

GEORGE MASON UNIVERSITY

Undergraduate Council NEW Certificate, Concentration, Minor, Track or Degree Program Coordination/Approval Form

(Please complete this form and attach any related materials. Forward it as an email attachment to the Secretary of the Undergraduate Curriculum Council. A printed copy of the form with signatures should be brought to the Undergraduate Curriculum Council Meeting. If no coordination with other units is required, simply indicate "None" on the form.

Title of Program/Certificate, etc: Bioinformatics Minor

Level (Master's/Ph.D.): Undergraduate

Please Indicate: ☐ Program ☐ Certificate ☐ Concentration ☐ Track
☒ Minor ☐ Degree

Description of certificate, concentration or degree program:

Please attach a description of the new certificate or concentration. Attach Course Inventory Forms for each new or modified course included in the program. **For new degree programs**, please attach the SCHEV Program Proposal submission.

Please list the contact person for this new certificate, concentration, track or program for incoming students: Glenda Wilson (703 993-8449, gwilson1@gmu.edu)

Approval from other units:

Please list those units outside of your own who may be affected by this new program. Each of these units must approve this change prior to its being submitted to the Graduate Council for approval.

Unit: MMB	Head of Unit's Signature:	Date:
Unit: CDS	Head of Unit's Signature:	Date:
Unit: ITE-CS	Head of Unit's Signature:	Date:
Unit:	Head of Unit's Signature:	Date:

Submitted by: Jennifer W Weller Email: jweller@gmu.edu

Undergraduate Curriculum Council approval: _____ Date: _____

Undergraduate Curriculum Council representative: _____ Date: _____

Provost Office representative: _____ Date: _____

**STATE COUNCIL OF HIGHER EDUCATION FOR VIRGINIA
PROGRAM PROPOSAL COVER SHEET**

1. Institution George Mason University	2. Program action (Check one): Spin-off proposal ☐ New program proposal ☒
3. Title of proposed program Bioinformatics Minor	4. CIP code
5. Degree designation Biology (or BioSciences) with minor in Bioinformatics	6. Term and year of initiation FALL 2007
7a. For a proposed spin-off, title and degree designation of existing degree program: BSc Bioinformatics	
7b. CIP code (existing program)	
8. Term and year of first graduates SPRING 2008	9. Date approved by Board of Visitors
10. For community colleges: date approved by local board date approved by State Board for Community Colleges	
11. If collaborative or joint program, identify collaborating institution(s) and attach letter(s) of intent/support from corresponding chief academic officers(s) NONE	
12. Location of program within institution (complete for every level, as appropriate). School(s) or college(s) of <u>College of Science</u> Division(s) of <u>Department of Bioinformatics and Computational Biology</u> Campus (or off-campus site) <u>Fairfax and Prince William</u> Distance Delivery (web-based, satellite, etc.) <u>web-based delivery</u>	
Name, title, telephone number, and e-mail address of person(s) other than the institution's chief academic officer who may be contacted by or may be expected to contact Council staff regarding this program proposal. Richard Diecchio ASSOCIATE DEAN FOR UNDERGRADUATE PROGRAMS COLLEGE OF SCIENCE GEORGE MASON UNIVERSITY 703-993-1209 rdiecchi@gmu.edu	

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BACKGROUND

The George Mason University College of Science has a department that provides quality graduate education in bioinformatics. This department prepares its students for careers as research professionals of bioinformatics and computational biology, and successfully supports human capital needs in the public and private sectors. However, there is no well-defined mechanism in place whereby undergraduate students in the various bioscience disciplines can gain the necessary theoretical and skills background to move into positions as technical and research assistant experts in the biotechnical and pharmaceutical industries. The discipline requires a strong informatics background along with a solid foundation in one of the biosciences, with biology providing the broadest range.

To address this shortcoming, it is proposed that the Bioinformatics and Computational Biology department develop a senior undergraduate two-semester lecture and lab series to provide the theoretical basis for and hands-on practice with the types of experiments and tools used in bioinformatics research and biotechnology development processes. The members of the department will collaborate to develop and teach these courses, so that students are exposed to the most up to date methods and questions, resulting in a minor specialization for a Biology degree. The curriculum will provide training in the technical aspects of carrying out bioinformatics experiments and the theoretical training to read and understand the bioinformatics literature.

DESCRIPTION OF PROPOSED PROGRAM

Program Mission

The proposed undergraduate BSc in Biology/Bioinformatics minor addresses both regional and national needs¹ for a cadre of technically trained scientists who will be able to participate as members of R & D teams of bioinformaticians in both the public and private sectors. Local corporations expected to hire graduates of the program include Celera, TIGR, Human Genome Sciences, The Venter Institute, and Gene Logic, as well as many other firms in the region's robust biotechnology community. The proposed minor includes a solid foundation in all aspects of bioinformatics, including familiarity with research issues, tools and techniques. The proposed minor is intended for:

- Students seeking to work in biological science centered careers that require an understanding of how bioinformatics and computational biology inform and support experimental research
- Students with undergraduate majors in either biological science or computational science who are planning to enter the field of bioinformatics as technicians or go on to graduate school and would like to demonstrate capability in the skill sets needed.

Although courses will initially be offered using lecture and computer lab facilities on the Fairfax and Prince William campuses, the capability to offer classes remotely to students inside and outside of Northern Virginia will be considered, as this will make it easier for local students to attend classes, and it will give the program both national and international footprints. Typical undergraduates will benefit from the personal attention of professors, but non-traditional students are often more competent to regulate schedules and seek help outside of a lecture venue.

Program Objectives

Bioinformatics refers to the application of information technology to the storage, retrieval and analysis of large amounts of data and information about biological sequences, structures and functions. As such, bioinformatics is an inherently multidisciplinary specialty that requires a background in both biology and computing.

¹ US Department of Labor, "The field of biology has progressively transitioned from a bench-based skill to a computer-based science. The bioinformatics sector represents the technological future of the biotech industry. Utilizing sophisticated computer equipment for gathering and analyzing biological information, bioinformatics holds the promise of significant advancements in health care. The sector will grow exponentially over the next decade and provide us new intelligence about our genetic structure, how our genes shape who we are, and how we function. This tremendous growth has created a need for workers at all levels, from basic tasks like creating and maintaining databases that hold biological data to more advanced occupations the demand for computational and biological expertise continues to grow." (underscore added for emphasis) (<http://www.careervoyages.gov/biotechnology-processingandinformatics.cfm#bioinformatics>).

Competence in the bioinformatics field requires an understanding of the tools, techniques, research questions and legal and ethical aspects of projects. At the time of completion, students should be able to:

- Demonstrate a sound theoretical knowledge about the technology and research questions relevant to the fields of bioinformatics,
- Possess a set of practical skills for R&D in commercial fields such as biomedicine and experimental pharmacology

Admission Criteria

The student must be in good academic standing working towards a Biology degree, and have taken certain prerequisites, put in place to that ensure that students have both biological and informatics foundations needed to be successful in the senior-level lecture and labs.

Program Structure

The general academic requirements for completion of the minor in Bioinformatics are organized into several areas:

- Biological Science Core Courses (4 credits) -- foundational courses in modern biology, biotechnology, genetics, etc.
- Informatics and mathematics Core Courses (9 credits)
- Bioinformatics lecture and Lab courses (8 credits) will acquaint the student with the tools and methods used for bioinformatics analysis, and methods for creating customized bioinformatics tools.
- Mentored senior research project (2 credits)

Curriculum Requirements

The proposed Bioinformatics minor consists of the following coursework:

BIOL 231 - Cell Structure and Function (4 credits)

IT 108 – Programming Fundamentals (3 credits)

IT 208 – Program Design and Data Structures (3 credits)

STAT 344 – Probability and Statistics for Scientists and Engineers I (3 credits)

BINF 401 - Bioinformatics and Computational Biology I (3 credits)

BINF 402 - Bioinformatics and Computational Biology II (3 credits)

BINF 403 - Bioinformatics and Computational Biology Lab I (1 credit)

BINF 404 - Bioinformatics and Computational Biology Lab II (1 credit)

BINF 491 - Senior Research in Bioinformatics and Computational Biology I (1 credit)

BINF 492 - Senior Research in Bioinformatics and Computational Biology II (1 credit)

Sample Course Schedule

(based on full time student taking 12 credit hours per semester):

1st semester (fall) or 2nd semester (spring): IT108

3rd semester (fall): IT208

4th semester (spring): BIOL231

5th semester (fall) or 6th semester (spring): STAT344

7th semester (fall): BINF401, BINF403, BINF491

8th semester (spring): BINF402, BINF404, BINF492

Faculty

Currently there are seven BCB tenure and tenure-track full-time faculty members and three adjunct and affiliate faculty members teaching the courses in the graduate programs.

Faculty Advisor

A BCB faculty member will be assigned annually to oversee the progress of students who have selected the minor and advise those interested in pursuing such a minor. Dr. Dmitri Klimov currently serves as undergraduate advisor to Biology students interested in the current Bioinformatics minor program. This advisor will work with the Biology department to correlate changes in programs and courses that impact students.

Senior Research Projects

Although not required for the completion of the minor we will begin a senior research project program, in which individual professors in BCB will direct student research projects, from the design phase through the summarization of results and writing of a report. Research Experience for Undergraduates is an activity highly thought of by funding agencies, and benefits students by allowing them to demonstrate to employers or recruiting committees in graduate schools their capabilities and competencies.

EVALUATION OF PROGRAM EFFECTIVENESS

Student achievement in the minor and the overall quality of the program will be measured in a number of ways, including:

- Annual reviews of students' academic progress.
- Annual review of graduates' academic outcomes.
- Annual exit interviews with graduates to assess satisfaction with the program. This can be analyzed in conjunction with data provided by employers and graduate admission committees concerning the preparedness of our students for the jobs/courses they are presented with.
- Annual monitoring of rate of acceptance to minor program.
- Annual data collection regarding success in obtaining or enhancing employment.
- Annual alumni satisfaction surveys (at least 85% satisfied or very satisfied).
- Meeting enrollment targets (maintaining minimum of 12 students, beginning in the third year).

JUSTIFICATION OF PROPOSED PROGRAM

Relations to Other GMU Programs

The proposed program complements existing GMU graduate programs related to Bioinformatics.

Comparison with Other Programs in Washington, D.C. Region

The George Washington University: GWU offers a B.S. (Computer Science) with Bioinformatics Option. This program, which resides within a Department of Computer Sciences, provides a strong emphasis on IT aspects on bioinformatics, including networks and operating systems. However, in contrast to the proposed minor at GMU the GWU program does not contain special bioinformatics courses.

Johns Hopkins University: JHU offers a Master of Health Science (MHS) program in bioinformatics managed by the Departments of Molecular Microbiology and Immunology and Biostatistics. This is a premier program in bioinformatics, which provides a broad theoretical and practical introduction. However, given a graduate standing of JHU program, the minor in bioinformatics proposed by us should complement the existing curriculum at JHU.

The University of Maryland: UMBC offers a BSc in bioinformatics and computational biology, which spans a number of departments. This program provides a good background in a number of disciplines related to bioinformatics, but does not offer specific bioinformatics courses similar to BINF401 and BINF402 proposed herein.

American University: AU offers a Professional Science Master program in Biotechnology, with the emphasis on theoretical and management skills in biotechnology. This program does not directly compete with the Bioinformatics minor proposed by us because it has graduate standing and put strong emphasis on management training.

Relevance of Proposed Degree for Northern VA

The Commonwealth of Virginia has a significant interest in increasing the number of skilled workers in bioinformatics in order to attract additional biotechnology companies to Virginia. Recent examples include the American Type Culture Collection (ATCC), which moved to Prince William County in 1997, and on September 6, 2006 the Howard Hughes Medical Institute opened its Janelia Farm Research Campus, a computational biology center in Loudon County that will ultimately employ approximately 300 scientists. Such companies depend on the availability of highly skilled employees, as well as the availability of continued professional education opportunities at all levels.

The Fairfax County Economic Development Authority (FCEDA) opened a 7,500-square foot biotechnology incubator, called BioAccelerator², in January 2003, with the goal of accelerating the growth of start-up companies involved in biosciences, including bioinformatics. The incubator will be a catalyst for growth of the bioinformatics and biotechnology industry in Fairfax County and Northern Virginia and further diversify the Fairfax County economic base.

Finally, the proposed minor will support the steady growth of the biotechnology industry in the Washington, D.C. region, and nationally³ as well.

Summary of Projected Enrollments in Proposed program

State Council of Higher Education for Virginia

Instructions:

Enter the appropriate dates at the top of each column.

Provide fall headcount enrollment (HDCT) and annual full-time equivalent student (FTE) enrollment. Round the FTE to the nearest whole number.

Note: Target Year refers to the year the institution anticipates the program will have achieved full enrollment. The Council will review for possible closure any program that has not met SCHEV's productivity standards within five years of the date of first program graduates. Programs that do not anticipate meeting SCHEV productivity standards should not be proposed.

Projected enrollment:

Year 1		Year 2		Year 3		Year 4		Target Year		
2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		
HDCT	FTES	HDCT	FTES	HDCT	FTES	HDCT	FTES	HDCT	FTES	GRAD
<u>6</u>	<u>4</u>	<u>8</u>	<u>6</u>	<u>10</u>	<u>8</u>	<u>12</u>	<u>10</u>	<u>12</u>	<u>10</u>	<u>10</u>

The assumptions used in determining the above figures are as follows:

² Fairfax County Economic Development Authority "Fairfax County EDA dedicates BioAccelerator to grow new bioscience companies" (January 24, 2003). (<http://www.fairfaxcountyeda.org/03releases/jan24-03.htm>)

³ Joseph Cortright and Heike Mayer, "Signs of Life: The Growth of Biotechnology Centers in the United States" The Brookings Institution Center on Urban and Metropolitan Policy, 2002
<http://www.brookings.edu/es/urban/publications/biotech.pdf>

95% rate of retention

80% full-time students and 20% part-time students

full-time students take 12 credit hours per semester

part-time students take an average of 4.5 credit hours per semester

full-time students graduate in four years, but a certain number will have the proper background in the first year. Not all students who take the course/lab series will choose a bioinformatics minor, as Biochemistry has already expressed an interest in having their students take it as a useful elective.

Definitions:

HDCT—fall headcount enrollment

FTES—annual full-time equated student enrollment

GRADS—annual number of graduates of the proposed program

CONCLUSION

Establishment of the proposed Bioinformatics minor undergraduate degree program would be advantageous to George Mason University, the Commonwealth of Virginia, and to the Washington, D.C. region. This program represents an extension of current resources devoted to the M.S. and Ph.D. programs in Bioinformatics as well as majors in the Biology and Information Technology departments. It is expected to provide courses needed for the Biology concentration in the Data Sciences undergraduate major. As such, George Mason has the resources in place to support this innovative, interdisciplinary degree, including faculty, library facilities, computer labs, networking, and general technology support. The proposed degree program is unique in Virginia and would expand the range of academic offerings in Bioinformatics at GMU.

The minor is expected to attract students enrolled in undergraduate programs in biology, computer science, engineering, information technology, and biochemistry. Graduates having the proposed minor will have opportunities to seek or continue employment in the biotechnology field in the Northern Virginia region. As the only school in the state to offer this innovative degree, George Mason is well positioned to enjoy significant student demand and to prepare students for challenging and exciting careers.

PROJECTED RESOURCE NEEDS

Institution: George Mason University
Program Title: Minor in Bioinformatics

Summary

The available program resources include seven BCB full time faculty members, and three 1st and 2nd year Bioinformatics Ph.D. students to help as GRAs in the core BINF classes. Currently BCB has one designated full-time classified person working at the administrative level and assisting with the existing BCB academic programs. There will be no anticipated financial aid available to the students at the departmental level. The two libraries available for the students are the Mercer Library on the Prince William campus and the Fenwick Library on the Fairfax campus. The students are expected to use BCB designated classrooms already being utilized for existing classes. On the Prince William campus, there are two computer labs dedicated to students taking BINF classes. Other resources that will be available include BCB conference rooms for committee discussions pertaining to student projects and research.

Infrastructure

The proposed program will use existing classrooms, libraries, laboratories and computational resources, on the Fairfax and PW Campuses.

Course Design

The proposed program requires course design for the 2-semester lecture series and accompanying labs. The related proposals for syllabi have already been submitted to the COS curriculum council. The proposed syllabi have been attached to the end of this document for the sake of completeness, but as of Nov 27th, 2006 have not been approved by the curriculum committee.

Teaching Resources

At the anticipated level of enrollment, the proposed program is not expected to require additional teaching resources, since staff effort currently devoted to the M.S and Ph.D. programs in Bioinformatics will be available to support the proposed minor, barring unexpected levels of interest.

PROJECTED RESOURCE NEEDS FOR PROPOSED PROGRAM

Part A: Answer the following questions about general budget information.

Has or will the institution submit an addendum budget request to cover one-time costs? Yes_____ No X

Has or will the institution submit an addendum budget request to cover operating costs? Yes_____ No X

Will there be any operating budget requests for this program that would exceed normal operating budget guidelines (for example, unusual faculty mix, faculty salaries, or resources) Yes_____ No X

Will each type of space for the proposed program be within projected guidelines? Yes X No_____

Will a capital outlay request in support of this program be forthcoming? Yes X No_____

Part B: Fill in the number of FTE positions needed for the program.

	Program initiation year 2007-2008		Total expected by target enrollment year 2011-2012	
	On-going and reallocated	Added (New)	On-going and reallocated	Added (New)
Full-time faculty	7	0	10	0
Part-time faculty	3	0	4	0
Graduate Assistants	2	0	3	0
Classified Positions	1	0	2	0
TOTAL	13	0	19	0

Part C: Estimated \$\$ resources to initiate and operate the program. *

	Program initiation year 2007-2008	Total expected by target enrollment year 2011-2012
Full-time faculty	0	0
Part-time faculty	0	0
Graduate assistants	0	0
Classified positions	0	0
Fringe benefits	0	0
Total personnel costs	0	0
Targeted financial aid	0	0
Equipment	0	0
Library	0	0
Telecommunication costs	0	0
Other resource needs (specify)	0	0
TOTAL	0	0

* There are no expected incremental costs associated with this proposed minor. All personnel are currently in place and will be utilized at same capacity.

CERTIFICATION STATEMENTS

The institution will require additional state funding to initiate and sustain this program.

_____ Yes

Signature of Chief Academic Officer



 X No

Signature of Chief Academic Officer

If “no,” please complete Items 1, 2, and 3 below.

1. Estimated \$\$ and funding source to initiate and operate the program.

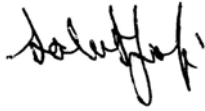
Funding Source	Program initiation year 2007-2008	Target enrollment year 2011-2012
Reallocation within the department or school (Note below the impact this will have within the school or department.)	Utilizing already existing resources. FTE for existing classes should increase accordingly.	Incremental increase in class size due to anticipate student population growth. No new sections or classes are expected.
Reallocation within the institution (Note below the impact this will have within the school or department.)	None	None
Other funding sources (Please specify and note if these are currently available or anticipated.)	None	None

1. Statement of Impact/Other Funding Sources.

The increased student enrollment anticipated by to this proposed program will create a more efficient use of departmental and institutional resources. The student growth is expected to increase FTEs counts, while the current staff resources exist to handle the student issues and recruitment efforts.

3. Secondary Certification.

If resources are reallocated from another unit to support this proposal, the institution will not subsequently request additional state funding to restore those resources for their original purpose.



 X Agree _____
Signature of Chief Academic Officer

 Disagree _____
Signature of Chief Academic Officer

Appendices

Appendix A - Catalogue Description of New Courses

BINF 401 (3:3:0) 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.

BINF402 (3:3:0) 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.

BINF 403 (1:0: 0) Catalog Description: Bioinformatics labs will complement the topics are presented in the BINF 401 lecture: 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.

BINF 404 (1:0:0) Catalog Description: Laboratories will introduce students to research bioinformatics tools relevant to lecture topics such as: the correspondence of measured fragments to parent biomolecules, inference methods for gene and protein networks, predicting system outputs given specified inputs.

BINF 491 (1:1:3) Catalog Description: Senior Research in Bioinformatics I. Prerequisites: the bioinformatics minor core classes and a previous passing grade or concurrent enrollment in BINF 401. An experimental design with materials and methods is completed under the guidance of a bioinformatics department faculty member. An oral progress report with a poster at the fall semester Student Research Day is required.

BINF 492 (1:1:3) Catalog Description: Senior Research in Bioinformatics II. Prerequisites: the student must be a Biology major with at least 90 credits and have the permission of the departmental research committee. An experimental design with materials and methods is completed under the guidance of a bioinformatics department faculty member. An oral progress report with a poster at the fall semester Student Research Day is required.

Appendix B - Qualifications of Faculty

Dept. of Bioinformatics and Computational Biology

The following faculty members are actively participating in the BCB Master's and Doctoral programs in Bioinformatics. As such, they are fully qualified to advise and instruct undergraduate level students.

John Grefenstette, Ph.D., Professor, Bioinformatics and Computational Biology. Dr. Grefenstette's research focuses on the application of artificial intelligence methods, especially evolutionary algorithms, to problems in bioinformatics and computational biology. He has published over 50 research papers, and is currently funded by the Office of Naval Research and the USDA. Dr. Grefenstette has taught graduate courses on machine learning, biological sequence analysis, and the analysis of gene expression data.
Web site: <http://www.scs-pw.gmu.edu/people/faculty/cvs/gref-cv.html>

Saleet Jafri, Ph.D., Professor, Bioinformatics and Computational Biology. Research interests: cellular signalling, cardiac physiology, protein structure, high-performance computing
Web site: <http://binf.gmu.edu/jafri/>

Jason M. Kinser, D.Sc., Associate Professor. Research interests include image and signal processing, pulse image processing, image signatures, associative memories, and applications in bioinformatics. Graduate level teaching has included biological sequencing, signal and image processing, and computer languages.
Web site: <http://ib3.gmu.edu/kinser/Public/JMK-CV.html>

Dmitri Klimov, Ph.D., Assistant Professor, Bioinformatics and Computational Biology. Research interests: Computational study of protein aggregation and mechanical unfolding of proteins.
Web site: <http://binf.gmu.edu/dklimov/>

Donald Seto, Ph.D., Associate Professor, Microbial Genomics and Diversity, Bioinformatics. Research interests: Comparative genomics; comparative virology; tools for annotation; tools for data mining; cancer genomics; Gene expression.
Web site: <http://www.scs-pw.gmu.edu/people/faculty/dseto.html>

Iosif Vaisman, Ph.D., Associate Professor, Bioinformatics and Computational Biology. Dr. Vaisman's research focuses on developing computational methods for protein structure analysis and classification. Computational geometry algorithms are applied to identify and characterize sequence-structure patterns in known protein structures. Information derived from these studies is used for protein structure alignment, comparison, and prediction.
Web site: <http://www.scs-pw.gmu.edu/vaisman/vaisman.html>

Jennifer Weller, Ph.D., Associate Professor, Bioinformatics and Computational Biology.
Research interests: Systematic investigation and evaluation of the behavior of the complex mixture of probes and targets on microarrays.
Web site: <http://binf.gmu.edu/weller/>

Non-full time BCB faculty with relevant backgrounds:

Jeffrey Solka, Ph.D., Contract Assistant Professor. Research interests: computational statistics. His day job probably will not permit the teaching of courses during the day at Fairfax.

James Willett, Ph.D., Professor of Biology, Applied Cell Biology and Genetics. Dr. Willett is developing a rapid assay for metabolic system effectors using the nematode *Caenorhabditis elegans*. Recording responses of biochemical pathways to physiologic state modifiers provides a means of studying the underlying mechanisms responsible for these changes. This is especially valuable in elucidating the mechanisms of action of neurotoxicants, and dietary supplements purported to have life extending properties. Willett's interest in this approach arose as a result of his studies of alterations in signaling arrays in nematodes as a function of age.
Web site: <http://www.scs-pw.gmu.edu/people/faculty/willett.html>

Appendix C Proposed Syllabi

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:

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	Mount Chapt 5

	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.	
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, 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	Pevzner Chapt 9
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

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:

BINF 402 Syllabus

Week	subject	Reading
1	Topic I: 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	Selected Chapters from D. Frankel and B. Smit

	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.	"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, measurement summaries, a variety of data and pathway representations and related information on the pathways previously introduced.	Chapter 3 from "Pathway Analysis and Optimization in Metabolic Engineering" by 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

3. "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

1. COURSE NUMBER AND TITLE:

BINF403 (1 credit) Bioinformatics and Computational Biology Lab I.

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

Corequisites: BINF 401

Catalog Description: Bioinformatics labs will complement the topics are presented in the BINF 401 lecture: 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 expose students to how bioinformatics and computational biology hypotheses are framed and how experiments are designed to test those hypotheses while exploring the data and tools commonly used by research scientists in the field. As with any other science, practical experience with the tools and personal experience examining the data are essential to providing the student with a true understanding of the theory. In addition, exposure to the common tools of the trade will better fit our graduates to compete for positions at biotechnology and pharmaceutical companies.

Course Necessity: Bioinformatics and computational biology are rapidly expanding research areas in both academic and commercial settings. The majority of life scientists are now required to understand the tools used to model biomolecules but the breadth of the field prevents a specialist in another discipline from having familiarity with more than the essentials for his own research. This course will allow students to experience the range of possibilities and make informed choices when faced with deciding on the best tools to achieve research or development goals. There is no existing undergraduate laboratory course at GMU that covers these research methods in a context that links the field effectively.

Course Relationship to Existing Programs: This course is proposed as the laboratory component matching the first of a two-semester lecture series intended to 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 while some of the fundamental methods are in common the application is quite different, thus there is 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 BINF 401 Syllabus

Week	subject	Databases, tools introduced
1	Topic I: Protein sequence and structure databases	PDB, PIR and SwissProt data models, data types and record formats will be introduced – how to download, view and interpret the available data.
2	Protein folding tools comparing de novo and other methods	Folding@ home project, the PFD database, the Structure Predictor Meta Server
3	Comparative structure frameworks for two-and three-dimensional protein structure comparison	Delauney tessellation as an exemplar method
4	Topic II: Nucleic acid sequence and structure databases The NCBI and EMBL sequence databaes	The NCBI and EMBL sequence databases, their data models and recored formats will be introduced, how to query for and download a target sequecne
5	Structural RNAs, energetics and phylogeny applied to conserved sequences and structures	RiboDB, the representation of structure in SMILE strings; mfold and tools for converting strings to 2-D structures
6	Sequence comparison methods will be discussed as well as some common evolutionary models used in sequence comparisons.	BLAST comparisons; motif finding tools such as PFAM: pattern-finding algorithms – limitations and assumptions, demonstrated with hands-on examples.
7	midterm	
8	Topic III: Gene structure prediction in prokaryotes and eukaryotes	Complex and fuzzy pattern-matching algorithms: work with hands-on examples
9	Prokaryotic genomes and operons.	Self-organizing maps and RescueNet; REGANOR
10	Eukaryotic genomes, introns, untranslated regions and different isoforms.	Hidden Markov Models and MHHgene; GenScan, EuGen'hom
11	Topic IV: Images of Biological Systems Images as Data vs images as summaries - For specific types of biomedical images the limits of resolution, precision and accuracy will be	Exercises will include the opening of a number of types of images, understanding headers and source directions.

	discussed.	
12	Diagnostic images are annotated from different points of view: the image modality (radiograph, MRI, etc) and its acquisition parameters (including time), the sample source and anatomical body part depicted by the image, related non-image data	Semantic Web standards; Flickr and the Dublin Core
13	Methods of image feature analysis	Fourier transforms and spectral decomposition as examples of techniques, presented as case studies
14	Final	

4. There are no comprehensive laboratory texts in this field, this will rely on expert notes from the instructors.

1. COURSE NUMBER AND TITLE:

BINF404 (1 credit) Bioinformatics and Computational Biology Lab II.

Prerequisites: BINF 401,403

Corequisites: BINF 402

Catalog Description: Laboratories will introduce students to research bioinformatics tools relevant to lecture topics such as: the correspondence of measured fragments to parent biomolecules, inference methods for gene and protein networks, predicting system outputs given specified inputs.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to give students hands-on experience with current tools used in bioinformatics research and give them an understanding of the underlying assumption, limitations and appropriate use of the tools. Practical experience applying the tools to both provided and student-acquired datasets will ensure that students truly understand the theory. Active practice with the accepted standard tools of the trade will better fit our graduates to compete for positions at biotechnology and pharmaceutical companies.

Course Necessity: Bioinformatics and computational biology are rapidly expanding research areas in both academic and commercial settings. The majority of life scientists are now required to understand the tools used to model biomolecules but the breadth of the field prevents a specialist in another discipline from having familiarity with more than the essentials for his own research. This course will allow students to experience the range of possibilities and make informed choices when faced with deciding on the best tools to achieve research or development goals. There is no existing undergraduate laboratory course at GMU that covers these research methods in a context that links the field effectively.

Course Relationship to Existing Programs: This course is proposed as the laboratory component matching the second of a two-semester lecture series intended to 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 while some of the fundamental methods are in common the application is quite different, thus there is 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:
BINF 402 Syllabus

Week	subject	Tools and tasks
1	Topic I: Genomics Platforms Sequence data	Interpreting DNA electropherograms; Phred, Phrap and Consed
2	Microarray data	Design tools (Picky), analysis tools (DRAGON)
3	Proteomics Data	Mass spec data and its interpretation, mapping to sequences; the ProteomeCommons
4	Topic 2: Inferring Biological Pathways Representing Genetic data	Linkage analysis and regulatory networks; LD Mapping, VitaPad and GeneVis
5	Representing Enzymatic pathways	Using EcoCyc and KEGG; PathwayTools
6	Representing Chemical reactions and the metabolome	Metabolome and BioPathways databases and the CORINA and ROTATE tools
7	midterm	
8	Topic 3: Simulation Methods for Dynamics of BioMolecules The basics of molecular dynamics	CHARMM and NAMD examples
9	How to obtain and interpret results from molecular dynamics simulations	Exercise involves setting up, running and interpreting a MD simulation using
10	The foundations of the Monte Carlo algorithm	Examples of MC simulations for biomolecular systems
11	Topic 4: Systems Biology Core metabolic and Signalling pathways	An exercise in diagramming the selected pathways for the targeted biomolecule using Gepasi
12	Primary and secondary pathway databases records	KEGG and EcoCyc records
13	Pathway representation	Using the Ingenuity package
14	Pathway dynamics	Using the Gepasi and Copasi packages

Required text: comprehensive lab texts do not exist for this level of this field, the notes and expertise of the instructors will guide the content.

1. COURSE NUMBER AND TITLE:

BINF491 (1 credit) Senior Research in Bioinformatics and Computational Biology I.

Prerequisites:

Corequisites: BINF 401

Catalog Description: BINF 491 Senior Research in Bioinformatics I (1,1,3) Prerequisites: the bioinformatics minor core classes and a previous passing grade or concurrent enrollment in BINF 401. An experimental design with materials and methods is completed under the guidance of a bioinformatics department faculty member. An oral progress report with a poster at the Fall semester Student Research Day is required.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to give students a mentored research experience in the research area of particular interest to a BCB faculty member. The student will learn to identify an important question, frame a hypothesis and devise an experimental plan, investigate the current literature, obtain data sets and identify the necessary tools to carry out the research. The student will then defend this plan of work by designing a poster and defending it to students and faculty at the end of semester BCB department Student Research Day.

Course Necessity: Bioinformatics and computational biology research require an unusual mixture of using modeling tools and large volumes of real data. However, unlike in many of the biological sciences, the students do not typically produce the data and the process of obtaining and vetting data produced at a number of disparate sites is challenging. In addition it is often difficult for students to understand how to formulate a problem such that they are really testing a hypothesis rather than running an algorithm through a number of parameter values. To qualify as well-trained scientists, our students must be able to not only critically evaluate the published research but be able to design experiments that will hold up to critical evaluation from their peers.

Course Relationship to Existing Programs: This course is proposed as an in-depth research experience for students who want to delve into a problem as an active, if junior, scientist. Research experience for undergraduates is a highly rated activity by many granting agencies since when well done it tends to draw students into post-graduate training and research careers. The mentoring aspect is known to be essential to the development of a passion for research. This will be the course that really rewards the most excellent of the students in the minor program, and the level of interest will indicate whether the undergraduate degree should be expanded from a minor to a major eventually. The department members currently have extensive experience directing Masters level students in projects and theses so this will be an extension of existing practices rather than a break with them. There are no programs at GMU outside of this department and course that offer this experience to undergraduates in this research area.

Course Relationship to Existing Courses: There are no undergraduate senior research offerings in this area in other departments.

3. SCHEDULING AND PROPOSED INSTRUCTORS:

Semester of Initial Offering: Fall 2007

Proposed instructors: Available full-time, adjunct and affiliate faculty members of the Bioinformatics and Computational Biology department.

TENTATIVE SYLLABUS: a week by week syllabus cannot be detailed since each professor will have a different field and the specific area of emphasis will change from year to year. The responsibilities of the faculty member are to meet with the student once a week (at least) for one hour, to provide introductory material in the area of the research field of focus during the first meeting along with 3-4 open questions the faculty mentor has some confidence the student can make progress on in a term, and a list of any software tools and their documentation that the student will need to become familiar with. The student should expect to spend 2-4 hours per week reading and 2-4 hours per week actively doing experiments, although the proportion of time spent on each activity will almost certainly vary week by week through the semester. The goal of the first semester is to have a concrete research plan that the student understands well enough to be able to defend in an open forum.

1. COURSE NUMBER AND TITLE:

BINF491 (1 credit) Senior Research in Bioinformatics and Computational Biology I.

Prerequisites: A Biology major with at least 90 credits.

Corequisites: the permission of the departmental research committee.

Catalog Description: BINF 491 Senior Research in Bioinformatics I (1,1,3). Prerequisites: the student must be a Biology major with at least 90 credits and have the permission of the departmental research committee. An experimental design with materials and methods is completed under the guidance of a bioinformatics department faculty member. An oral progress report with a poster at the fall semester Student Research Day is required.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to give students a mentored research experience in the research area of particular interest to a BCB faculty member. The student will learn to identify an important question, frame a hypothesis and devise an experimental plan, investigate the current literature, obtain data sets and identify the necessary tools to carry out the research. The student will then defend this plan of work by designing a poster and defending it to students and faculty at the end of semester BCB department Student Research Day.

Course Necessity: Bioinformatics and computational biology research require an unusual mixture of using modeling tools and large volumes of real data. However, unlike in many of the biological sciences, the students do not typically produce the data and the process of obtaining and vetting data produced at a number of disparate sites is challenging. In addition it is often difficult for students to understand how to formulate a problem such that they are really testing a hypothesis rather than running an algorithm through a number of parameter values. To qualify as well-trained scientists, our students must be able to not only critically evaluate the published research but be able to design experiments that will hold up to critical evaluation from their peers.

Course Relationship to Existing Programs: This course is proposed as an in-depth research experience for students who want to delve into a problem as an active, if junior, scientist. Research experience for undergraduates is a highly rated activity by many granting agencies since when well done it tends to draw students into post-graduate training and research careers. The mentoring aspect is known to be essential to the development of a passion for research. This will be the course that really rewards the most excellent of the students in the minor program, and the level of interest will indicate whether the undergraduate degree should be expanded from a minor to a major eventually. The department members currently have extensive experience directing Masters level students in projects and theses so this will be an extension of existing practices rather than a break with them. There are no programs at GMU outside of this department and course that offer this experience to undergraduates in this research area.

Course Relationship to Existing Courses: There are no undergraduate senior research offerings in this area in other departments.

3. SCHEDULING AND PROPOSED INSTRUCTORS:

Semester of Initial Offering: Fall 2007

Proposed instructors: Available full-time, adjunct and affiliate faculty members of the Bioinformatics and Computational Biology department.

TENTATIVE SYLLABUS: a week by week syllabus cannot be detailed since each professor will have a different field and the specific area of emphasis will change from year to year. The responsibilities of the faculty member are to meet with the student once a week (at least) for one hour, to provide introductory material in the area of the research field of focus during the first meeting along with 3-4 open questions the faculty mentor has some confidence the student can make progress on in a term, and a list of any software tools and their documentation that the student will need to become familiar with. The student should expect to spend 2-4 hours per week reading and 2-4 hours per week actively doing experiments, although the proportion of time spent on each activity will almost certainly vary week by week through the semester. The goal of the first semester is to have a concrete research plan that the student understands well enough to be able to defend in an open forum.

1. COURSE NUMBER AND TITLE:

BINF492 (1 credit) Senior Research in Bioinformatics and Computational Biology II.

Prerequisites: BINF 491

Corequisites: permission of the instructor

Catalog Description: BINF 492 Senior Research in Bioinformatics II (1,1,3) Prerequisites: BINF 491 and permission of the instructor. The research project designed the previous semester (in BINF 491) is completed under the guidance of a faculty mentor. A written report in approved format is required for course completion.

2. COURSE JUSTIFICATION:

Course objectives: This course is designed to allow students to complete an independent research project under the guidance of a faculty mentor, having first spent a semester learning how to formulate the hypothesis and collect the appropriate data set and tools. In addition to performing the research the student will learn to summarize results and present a discussion as to how the results support or contradict the initial hypothesis and what additional experiments might be suggested. The student will learn to write the experiment in the form of a peer-reviewed publication, which will constitute part of the work to be judged.

Course Necessity: To qualify as well-trained scientists an individual must be able to not only carry out experiments but learn to summarize the results succinctly and clearly and communicate these results to a critical peer-level audience. Communication skills, both verbal and written, are known to have an even greater impact on the career of a scientist than technical skills, and paradoxically are given the least attention in most undergraduate and graduate science education programs. Students who have had experience and a focused critic helping them improve oral and written research will have been provided with a very competitive edge in achieving success in their careers.

Course Relationship to Existing Programs: This course provides a student with the experience of carrying out an experiment designed by the student with the help of a faculty mentor, where there is depth of focus to the work. Thus it complements the senior-level Bioinformatics Lecture and Lab courses which are designed to be broad and provide an understanding of how a number of research areas integrate, but therefore cannot be deep in any one area. By producing a well-written final paper the student will also have a document to submit with graduate school or professional applications demonstrating his ability to acquire skills, and communicate effectively. This focus is not provided by any other courses in the department or by other departments. The department members currently have extensive experience directing Masters level students in projects and theses so this will be an extension of existing practices rather than a break with them.

Course Relationship to Existing Courses: There are no undergraduate senior research offerings in this area.

3. SCHEDULING AND PROPOSED INSTRUCTORS:

Semester of Initial Offering: Spring 2008

Proposed instructors: Available faculty, adjunct and affiliate faculty members of the Bioinformatics and Computational Biology department.

TENTATIVE SYLLABUS: a week by week syllabus cannot be detailed since each professor will have a different field and the specific area of emphasis will change from year to year. The responsibilities of the faculty member are to meet with the student once a week (at least) for one hour in order to survey progress and

help the student overcome roadblocks or choose strategies, to guide the student in completing the work in a timely fashion, provide models of good data summarization techniques for both visualization and discussion, and to be an active and engaged editor of the final report. The student should expect to spend 6-8 hours a week actively executing the research, or in the later phases writing the research report. The goal of the second semester is to have completed the work proposed in the research plan put together in the first semester and to have provided a coherent journal-format ready paper based on the research that the student is able to defend to a peer community.