

Brief Course Description
(50-words or less)

Application of discrete algorithms to computational problems in molecular biology. Topics are drawn from such areas as classical sequence comparison, multiple sequence alignment, DNA sequence assembly, DNA physical mapping, genome rearrangement, evolutionary tree construction, and protein folding. Background in molecular biology is not required.

**Extended Course
Description / Comments**

N/A

**Pre-Requisites and/or Co-
Requisites**

CSCI 4470
Algorithms

**Required, Elective or
Selected Elective**

Selected Elective Course

Approved Textbooks
(if more than one listed, the
textbook used is up to the
instructor's discretion)

Author(s): Jones and Pavzner
Title: *Introduction to Bioinformatics Algorithms*
Edition: 1st
ISBN-13: 978-0-262-10106-6

**Specific Learning Outcomes
(Performance Indicators)**

1. Use exhaustive search strategies to solve Motif Finding and Center String problems.
2. Use greedy strategies to solve Sorting By Reversal problem in genome rearrangement.
3. Apply dynamic programming techniques to solve the problems of Pairwise Alignment, Multiple Alignment, Exon Chaining, and hidden Markov model based Gene Finding.
4. Apply divide-and-conquer strategies to save memory space for dynamic programming algorithms
5. Use basic graph algorithms for genome Sequence Assembly
6. Apply combinatorial algorithms for Repeat Finding on genomes
7. Use probabilistic model for Phylogeny Reconstruction
8. Use statistical models for sequence and structure pattern identification algorithm development.

Relationship Between Student Outcomes and Learning Outcomes

		Student Outcomes										
		a	b	c	d	e	f	g	h	i	j	k
Learning Outcomes	1	●	●							●	●	
	2	●	●							●	●	
	3	●	●							●	●	
	4	●	●							●	●	
	5	●	●							●	●	
	6	●	●							●	●	
	7	●	●							●	●	
	8	●	●							●	●	

Major Topics Covered
(Approximate Course Hours)

3 credit hours = 37.5 contact hours

4 credit hours = 50 contact hours

Note: Exams count as a major topic covered

Asymptotic notations (4-hours)

Exhaustive search for motif finding and other applications (7-hours)

Greedy algorithms for genome rearrangement (4-hours)

Dynamic programming for sequence alignment and gene finding (8-hours)

Divide-and-conquer (4-hours)

Combinatorial algorithms for repeat finding (4-hours)

Graph algorithms for sequence assembly (5-hours)

Probabilistic modeling for phylogeny reconstruction (6-hours)

Hidden Markov model, Viterbi's algorithm, forward, backward, forward-backward algorithms (8-hours)

Course Master

Dr. Liming Cai