CALIFORNIA STATE UNIVERSITY CHANNEL ISLANDS

NEW COURSE PROPOSAL

PROGRAM AREA

1. Catalog Description of the Course. BINF 500 DNA AND PROTEIN SEQUENCE ANALYSIS (3) Three hours of lecture per week. Prerequisite BIOL 400 or permission of instructor.

This course will introduce the computational aspects of biological inference from nucleic acid and protein sequences. Pairwise sequence comparison and multiple sequence alignment will be studied in detail. Additional topics include: RNA structure prediction, conserved sequence pattern recognition (sequence profile analysis), phylogenetic analysis algorithms, sequence data as a means to study molecular evolution, models and algorithms for genetic regulation, contig assembly, PAM and BLOSUM matrices, protein three dimensional structure prediction.

2. Mode of Instruction.

Lecture	Units	Hours per Unit 1	Benchmark Enrollment 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 a required element of the core curriculum for the proposed Professional Science Masters degree in Bioinformatics

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

- Explain the algorithms used in DNA sequence alignment
- Explain the significance of scoring in DNA sequence alignment
- Write Perl scripts that perform basic manipulations of nucleic acid and protein sequence data
- Evaluate the merits and disadvantages of probabilistic and non-probabilistic tree-finding methods
- Use a profile hidden Markov model to score how well an unknown protein sequence fits a family motif
- Demonstrate facility using BLAST and PSI-BLAST.

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]

Markov chains and hidden Markov models Pairwise alignment Profile hidden Markov models for sequence families Multiple sequence alignment methods Phylogeny reconstruction and assessment Evolutionary models RNA structure analysis Gene prediction Protein classification and structure prediction

NEWCRSFR 9/30/02

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

Durbin, R., Eddy, S., Krogh, A., and Mitchison, G. 1998. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, ISBN 0-521-62971-3

Ewens, W. and Grant, G. 2001. Statistical Methods in Bioinformatics. Springer-Verlag, ISBN 0-387-95229-2

Mount, D. Bioinformatics: Sequence and Genome Analysis. 2001. Cold Spring Harbor Laboratory Press, ISBN 0-87969-608-7

Tisdall, J. Beginning Perl for Bioinformatics. 2001. O'Reilly and Associates, ISBN 0-596-00080-4

7. List Faculty Qualified to Teach This Course.

Biology faculty

8. Frequency.

a. Projected semesters to be offered: Fall _X____ Spring _____ 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.

Attach consultation sheet from all program areas, Library, and others (if necessary)

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

Amy Denton

31 October 2003

Proposer of Course

Date