LONG SIGNATURE SHEET

UNC CHARLOTTE

Proposal Number: __BINF 2-03-12____

Proposal Title: **Revisions of Graduate Curriculum for the Department of Bioinformatics and Genomics**

Originating Department: _____Bioinformatics and Genomics_____

TYPE OF PROPOSAL: UNDERGRADUATE_____ GRADUATE__x___ UNDERGRADUATE & GRADUATE____
(Separate proposals sent to UCCC and Grad. Council)

DATE RECEIVED	DATE CONSIDERED	DATE FORWARDED	ACTION	SIGNATURES
			Approved	DEPARTMENT CHAIR [print name here] LARRY
			Approved	COLLEGE CURRICULUM COMMITTEE CHAIR [print name here] ANTHONY
			Approved	COLLEGE FACULTY CHAIR (if applicable) [print name here] BARRY Wilkenson
			Approved	COLLEGE DEAN [print name here] DEAN Yi Deng
			Approved	GENERAL EDUCATION (for General Education courses) [print name here]
			Approved	UNDERGRADUATE COURSE & CURRICULUM COMMITTEE CHAIR (for undergraduate courses) N/A
2-28-12	3-13-12	5-2-12	*Approved*	GRADUATE COUNCIL CHAIR (for graduate courses) Rob Roy McGregor
			Approved	FACULTY GOVERNANCE ASSISTANT (Faculty Council approval on Consent Calendar)
				FACULTY EXECUTIVE COMMITTEE (if decision is appealed)

Revised 08/01/11
OAA/lz

University of North Carolina at Charlotte BINF 2-03-12

Revised Graduate Curriculum

Course and Curriculum Proposal from: Department of Bioinformatics and Genomics.

"Revisions of Graduate Curriculum for the Department of Bioinformatics and Genomics"

A. PROPOSAL SUMMARY AND CATALOG COPY

1. Summary

The Department of Bioinformatics and Genomics within the College of Computing and Informatics seeks to modify its graduate curriculum. The proposed changes primarily affect program requirements and course offerings for the Professional Science Masters (PSM) in Bioinformatics, the Graduate Certificate in Bioinformatics Applications, and the Graduate Certificate in Bioinformatics Technology. These changes to the graduate curriculum are required to ensure that our students graduate with a common skill set, which includes current core technological competencies in our rapidly changing field. In conjunction with updating the program requirements, we propose to add four courses that will enhance the current offerings for students enrolled in our PSM and Ph.D. programs.

a. We propose to create the following new courses:

- BINF 6152 – Program and Professional Orientation
- BINF 6153 – Career Development
- BINF 6318/BINF 8318 – Computational Proteomics and Metabolomics
- BINF 6382/BINF 8382 – Accelerated Bioinformatics Programming

b. We propose to modify the catalog copy of the following courses:

- BINF 6151/GRAD 6151 – Professional Communication
- BINF 6203/BINF 8203/ITSC 8203 – Genomics
- BINF 6111/BINF 8111/ITSC 8111 – Bioinformatics Programming I
- BINF 6112/BINF 8112/ITSC 8112 – Bioinformatics Programming II
- BINF 6380/BINF 8380/ITSC 8380 – Bioinformatics Programming III (changed title and catalog copy)
- We will also remove ITSC course numbers from all courses; these were placeholder numbers created while BINF was still a track within ITSC, and are no longer needed.

c. We propose to change the core requirements of the PSM in Bioinformatics:

- The total number of required credit hours will increase to 40.
- All PSM students will be required to enroll in BINF 6152 – Program and Professional Orientation (1cr), BINF 6151 – Professional Communications (1cr) and BINF 6153 – Career Development (1cr). These courses, taken together, will provide ongoing support for PSM in Bioinformatics students to learn to recognize and use key resources and networks specific to their field, and to develop a professional self-presentation that will help them transition to jobs in business and industry environments.
- All PSM students will now be required to take a common core of seven BINF courses. Depending on their undergraduate training, students will enroll in either BINF 6100 – Biological Basis of Bioinformatics

or BINF 6111 – Bioinformatics Programming I. Concurrently with and subsequently to these courses, all PSM students will enroll in BINF 6101 – Energy and Interaction in Biological Modeling, BINF 6111 – Bioinformatics Programming II, BINF 6200 – Statistics for Bioinformatics, BINF 6201 – Molecular Sequence Analysis, BINF 6203 – Genomics, and BINF 6211 – Design and Implementation of Bioinformatics Databases.

The remaining requirements of the PSM in Bioinformatics, including the PLUS Elective, internship requirement, and advanced elective requirements, will remain unchanged, resulting in a requirement of 40 total credit hours, The curriculum as modified can be completed by a full-time student in two years.

d. We propose to change the core curriculum of the Graduate Certificate in Bioinformatics Applications

All Bioinformatics Applications certificate students will now be required to take a common core of three BINF courses. All students will enroll in BINF 6200 – Statistics for Bioinformatics, BINF 6201 – Molecular Sequence Analysis, and BINF 6203 – Genomics, and will choose as their fourth course either BINF 6350 – Biotechnology and Genomics Laboratory, or BINF 6211 – Design and Implementation of Bioinformatics Databases.

e. We propose to change the core curriculum of the Graduate Certificate in Bioinformatics Technology

All Bioinformatics Technology certificate students will now be required to take a common core of four BINF courses. Depending on their undergraduate training, students will enroll in either BINF 6100 – Biological Basis of Bioinformatics or BINF 6111 – Bioinformatics Programming I. Concurrently with and subsequently to these courses, all students will enroll in BINF 6112 – Bioinformatics Programming II, BINF 6200 – Statistics for Bioinformatics, and BINF 6203 – Genomics, and will choose as their fifth course either BINF 6201 – Molecular Sequence Analysis or BINF 6211 – Design and Implementation of Bioinformatics Databases.

2. Proposed Catalog Copy

PROFESSIONAL SCIENCE MASTER'S IN BIOINFORMATICS

Additional Admission Requirements

In addition to the general requirements for admission to the Graduate School, the following are required for study toward the Professional Science Masters (PSM) in Bioinformatics:

Under most circumstances, students admitted to the program will have:

1) A baccalaureate degree from an accredited college or university in Biology, Biochemistry, Chemistry, Physics, Mathematics, Statistics, Computer Science, or another related field that provides a sound background in life sciences, computing, or both.
2) A minimum undergraduate GPA of 3.0 (4.0 scale) and 3.0 in the major.
3) A minimum combined score of 1000 on the verbal and quantitative portions of the GRE, and acceptable scores on the analytical and discipline-specific sections of the GRE.
4) A combined TOEFL score of 220 (computer-based), 557 (paper-based), or 83 (Internet-based) is required if the previous degree was from a country where English is not the common language.
5) Positive letters of recommendation.

Degree Requirements

The Professional Science Masters (PSM) in Bioinformatics degree requires a minimum of 40 graduate credit hours, and a minimum of 36 credit hours of formal coursework. A minimum of 24 credit hours presented toward a PSM in Bioinformatics must be from courses numbered 6000 or higher. A maximum of 6 hours of graduate credit may be transferred from other institutions.

Total Hours Required

The program requires 40 post-baccalaureate credit hours. Because of the interdisciplinary nature of this program, which is designed to provide students with a common graduate experience during their professional preparation for the PSM in Bioinformatics degree, all students will be required to take a general curriculum that includes a two-year sequence of courses as described below:

Core Requirements

a) Gateway Course

The **Gateway** courses are intensive graduate-level courses designed to provide accelerated training in a second discipline that complements the student's undergraduate training. Students entering the program are expected to have achieved proficiency in either Biological Sciences or Computing, and to take the **Gateway** course that is appropriate for their background. For students entering from computing backgrounds, BINF 6100 (Biological Basis of Bioinformatics), should be chosen, while students entering from biological science backgrounds should choose BINF 6111 (Bioinformatics Programming I).

b) Core Bioinformatics Courses

Gateway courses prepare students for the required **Core** courses. All students must take BINF 6101 (Energy and Interaction in Biological Modeling, BINF 6112 (Bioinformatics Programming II), BINF 6200 (Statistics for Bioinformatics), BINF 6201 (Molecular Sequence Analysis), BINF 6203 (Genomics), and BINF 6211 (Design and Implementation of Bioinformatics Databases). A student who has previously taken a course with a syllabus that closely follows one of the course courses may test out of the core requirement by passing a written exam, and may then substitute an advanced elective for the required core course.

c) Professional Preparation Requirement

Students are required to take at least 6 credit hours of electives designed to prepare them to function effectively and ethically in a professional environment. All Bioinformatics PSM students are required to enroll in BINF 6152 (Program and Professional Orientation) (1cr), BINF 6151 (Professional Communications) (1cr) and BINF 6153 (Career Development) (1cr). The remaining PLUS credits may be chosen from a list of recommended electives, which include BINF 5171 (Business of Biotechnology), BINF 5191 (Biotechnology and the Law), PHIL 6050 (Research Ethics), and ITIS 6362 (Information Technology Ethics, Policy, and Security). Additional elective choices that may fulfill this requirement can be identified by the student and the PSM Advisory Committee.

d) The remaining credit hours of formal coursework can be completed in elective coursework. The PSM Advisory Committee will review the student's plan of study each semester.

Bioinformatics Electives

Any courses with BINF numbers, with the exception of **Fundamentals** courses, which require approval, are open to PSM students seeking to complete their coursework requirements.

Recommended Electives Offered By Other Departments

A wide range of courses in Biology, Chemistry, Computer Science, Software and Information Systems, and other departments may be appropriate electives for PSM in Bioinformatics students. As course offerings change frequently, the Bioinformatics Program maintains a list of current recommended electives, which can be found online at bioinformatics.uncc.edu.

Elective Clusters

Students are encouraged to choose their electives with a topical focus that reflects their scientific and career interests. Courses from one of the following recommended clusters of advanced electives can be selected, or the student can design his or her own elective focus with the approval of the PSM Advisory Committee.

Genomic Biology Cluster

BINF 6205 Computational Molecular Evolution

BINF 6305 Biotechnology and Genomics Laboratory
BINF 6310 Advanced Statistics for Genomics
BINF 6318 Computational Proteomics and Metabolomics

Modeling and Simulation Cluster
BINF 6202 Computational Structural Biology
BINF 6204 Mathematical Systems Biology
BINF 6210 Numerical Methods and Machine Learning in Bioinformatics
BINF 6311 Biophysical Modeling

Computing and Technology Cluster
BINF 6210 Numerical Methods and Machine Learning in Bioinformatics
BINF 6310 Advanced Statistics for Genomics
BINF 6380 Advanced Bioinformatics Programming
BINF 6382 Accelerated Bioinformatics Programming

e) Other Requirements

Bioinformatics Seminar
In addition to 33 hours formal coursework, students are required to enroll in the Bioinformatics Program seminar (BINF 6600) for at least one semester (1 credit hour) and to enroll in either an approved internal or external internship (BINF 6400) or a faculty-supervised original research project leading to a thesis (BINF 6900).

Grade Requirements
An accumulation of three C grades will result in suspension of the student's enrollment in the graduate program. If a student makes a grade of U in any course, enrollment in the program will be suspended.

Amount of Transfer Credit Accepted
A maximum of 6 credit hours of coursework from other institutions will count toward the PSM in Bioinformatics degree requirements. Only courses with grades of A or B from accredited institutions are eligible for transfer credit.

GRADUATE CERTIFICATE IN BIOINFORMATICS APPLICATIONS

The purpose of the Graduate Certificate in Bioinformatics Applications is to train individuals in the application of established bioinformatics methods for analysis of biological sequence, structure, and genomic data. The certificate requires twelve (12) credit hours of coursework. The certificate may be pursued concurrently with a related graduate degree program at UNC Charlotte or as a standalone program.

Admission Requirements

For admission into the certificate program, applicants must meet the following requirements:
1) A bachelor's degree in a life science discipline, that includes advanced coursework in molecular biology and genetics.
2) Practical experience and confidence with computers, for instance use of common web browsers, word processing, plotting, and spreadsheet applications.

Program Requirements

Students will take four courses that introduce core methods for analysis of molecular biological data:

BINF 6200 Statistics for Bioinformatics (3)
BINF 6201 Molecular Sequence Analysis (3)
BINF 6203 Genomics (3)

And one of the following:

BINF 6211 Design and Implementation of Bioinformatics Databases (3)
BINF 6350 Biotechnology and Genomics Laboratory (3)

If a student wishes to enter the program having completed coursework that is equivalent to one or more of the core requirements, the requirements may be waived at the discretion of the certificate coordinator. In this case, the required 12

credit hours may be selected from other advanced graduate courses offered by the Department of Bioinformatics and Genomics.

Transfer credit may not be applied toward this certificate.

It is suggested that students in the Graduate Certificate Program arrange formal co-mentorship by a Department of Bioinformatics and Genomics faculty member, if the student is concurrently enrolled in another thesis-based degree program on campus and intends to extend or enable their thesis research through the application of bioinformatic methods.

GRADUATE CERTIFICATE IN BIOINFORMATICS TECHNOLOGY

The purpose of the Graduate Certificate in Bioinformatics Technology is to train individuals in method development for analysis of large-scale biological data and modeling of complex biological systems, with a focus on acquiring complementary skill sets in life sciences and in programming, statistical analysis, and database development. The certificate requires fifteen (15) credit hours of coursework. The certificate may be pursued concurrently with a related graduate degree program at UNC Charlotte.

Admission Requirements

For admission into the certificate program, applicants must meet the following requirements:

1) A bachelor's degree in related field, including, but not limited to, a life science, physical science, mathematics, or computing discipline.
2) Practical experience and confidence with computers, for instance use of common web browsers, word processing, plotting, and spreadsheet applications.

Program Requirements

Students will follow one of two pathways through the program, depending on their bachelor's degree field and previous experience. The following courses make up the required core:

If the bachelor's degree is in life sciences:
BINF 6200 Statistics for Bioinformatics (3)
BINF 6110 Bioinformatics Programming I (3)
BINF 6111 Bioinformatics Programming II (3)
BINF 6203 Genomics (3)

If the bachelor's degree is in computing or mathematics:
BINF 6200 Statistics for Bioinformatics (3)
BINF 6100 Biological Basis of Bioinformatics (3)
BINF 6111 Bioinformatics Programming II (3)
BINF 6203 Genomics (3)

And one of the following courses:
BINF 6201 Molecular Sequence Analysis (3)
BINF 6211 Design and Implementation of Bioinformatics Databases (3)

If a student wishes to enter the program having completed coursework that is equivalent to the core course requirements, the core requirements may be waived at the discretion of the certificate coordinator. In this case, the required 15 coursework hours may be selected from the electives listed above, or from other advanced graduate courses offered by the Department of Bioinformatics and Genomics.

Transfer credit may not be applied toward this certificate.

It is suggested that students in the Graduate Certificate Program arrange formal co-mentorship by a Department of Bioinformatics and Genomics faculty member, if the student is concurrently enrolled in another thesis-based degree program on campus and intends to extend or enable their thesis research through the application of bioinformatic methods.

COURSES IN BIOINFORMATICS (BINF)

BINF 5171. Business of Biotechnology. (3) Prerequisite: Admission to a graduate program. Introduces students to the field of biotechnology and how biotech businesses are created and managed. Students should be able to define biotechnology and understand the difference between a biotech company and a pharmaceutical company. Additional concepts covered will include platform technology, biotechnology's history, biotechnology products and development processes, current technologies used by biotech companies today, biotechnology business fundamentals, research and development within biotech companies, exit strategies, and careers in the biotech field. *(On demand)*

BINF 5191. Biotechnology and the Law. (3) Prerequisite: Admission to a graduate program. At the intersection of biotechnology and the law, an intricate body of law is forming based on constitutional, case, regulatory and administrative law. This body of legal knowledge is interwoven with ethics, policy and public opinion. Because biotechnology impacts everything in our lives, the course will provide an overview of salient legal biotechnology topics, including but not limited to: intellectual property, innovation and approvals in agriculture, drug and diagnostic discovery, the use of human and animal subjects, criminal law and the courtroom, agriculture (from farm to fork), patient care, bioethics, and privacy. The body of law is quite complex and it is inundated with a deluge of acronyms. The course will provide a foundation to law and a resource to help students decipher laws and regulation when they are brought up in the workplace. *(On demand)*

BINF 6010. Topics in Bioinformatics. (3) Prerequisite: permission of the department. Topics in bioinformatics and genomics selected to supplement the regular course offerings. A student may register for multiple sections of the course with different topics in the same semester or in different semesters. *(On demand)*

BINF 6100. Biological Basis of Bioinformatics. (3) Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. This course provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. *(Fall)*

BINF 6101. Energy and Interaction in Biological Modeling. (3) Prerequisite: Admission to graduate standing in Bioinformatics. This course covers: (a) the major organic and inorganic chemical features of biological macromolecules; (b) the physical forces that shape biological molecules, assemblies and cells; (c) the chemical driving forces that govern living systems; (d) the molecular roles of biological macromolecules and common metabolites; (e) and the pathways of energy generation and storage. Each section of the course builds upon the relevant principles in biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. *(Spring)*

BINF 6111. Bioinformatics Programming I. (3) Prerequisite: Admission to graduate standing in Bioinformatics or permission of instructor. Introduces fundamentals of programming for bioinformatics using a high-level object-oriented language such as Java or Python. The course introduces object-oriented programming, analysis of algorithms and fundamental sequence alignment methods. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. *(Fall)*

BINF 6112. Bioinformatics Programming II. (3) Prerequisite: BINF 6111 or permission of instructor. Continuation of BINF 6111. In this second semester, students practice and refine skills learned in the first semester. New topics include: (a) programming as part of a team, using sequence analysis algorithms in realistic settings; (b) writing maintainable and re-usable code; and (c) graphical user interface development. *(Spring)*

BINF 6151. Professional Communication. (1) Cross-listed as GRAD 6151. Principles and useful techniques for effective oral presentations, poster presentations, scientific writing, use of references, and avoiding plagiarism. Students in the course critique and help revise each other's presentations and learn how to avoid common pitfalls. In addition, students learn how to properly organize and run a meeting. *(Fall)*

BINF 6152. Program and Professional Orientation. (1) Students in the course learn to identify key Bioinformatics skill sets and where they are applied in research and industry settings, join appropriate professional networks, use the major professional and research journals in the field, identify key organizations and companies driving intellectual and technology development in Bioinformatics, and achieve beginner-level proficiency with key molecular data repositories. *(Fall)*

BINF 6153. Career Development in Bioinformatics. (1) Students in the course will prepare intensively for the job search, from developing a resume, to identifying appropriate opportunities, to preparing for the interview. Students are expected to complete a final interview practicum with faculty and members of the PSM Advisory Board. *(Fall)*

BINF 6200. Statistics for Bioinformatics. (3) Introduces students to statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. *(Fall)*

BINF 6201. Molecular Sequence Analysis. (3) Prerequisite: BINF 6100 or equivalent. Introduction to bioinformatics methods that apply to molecular sequence and to biological databases online. Sequence databases, molecular sequence data formats, sequence data preparation and database submission. Local and global sequence alignment, multiple alignment, alignment scoring and alignment algorithms for protein and nucleic acids, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. *(Fall)*

BINF 6202. Computational Structural Biology. (3) Prerequisites: BINF 6101 and BINF 6201 or their equivalents. This course covers: (a) the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); (b) structural databases and software for structure visualization; (c) Structure determination and quality assessment; (d) protein structure comparison and the hierarchical nature of biomacromolecular structure classification; (e) protein structure prediction and assessment; and (f) sequence- and structure-based functional site prediction. *(Fall)*

BINF 6203. Genomics. (3) Prerequisite: BINF 6100 or equivalent. Surveys the application of high-throughput molecular biology and analytical biochemistry methods and data interpretation for those kinds of high volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern genomics technology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: genome sequencing and assembly, annotation, and comparison; genome evolution and individual variation; function prediction; gene ontologies; transcription assay design, data acquisition, and data analysis; metabolic pathways and databases and their role in genome analysis. *(Spring)*

BINF 6204. Mathematical Systems Biology. (3) Prerequisites: BINF 6200 and BINF 6210 or equivalents. Introduces basic concepts, principles and common methods used in systems biology. Emphasizes molecular networks, models and applications, and covers the following topics: (a) the structure of molecular networks; (b) network motifs, their system properties and the roles they play in biological processes; complexity and robustness of molecular networks; (c) hierarchy and modularity of molecular interaction networks; kinetic proofreading; (d) optimal gene circuit design; and (e) the rules for gene regulation. *(Spring)*

BINF 6205. Computational Molecular Evolution. (3) Prerequisites: BINF 6201 and BINF 6200 or permission of the instructor. Covers major aspects of molecular evolution and phylogenetics with an emphasis on the modeling and computational aspects of the fields. Topics will include: models of nucleotide substitution, models of amino acid and codon substitution, phylogenetic reconstruction, maximum likelihood methods, Bayesian methods, comparison of phylogenetic methods and tests on trees, neutral and adaptive evolution and simulating molecular evolution. Students will obtain an in-depth knowledge of the various models of evolutionary processes, a conceptual understanding of the methods associated with phylogenetic reconstruction and testing of those methods and develop an ability to take a data-set and address fundamental questions with respect to genome evolution. *(On demand)*

BINF 6210. Numerical Methods and Machine Learning in Bioinformatics. (3) Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++) and Calculus. Focuses on commonly used numerical methods and machine learning techniques. Topics will include: solutions to linear systems, curve fitting, numerical differentiation and integration, PCA, SVD, ICA, SVM, PLS. Time permitting, Hidden Markov Chains and Monte Carlo simulations will be covered as well. Students learn both the underlying theory and how to apply the theory to solve problems. *(Fall)*

BINF 6211. Design and Implementation of Bioinformatics Databases. (3) Students learn the necessary skills to access and utilize public biomedical data repositories, and are expected to design, instantiate, populate, query and maintain a personal database to support research in an assigned domain of bioinformatics. Topics include common data models and representation styles, use of open-source relational DBMS, and basic and advanced SQL. Focuses on how data integration is achieved, including the use of standardized schemas, exchange formats and ontologies. Examines large public biomedical data repositories such as GenBank and PDB, learn how to locate and assess the quality of data in Web-accessible databases, and look at representation, standards, and access methods for such databases. *(Spring)*

BINF 6310. Advanced Statistics for Genomics. (3) Prerequisite: BINF 6200 or equivalent. The first half of this course emphasizes canonical linear statistics (t-test, ANOVA, PCA) and their non-parametric equivalents. The second half of the course emphasizes Bayesian statistics and the application of Hidden Markov Models to problems in bioinformatics. Students

should have fluency in a high-level programming language (PERL, Java, C# or equivalent) and will be expected, in assignments, to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. *(On demand)*

BINF 6311. Biophysical Modeling. (3) This course covers: (a) overview of mechanical force fields; (b) energy minimization; (c) dynamics simulations (molecular and coarse-grained); (d) Monte-Carlo methods; (e) systematic conformational analysis (grid searches); (f) classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Colombic); (g) free energy decomposition schemes; and (h) hybrid quantum/classical (QM/MM) methods. *(On demand)*

BINF 6312. Computational Comparative Genomics. (3) Prerequisite: BINF 6201 or equivalent. Introduces computational methods for comparative genomics analysis. Covers the following topics: (a) the architecture of prokaryotic and eukaryotic genomes; (b) the evolutionary concept in genomics; (c) databases and resources for comparative genomics; (d) principles and methods for sequence analysis; evolution of genomes; (e) comparative gene function annotation; (f) evolution of the central metabolic pathways and regulatory networks; (g) genomes and the protein universe; (h) cis-regulatory binding site prediction; (i) operon and regulon predictions in prokaryotes; and (j) regulatory network mapping and prediction. *(On demand)*

BINF 6313. Structure, Function, and Modeling of Nucleic Acids. (3) Prerequisites: BINF 6100 and BINF 6101 or their equivalents. Covers the following topics: (a) atomic structure, macromolecular structure-forming tendencies and dynamics of nucleic acids; (b) identification of genes which code for functional nucleic acid molecules, cellular roles and metabolism of nucleic acids; (c) 2D and 3D abstractions of nucleic acid macromolecules and methods for structural modeling and prediction; (d) modeling of hybridization kinetics and equilibria; and (e) hybridization-based molecular biology protocols, detection methods and molecular genetic methods, and the role of modeling in designing these experiments and predicting their outcome. *(On demand)*

BINF 6318. Computational Proteomics and Metabolomics. (3) Prerequisites: BINF 6200 or equivalent. The aim of this 3-credit course is to introduce commonly used computational algorithms and software tools for analyzing mass spectrometry-based proteomics and metabolomics data. Chromatography and mass spectrometry will be covered at the beginning of the course to provide background information for the students to understand the nature of mass spectrometry data. *(On demand)*

BINF 6350. **Biotechnology and Genomics Laboratory. (3)** Teaches basic wet-lab techniques commonly used in biotechnology to generate genomics data. Lectures cover methods for sample isolation, cell disruption, nucleic acid and protein purification, nucleic acid amplification, protein isolation and characterization, molecular labeling methods and commonly used platforms for characterizing genome-wide molecular profiles. In particular, students discuss and learn to perform: tissue culture and LCM isolation of cells, DNA sequencing methods, DNA fingerprinting methods, RT-qPCR and microarrays of cDNA, 1D and 2D gels for protein separation, protein activity assays, and proteomics platforms. Lectures describe emerging methodologies and platforms, and discuss the ways in which the wet-lab techniques inform the design and use of bioinformatics tools, and how the tools carry out the processing and filtering that leads to reliable data. This course also discusses the commercial products beginning to emerge from genomics platforms. *(Spring)*

BINF 6380. Advanced Bioinformatics Programming. (3) Prerequisite: BINF 6112 or equivalent or permission of instructor. Advanced algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest, but may include assembly of short read fragments from next-generation sequencing platforms, clustering algorithms, machine learning, development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and "cloud" supercomputers. Students are expected to complete a significant independent project. *(On demand)*

BINF 6382. Accelerated Bioinformatics Programming. (3) Prerequisite: BINF 6112 or equivalent. Prerequisite: BINF 6112 or equivalent or permission of instructor. Computationally intensive algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing using modern hardware processor accelerators such as GPUs and FPGAs. Topics covered depend on instructor expertise and student interest but may include multi-threaded applications and developing for multi-core processors and for large clusters and other "cloud" computers. Students will be expected to complete a significant independent project. *(On demand)*

BINF 6400. Internship Project. (1-3) Prerequisite: Admission to graduate standing in Bioinformatics. Project is chosen and completed under the guidance of an industry partner, and results in an acceptable technical report. *(Fall, Spring)*

BINF 6600. Seminar. (1) Prerequisite: Admission to graduate standing in Bioinformatics. Weekly seminars are given by bioinformatics researchers from within the University and across the world. *(Fall, Spring)*

BINF 6601. Journal Club. (1) Prerequisite: Admission to graduate standing in Bioinformatics. Each week, a student in the course is assigned to choose and present a paper from the primary bioinformatics literature. *(Fall, Spring)*

BINF 6880. Independent Study. (1-3) Faculty supervised research experience to supplement regular course offerings.

BINF 6900. Master's Thesis. (1-3) Prerequisites: 12 graduate credits and permission of instructor. Project is chosen and completed under the guidance of a graduate faculty member, and will result in an acceptable master's thesis and oral defense. *(On demand)*

BINF 7999. Master's Degree Graduate Residency Credit. (1) *(Fall, Spring, Summer)*

BINF 8100. Biological Basis of Bioinformatics. (3) Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. This course provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. (Fall)

BINF 8101. Energy and Interaction in Biological Modeling. (3) Prerequisites: Admission to graduate standing in Bioinformatics. This course covers: (i.) the major organic and inorganic chemical features of biological macromolecules; (ii.) the physical forces that shape biological molecules, assemblies and cells; (iii.) the chemical driving forces that govern living systems; (iv.) the molecular roles of biological macromolecules and common metabolites; (v.) and the pathways of energy generation and storage. Each section of the course builds upon the relevant principles in biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. (Spring)

BINF 8111. Bioinformatics Programming I. (3) Prerequisite: Admission to graduate standing in Bioinformatics or permission of instructor. Introduces fundamentals of programming for bioinformatics using a high-level object-oriented language such as Java or Python. The course introduces object-oriented programming, analysis of algorithms and fundamental sequence alignment methods. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. *(Fall)*

BINF 8112. Bioinformatics Programming II. (3) Prerequisite: BINF 8111 or permission of instructor. Continuation of BINF 6111. In this second semester, students practice and refine skills learned in the first semester. New topics include: (a) programming as part of a team, using sequence analysis algorithms in realistic settings; (b) writing maintainable and re-usable code; and (c) graphical user interface development. *(Spring)*

BINF 8151. Professional Communications. (1) This course covers: Principles and useful techniques for effective oral presentations, poster presentations, scientific writing, use of references and avoiding plagiarism. Students in the class will critique and help revise each other's presentations and learn how to avoid common pitfalls. In addition, students will learn how to properly organize and run a meeting. Students will prepare a CV, job application letter and job talk. (Fall).

BINF 8200. Statistics for Bioinformatics. (3) This course aims to introduce statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. (Fall)

BINF 8201. Molecular Sequence Analysis. (3) Prerequisite: BINF 8100 or equivalent. BINF 8100 or equivalent. Introduction to bioinformatics methods that apply to molecular sequence. Intro to biological databases online. Sequence databases, molecular sequence data formats, sequence data preparation and database submission. Local and global sequence alignment, multiple alignment, alignment scoring and alignment algorithms for protein and nucleic acids, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. (Fall)

BINF 8202. Computational Structural Biology. (3) Prerequisite: BINF 8101, 8201 or equivalents. This course covers: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** structural databases and software for structure visualization; **(c)** structure determination and quality assessment; **(d)** protein structure comparison and the hierarchical nature of biomacromolecular structure classification; **(e)** protein structure prediction and assessment; and **(f)** sequence- and structure-based functional site prediction. *(Fall)*

BINF 8203. Genomics. (3) Prerequisite: BINF 8100 or equivalent. Surveys the application of high-throughput molecular biology and analytical biochemistry methods, and data interpretation for those kinds of high volume biological data most

commonly encountered by bioinformaticians. The relationship between significant biological questions, modern genomics technology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: genome sequencing and assembly, annotation, and comparison; genome evolution and individual variation; function prediction; gene ontologies; transcription assay design, data acquisition, and data analysis; metabolic pathways and databases and their role in genome analysis. *(Spring)*

BINF 8204. Mathematical Systems Biology. (3) Prerequisites: BINF 8200 and 8210 or equivalents. This course introduces basic concepts, principles and common methods used in systems biology. The class emphasizes on molecular networks, models and applications, and covers the following topics: the structure of molecular networks; network motifs, their system properties and the roles they play in biological processes; complexity and robustness of molecular networks; hierarchy and modularity of molecular interaction networks; kinetic proofreading; optimal gene circuit design; the rules for gene regulation. (Spring)

BINF 8205. Computational Molecular Evolution. (3) Pre-requisites: BINF 8201 (Molecular Sequence Analysis) and BINF 8200 Statistics for Bioinformatics (or permission of the instructor). This course will cover major aspects of molecular evolution and phylogenetics with an emphasis on the modeling and computational aspects of the fields. Topics will include: models of nucleotide substitution, models of amino acid and codon substitution, phylogenetic reconstruction, maximum likelihood methods, Bayesian methods, comparison of phylogenetic methods and tests on trees, neutral and adaptive evolution and simulating molecular evolution. Students will obtain an in-depth knowledge of the various models of evolutionary processes, a conceptual understanding of the methods associated with phylogenetic reconstruction and testing of those methods and develop an ability to take a data-set and address fundamental questions with respect to genome evolution. (On demand)

BINF 8210. Numerical Methods and Machine Learning in Bioinformatics. (3) Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++), Calculus. This course focuses on commonly used numerical methods and machine learning techniques. Topics will include: solutions to linear systems, curve fitting, numerical differentiation and integration, PCA, SVD, ICA, SVM, PLS. Time permitting, hidden markov chains and Monte Carlo simulations will be covered as well. Students will learn both the underlying theory and how to apply the theory to solve problems. *(Fall)*

BINF 8211. Design and Implementation of Bioinformatics Databases. (3) In this course students will acquire skills needed to access and utilize public biomedical data repositories, and will be expected to design, instantiate, populate, query and maintain a personal database to support research in an assigned domain of bioinformatics. The course content includes common data models and representation styles, use of open-source relational DBMS, and basic and advanced SQL. The course focuses on how data integration is achieved, including the use of standardized schemas, exchange formats and ontologies. We will examine large public biomedical data repositories such as GenBank and PDB, learn how to locate and assess the quality of data in Web-accessible databases, and look at representation, standards and access methods for such databases. *(Spring)*

BINF 8310. Advanced Statistics. (3) Prerequisite: BINF 8200 or equivalent. The first half of this course emphasizes canonical linear statistics (t-test, ANOVA, PCA) and their non-parametric equivalents. The second half of the course emphasized Bayesian statistics and the application of Hidden Markov Models to problems in bioinformatics. Students should have fluency in a high-level programming language (PERL, Java, C# or equivalent) and will be expected in assignments to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. *(Spring)*

BINF 8311. Biophysical Modeling. (3) This course covers: **(a)** an overview of mechanical force fields; **(b)** energy minimization; **(c)** dynamics simulations (molecular and coarse-grained); **(d)** Monte-Carlo methods; **(e)** systematic conformational analysis (grid searches); **(f)** classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Coulombic); **(g)** free energy decomposition schemes; and **(h)** hybrid quantum/classical (QM/MM) methods. *(On demand)*

BINF 8312. Computational Comparative Genomics. (3) Prerequisite: BINF 8201 or equivalent. This course introduces computational methods for comparative genomics analyses. The course covers the following topics: the architecture of prokaryotic and eukaryotic genomes; the evolutionary concept in genomics; databases and resources for comparative genomics; principles and methods for sequence analysis; evolution of genomes; comparative gene function annotation; evolution of the central metabolic pathways and regulatory networks; genomes and the protein universe; *cis*-regulatory binding site prediction; operon and regulon predictions in prokaryotes; regulatory network mapping and prediction. *(On demand)*

BINF 8313. Structure, Function, and Modeling of Nucleic Acids. (3) Prerequisite: BINF 8100-8101 or equivalent. The course covers the following topics: atomic structure, macromolecular structure-forming tendencies and dynamics of nucleic acids; identification of genes which code for functional nucleic acid molecules, cellular roles and metabolism of nucleic acids; 2D and 3D abstractions of nucleic acid macromolecules and methods for structural modeling and prediction; modeling of hybridization kinetics and equilibria; hybridization-based molecular biology protocols, detection methods and molecular genetic methods, and the role of modeling in designing these experiments and predicting their outcome. *(On demand)*

BINF 8318. Computational Proteomics and Metabolomics. (3) Prerequisites: BINF 8200 or equivalent. The aim of this 3-credit course is to introduce commonly used computational algorithms and software tools for analyzing mass spectrometry-based proteomics and metabolomics data. Chromatography and mass spectrometry will be covered at the beginning of the course to provide background information for the students to understand the nature of mass spectrometry data. *(On demand)*

BINF 8350. Biotechnology and Genomics Laboratory. (3) Prerequisite: none. This course teaches basic wet-lab techniques commonly used in biotechnology to generate genomics data. Lectures will cover methods for sample isolation, cell disruption, nucleic acid and protein purification, nucleic acid amplification, protein isolation and characterization, molecular labeling methods and commonly used platforms for characterizing genome-wide molecular profiles. In particular we will discuss and learn to perform: tissue culture and LCM isolation of cells, DNA sequencing methods, DNA fingerprinting methods, RT-qPCR and microarrays of cDNA, 1D and 2D gels for protein separation, protein activity assays, and proteomics platforms. Lectures will describe emerging methodologies and platforms, and will discuss the ways in which the wet-lab techniques inform the design and use of bioinformatics tools, and how the tools carry out the processing and filtering that leads to reliable data. The course will also discuss the commercial products beginning to emerge from genomics platforms. *(Spring)*

BINF 8380. Advanced Bioinformatics Programming. (3) Prerequisite: BINF 8112 or equivalent or permission of instructor. Advanced algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest, but may include assembly of short read fragments from next-generation sequencing platforms, clustering algorithms, machine learning, development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and "cloud" supercomputers. Students are expected to complete a significant independent project. *(On demand)*

BINF 8382. Accelerated Bioinformatics Programming. (3) Prerequisite: BINF 8112 or equivalent or permission of instructor. Computationally intensive algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing using modern hardware processor accelerators such as GPUs and FPGAs. Topics covered depend on instructor expertise and student interest but may include multi-threaded applications and developing for multi-core processors and for large clusters and other "cloud" computers. Students will be expected to complete a significant independent project. *(On demand)*

BINF 8600. Seminar. (1)
Prerequisites: Admission to graduate standing in Bioinformatics. Departmental seminar. Weekly seminars will be given by bioinformatics researchers from within the university and across the world. *(Fall, Spring)*

BINF 8601. Journal Club. (1)
Prerequisites: Admission to graduate standing in Bioinformatics. Each week, a student in the class is assigned to choose and present a paper from the primary bioinformatics literature. *(Fall, Spring)*

BINF 8911 Research Rotation I (2), BINF 8912 Research Rotation II (2).
Faculty supervised research experience in bioinformatics to supplement regular course offerings.

B. JUSTIFICATION

1. Need for proposed courses.

As our department has continued to grow in terms of both faculty and students, we have received feedback on our curriculum both from graduates and from potential employers. In response to changes and growth in some areas in the field, we propose to add a fourth semester of coursework that covers the growing use of hardware-accelerated code in Bioinformatics (BINF 6382/BINF 8382). We propose to remove the proteomics and metabolomics material from BINF 6203/BINF 8203 Genomics, and create a new course that provides more extensive coverage of that material (BINF 6318/BINF 8318).

In the Professional Science Masters program we have found that our entering students need more support as they orient themselves to the program of study and learn to identify domain-specific resources – from professional societies and journals to data resources. In response, we propose to create a required 1 credit course, BINF 6152 (Program and Professional Orientation). We propose to offer this course as a 4 week, intensive module at the beginning of the Fall semester so that incoming students can quickly understand the Bioinformatics field and the context for their degree requirements. We will create a second 1 credit course, BINF 6153 (Career Development in Bioinformatics) which will prepare students for the job search and interview, including an interview practicum with potential employers in the field.

Finally, we propose minor modifications to the descriptions of a number of courses (BINF 6151/8151, BINF 6203/8203, BINF 6111/8111, BINF 6112/8112, and BINF 6380/8380) in order to more accurately capture their contents now that our faculty have had the opportunity to teach these courses multiple times.

The most significant change proposed here is the standardization of degree requirements for the Professional Science Masters, the Graduate Certificate in Bioinformatics Applications, and the Graduate Certificate in Bioinformatics Technology. Feedback from graduates has helped us to focus the program on key skill sets, suggesting that all students should take BINF 6203/8203 (Genomics), and preferably take it early in the program; similarly, BINF 6201/8201 (Molecular Sequence Analysis) and BINF 6211/8211 (Design and Implementation of Bioinformatics Databases) provide skills that our graduates have found valuable in their subsequent employment. Our experience with several classes of entering students has suggested modifications to the core – for example, that all students, including those entering from a computing background, benefit from taking our BINF 6112/8112 (Bioinformatics Programming II) offering, and that many bioscience students benefit from taking BINF 6101/8101 (Energy and Interaction in Biological Modeling). Each of these courses had originally been envisioned as "Gateway" courses but are now part of the core for all students. Changes to the Certificate courses mirror the changes made to the Professional Science Masters, and for the same reasons.

2. Prerequisites and corequisites.

All of the new classes require good standing within our PSM or Ph.D. program. In addition, Computational Proteomics and Metabolomics (BINF 6318/BINF 8318) requires Statistics for Bioinformatics (BINF 6200/8200). Accelerated Bioinformatics Programming (BINF 6382/8382) requires Bioinformatics Programming II (BINF 6112/8112). These requirements are reasonable given the course content.

3. Justification of course numbering scheme.

Two of the proposed courses are PLUS courses designed specifically for students enrolled in the Professional Science Masters (PSM) in Bioinformatics, and have been numbered with 6000 numbers only. Two of the proposed courses are available to either Ph.D. or PSM students and have been given dual 6000/8000 numbers. In both cases, second digits follow the guidelines for course numbers described in the 2005-2007 Graduate

Catalog. We have generally followed the numbering scheme laid out in the original bioinformatics curriculum proposal, in which fundamental courses have a second digit of "1", core bioinformatics courses have a second digit of "2" and electives have a second digit of "3" or higher.

4. Improvements to the scope and quality of instruction.

As outlined above, the changes to these courses will make our curriculum more relevant to recent changes in the biotechnology industry, will better reflect the skills and research interests of our growing department and will incorporate our experiences in teaching these courses to our growing graduate student population over the last several years.

2. IMPACT.

A. Students served.

We currently have 24 Ph.D. students and 20 PSM students enrolled in our program. We anticipate another 2-4 Ph.D. students, 10 PSM students, and 10 graduate certificate students to enroll in the 2012-2013 academic year. Most of the students taking our classes are enrolled in our degree programs, although we have also had significant enrollment from students in other graduate programs (including Biology and Computer Science) as well as post-baccalaureate students.

B. Impact on other courses.

The proposed changes can be taught by current faculty, with minor changes to teaching assignments that will allow us to continue to offering existing courses. Offerings of other courses will be unaffected.

C. Anticipated enrollments.

We anticipate between 7 and 12 students enrolling in these courses in the near term. However, with the continued growth of our PSM program we expect eventual enrollment to be 15-20 students in the BINF 6152 and BINF 6153. Both PSM and the Ph.D. will fill BIN and BINF 6200/8200 series courses.

D. Effect of enrollment in other courses.

The courses offered by our department have little overlap with the efforts of other departments on campus and as such will not affect the enrollment of the courses of other programs.

E. Experience offering these courses as special topics.

Topics covered in BINF 6152 and BINF 6153 have been previously covered in non-mandatory orientations and student information sessions. BINF 6318/BINF 8318 (Computational Proteomics and Metabolomics) has previously been offered as a special topics course by Dr. Xiuxia Du. Content to be presented in BINF 6382/BINF 8382 (Accelerated Bioinformatics Programming) has previously been offered by Dr. Shannon Schlueter in a semester when he taught BINF 6380/BINF 8380 (Advanced Bioinformatics Programming).

F. Impact on catalog copy.

We have drafted catalog copy (see above) that should be inserted into the College of Computing and Informatics section of the catalog.

3. Resources Required to Support Proposal.

A. Personnel

a. Specify requirements for new faculty, part-time teaching, student assistant and/or increased load on present faculty.

As described above, we have 12 active faculty within our department and 1 additional faculty member will join in July 2012. We are adequately staffed to teach the newly proposed courses.

b. List by name qualified faculty members interested in teaching the courses.

We here list faculty interested in teaching the new classes:

- BINF 6152 – Program and Professional Orientation (All program faculty)
- BINF 6153 – Career Development (All program faculty)
- BINF 6318/BINF 8318 – Computational Proteomics and Metabolomics (Dr. Xiuxia Du)
- BINF 6382/BINF 8382 – Accelerated Bioinformatics Programming (Dr. Shannon Schlueter)

B. Physical Facility. Our recently constructed Bioinformatics building has state of the art classroom facilities and student computer workrooms. All classes will be taught in this building.

C. Equipment and Supplies. No new equipment.

D. Computer. No new computer equipment is required beyond what is already in the Bioinformatics building.

E. Audio-Visual. No new audio-visual equipment is requested beyond the state-of-the-art presentation facilities in the Bioinformatics building.

F. Other Resources. No other new resources are required for the teaching of these courses.

4. Consultation with the Library and Other Departments or Units.

a. Library Consultation is pending

b. Letters from chairs. We have sought consultation letters from the Departments of Biology, Chemistry, Mathematics and Statistics, Software and Information Systems, and Computer Science, and have so far received consultation letters from Biology, Mathematics and Statistics, and Computer Science, which are appended to this document.

5. Initiation and Consideration of the Proposal

a. Originating Unit.

This proposal was originated by the department of Bioinformatics and Genomics on February 3, 2012.

b. Other Considering Units.

The proposal will be considered by the College of Computing and Informatics at the next faculty meeting.

6. Attachments:

- Proposal for BINF 6152 – Program and Professional Orientation
- Proposal for BINF 6153 – Career Development
- Proposal for BINF 6318/BINF 8318 – Computational Proteomics and Metabolomics
- Proposal for BINF 6382/BINF 8382 – Accelerated Bioinformatics Programming

BINF 6153, CAREER DEVELOPMENT IN BIOINFORMATICS SYLLABUS

A. COURSE DESCRIPTION

Preparations for the job search, from developing a resume, to identifying appropriate opportunities, to preparing for the interview, for students enrolled in Professional Science Masters in Bioinformatics. (1 credit hour)

B. PRE- OR CO-REQUISITES

Prerequisite: Enrollment in the Professional Science Masters or certificate programs in Bioinformatics.

C. OBJECTIVES OF THE COURSE

Having successfully completed this course, the student will be able to:

1. Develop a current resume that highlights their strengths
2. Effectively seek and communicate with references
3. Network with potential employers online and in person
4. Identify job postings that are a good fit with their training
5. Think on their feet in a "simulated interview" situation
6. Anticipate and solve problems that may be encountered in a technical interview

D. INSTRUCTIONAL METHOD

The course will be presented in a hybrid lecture/demonstration and discussion format.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their participation in course activities.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 6153:

1. UNIVERSITY INTEGRITY

All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online at: http://www.legal.uncc.edu/policies/ps-105.html. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website: http://library.uncc.edu/display/?dept=instruction&format=open&page=920.

2. ATTENDANCE

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency. Excessive absences will negatively impact the overall course grade.

3. GRADING POLICY

Grades will be based on required written assignments (60%) and participation in classroom exercises and discussions (40%). Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=65-80%
U=0-65%

4. ADDITIONAL POLICIES.
The use of cell phones, beepers, or other communication devices is disruptive, and is therefore prohibited during class. Except in emergencies, those using such devices must leave the classroom for the remainder of the class period. Students are permitted to use computers during class for note-taking and class-related work.

G. PROBABLE TEXTBOOKS OR RESOURCES

Readings from current news and online sources will be assigned as appropriate

H. TOPICAL OUTLINE OF COURSE CONTENT

- Introduction to the Bioinformatics Program
- A Brief Introduction to DNA and Genome Science
- Introduction to key resources and players in the field

I. DAY-BY-DAY SCHEDULE

The course will be presented in five 3 hour sessions at the beginning of Fall semester.

DATE	TOPIC	READINGS	ASSIGNMENT
Session 1	Resume Development		Prepare a CV that highlights student's bioinformatics training
Session 2	Job Search Resources		Identify and develop mock applications to posted opportunities that fit the applicant's expertise
Session 3	Networking Resources in Bioinformatics		Identify and develop profiles on professional networking sites and join bioinformatics related subgroups
Session 4	Interview Preparation		Discuss and prepare for a practice interview with faculty and advisory board members

Session 5	FINAL INTERVIEW PRACTICUM		

BINF 6152, PROGRAM AND PROFESSIONAL ORIENTATION SYLLABUS

A. COURSE DESCRIPTION

This course provides an orientation to degree subject matter and field-specific resources, for students enrolled in Professional Science Masters in Bioinformatics. (1 credit hour)

B. PRE- OR CO-REQUISITES

Prerequisite: Enrollment in the Professional Science Masters or certificate programs in Bioinformatics.

C. OBJECTIVES OF THE COURSE

Having successfully completed this course, the student will be able to:

1. Understand and describe current significant research areas in Bioinformatics and Genomics
2. Recognize and understand where particular skill sets are applied in research and industry settings
3. Identify and join key professional networks
4. Identify and use the main professional and research journals in the field
5. Identify and achieve beginner-level proficiency with key genomic data repositories
6. Identify centers, organizations and companies driving intellectual and technology development in the field.

D. INSTRUCTIONAL METHOD

The course will be presented in a hybrid lecture/demonstration and discussion format.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their participation in course activities.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 6152:

1. UNIVERSITY INTEGRITY

All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online at: http://www.legal.uncc.edu/policies/ps-105.html. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website: http://library.uncc.edu/display/?dept=instruction&format=open&page=920.

2. ATTENDANCE

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency. Excessive absences will negatively impact the overall course grade.

3. GRADING POLICY

Grades will be based on required written assignments (60%) and participation in classroom exercises and discussions (40%). Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=65-80%
U=0-65%

4. ADDITIONAL POLICIES.

The use of cell phones, beepers, or other communication devices is disruptive, and is therefore prohibited during class. Except in emergencies, those using such devices must leave the classroom for the remainder of the class period. Students are permitted to use computers during class for note-taking and class-related work.

G. PROBABLE TEXTBOOKS OR RESOURCES

Readings from current news and online sources will be assigned as appropriate

H. TOPICAL OUTLINE OF COURSE CONTENT

- Introduction to the Bioinformatics Program
- A Brief Introduction to DNA and Genome Science
- Introduction to key resources and players in the field

I. DAY-BY-DAY SCHEDULE

The course will be presented in five 3 hour sessions at the beginning of Fall semester.

DATE	TOPIC	READINGS	ASSIGNMENT
Session 1	Introduction to the UNCC program A brief history of DNA and genome science Research topics		Bioinformatics Discovery: identify a recent newsworthy scientific story where bioinformatics and genomics methods were involved
Session 2	Core aims of genome science A brief history of bioinformatics, key problems and solutions Research topics		Bioinformatics Discovery: Identify the top scientific and industry journals in your field
Session 3	Key public data sources for bioinformaticians Researc topics: construction of a genome browser		UCSC Genome Browser tutorial
Session 4	The sequencing revolution: centers of innovation, key		Bioinformatics Discovery: Identify

	individuals and organizations driving bioinformatics innovation Research topics		your professional societies and key conferences; identify key deadlines for internship program applications
Session 5	FINAL EXAM		Essay exam: Write up a detailed timeline of key tasks that you will pursue during the different semesters of your PSM program, to help you secure an internship and later a job. Name resources that you will use to find jobs, organizations or companies that you might be interested in working for, and skills you are particularly interested in developing.

Syllabus

BINF 6318 / ITSC 8318
Computational Proteomics and Metabolomics
Spring 2013

Instructor

Xiuxia Du
Xiuxia.Du@uncc.edu, (704) 250-5754

Textbook

No textbook is required

Course Description

The aim of this 3-credit course is to introduce commonly used computational algorithms and software tools for analyzing mass spectrometry-based proteomics and metabolomics data. Chromatography and mass spectrometry will be covered at the beginning of the course to provide background information for the students to understand the nature of mass spectrometry data.

Course Content

- Instrumentation
- Isotopes and mass measurement
- Protein identification
- Assigning statistical significance to protein identifications
- Protein quantitation
- Metabolite identification and quantitation

Course Objective

- Learn what mass spectrometry (MS) measures and how mass spectrometry does it.
- Understand isotopes and mass measurement accuracy.
- Learn top-down and bottom-up proteomics.
- Learn how to identify proteins using top-down and bottom-up proteomics approach.
- Learn how to assign statistical confidence to protein identifications.
- Understand quantitative proteomics and how to extract quantitative information of proteins from MS data.
- Become familiar with software tools for identifying and quantifying proteins. These include SEQUEST, MASCOT, and OMSSA.
- Understand mass spectrometry-based metabolomics.
- Learn how to extract qualitative and quantitative information of metabolites from MS data and become familiar with software tools that include AMDIS and XCMS.
- Learn multivariate statistical analysis of quantitative protein and metabolite data.

Pre-requisites

Statistics. Specifically, students are expected to be able to carry out univariate and multivariate statistical analyses. Univariate analysis includes calculation of p-value, q-value, and false discovery rate. Multivariate analysis techniques include MANOVA, linear regression, principle component analysis (PCA), discriminant analysis, and clustering.

Grading

Evaluation will be based on understanding of concepts and the ability to apply theory in solving practical problems.

- Two homework assignments: 50%
- Midterm: 20%
- Final: 25%

- Classroom participation: 5%

Students taking ITSC 8318 are required to do more reading and homework problems, and answer more exam questions.

Attendance

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency. Excessive absences will result in a reduced classroom participation score at the instructor's discretion, and will negatively impact the overall course grade.

University Integrity

All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online at: http://www.legal.uncc.edu/policies/ps-105.html. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website:

http://library.uncc.edu/display/?dept=instruction&format=open&page=920.

Hardware Accelerated Bioinformatics Programming

BINF 6382 / BINF 8382

Fall ----

Catalog Description: This course emphasizes implementation of computationally intensive bioinformatics algorithms in the context of parallel processing using modern hardware processor accelerators such as GPUs and FPGAs. Topics covered depend on instructor expertise and student interest but may include multi-threaded applications and developing for multi-core processors and for large clusters and other "cloud" computers. Students will be expected to complete a significant independent project.

Course Instructor

Name	*Office*	*Phone*	*Email Address*
Shannon D. Schlueter, Ph.D.	BINF 263	704-687-7698	s.schlueter@uncc.edu

Course Description and/or Theme

In this course students will explore parallel programming primitives and bioinformatic algorithms in the context of GPU acceleration. NVIDIA processors and the CUDA C programming library extensions will be taught through hands-on exercise. Profiling of modern bioinformatics applications will demonstrate areas amenable to GPU acceleration.

Course Audience

This is a graduate level course for students interested in the development of General Purpose GPU programming skills and an introduction to parallel processing enabled algorithm development with emphasis on the bioinformatic computation domain.

Course Requirements and Learning Assessment

Knowledge	Students are expected to demonstrate an understanding of computational algorithm development and CUDA enabled programming that exceeds typical memorization and mechanical application. Examinations will be used to assess this level of learning.
Techniques	Students are expected to demonstrate the application of course materials presented. Homework problems will be used to assess this level of learning.
Application	Students are expected to be able to apply the concepts and techniques of CUDA programming. A capstone project will be used to assess this level of learning

Texts and Course Materials

Required texts:

Sanders and Kandrot (2010), *CUDA By Example: An Introduction to General-Purpose GPU Programming,* Addison-Wesley

Online materials:

Course materials and information about assignments will be made available via Moodle (moodle.uncc.edu).

Recommended references:

NVIDIA CUDA Programming Guide
http://developer.download.nvidia.com/compute/cuda/3_0/toolkit/docs/NVIDIA_CUDA_ProgrammingGuide.pdf

NVIDIA CUDA Reference Manual
http://developer.download.nvidia.com/compute/cuda/3_0/toolkit/docs/CudaReferenceManual.pdf

NVIDIA CUDA Library Documentation
http://developer.download.nvidia.com/compute/cuda/3_1/toolkit/docs/online/index.html

How Final Grades will be Determined (subject to change with notice)

Points and/or Weights

Assessment Mechanism	*Total Points*	*Weighting*[1]
Examination	100 points	50/30/15%
Homework	100 points	50/30/15%
Project	100 points	50/30/15%
Class Participation	5 points	5%

Notes and Comments

1. As students tend to differ in their preferred learning style so to do they differ in effective assessment methodology, therefore of the three primary assessment mechanisms student grades will be determined by assigning weights (50/30/15%) to the scoring mechanisms in order of individual student performance.
2. Incompletes will only be given under (1) extenuating circumstances that caused the student to be absent for an extended period of time, or (2) failure to complete the semester project. Extended absences must be documented through the Dean of Students Office and will be validated by the instructor. Project-based incompletes will be penalized a minimum of one letter grade for the course.

EXPECTATIONS OF BINF 8382 PARTICIPANTS:

As participation in 8000 level coursework entails the development of research philosophy and critical thinking skills, course participants registered for BINF 8382 will be required to complete weekly readings and reports related to current accelerated code development in the field of bioinformatics in addition to the coursework undertaken by BINF 6382 participants.

REVISION OF THE SYLLABUS:

The standards and requirements set forth in this syllabus may be modified at any time by the course instructor. Notice of such changes will be by announcement in class or by changes to this syllabus posted on the course website in Blackboard.

INSTRUCTOR ABSENCE/LATENESS:

I will let you know by e-mail in advance of class time if I will be absent due to illness or unavoidable conflict. I will make materials available through the website so you have access to assignments, etc. If I am late and haven't warned you, please wait for 10 minutes.

STUDENT ABSENCE/LATENESS:

Regular attendance is expected, and skipping class regularly will affect the participation component of your grade. If a single class session must be missed due to an illness or other conflict, the student is responsible for studying the notes and readings associated with that lecture and obtaining additional notes from classmates or help from the instructors if needed. If class must be missed for an extended period due to an illness or family problem a doctor's note or other documentation should be provided and arrangements for makeup work made with the instructors.

DISABILITY ISSUES:

Students in this course seeking accommodations to disabilities must first consult with the Office of Disability Services and follow the instructions of that office for obtaining accommodations.

ACADEMIC INTEGRITY:

All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online at: http://www.legal.uncc.edu/policies/ps-105.html. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website: http://library.uncc.edu/display/?dept=instruction&format=open&page=920.

This course is not writing intensive. Therefore, the main things to avoid are a) copying other students' short answers, figures, and problem solutions directly, and b) cut and pasting text from websites or copying it from your textbook, instead of writing your short answers in your own words. If I see something that stands out as different from your own writing style I will plug it into Google.

USE OF CELL PHONES AND OTHER DEVICES IN CLASS:

The use of cell phones, beepers, or other communication devices is disruptive, and is

therefore prohibited during class. Except in emergencies, those using such devices must leave the classroom for the remainder of the class period. Students are permitted to use computers during class for note-taking and other class-related work only. Those using computers during class for work not related to that class must leave the classroom for the remainder of the class period.

Subject: RE: Request for consultation letter on Bioinformatics graduate curriculum revision

Date: Wednesday, February 8, 2012 5:54:15 PM ET

From: Ribarsky, William

To: Gibas, Cynthia

CC: Mays, Larry

Cynthia,
We have no specific comments or objections. Go for it.
Bill

Dr. William Ribarsky
Bank of America Endowed Chair in Information Technology
Chair, Computer Science Department
Director, Charlotte Visualization Center
College of Computing and Informatics
University of North Carolina at Charlotte
www.viscenter.uncc.edu

From: Gibas, Cynthia
Sent: Wednesday, February 08, 2012 4:00 PM
To: Ribarsky, William
Cc: Mays, Larry
Subject: Request for consultation letter on Bioinformatics graduate curriculum revision

Bill,

Bioinformatics and Genomics is preparing a long form curriculum modification proposal and we would like to request your comments.

While the proposal is such that it requires a long form and consultation, only a few new courses are actually proposed. The primary purpose of the proposal is to redefine the core curriculum in the Professional Science Masters degree and in the Graduate Certificates. The new requirements will constrain students to a single set of core courses, so that graduates will have a more predictable skill set that fits well with current needs in the field.

If you have specific comments on the proposal please send them to me as soon as possible. If you have no specific comments, all we need is a brief note stating that you've reviewed the proposal and have no objections.

Thanks,
Cynthia

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Dr. Cynthia J. Gibas
Department of Bioinformatics and Genomics
University of North Carolina at Charlotte
ph: 704.687.8378 e: cgibas@uncc.edu

Subject: RE: Request for consultation letter on Bioinformatics graduate curriculum revision

Date: Wednesday, February 8, 2012 6:58:03 PM ET

From: Dow, Alan

To: Gibas, Cynthia

CC: Mays, Larry

Hello Cynthia,

Thank you for the consultation concerning the curriculum changes in the Professional Science Masters degree program in Bioinformatics. I have reviewed the proposal and have no objections.

Sincerely
Alan Dow

--

Alan Dow, Ph.D. | Professor of Mathematics
UNC Charlotte | Dept. of Mathematics and Statistics
9201 University City Blvd. | Charlotte, NC 28223
Phone: 704-687-4560 | Fax: 704-687-6416

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UNC CHARLOTTE

Department of Biology
9201 University City Boulevard
Charlotte, NC 28223-0001
Ph. (704) 687-8686 ~ Fax. (704) 687-3128

Memorandum

TO: Larry Mays, PhD
Professor and Chair
Department of Bioinformatics and Genomics

FROM: Martin G. Klotz, Ph.D.
Professor and Chair
Department of Biology

RE: **Long Form and consultation, PSM and Graduate Certificates**

DATE: February 9, 2012

This note is to express support by the Biology department for the redefinition of the core curriculum in the Professional Science Masters degree and Graduate Certificate programs to be offered by the Department of Bioinformatics and Genomics. The course and curriculum proposal dated "BINF-2-03-12" does not contain the offering of new, the inclusion of existing or the request of prerequisite BIOLOGY courses and it does not require direct participation of the Department of Biology. The proposed curricula do not include any specific prerequisites that a UNC Charlotte Biology BA or BS graduate would need to acquire in order to satisfy the requirements for admission in to these PSM or certificate programs and we agree with the comment in the proposal that "many bioscience students [will] benefit from taking BINF 6101/8101 (Energy and Interaction in Biological Modeling)." As stewards of the BIOLOGY curriculum at UNC Charlotte, the Biology Department needs to evaluate carefully all course offers that include the subject "Biology" or "biological" as a qualifier. The proposed BINF curriculum offers four courses in this category:

- BINF 6100/8100 Biological Basis of Bioinformatics,
- BINF 6101/8101 Energy and Interaction in Biological Modeling,
- BINF 6202/8202 Computational Structural Biology, and
- BINF 6204/8204 Mathematical Systems Biology.

Review of the proposed course descriptions/syllabi indicates that **none of these courses has a replace-equivalent in the Biology Department curriculum**. The "Biological Basis" course BINF 6100/8100 has the stated aim to provide "a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics." This correlates with the stated course target namely students with a "bachelor's degree in computing or mathematics" as well as the exemption from taking the course for BINF students with a bachelor's degree in the life sciences. In contrast, the pertinent graduate course "BIOL 6102/8102: Cell and Molecular Biology" offered by the Department of Biology is designed to build on foundations and provide depth. The other three courses listed above are focused on explaining the modeling, computational processing as well as the mathematical/statistical representation of biological data whereas related courses in Biology are designed to explain the biology of organisms and their viruses. Therefore the Department of Biology has no objections or suggested amendments to the proposed curriculum. Instead, the proposed curricula appear to represent valuable career choices for students graduating with a Bachelor's degree in Biology and who have an interest in graduate studies in Bioinformatics and Genomics.

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: Reese Manceaux

From: Dr. Cynthia Gibas
College of Computing and Informatics
Department of Bioinformatics and Genomics

Date: February 17, 2012

Subject: **Revisions of Graduate Curriculum for the Dept. of Bioinformatics**
NEW COURSES PROPOSED:
BINF 6152 – Program and Professional Orientation
BINF 6153 – Career Development
BINF 6318/BINF 8318 – Computational Proteomics and Metabolomics
BINF 6382/BINF 8382 – Accelerated Bioinformatics Programming

Summary of Librarian's Evaluation of Holdings:

Evaluator: ___Reese Manceaux_____ Date: ___2/17/2012_____

Please Check One:

Holdings are superior	____
Holdings are adequate	__☑___
Holdings are adequate only if Dept. purchases additional items.	_____
Holdings are inadequate	_____

Comments:

This is a proposal for a change in the Graduate Curriculum in Bioinformatics. This is proposing four new courses in addition to numerous modifications of the catalog and changing of core requirements of the Professional Science Masters in Bioinformatics, the Graduate Certificate in Bioinformatics Applications, and the Graduate Certificate in Bioinformatics Technology.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A sampling of the related subjects retrieved over 2,000 pertinent items.

In addition to books, the Library has electronic access to periodicals and other electronic resources (e-books from NCLIVE & Skillport/Books 24x7) that support these courses. Also, the library has many electronic databases such as Springer Link, Oxford Journals, Web of Science , ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to
Revision of Graduate Curriculum in Bioinformatics

Library of Congress Subject Headings	Books	Journals
Bioinformatics/ Genomics/ Computational Biology	300	71
Bioethics	253	17
Genetics	562	55
Medical Informatics / Biology – Data Processing / Medicine – Data Processing	150	25
Proteomics / Metabolism – Research / Molecular biology	502	115
TOTAL	**1767**	**283**

Reese A. Manceaux

Evaluator's Signature

February 17, 2012
Date