CALIFORNIA STATE UNIVERSITY CHANNEL ISLANDS COURSE MODIFICATION PROPOSAL Courses must be submitted by October 15, 2013, and finalized by the end of the fall semester to make the next catalog (2014-15) production

Date (Change date each time revised): 10/13/13; rev 11.5.13

PROGRAM AREA(S): BIOL

Directions: All of sections of this form must be completed for course modifications. Use YELLOWED areas to enter data. All documents are stand alone sources of course information.

1. Indicate Changes and Justification for Each. [Mark an X by all change areas that apply then please follow-up your X's with justification(s) for each marked item. Be as brief as possible but, use as much space as necessary.]

	Course title	X Course Content				
	Prefix/suffix	X Course Learning Outcomes				
	Course number	x References				
	Units	GE				
	Staffing formula and enrollment limits	X Other ADD GWAR designation				
	Prerequisites/Corequisites	Reactivate Course				
X C	Catalog description					

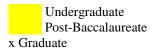
Justification: The original course proposal was written in 2003 and because the field of bioinformatics advances rapidly, significant changes to the references, content, and learning outcomes is required to update course documentation. This course requires that students demonstrate proficiency in writing appropriate to masters-level students through several assigned literature reviews and research reports.

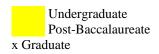
2. Course Information.

Mode of Instruction

[Follow accepted catalog format.] (Add additional prefixes i f cross-listed)

OLD	NEW
Prefix BINF Course# 500	Prefix BINF Course# 500
Title DNA AND PROTEIN SEQUENCE ANALYSIS Units	Title DNA AND PROTEIN SEQUENCE ANALYSIS
(3)	Units (3)
3 hours lecture per week	3 hours lecture per week
hours blank per week	hours blank per week
x Prerequisites: BIOL 400 or 501	x Prerequisites: BIOL 400 or 501
Consent of Instructor Required for Enrollment Corequisites:	Consent of Instructor Required for Enrollment Corequisites:
Catalog Description (Do not use any symbols):	Catalog Description (Do not use any symbols):
This course will introduce the computational aspects of	Introduces the computational aspects of biological
biological inference from nucleic acid and protein sequences.	inference from nucleic acid and protein sequences, and the
Pairwise sequence comparison and multiple sequence	access and manipulation of genomic data from public
alignment will be studied in detail. Additional topics include:	databases. Pairwise sequence comparison and multiple
RNA structure prediction, conserved sequence pattern	sequence alignment will be studied in detail. Additional
recognition (sequence profile analysis), phylogenetic analysis	topics include: RNA structures, conserved sequence pattern
algorithms, sequence data as a means to study molecular	recognition and gene prediction, phylogenetic analysis, sequence data as a means to study molecular evolution, and
evolution, models and algorithms for genetic regulation, contig assembly, PAM and BLOSUM matrices, protein three	human genome science. Meets graduate writing assessment
dimensional structure prediction.	requirement (GWAR).
General Education Categories:	General Education Categories:
Grading Scheme (Select one below):	Grading Scheme (Select one below):
x A – F	x A - F
Credit/No Credit	Credit/No Credit
Optional (Student's Choice)	Optional (Student's Choice)
Repeatable for up to units Total Completions	Repeatable for up to units Total Completions
Multiple Enrollment in Same Semester Y/N	Multiple Enrollment in Same Semester Y/N
Course Level:	Course Level:





(Provided by the Provost Office)

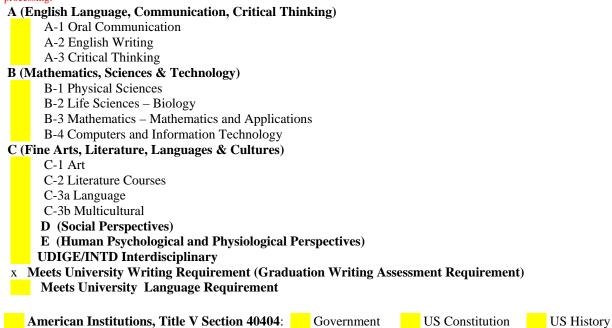
3. Mode of Instruction (Hours per Unit are defaulted)

Hegis Code(s)

Existing				Proposed						
	Units	Hours Per Unit	Default Section Size	Graded		Units	Hours Per Unit	Default Section Size	Graded	CS No. (filled out by Provost Office)
Lecture	<u>3</u>	<u>1</u>	<u>24</u>	Х	Lecture	<u>3</u>	<u>1</u>	<u>24</u>	Х	
Seminar		<u>1</u>			Seminar		<u>1</u>			
Lab		<u>3</u>			Lab		<u>3</u>			
Activity		<u>2</u>			Activity		<u>2</u>			
Field Studies					Field Studies					
Indep Study					Indep Study					
Other blank					Other blank					
Online					Online					

4. Course Attributes:

General Education Categories: All courses with GE category notations (including deletions) must be submitted to the GE website: http://summit.csuci.edu/geapproval. Upon completion, the GE Committee will forward your documents to the Curriculum Committee for further processing.



Service Learning Course (Approval from the Center for Community Engagement must be received before you can request this course attribute).

Online Course (Answer YES if the course is ALWAYS delivered online).

5. Justification and Requirements for the Course. [Make a brief statement to justify the need for the course]

OLD	NEW
This course is a required element of the core curriculum for the	This course is a required element of the core curriculum for a
proposed Professional Science Masters degree in	emphases within the MS Biotechnology and Dual MS/MBA
Bioinformatics	degrees.
x Requirement for the Major/Minor	x Requirement for the Major/Minor
Elective for the Major/Minor	Elective for the Major/Minor

Free Elective

Submit Program Modification if this course changes your program.

6. Student Learning Outcomes. (List in numerical order. Please refer to the Curriculum Committee's "Learning Outcomes" guideline for measurable outcomes that reflect elements of Bloom's Taxonomy: <u>http://senate.csuci.edu/comm/curriculum/resources.htm</u>. The committee recommends 4 to 8 student learning outcomes, unless governed by an external agency (e.g., Nursing).

Free Elective

Upon completion of the course, the student will be able to: **OLD**Upon completion of the course, the student 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.

- describe the techniques used to collect sequence and gene expression data.
- identify appropriate biological databases for specific analyses.
- query databases and search for molecular sequences.
- identify sequences homologous to a known sequence using BLAST.
- describe the regulation of gene expression and the applications of gene expression profiling.
- use sequence alignment and tree building tools.
- explain the principles used to predict and to model protein structures from amino acid sequences.
- Communicate scientific information effectively in written format

No x

7. Course Content in Outline Form. (Be as brief as possible, but use as much space as necessary) OLD NEW

Markov chains and hidden Markov models	Biological databases
Pairwise alignment	Pairwise sequence alignment
Profile hidden Markov models for sequence families	Basic local alignment search tool (BLAST)
Multiple sequence alignment methods	Advanced BLAST and searching techniques
Phylogeny reconstruction and assessment	Multiple Sequence Alignment
Evolutionary models	Phylogenetic Analysis
RNA structure analysis	Short nucleotide sequences
Gene prediction	Bioinformatic approaches to genes and gene expression
Protein classification and structure prediction	Eukaryotic genes and gene-finding methods
	RNA resources
	Protein databases
	Human genome

Does this course content overlap with a course offered in your academic program? Yes _____ No x If YES, what course(s) and provide a justification of the overlap.

all

Does this course content overlap a course offered in another academic area? Yes If YES, what course(s) and provide a justification of the overlap.

Overlapping courses require Chairs' signatures.

8. Cross-listed Courses (Please note each prefix in item No. 1) Beyond three disciplines consult with the Curriculum Committee.

- A. List cross-listed courses (Signature of Academic Chair(s) of the other academic area(s) is required).
- B. List each cross-listed prefix for the course:
- C. Program responsible for staffing: Biology
- 9. References. [Provide 3-5 references]

OLD

Durbin, R., Eddy, S., Krogh, A., and Mitchison, G. 1998. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, <u>Cambridge University Press</u>.

Ewens, W. and Grant, G. 2001. Statistical Methods in Bioinformatics. Springer-Verlag.

Mount, D. Bioinformatics: Sequence and Genome Analysis. 2001. Cold Spring Harbor Laboratory Press.

Tisdall, J. Beginning Perl for Bioinformatics. 2001. O'Reilly and Associates.

NEW

Agostino, Michael. 2013. <u>Practical Bioinformatics</u>. Garland Science Pevsner, Jonathan. 2009. <u>Bioinformatics and Functional Genomics (2nd edition)</u>. John Wiley & Sons, Inc. Lesk, Arthur M. 2011. <u>Introduction to Genomics (2nd ed.)</u>. Oxford University Press. Lesk, Arthur M. 2008. <u>Introduction to Bioinformatics (3rd edition)</u>. Oxford University Press. Campbell, A. Malcolm and Laurie J. Heyer. 2007. <u>Discovering Genomics, Proteomics and Bioinformatics (2nd ed.)</u>. Pearson/Benjamin Cummings

- **10.** Tenure Track Faculty qualified to teach this course. Amy Denton, Erich Fleming
- 11. Requested Effective Date or First Semester offered: Fall 2014
- 12. New Resource Requested: Yes No x If YES, list the resources needed.
 - A. Computer Needs (data processing, audio visual, broadcasting, other equipment, etc.)
 - B. Library Needs (streaming media, video hosting, databases, exhibit space, etc.)
 - C. Facility/Space/Transportation Needs:
 - D. Lab Fee Requested: Yes _____ No ____ (Lab fee requests should be directed to the Student Fee Committee)
 - E. Other.
- 13. Will this course modification alter any degree, credential, certificate, or minor in your program? Yes x No If, YES attach a program update or program modification form for all programs affected. Priority deadline for New Minors and Programs: October 1, 2013 of preceding year. Priority deadline for Course Proposals and Modifications: October 15, 2013. Last day to submit forms to be considered during the current academic year: April 15th.

Amy Denton

<mark>10/13/13</mark>

Proposer(s) of Course Modification Type in name. Signatures will be collected after Curriculum approval. Date

Approval Sheet

Course: BINF 500

If your course has a General Education Component or involves Center affiliation, the Center will also sign off during the approval process.

Multiple Chair fields are available for cross-listed courses.

The CI program review process includes a report from the respective department/program on its progress toward accessibility requirement compliance. By signing below, I acknowledge the importance of incorporating accessibility in course design.

Program Chair		
	Signature	Date
Program Chair		
	Signature	Date
Program Chair		
	Signature	Date
General Education Chair		
	Signature	Date
Center for Intl Affairs Director		
	Signature	Date
Center for Integrative Studies Director		
	Signature	Date
Center for Multicultural Engagement Director		
	Signature	Date
Center for Civic Engagement and Service Learning Director		
	Signature	Date
Curriculum Chair		
	Signature	Date
AVP		