

CHEM185/CHEM285: Computational Chemistry

General Course Information

Course Number CHEM185 / CHEM285, 4 units

Course Faculty

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Class sessions: Keck II Center, 2205 Urey Hall
Tuesdays 12:30 – 1:50 PM
Thursdays 12:30 – 1:50 PM

Office Hours: 3234 Urey Hall
Wednesdays 11am – 1pm and by appointment

Course Philosophy

The course will be structured around ability-based education. Students will integrate knowledge, attitudes, and skills and in a variety of ways to accomplish the course outcomes.

The procedures in ability-based education are:

- Clearly define and make public the *ability outcome and objectives* students are expected to achieve during the course
- Give students multiple opportunities to achieve the course objectives
- Provide clear criteria so students can know how well they are performing the abilities during their practices
- Provide feedback from the faculty, peers, and self to determine how successfully students are meeting the criteria

The overall goal of this course is to enable students to gain an understanding of protein structure and dynamics, set up and run molecular dynamics simulations, and search for small molecule inhibitors using state-of-the-art methods in computer-aided drug discovery.

Course Description

This graduate-level seminar course will walk students through the basic techniques of biomolecular simulation and computer-aided drug design, including application of massively parallel molecular and Brownian dynamics simulations on large-scale high performance computing clusters and GPU architectures, as well as analysis techniques to enable new discoveries within the vast quantity of digital data, such as finding new potential drug leads through virtual screening and small molecule docking. Lectures on course concepts will be closely combined with hands-on tutorials that allow the practical application of computational methods and statistical data analysis in a project-based format. Students will be granted access to the national supercomputers centers as well as the local Keenelane GPU cluster to run their simulations and analyze the data.

Course Ability Outcomes and Objectives

At the conclusion of the course, students shall be able to:

1. Understand the basic principles and concepts of protein structure, molecular dynamics simulations, and computer-aided drug discovery
2. Set up and run their own protein / biomolecular system MD / BD simulations on both personal computers, cluster architectures, and using CPUs and GPUs

3. Perform and understand the interpretation of basic (statistical) analysis techniques on the resulting MD / BD trajectories
4. Perform and understand the results of docking and virtual screening experiments

Grading

This is a project-based course with no formal exams. Attendance and class participation in the 10 class sessions constitute a substantial portion of the final grade.

Assessment Tool	Percentage of Grade
Attendance	20%
Participation	20%
Project	60%

Optional Textbooks

There are no required textbooks for this course. However, a list of helpful reading materials will be presented during course lectures, and the broadest references are included here (and kept on reserve in the Geisel library or available online):

Introduction to Protein Structure: Second Edition, by Carl Branden and John Tooze
<http://www.amazon.com/Introduction-Protein-Structure-Carl-Branden/dp/0815323050>

Molecular Modelling: Principles and Applications, by Andrew Leach
<http://www.amazon.com/Molecular-Modelling-Applications-Andrew-Leach/dp/0582239338>

Molecular Modeling and Simulation, by Tamar Schlick
<http://www.amazon.com/Molecular-Modeling-Simulation-Tamar-Schlick/dp/038795404X>

Course Schedule

Week	Lecture Topics (L)	Practicals (P)
1 09-27-12 (L) 10-02-12 (P)	Introduction to unix, protein structure and visualization, 3D viz	Logins, unix primer, "Using VMD" & "VMD Images and Movies", MultiSeq tutorials
2 10-04-12 (L) 10-09-12 (P)	Introduction to molecular dynamics simulation methods, part 1	NAMD tutorial, parts 1 & 2, "Membrane Proteins tutorial"
3 10-11-12 (L) 10-16-12 (P)	Introduction to molecular dynamics simulation methods, part 2, XSEDE logins	AMBER MD tutorial: A8, XSEDE login
4 10-18-12 (L) 10-23-12 (P)	Introduction to molecular dynamics analysis methods in AMBER, generalized Born MD	AMBER GB MD tutorials (B1 & B3), AMBER analysis (B5) & clustering
5 10-25-12 (L) 10-30-12 (P)	Force fields and parameterization (Amber and Charmm) <i>*Guest lecturer: Dr. Jesper Sorensen</i>	Parameterization tutorial: AMBER tutorials B4, A1 Amarolab tutorial
6 11-1-12 (L) 11-6-12 (P)	Computer-aided drug design, solvent mapping, docking methods	AutoDockTools tutorial, FTProd tutorial
7 11-08-12 (L) 11-13-12 (P)	Ensemble-based methods, including the relaxed complex scheme, free energies of binding	Relaxed complex scheme tutorial, AMBER tutorial A3

8 11-15-12 (L) 11-20-12 (P)	GPU computing and homology modeling	Nvidia GPU benchmarking, DelEnsembleElec
9* L on Tue 11-27-12 (L) 11-29-12 (P)	Brownian dynamics simulations, protein- protein docking	BrownDye tutorial, Project time
10 12-4-12 (L) 12-6-12 (P)	Enhanced sampling (aMD) and non- equilibrium approaches <i>*Guest lecturer Dr. Robert Swift</i>	aMD tutorial, Project time
11-FINAL 12-14-12	PROJECT PRESENTATIONS	11:30 AM – 2:20 PM 2205 Urey Hall (KeckII)