequence search tools/ Sequence databases/ MSA / Phylogenetic trees / file types Annotation, names, ontology		PyMOL image
4	Structural Bioinformatics CONSURF, PISA – oligomeric states	Bioinformatics Tutorial Complete on your own	PyMOL image
5	Computational Methods Homology modeling Ab initio Rosetta Molecular dynamics		Journal Club PyMOL image
6	Functional Assignment BRENDA String database Microarray datasets Literature searches		Journal Club PyMOL image
	READING WEEK		
7	X-ray / EM		Journal Club Homology modelling
8	X-ray / EM		Journal Club
9	X-ray / EM		Journal Club
10	NMR		Structural Annotation Assignment manuscript
11	NMR	Review / Revise	Final Submission
12			Presentations Structural Annotation Assignment

Grade Assessment
Miniassignments:
        PyMOL & Modelling: **15%**
Journal Club:
        Presentation: **20%**
        Participation: **10%**
Structural Annotation:
        Written   **40%**
        Oral Presentation   **15%**

PyMOL Tutorial, PyMOL Image and Homology Modelling:
Protein structure visualization is an extremely important skill in structural biology. The purpose of the tutorial is to familiarize students with the use of the very powerful, general-purpose macromolecular structure viewing, analysis and documenting program called PyMOL.

The Image assignments are designed to assess your mastery of PyMOL as well as some ancillary programs and concepts. The value of these assignments will be measured in your improved presentations for your proposals and thesis defences and the quality of the figures you submit for your publications.

The homology modelling assignment will introduce you to the techniques used to take a sequence with high identity to a known structure and create a plausible structural model. PyMOL will be used to show the new structure and how it relates to its template, and a pseudo-energy function will be used to show what problem areas may exist in the model structure.

Journal Club Presentations:
Each student will present a research paper which focuses on some particular structure-function relations problem. One student will be assigned to lead the discussion; this student should be deeply familiar with the paper, have done any additional reading required to understand the material being analysed, and should be looking to stimulate a meaningful discussion with their peers. The primary focus should be on this discussion; the leader may optionally use PowerPoint or PyMOL to show figures from the paper, the whiteboard, etc. if they feel that it helps foster the discussion, but these materials will not be the focus of the evaluation. All students are expected to be able to intelligently discuss the content of the paper, and therefore need to be familiar with its content and have done some further reading into the background to the problem. Students are expected to have informed opinions about the methodology, its applicability to the problem, the quality of the results obtained and the appropriateness of the interpretation.

Structure Annotation Paper:
The final assignment for the course is a structure annotation assignment. Students will be assigned a recently deposited structure in the protein data bank. This structure, determined as part of a structural genomics effort, will have minimal analysis completed, and no associated paper published. Students will then analyse the structure and sequence using sequence and structure based bioinformatics tools (including, but not limited to, those discussed in class), searches of the relevant literature and functional databases. This analysis will be centered on documenting the structure (using PyMOL and other tools to produce publication quality figures), and to objectively evaluate the existing evidence for various candidate functions for the protein. The results of this analysis will be presented as a scientific manuscript, and presented in-class using standard scientific presentation methods.

Participation:

Students are expected to participate actively in discussions, and their participation will be reflected in their presentation marks. Note that the quality of the participation counts as well as the quantity. The mark will also reflect the degree to which students have read and critically assessed the assigned readings.

Late Policy:

Assignments that are late will be given a penalty of 10% per day unless a valid reason is given. Assignments will not be accepted five days after the due date.

Academic Misconduct:

The University of Guelph is committed to upholding the highest standards of academic integrity and it is the responsibility of all members of the University community – faculty, staff, and students – to be aware of what constitutes academic misconduct and to do as much as possible to prevent academic offences from occurring. University of Guelph students have the responsibility of abiding by the University's policy on academic misconduct regardless of their location of study; faculty, staff and students have the responsibility of supporting an environment that discourages misconduct. Students need to remain aware that instructors have access to and the right to use electronic and other means of detection. The Academic Misconduct Policy is detailed in the Graduate Calendar:
http://www.uoguelph.ca/registrar/calendars/graduate/current/genreg/sec_d0e1702.shtml