CALIFORNIA STATE UNIVERSITY CHANNEL ISLANDS

NEW COURSE PROPOSAL

PROGRAM AREA _____

1. Catalog Description of the Course.
BINF 514 STATISTICAL METHODS IN COMPUTATIONAL BIOLOGY (3)
Three hours lecture per week.
Prerequisite MATH 151, BIOL 202, or permission of instructor.

Techniques in statistical inference and stochastic modeling required for the interpretation and utilization of genomic data, including biological sequence alignment and analysis, sequence structure and function prediction, database searching, gene expression profiling, statistical genetics, phylogenetic inference and genetic epidemiology.

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:
- select, apply and interpret descriptive statistics to significant research problems in bioinformatics
- apply quantitative problem-solving skills to biological problems and issues
- describe statistical approaches to the analysis of molecular genetic data
- exercise problem solving capabilities and communication skills for effective research

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]*
Representation and summary of data
Random variables: independence, distributions
Statistical inference: classical and Bayesian methods, likelihood
Stochastic processes: Poisson processes, random walks, Markov chains
Hidden Markov models
Evolutionary models
Phylogenetic tree estimation
Computationally intensive methods

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

Markov Chains, James R. Norris (Author), 1998.; K.L. Chung. **A Course in Probability Theory**. New York: Academic, 1974.

Ewens, W. and G. Grant. 2001**. Statistical Methods in Bioinformatics**: An Introduction. Springer-Verlag, ISBN: 0387952292

Raymer, M and D. Krane. 2002. **Fundamental Concepts of Bioinformatics**. Benjamin Cummings, ISBN: 0805346333

Waterman, M**. Introduction to Computational Biology**: Maps, Sequences and Genomes. 1995. CRC Press, ISBN: 0412993910

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

7. **List Faculty Qualified to Teach This Course.**

Mathematics faculty, 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
Jorge Garcia   31 October 2003
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Proposer of Course   Date