

Please complete this form and attach a copy of the syllabus and catalog description for new courses. Forward the form and attachments to your departmental curriculum committee for approval, and then to your College/School curriculum committee, or Dean's office, for final approval. The approved form should then be forwarded to the Academic Scheduling Office, MS 3D1. This is for ***undergraduate course approval only***. Please see the Provost Office/Graduate Council website to obtain a copy of the Graduate Course Approval Form and for details about the graduate course approval process.

Please indicate: **New** **N** **Modify** **Delete**

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Effective Term (New/Modified Courses only): Fall 2007 **Final Term** (deleted courses only): _____

IP)

Repeat Status*(check one): X NR-Not repeatable _____ RD-Repeatable within degree _____ RT-Repeatable within term _____

***Note:** Used only for special topics, independent study, or internships courses

Schedule Type Code(s): 1. LEC LEC=Lecture SEM=Seminar STU=Studio INT=Internship IND=Independent Study
2. _____ LAB=Lab RCT=Recitation (second code used only for courses with Lab or Rct component)

Prereq ☒ **Coreq** _____ (Check one): BIO231, IT108, IT208, STAT344

Note: Modified courses - review prereq or coreq for necessary changes; Deleted courses - review other courses to correct prereqs that list the deleted course.

Description of Modification (for modified courses): _____

Special Instructions (major/college/class code restrictions, if needed): _____

Approval Signatures:

Department or Unit: _____ Date: _____
(Signature)

College/School Committee: _____ **Date:** _____
(Signature)

Approval from other units:

Please list those units outside of your own which may be affected by this new, modified, or deleted course. Each of these units should approve this action prior to its being submitted to the COS Curriculum Committee for approval.

Unit: BIO (relevant course: 580)	Head of Unit's Signature:	Date:
Unit:	Head of Unit's Signature:	Date:
Unit:	Head of Unit's Signature:	Date:
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Unit:	Head of Units Signature:	Date:

COS Curriculum Committee approval: _____ Date: _____

Course Proposal Submitted to the Curriculum Council

by

The College of Science

1. COURSE NUMBER AND TITLE:

BINF401 (3 credits) Bioinformatics and Computational Biology I.

Prerequisites: Prerequisites: BIO231, IT108, IT208, STAT344.

Catalog Description: Bioinformatics topics are presented as 3-4 week units: protein sequence, structure prediction and modeling methods; nucleic acid sequence and structure prediction and evolutionary models; gene structure prediction in prokaryotes and eukaryotes; image analysis and biomedical applications.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to provide a survey of the outstanding research problems in the fields of bioinformatics and computational biology for senior-level undergraduate students who have an appropriate background in the biological sciences and sufficient quantitative and programming skills to benefit from exposure to the opportunities presented in an emerging scientific field. The course is intended to be taken in concert with a computational lab class in which the students receive practical experience framing a scientific hypothesis and using the existing tools to understand how particular research problems are approached. While individual components of this course may be taught in upper-level courses in other departments (for example sequence analysis is a mainstay of evolutionary biology), the framework in which the problems are presented is quite different and the integrating principles that connect the field will not be considered in those courses. Many of these concepts and the associated tools have become essential to biotechnology companies as they develop products, so exposure of students to both theory and practice will make them better suited to compete for positions with such employers as well as more competitive in applying to graduate schools.

Course Necessity: Bioinformatics and computational biology are research areas in which both the behavior of individual biomolecules and their role in living cells and ecosystems may be considered. It is likely to be the predominant research science of the early part of the 21st century. The intellectual disciplines from which a computational biologist draws in order to perform research are very diverse. Courses taught in those diverse fields do not provide the intellectual connections that are identified as important by a computational biologist. It is important that undergraduates be given exposure to a consistent and coherent description of the discoveries, methods and theoretical framework used in this scientific discipline. There is no existing undergraduate course at GMU that covers these topics as a connected and integrated discipline.

Course Relationship to Existing Programs: This course is proposed as the first of a two-semester lecture series that will anchor an undergraduate minor in bioinformatics for a Biology (or closely related biosciences field) major. It is part of the first undergraduate program to be developed by the Bioinformatics and Computational Biology department. Interest in these lectures will determine to what extent a more extensive set of undergraduate courses is developed.

Course Relationship to Existing Courses: The only existing undergraduate course at GMU with a similar title is BINF 354 (Foundations in Mathematical Biology), which was developed by professors at the Krasnow Institute, without reference to any of the professors in the Bioinformatics and Computational Biology department, when we were still a program in SCS. BINF 354 is a research methods course with emphasis on the concepts and techniques required in neurosciences research and has no overlap with the proposed course(s). A second course, BIOL 580 (Computer Applications for the Life Sciences), might be suitable for senior undergraduates, and is listed in the GMU catalog, however this course has not been taught in several years and in fact we were approached to develop a syllabus for and teach this course in Spring 2007.

3. **SCHEDULING AND PROPOSED INSTRUCTORS:**

Semester of Initial Offering: Fall 2007

Proposed instructors: Three-week commitments from each professor in Bioinformatics and Computational Biology (Vaisman, Seto, Weller, Kinser in semester 1, Weller, Klimov, and Willett in semester 2).

4. **TENTATIVE SYLLABUS:** See attached.

BINF 401 Syllabus

Week	subject	Reading
1	Topic I: Protein sequence, structure prediction and modeling Introduce/review the chemical and biochemical properties of proteins, the experimental methods by which these properties are measured and ways in which the information is represented. The ways in which proteins are compared will be presented; primary sequence comparison will be presented in depth.	Mount Chapt 1
2	Three--dimensional folding of proteins, the methods for measuring such folding, the processes that can disrupt such folding and the consequences of such disruption. Methods for predicting structure and the identification of important motifs for correct structure and function will be discussed.	Mount Chapt 9
3	Methods for imposing a computational framework on a three-dimensional structure of a protein in order to allow sequence-separated but spatially correlated components to be identified.	Mount Chapt 9
4	Topic II: Nucleic Acid sequence and structure prediction, sequence comparison Review of the Central Dogma of Molecular Biology, emphasizing the relevant chemical characteristics of DNA and RNA. The relationship between the two types of code will be introduced as well as the implication of the chemistry in the allowed structural forms. The ways in which the information is represented and the databases in which the information is stored will be presented.	Mount Chapt 1
5	The experimental basis of nucleic acids as the hereditary material and the ways in which the coded information can be dispersed. Working definitions of genes will be presented, including those that are eventually translated into protein and those that function as structural RNAs. The energetic and chemical basis for the structural prediction programs for functional RNAs will be presented.	Mount Chapt 5
6	The sequence signals by which genes are recognized against the background of a large amount of non-gene sequence information will be discussed, as well as the pitfalls and unknowns to the computational and experimental approaches. Sequence comparison methods will be discussed as well as some common evolutionary models used in sequence comparisons.	Mount Chapt 10
7	midterm	
8	Topic III: Gene structure prediction in prokaryotes and eukaryotes What is known about the long- and short-range organization of chromatin and DNA sequence in genomes. The organizational differences in eukaryotes and prokaryotes will be described along with the experimental methods used in determining particular features.midterm questions	Mount Chapt 2
9	Prokaryotic genomes and the arrangement of genes as operons and the presence of possibly overlapping genes along with the sequence motifs that characterize these structures and software programs used to predict/identify them.	Pevzner Chapt 8
10	Eukaryotic genomics and the presence of introns,	Pevzner Chapt 9

	untranslated regions and other structure important to regulation, along with the sequence signal used to identify such components and software programs used to predict and identify them. Topic IV: Image analysis and biomedical applications	
11	Topic IV: Images of Biological Systems The types of biomedical data commonly stored as images, from whole-organism subsystem such as skeletal x-rays to tissue- and cell-specific microscopic methods. The techniques for developing molecule- specific visual markers and the limits of resolution, precision and accuracy will be discussed.	Web resources and papers from clinical journals
12	General approaches to the annotation of biomedical images including the use of expert-provided tags as well more general feature-recognition	Web resources and papers from clinical journals
13	The basis for image decomposition to extract important structural data and image layering to achieve multi-dimensional information with a common location , or neighborhood information as a three-dimensional construct.	Web resources and papers from clinical journals
14	Final	

Required course texts

1. Bioinformatics: Sequence and Genome Analysis ed 2, David Mount, CSHL Press
2. Computational Molecular Biology: an algorithmic approach ed 1, Pavel Pevzner, The MIT Press