The University of Georgia

Department of Computer Science

*Course Information Sheet*
# CSCI 4490
Algorithms for Computational Biology

| | |
|---|---|
| **Brief Course Description**<br>(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**<br><br>Use this section to put additional information that's relevant to whom this course is targeting | |
| **Pre-Requisites and/or Co-Requisites** | CSCI 4470<br>Algorithms<br><br>Or permission of department |
| **Approved Textbooks**<br>(If more than one, course text used during a semester is at the discretion of the instructor) | Author(s): Jones and Pavzner<br>Title: Introduction to Bioinformatics Algorithms<br>Edition: 1st<br>ISBN-13: 978-0-262-10106-6 |
| **Specific Learning Outcomes**<br>**(Performance Indicators)** | This course studies discrete algorithms for solving computational biology problems and algorithmic principles driving advances in bioinformatics most relevant to students studying computer engineering. At the end of the semester, all students will be able to do the following:<br>1. Use exhaustive search strategies to solve Motif Finding and Center String problems.<br>2. Use greedy strategies to solve Sorting By Reversal problem in genome rearrangement.<br>3. Apply dynamic programming techniques to solve the problems of Pairwise Alignment, Multiple Alignment, Exon Chaining, and hidden Markov model based Gene Finding.<br>4. Apply divide-and-conquer strategies to save memory space for dynamic programming algorithms<br>5. Use basic graph algorithms for genome Sequence Assembly<br>6. Apply combinatorial algorithms for Repeat Finding on genomes<br>7. Use probabilistic model for Phylogeny Reconstruction<br>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 |
| 1 | • | • | | | | | | | • | • | |
| 2 | • | • | | | | | | | • | • | |
| 3 | • | • | | | | | | | • | • | |
| 4 | • | • | | | | | | | • | • | |
| 5 | • | • | | | | | | | • | • | |
| 6 | • | • | | | | | | | • | • | |
| 7 | • | • | | | | | | | • | • | |
| 8 | • | • | | | | | | | • | • | |

*Learning Outcomes*

**Program Outcomes**

a. An ability to apply knowledge of computing and mathematics appropriate to the discipline.
b. An ability to analyze a problem, and identify and define the computing requirements appropriate to its solution.
c. An ability to design, implement, and evaluate a computer-based system, process, component, or program to meet desired needs.
d. An ability to function effectively on teams to accomplish a common goal.
e. An understanding of professional, ethical, legal, security and social issues and responsibilities.
f. An ability to communicate effectively with a range of audiences.
g. An ability to analyze the local and global impact of computing on individuals, organizations, and society.
h. Recognition of the need for and an ability to engage in continuing professional development.
i. An ability to use current techniques, skills, and tools necessary for computing practice.
j. An ability to apply mathematical foundations, algorithmic principles, and computer science theory in the modeling and design of computer-based systems in a way that demonstrates comprehension of the tradeoffs involved in design choices.
k. An ability to apply design and development principles in the construction of software systems of varying complexity.

| | |
|---|---|
| **Major Topics Covered**<br>(Approximate Course Hours)<br><br>3 credit hours = 37.5 contact hours<br>4 credit hours = 50 contact hours<br><br>Note: Exams count as a major topic covered | Asymptotic notions (4-hours)<br>Exhaustive search for motif finding and other applications (7-hours)<br>Greedy algorithms for genome rearrangement (4-hours)<br>Dynamic programming for sequence alignment and gene finding (8-hours)<br>Divide-and-conquer (4-hours)<br>Combinatorial algorithms for repeat finding (4-hours)<br>Graph algorithms for sequence assembly (5-hours)<br>Probabilistic modeling for phylogeny reconstruction (6-hours)<br>Hidden Markov model, Viterbi's algorithm, forward, backward, forward-backward algorithms (8-hours) |
| **Assessment Plan for this Course** | Each time this course is offered, the class is initially informed of the Course Outcomes listed in this document, and they are included in the syllabus. At the end of the semester, an anonymous survey is administered to the class where each student is asked to rate how well the outcome was achieved. The choices provided use a 5-point Likert scale containing the following options: Strongly agree, Agree, Neither agree or disagree, disagree, and strongly disagree. The results of the anonymous survey are tabulated and results returned to the instructor of the course.<br><br>The course instructor takes the results of the survey, combined with sample student responses to homework and final exam questions corresponding to course outcomes, and reports these results to the ABET committee. If necessary, the instructor also writes a recommendation to the ABET committee for better achieving the course outcomes the next time the course is offered. |
| **How Data is Used to Assess Program Outcomes** | Each course Learning Outcome, listed above, directly supports one or more of the Student Outcomes, as is listed in "Relationships between Learning Outcomes and Student Outcomes". For CSCI 4490, Student Outcomes (a), (b), (i), and (j) are supported. |
| **Course Master** | Dr. Liming Cai |
| **Course History** | |