

CS 686-02 - Bioinformatics

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1 Course Description

Bioinformatics, one of the fastest growing application areas in science, is the realm where computer science meets molecular biology. This course will build on students' expertise in either computer science or natural sciences and prepare them to enter bioinformatics in either research or industry. Students will be brought up to speed in the content area which is unfamiliar to them. Students will be introduced to genomics, proteomics and software tools of the trade such as Pymol and Blast. They will learn bioinformatics algorithms such as dynamic programming, hidden markov models and monte carlo.

2 Learning Outcomes

On completion of this course the student should be able to accomplish the following:

- Explain concepts of genomics and proteomics
- Describe bioinformatics algorithms such as dynamic programming, hidden markov models and monte carlo
- Utilize bioinformatics tools such as Pymol, Blast, and ClustalW
- Code solutions to bioinformatics problems utilizing tools such as R, biopython, bioperl
- Perform research in bioinformatics
- Present research in bioinformatics

3 Prerequisites

proficiency in one of the following fields: computer science, biology, chemistry or physics.

4 Course Text

Introduction to Bioinformatics by Arthur M. Lesk (Jun, 2008)

5 Suggested Reading

Bioinformatics Resources: research papers, textbooks, software, slides are listed in Bioinformatics Resources: <http://www.cs.usfca.edu/~pfrancislyon/resources.html>

6 Weekly Breakdown

Week 1	Introduction to Bioinformatics / Basic programming / Molecular biology basics
Week 2	Probability/ Algorithms / Genetics
Week 3	Sequence alignment: dynamic programming, Needleman-Wunsch, Smith-Waterman algorithms
Week 4	Research in bioinformatics / Cancer genomics / Promoters and Transcription Factors
Week 5	Bacteria, viruses, cellular functioning / Visualization of DNA, RNA and proteins: pymol
Week 6	open Reading Frames / Gene finding / Blast
Week 7	Multiple sequence alignment: ClustalW
Week 8	Profiles / PsiBlast / Hidden markov models
Week 9	HMM definition and forward algorithm
Week 10	Protein secondary structure prediction / Neural Networks
Week 11	Energy of protein structures / Protein tertiary structure prediction
Week 12	SupportVector Machines / ROC curves / Research reports
Week 13	Phylogenetic trees / Research reports
Week 14	Databases in Bioinformatics / Research reports
Week 15	Moecular Dynamics / tools: R, biopython, bioperl/ Research reports

7 Grading

- quizzes: 10% (lowest third of scores are dropped to cover both absences and low scores).
- paper presentation and participation: 10%
- assignments: 30%
- midterm: 25%
- project and CS Night presentation: 25%

8 Assignments and Assessments

- All students are expected to participate in class discussions, including presentations by fellow students.
- An in-class midterm will be administered. A make-up exam will be given only in the case of a medical emergency documented by a doctor's note.
- Each student will present one bioinformatics research paper on a topic of their choosing.
- Each student will implement a bioinformatics project of their choosing and present it at CS Night. For example, a student interested in Machine Learning can do gene-finding, or predict-protein interactions.
- In general, late work will not be accepted. If an emergency arises and you are unable to meet a deadline, please notify the instructor beforehand to avoid a grade penalty.
- Students are responsible for keeping backups of written assignments and project files until the course is over. Extensions will not be granted for lost work.

9 Academic Honesty

We will adhere to the University's Student Academic Honesty Policy available at: www.usfca.edu/catalog/policies/honor. In this course you must do your own work on exams and homework, unless explicitly specified otherwise.

Note: This syllabus is subject to change.