

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**

Submitted by: Jennifer W Weller **Ext:** 3-8329 **Email:** jweller@qmu.edu

Effective Term (New/Modified Courses only): Spring 2008 **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 X Coreq _____ (Check one): BINF 401,403

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:
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Unit:	Head of Units Signature:	Date:

COS Curriculum Committee approval: _____ Date: _____

Course Proposal Submitted to the Registrar
by
Dept. Bioinformatics and Computational Biology, COS

1. COURSE NUMBER AND TITLE:

BINF402 (3 credits) Bioinformatics and Computational Biology II.

Prerequisites: Prerequisites: BINF 401, BINF 403.

Catalog Description: Bioinformatics topics are presented as 3-week units: the design and use of parallel genomics platforms, mapping the measurements to biomolecules; approaches for inferring biological pathways; simulation methods for the dynamics of biomolecules; systems approaches to biology.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to provide a survey of the newest research problems in the fields of bioinformatics and computational biology for senior-level undergraduate students who have already taken the first bioinformatics course. The course is intended to be taken in concert with a computational lab class in which the students receive practical experience working with the data and gaining familiarity with the tools that have been developed so far. IN this course students will be exposed to the types of data and analysis paradigms that are at the forefront of research areas emphasized by the NIH and NSF.

Course Necessity: The high throughput and parallel generation of entire sets of biomolecules has both challenged existing paradigms in the biosciences and provided unprecedented modeling opportunities to *in silico* biologists. No previous generation of computational biologists had access to amount or types of data that would allow realistic modeling of the networks that provide both the buffering against and the response of living organisms to the environment and their own development. This is the predominant open research field in biology at the current time. It is important that our graduating students understand the new biology and understand the methods required to participate in one of the most exciting research and development areas of science in the 21st century. 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 second 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 lecture courses 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: Spring 2008

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 402 Syllabus

Week	subject	Reading
1	Topic 1: Highly Parallel genomics platforms Strategies for the high-throughput sequencing of DNA and RNA, the characteristics of the resulting data and the steps required to cleanse, assemble and annotate such information.	Pevzner Chapt 1
2	Microarray platforms for the analysis of transcript and genomic structure, and how to map the measurement back to a genome.	Pevzner Chapt 5
3	Proteomics platforms for the analysis of protein profiles, how to map the measurement back to the genome and how to compare it to the transcriptome.	Pevzner Chapt 11
4	Topic 2: Inferring Biological Pathways Genetic pathways, the experimental approaches to obtaining the data and the ways in which to represent the information and the ways in which the measurements are captured as relationships that are amenable to computational analysis.	Chapter 4 from “Systems Biology: Properties of Reconstructed Networks” by Palsson
5	Enzymatic pathways, the experimental approaches to obtaining the kinetic and regulatory data and the ways in which the measurements are represented and put into computationally accessible frameworks.	Chapter 3 from “Systems Biology: Properties of Reconstructed Networks” by Palsson
6	The metabolome and the ways in which the reactants and products of chemical reactions tie together the metabolic and gene regulatory network pathways, how the measurement of pools and flux are represented and how they are incorporated into computational analyses of cell responses.	Chapter 5 from “Systems Biology: Properties of Reconstructed Networks” by Palsson
7	midterm	
8	Topic 3: Simulation Methods for Dynamics of BioMolecules The basics of molecular dynamics including (1) Introduction to molecular dynamics, (2) a review of the methods of integrating Newton equations of motion and computation of energy function (3) design and structure of popular biomolecular force fields.	Selected Chapters from D. Frankel and B. Smit "Understanding Molecular Simulations: From Algorithms to Applications"
9	How to obtain and interpret results from molecular dynamics simulations, including (1) the steps and procedures for preparing biomolecular systems for simulations. Solvation of proteins and polynucleotides, (2) procedures for performing typical molecular dynamics simulation and the analysis of simulation results (3) examples of molecular dynamics simulations.	Selected Chapters from D. Frankel and B. Smit "Understanding Molecular Simulations: From Algorithms to Applications"
10	The foundations of the Monte Carlo algorithm including (1) the concept and basics of Monte Carlo simulations, (2) trial moves (3) applications of the Monte Carlo algorithm in biomolecular systems, (4) examples of applications of the Monte Carlo algorithm in computational biology.	Selected Chapters from: D. Frankel and B. Smit "Understanding Molecular Simulations: From Algorithms to Applications"
11	Topic 4: Systems Biology Focusing on those metabolic pathways known to be fundamental to all cellular systems (including core metabolic pathways and signaling networks) these lectures will emphasize the cross-communication between pathways, including chemical messengers, localization and targeting of enzymes and products, and time scales.	Chapter 2 from “Pathway Analysis and Optimization in Metabolic Engineering” by Torres and Voit
12	Students will learn about the contents of primary and secondary pathway databases and other electronic information systems that contain original measurements,	Chapter 3 from “Pathway Analysis and Optimization in Metabolic Engineering” by

	measurement summaries, a variety of data and pathway representations and related information on the pathways previously introduced.	Torres and Voit
13	Students will be introduced to the ways in which pathways are represented in order to be amenable to computational analysis and how software tools contribute to the process. Important questions for the computational biologist include the extraction of data from the databases previously discussed, the comparability of data from different sources, the use and limitations of such data in formulating new hypotheses.	Selected parts of “Computational Cell Biology” by Marland Wagner and Tyson
14	Lectures will present the current research frameworks in which network modeling is conducted, in which individual pathways at particular layers, such as the gene regulatory pathways (circuit diagrams produced by Hood, Ericson and Istrail) and enzyme-metabolite pathways (Karp and co-workers) are integrated within the layer and how these networks are then integrated between layers such that system-wide effects are predicted.	Selected parts of “Computational Cell Biology” by Marland Wagner and Tyson

Required text

1. “Computational Molecular Biology: an algorithmic approach” ed 1, Pavel Pevzner, The MIT Press

Recommended but not required

1. “Systems Biology: Properties of Reconstructed Networks” by Palsson
2. “Computational Cell Biology” by Marland Wagner and Tyson
3. “Pathway Analysis and Optimization in Metabolic Engineering” by Torres and Voit
4. "Understanding Molecular Simulations: From Algorithms to Applications" Frankel and Smit