

CALIFORNIA STATE UNIVERSITY CHANNEL ISLANDS
COURSE MODIFICATION PROPOSAL
Courses must be submitted by November 3, 2008,
to make the next catalog (2009-2010) production

DATE (CHANGE DATE EACH TIME REVISED): 10-20-08 REV 11.3.08

PROGRAM AREA(S): BIOLOGY

Directions: All of sections of this form must be completed for course modifications. All documents are stand alone sources of course information.

1. Course Information.

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

OLD				NEW			
Prefix	BIOL	Course#	502	Prefix	BIOL	Course#	502
Title	TECHNIQUES IN GENOMICS/PROTEOMICS			Title	TECHNIQUES IN GENOMICS/PROTEOMICS		
Units	(2)			Units	(3)		
hours lecture per week				hours lecture per week	1		
hours laboratory per week	6			hours laboratory per week	6		
X Prerequisites: BIOL401 X Consent of Instructor Required for Enrollment Corequisites:				X Prerequisites: BIOL401 X Consent of Instructor Required for Enrollment Corequisites:			
Catalog Description (Do not use any symbols): This laboratory course introduces students to the current techniques and methodologies in the fields of comparative and functional genomics and proteomics. Topics and techniques covered include genome sequencing, micorarrays, mutagenesis, transgenic plants and animals, single nucleotide polymorphism (SNP) discovery and analysis. Students will gain hands-on lab bench experience and will make on-site visits to high volume regional biotechnology facilities.				Catalog Description (Do not use any symbols): Provides students with theoretical foundations and practical skills needed for general bioinformatics, genomics, and proteomics analysis. Intensive lab sessions, emphasize applied techniques. Field trips to various local biotechnology facilities will augment the training.			
General Education Categories		Graded		General Education Categories		Graded	
Lab Fee Requested		CR/NC		Lab Fee Requested		CR/NC	
		X A - F				X A - F	
Course Level:		Repeatable for up to		Course Level:		Repeatable for up to	
Undergraduate		units		Undergraduate		units	
Post-bac/Credential		Total Completions		Post-bac/Credential		Total Completions	
X Graduate		Multiple Enrollment in same semester		X Graduate		Multiple Enrollment in same semester	

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

Hegis Code(s) _____
 (Provided by the Dean)

Existing

Proposed

	Units	Hours Per Unit	Benchmark Enrollment	Graded		Units	Hours Per Unit	Benchmark Enrollment	Graded	CS No. (filled out by Dean)
Lecture					Lecture	1	1	24	X	
Seminar					Seminar					
Lab	2	3	15	X	Lab	2	3	24	X	
Activity					Activity					
Field Studies					Field Studies					
Indep Study					Indep Study					
Other blank					Other blank					

3. 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.

A (English Language, Communication, Critical Thinking)

- A-1 Oral Communication
- A-2 English Writing
- A-3 Critical Thinking

B (Mathematics, Sciences & Technology)

- B-1 Physical Sciences
- B-2 Life Sciences – Biology
- B-3 Mathematics – Mathematics and Applications
- B-4 Computers and Information Technology

C (Fine Arts, Literature, Languages & Cultures)

- C-1 Art
- C-2 Literature Courses
- C-3a Language
- C-3b Multicultural

D (Social Perspectives)

E (Human Psychological and Physiological Perspectives)

UDIGE/INTD Interdisciplinary

Meets University Writing Requirement

Meets University Language Requirement

American Institutions, Title V Section 40404: Government US Constitution US History
Refer to website, Exec Order 405, for more information: <http://senate.csuci.edu/comm/curriculum/resources.htm>

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

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

OLD

This course is a required element of the core curriculum for the proposed Professional Science Masters degree in Bioinformatics

NEW

This course is a required course for the MS in Biotechnology and Bioinformatics degree program. The course will familiarize students with techniques used in the fields of modern genomics and proteomics. The course actively explores basic biology in the context of applied research and provides students the opportunity to conduct pertinent experiments and analyze the results by a variety of techniques.

☒ Requirement for the Major/Minor

☐ Elective for the Major/Minor

☒ Requirement for the Major/Minor

☐ Elective for the Major/Minor

Submit Program Modification if this course changes your program.

5. Learning Objectives. (List in numerical order)

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

OLD

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

- Generate, edit and annotate a genomic DNA sequence
- Use Clustal to align several DNA sequences
- Compare and contrast the major techniques used in transcriptome profiling
- Use the xProfiler at NCBI online
- Perform and interpret a northern blot
- Interpret a DNA fingerprint and explain the fundamental populations genetics that underlie data
- Navigate and interpret a QTL map

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

NEW

Students who successfully complete this course will be able to:

- Utilize the concepts of genomics and proteomics toward biotechnological applications
- Demonstrate their ability to reason both inductively and deductively with experimental information and data.
- Explain the theory and practice of a variety of experimental techniques.
- Select and apply experimental procedures to the spectrum of fields making use of biotechnology

- Design strategies for successful experimentation

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

OLD

Genome sequencing and annotation (automated DNA sequencing, high-throughput sequencing, contig assembly, hierarchical and shotgun sequencing, EST sequencing)
 Analysis of gene expression (cDNA microarrays, oligonucleotide microarrays, microbeads, SAGE, differential display, quantitative PCR)
 Protein methods (2D-PAGE, protein microarrays)
 Functional genomics (reverse genetics, transgenic plants and animals, fingerprinting, fine-structure genetics)
 SNPs (QTL mapping, linkage disequilibrium mapping, SNP detection via hybridization, Invader assays)

NEW

The entire course will focus on three modules:
 1. Detection of protein-protein interactions: This will involve elements such as primer design, gene cloning, PCR, mammalian cell culture and affinity chromatography.
 2. Gene silencing by RNA interference: This will involve mammalian cell cultures, gene silencing by siRNAs, northern and western blots, SDS-PAGE, RT-PCR and fluorescence microscopy.
 3. Random mutagenesis and protein purification: This will involve synthesis of megaprimers, gene cloning, protein expression and purification using affinity columns.

Does this course content overlap with a course offered in your academic program? Yes ☐ No ☒

If YES, what course(s) and provide a justification of the overlap.

Does this course content overlap a course offered in another academic area? Yes ☐ No ☒

If YES, what course(s) and provide a justification of the overlap.

Overlapping courses require Chairs' signatures.

7. Cross-listed Courses (Please note each prefix in item No. 1)

- List cross-listed courses (Signature of Academic Chair(s) of the other academic area(s) is required).
- List each cross-listed prefix for the course:
- Program responsible for staffing:

8. References. [Provide 3-5 references]

OLD Isaac S. Kohane, Alvin Kho, Atul J. Butte. (2002). Microarrays for an Integrative Genomics. MIT Press.
 Richard J. Simpson (2002). Proteins and Proteomics: A Laboratory Manual. Cold Spring Harbor Laboratory.
 Ewing B, Hillier L, Wendl M, Green P: Basecalling of automated sequencer traces using phred. I. Accuracy assessment. Genome Research 8, 175-185 (1998).

Ewing B, Green P: Basecalling of automated sequencer traces using phred. II. Error probabilities. Genome Research 8, 186-194 (1998).

Jakt LM, Cao L, Cheah KS, and Smith DK: Assessing Clusters and Motifs from Gene Expression Data. Genome Research 11, 112-123 (2001).

A. Malcolm Campbell, Laurie J. Heyer (2002). Discovering Genomics, Proteomics, and Bioinformatics. Benjamin/Cummings.
 Cecilia Saccone, Graziano Pesole (2003). Handbook of Comparative Genomics : Principles and Methodology. Wiley-Liss
 Stephen P. Hunt, Frederick J. Livesey, F. M. Livesey, Rick Livesey. (2001). Functional Genomics: A Practical Approach (Practical Approach Series). Oxford University Press

NEW

- "Discovering Genomics, Proteomics and Bioinformatics", 2nd edition, by A. Malcolm Campbell and Laurie J. Heyer; Publisher: Benjamin Cummings; ISBN-10: 0805382194 ; ISBN-13: 9780805382198
- RNA Interference in Practice: Principles, Basics, and Methods for Gene Silencing in C.elegans, Drosophila, and Mammals (Hardcover) by Ute Schepers. Wiley-VCH; 1 edition (2005)
- The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification Oscar Puig et al. Methods, Vol 24 (3): 218-229 (2001)
- EZ cloning. Strategies, Vol 20 (2). Stratagene

9. Tenure Track Faculty qualified to teach this course.

Biology faculty

10. Requested Effective Date or First Semester offered: **Spring, 2009**

11. New Resource Requested: Yes ☐ No ☒

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 ☐ (Refer to the Dean's Office for additional processing)

E. Other.

12. Indicate Changes and Justification for Each. [Check all that apply and follow with justification. Be as brief as possible but, use as much space as necessary.]

<input type="checkbox"/> Course title	<input checked="" type="checkbox"/> Course Content
<input type="checkbox"/> Prefix/suffix	<input checked="" type="checkbox"/> Course Learning Objectives
<input type="checkbox"/> Course number	<input checked="" type="checkbox"/> References
<input checked="" type="checkbox"/> Units	<input type="checkbox"/> GE
<input type="checkbox"/> Staffing formula and enrollment limits	<input type="checkbox"/> Other
<input type="checkbox"/> Prerequisites/Corequisites	<input type="checkbox"/> Reactivate Course
<input checked="" type="checkbox"/> Catalog description	
<input checked="" type="checkbox"/> Mode of Instruction	

Justification:

1. UNITS: Presently, the course is offered as an intensive lab course. Although designated as a 2 unit course when first proposed (involving two 3 hour lab sessions), labs typically go for 7.5-8 hours per week due to the detailed nature of the experimental protocols. In the lab sessions conducted at present, the first 45-60min. are spent on lecturing students about the principles behind each experimental protocol and the methodologies involved. Students get a better grasp of the subject and are able to conduct experiments more efficiently when they are provided with enough background material about each of the techniques utilized. This is a very labor intensive lab and requires a significant input of time in preparation and presentation of the material to the students. Hence, it is recommended that a one hour lecture component be added to the existing lab course so that enough time is available for complete dedication to the experimental section rather than being partially overlapped by a lecture as is happening presently.

2. MODE OF INSTRUCTION: A lecture component is requested to be added to the lab course because of the sheer intense nature of the course itself which typically requires a significant element of presentation of the theoretical principles to the students which takes up their lab time.

3. CATALOG DESCRIPTION: Based on the nature of experiments conducted, the catalog description is required to be changed which covers broader aspects of genomics and proteomics while addressing specific goals.

4. COURSE CONTENT: Course content is required to be changed in order to provide a holistic view of techniques in genomics and proteomics today and be in alignment with the overall objectives of the course.

5. COURSE LEARNING OBJECTIVES: A change is being requested so that the student learning outcomes are in alignment with the course content.

6. REFERENCES: References are being changed because of the different type of experiments being conducted.

13. Will this course modification alter any degree, credential, certificate, or minor in your program? Yes ☒ No ☐

If, YES attach a program update or program modification form for all programs affected.

Priority deadline for New Minors and Programs: **October 6, 2008** of preceding year.

Priority deadline for Course Proposals and Modifications: **November 3, 2008**.

Last day to submit forms to be considered during the current academic year: **April 15th**.

Nitika Parmar

101608

Type in name. Signatures will be collected after Curriculum approval.

Approval Sheet

Course:

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.

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
Dean of Faculty		
	Signature	Date