

NEW COURSE PROPOSAL

PROGRAM AREA _____

1. Catalog Description of the Course.

BINF 512 ALGORITHMS FOR BIOINFORMATICS

Three hours lecture per week

Prerequisite BINF 500 or permission of instructor

This course will cover advanced theory in the area of biological informatics and will build on concepts introduced in BINF 500. Topics include: methods to support construction and application of combinatorial biochemical libraries, applications of algorithmic information theory, string matching, dynamic programming, prediction of three-dimensional protein structure from peptide sequence.

2. Mode of Instruction.

	Units	Hours per Unit	Benchmark Enrollment
Lecture	____3____	____1____	____15____
Seminar	_____	_____	_____
Laboratory	_____	_____	_____
Activity	_____	_____	_____

3. Justification and Learning Objectives for the Course. (Indicate whether required or elective, and whether it meets University Writing, and/or Language requirements) *[Use as much space as necessary]*

This course is an elective element of the bioinformatics emphasis for the proposed Professional Science Masters degree in Bioinformatics

Upon completion of this course, students will be able to:

- implement algorithms
- explain what is meant by an NP-complete problem and their relevance to reconstruction of phylogenetic trees
- construct a generalized suffix tree for a set of strings
- discuss the fundamental string problem
- generate three-dimensional models of protein structures using a web-based application and explain the computational elements upon which the application is based
- explain theoretical issues in the analysis, interpretation, and utilization of genomic data that require specialized algorithmic solutions.

4. Is this a General Education Course NO

If Yes, indicate GE category:

A (English Language, Communication, Critical Thinking)	
B (Mathematics & Sciences)	
C (Fine Arts, Literature, Languages & Cultures)	
D (Social Perspectives)	
E (Human Psychological and Physiological Perspectives)	

5. Course Content in Outline Form. *[Be as brief as possible, but use as much space as necessary]*

Exact string matching (preprocessing, comparison based methods, seminumerical methods)

Suffix trees (linear time construction, constant time construction, applications)

Inexact matching (core string edits, alignment, dynamic programming, multiple sequence comparison, applications)

Physical mapping

Evolutionary trees

Gene prediction

Genome rearrangements

6. References. *[Provide 3 - 5 references on which this course is based and/or support it.]*

- Gusfield, D. 1997. Algorithms on strings, trees, and sequences: computer science and computational biology. Cambridge University Press, ISBN: 0521585198
- Setubal, J. and Meidanis, J. 1997. Introduction to Computational Molecular Biology. Brooks Cole Publishing, ISBN: 0534952623
- Felsenstein, J. 2003. Inferring Phylogenies. Sinauer Associates, ISBN: 0878931775
- Durbin, R., Eddy, S., Krogh, A., and Mitchison, G. 1998. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, ISBN 0521629713
- Gibas, C., and P. Jambeck. 2001. Developing Bioinformatics Computer Skills. O'Reilly & Associates, ISBN: 1565926641
- Waterman, M. Introduction to Computational Biology: Maps, Sequences and Genomes. 1995. CRC Press, ISBN: 0412993910

7. List Faculty Qualified to Teach This Course.

Computer science faculty and/or computer science professionals

8. Frequency.

- a. Projected semesters to be offered: Fall _ ____ Spring _X____ Summer ____

9. New Resources Required.

- a. Computer (data processing), audio visual, broadcasting needs, other equipment
- b. Library needs
- c. Facility/space needs

None.

10. Consultation.

Dr. Peter Smith, Professor of Computer Science, has been consulted regarding the content and requirements of this course.

11. If this new course will alter any degree, credential, certificate, or minor in your program, attach a program modification.

Amy Denton
William Wolfe

31 October 2003

Proposer of Course

Date