

COLLEGE OF CHEMISTRY COURSE GUIDE (../INDEX.HTML)

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BIOE 144 - INTRODUCTION TO PROTEIN INFORMATICS (4 UNITS)

(Taken from the UC Berkeley Course Guide (<http://guide.berkeley.edu>))

COURSE OVERVIEW

SUMMARY

This course will introduce students to the bioinformatics algorithms used by biologists to identify homologs, construct multiple sequence alignments, predict protein structure, estimate phylogenetic trees, identify orthologs, predict protein-protein interaction, and build hidden Markov models. The focus is on the algorithms used, and on the sources of various types of errors in these methods.

PREREQUISITES

Prior coursework in algorithms. No prior coursework in biology is required. This course includes no programming projects and prior experience in programming is not required

TOPICS COVERED

This course is designed to provide a theoretical framework for protein sequence and structure analysis using bioinformatics software tools. Students completing this course will be prepared for subsequent in-depth studies in bioinformatics, for algorithm development, and for the use of bioinformatics methods for biological discovery. It is aimed at two populations: students in the life sciences who need to become expert users of bioinformatics tools, and students in engineering and mathematics/computer science

who wish to become the developers of the next generation of bioinformatics methods. As virtually all the problems in this field are very complex, there are many opportunities for research and development of new methods.

Students completing this course are likely to find several potential areas of research of interest, which they may want to work on as independent study projects during undergraduate work, or take on as Master's or Ph.D. thesis topics for advanced work.

WORKLOAD

TIME COMMITMENT

3 hours of lecture and 1 hour of discussion per week.

UC Berkeley Course Guide (<http://guide.berkeley.edu>)

COLLEGE OF CHEMISTRY PEER SERVICES

Made by Angela Lee, c/o 2019



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