LONG SIGNATURE SHEET

UNCCHARLOTTE

Proposal Number: BINF ~~2/16/2010~~ 1-29-10

Proposal Title Bioinformatics Track Curriculum Modifications

Originating Department Department of Bioinformatics and Genomics

TYPE OF PROPOSAL: UNDERGRADUATE_____ GRADUATE ✓ UNDERGRADUATE & GRADUATE____

DATE RECEIVED	DATE CONSIDERED	DATE FORWARDED	ACTION	SIGNATURES
2/2/10	2/4/10	2/4/10	approved	DEPARTMENT CHAIR
2/4/10	2/8/10	2/8/10	approved	COLLEGE CURRICULUM COMMITTEE CHAIR
				TEACHER EDUCATION COMMITTEE CHAIR (Teacher Education Program proposals only) N/A
2/9/10	2/16/10	2/16/10	approved	COLLEGE FACULTY CHAIR
[illegible]	[illegible]	2/17/10	approved	COLLEGE DEAN
				UNDERGRADUATE COURSE & CURRICULUM COMMITTEE CHAIR (for undergraduate courses) N/A
2/17/10	3/2/10	3/10/10	Approved	GRADUATE COUNCIL CHAIR (for graduate courses) Rob Roy McGregor
				FACULTY GOVERNANCE SECRETARY (noting Faculty Council approval on Consent Calendar)
				FACULTY EXECUTIVE COMMITTEE (if decision is appealed)

COPY
MADE

Grad School cp

Revised 4/08/03
OAA/jdp

University of North Carolina at Charlotte BINF 1-29-10

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. Technology in the fields of bioinformatics and genomics is rapidly changing the state-of-the art of our science. These changes to the graduate curriculum are required to ensure that our students receive up-to-date training. These changes also reflect the expertise and addition of eight new faculty that have been added to our department since our initial graduate curriculum was approved in 2007. In conjunction with updating the course curriculum, we propose to also update the required courses for the Ph.D. and PSM degrees.

We propose to create the following classes:

BINF 6151/BINF 8151*/ITSC 8151/GRAD 6151/8151 – Professional Communications

BINF 6171/BINF 8171*/ITSC 8171 – Business of Biotechnology

BINF 6205/BINF 8205*/ITSC 8205 - Computational Molecular Evolution

BINF 6350/BINF 8350*/ITSC 8350 – Biotechnology and Genomics Laboratory

BINF 6380/BINF 8380*/ITSC 8380 – Bioinformatics Programming III

BINF 6880 – Independent Study

BINF 8911*/ITSC 8911 – Research Rotation I

BINF 8912*/ITSC 8912 – Research Rotation II

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

BINF 6101/BINF 8101*/ITSC 8101 – Energy and Interaction in Biological Modeling (new title and catalog copy; was "Energy and Information in Biological Modeling")

BINF 6111/BINF 8111*/ITSC 8111 – Bioinformatics Programming I (new catalog copy)

BINF 6112/BINF 8112*/ITSC 8112 – Bioinformatics Programming II (new catalog copy)

BINF 6200/BINF 8200*/ITSC 8200 – Statistics for Bioinformatics (new catalog copy)

BINF 6202/BINF 8202*/ITSC 8201 – Computational Structural Biology (new catalog copy)

BINF 6203/BINF 8203*/ITSC 8203 – Genomics (new title and catalog copy; was “Genomics, Transcriptomics & Proteomics”)

BINF 6204/BINF 8204*/ITSC 8204 – Mathematical Systems Biology (new catalog copy)

BINF 6210/BINF 8210*/ITSC 8210 – Numerical Methods and Machine Learning for Bioinformatics (new title and catalog copy was “Numerical Methods in Bioinformatics”)

BINF 6211/BINF 8211*/ITSC 8211 – Design and Implementation of Bioinformatics Databases (new title and catalog copy)

BINF 6310/BINF 8310*/ITSC 8310 – Advanced Statistics for Genomics (new title and catalog copy; was “Analysis of Microarray Data”)

BINF 6312/BINF 8312*/ITSC 8312 – Computational Comparative Genomics (new catalog copy)

We propose to keep the following courses in their current form:

BINF 6100/BINF 8100*/ITSC 8100 – Biological Basis of Bioinformatics

BINF 6201/8201 – Molecular Sequence Analysis

BINF 6311/BINF 8311*/ITSC 8311 – Biophysical Modeling

BINF 6313/BINF 8313*/ITSC 8313 – Structure, Function, and Modeling of Nucleic Acids

BINF 6400 – Internship Project

BINF 6600/BINF 8600*/ITSC 8699 – Seminar

BINF 6601/BINF 8601*/ITSC 8601 – Journal Club

BINF 6900 – Masters’ Thesis

2. PROPOSED CATALOG COPY. (Starts on the following page)

BIOINFORMATICS

Department of Bioinformatics and Genomics
Bioinformatics Building, Room 309
704-687-8541
http://bioinformatics.uncc.edu/

Degrees

Professional Science Masters in Bioinformatics
Ph.D. in Information Technology (Bioinformatics Track)

Program Director

Dr. Lawrence Mays

Graduate Faculty

Xiuxia Du, Assistant Professor
Anthony Fodor, Assistant Professor
Cynthia Gibas, Associate Professor
Jun-tao Guo, Assistant Professor
Dennis Livesay, Associate Professor
Ann Loraine, Associate Professor
Lawrence Mays, Professor
Jessica Schlueter, Assistant Professor
Shannon Schlueter, Assistant Professor
Susan Sell, Professor
ZhengChang Su, Assistant Professor
Jennifer Weller, Associate Professor

Ph.D. in INFORMATION TECHNOLOGY (BIOINFORMATICS TRACK)

The Department of Bioinformatics and Genomics admits students seeking the Ph.D. degree under the Ph.D. in Information Technology (Bioinformatics Track). All requirements for the Ph.D. in Information Technology are described later in this section of the Catalog under the Information Technology heading. The Bioinformatics Track follows all of the common requirements of the Information Technology Ph.D. program with the exceptions stated below.

Bioinformatics Track Requirements

Students will be required to demonstrate competence in the areas of biochemistry, cellular and molecular biology, genetics, statistics, and computer science related to core concepts in bioinformatics. The student's advisor and at least one other dissertation committee member must be faculty in the Bioinformatics track.

Core Requirements

Plans of Study for Bioinformatics Ph.D. students are developed on an individual basis, by the student and his or her advisory committee. However, all students must take the following courses:

- BINF 8100*/ITSC 8100 Biological Basis of Bioinformatics
- BINF 8101*/ITSC 8101 Energy and Interaction in Biological Modeling
- BINF 8200*/ITSC 8200 Statistics for Bioinformatics
- BINF 8201*/ITSC 8201 Molecular Sequence Analysis
- BINF 8202*/ITSC 8202 Computational Structural Biology
- ITSC 8110 Introduction to IT Research
- BINF 8111*/ITSC 8111 Bioinformatics Programming I
- BINF 8112*/ITSC 8112 Bioinformatics Programming II
- BINF 8911*/ITSC 8911 Research Rotation I and BINF 8912*/ITSC 8912 Research Rotation II

However, all students must take BINF 8600*/ITSC 8699 Graduate Research Seminar every semester until advancing to PhD candidacy (unless they are taking ITSC 8110). Students with exceptionally strong backgrounds in specific disciplines may be excused from one or more of the required didactic classes (except ITSC 8110) at the discretion of the bioinformatics track coordinator.

Qualifying Examination

The Qualifying Examination must be passed prior to the 5th semester. The qualifying examination for the bioinformatics track is composed of three components: (i.) written exam, (ii.) oral exam, and (iii.) original written research contribution. The Qualifying Examination Committee will have the same members in any given semester. The written component will have three sections (Molecular Sequence Analysis, Structural Bioinformatics and Research Methods). The material covered by the qualifying exam will be based on material in the required courses listed above. Each student must pass all three sections in order to advance; failure to do so requires that the student attempt the failed sections the following semester. Passed sections carry forward from one exam to the next and three attempts are permitted. After passing the three written sections, students must pass an oral exam on the same topics, for which three attempts are also permitted. Students must pass both the written and oral components of the exam. (Note: if the written component is passed, but not the oral component, then only the oral component must be retaken.) Students must also prepare an "original written research contribution," which can be a write-up from a lab rotation (assuming it was given a passing grade), a research paper submitted or published in a journal, etc. Students must pass all components of the qualifying exam by the end of the fifth semester to continue in the program.

Dissertation Proposal

Each student must present and defend a Ph.D. dissertation proposal no more than three semesters after passing the qualifying exam. The proposal defense will be conducted by the student's Dissertation Committee and will be open to the Ph.D. IT faculty and students. At the discretion of the Dissertation Committee, the defense may include questions that cover the student's program of study and background knowledge in the area of the proposal. A student can retake the proposal defense if he/she does not pass it the first time. The second failed defense of a dissertation proposal will result in the termination of the student's enrollment in the Ph.D. program. A doctoral student advances to Ph.D. candidacy after the dissertation proposal has been successfully defended. For complete details and the required forms, see the sections entitled "Proposal Defense" and "Ph.D. Candidacy" online at www.cci.uncc.edu/coit_new/phd/phd_reqs.cfm.

Dissertation

Each student must complete a research program approved by the student's Dissertation Advisor(s) that yields a high quality, original and substantial piece of research. The Ph.D. dissertation describes this research and its results. The dissertation defense is a public presentation. A written copy of the dissertation must be made available to each member of the student Ph.D. Dissertation Committee, to the Ph.D. Steering Committee, and to the UNC Charlotte Library at least three weeks before the public defense. The date of the defense must be publicly announced at least three weeks prior to the defense. The student must present the dissertation and defend it in a manner accepted by the Dissertation Committee. The dissertation will be graded as pass/fail by the Dissertation Committee and must be approved by the Dean of the Graduate School. A student who fails the defense of a dissertation twice will be terminated from the Ph.D. program. For complete details and the required forms, see the section entitled "Dissertation" online at www.cci.uncc.edu/coit_new/phd/phd_reqs.cfm.

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 admission to the Professional Science Master's (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 37 graduate credit hours, and a minimum of 33 credit hours of formal course work. A minimum of 24 credit hours presented toward a PSM in Bioinformatics must be numbered 6000 or higher. A maximum of 6 hours of graduate credit may be transferred from other institutions.

1. Total hours required. The program requires 37 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:

2. Core Requirements.

a. Fundamentals Courses

The **Fundamentals** course sequences 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 require at most two of the **Fundamentals** courses.

Fundamental Biology track: This course sequence is designed for students entering with a degree in Computer Science or another quantitative science discipline. The Fundamental Biology course sequence provides accelerated training in Genetics, Cell and Molecular Biology, and Biochemistry for students entering Bioinformatics from computer science or a quantitative science. BINF 6100 (Biological Basis of Bioinformatics), 6101 (Energy and Interaction in Biological Modeling).

Fundamental Computing track: The Fundamental Computing track is designed for students entering with a degree in a life science discipline. The Fundamental Computing course sequence provides accelerated training in programming and data structures for students entering Bioinformatics from life sciences. BINF 6111, 6112 (Bioinformatics Programming I and II).

b. Core Bioinformatics Courses

Fundamentals courses prepare students for the required **Core** courses. All students must take BINF 6200, Statistics for Bioinformatics. In addition, students must take 6 additional credit hours of **Core Genomics** courses from among BINF 6201 (Molecular Sequence Analysis), BINF 6203 (Genomics), BINF 6205 (Computational Molecular Evolution) and BINF 6350 (Biotechnology and Genomics Laboratory) and 6 credit hours from the **Core Computational** courses from among 6202 (Computational Structural Biology), BINF 6204 (Mathematical Systems Biology), BINF 6210 (Numerical Methods and Machine Learning for Bioinformatics) and BINF 6310 (Advanced Statistics for Genomics).

c. Professional Preparation Requirement

Students are required to take at least 3 credit hours of electives designed to prepare them to function effectively and ethically in a professional environment. Some recommended electives in this category include BINF 6171, Business of Biotechnology, BINF 6151, Professional Communications, 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 student’s Advisory Committee.

d. The remaining credit hours of formal course work can be completed in additional **Core Bioinformatics** courses and/or other recommended program electives.

The student’s 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 units: 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.

e. Other requirements

- *Bioinformatics Seminar.* In addition to 33 hours of 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).

- *Grades required.* 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.

COURSES IN BIOINFORMATICS

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)
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 6111. Bioinformatics Programming I. (3)
Prerequisites: Admission to graduate standing in Bioinformatics. This course introduces fundamentals of programming for bioinformatics using a high-level object-oriented language such as python. The first weeks cover core data types, syntax, and functional programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. The course will cover object-oriented programming, introduce analysis of algorithms and sequence alignment methods, and introduce computational environments that are particularly useful in bioinformatics analyses such as R, BioPython, and Web services in bioinformatics. By the end of the class, students will have gained the ability to analyze data within the python interpreter (for example) and write well-documented, well-organized programs. (Fall)

BINF 6112. Bioinformatics Programming II. (3)
Prerequisite: BINF 6111. This course is the second semester of Introduction to Bioinformatics Programming I. In this semester, students will practice and refine skills learned in the first semester. New topics introduced will include: programming as part of a team, using sequence analysis algorithms in realistic settings; writing maintainable and re-usable code; Web programming; and graphical user interface development. At the end of the semester, students will be able to evaluate and deploy computer languages, tools, and software engineering techniques in bioinformatics research. (Spring)

BINF 6151/GRAD 6151. 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 6171. **Business of Biotechnology. (3)** This course introduces students to the field of biotechnology and how biotech businesses are created and managed. The 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, biotechnology business fundamentals, research and development within biotech companies, exit strategies, and careers in the biotech field. (Summer)

BINF 6200. Statistics for Bioinformatics. (3)
This course aims to introduce 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. 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 6202. Computational Structural Biology. (3)
Prerequisite: BINF 6101, 6201 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 6203. Genomics. (3)
Prerequisite: BINF 6100 or equivalent. This course 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. Proteomics methods. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

BINF 6204. Mathematical Systems Biology. (3)
Prerequisites: BINF 6200 and 6210 or equivalents. This course introduces basic concepts, principles and common methods used in systems biology. The class emphasizes 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 6205. Computational Molecular Evolution. (3)
Prerequisites: BINF 6201 (Molecular Sequence Analysis) and BINF 6200 Statistics for Bioinformatics (or permission of the instructor). This course 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++), 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 6211. Design and Implementation of Bioinformatics Databases. (3)
In this course students learn the necessary skills 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 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 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. *(Spring)*

BINF 6311. 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 6312. Computational Comparative Genomics. (3)
Prerequisite: BINF 6201 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 6313. Structure, Function, and Modeling of Nucleic Acids. (3)
Prerequisite: BINF 6100-6101 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 6350. 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 6380. Programming III. (3) Prerequisite: BINF 6112 or equivalent.
This course emphasizes implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest but may include development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and "cloud" supercomputers. Students will be expected to complete a significant independent project (Fall).

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 will result in an acceptable technical report. *(Fall, Spring)*

BINF 6600. Seminar. (1)
Prerequisite: 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 6601. 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 6900. Masters' Thesis. (1-3)
Prerequisites: Twelve 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 6880. Independent Study. (1-3) Faculty supervised research experience to supplement regular course offerings.

BINF 8100*/ITSC 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*/ITSC 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*/ITSC 8111. Bioinformatics Programming I. (3)
Prerequisite: Admission to graduate standing in Bioinformatics. This course introduces fundamentals

of programming for bioinformatics
using a high-level object-oriented language such as python. The first weeks cover core data types, syntax, and functional programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. The course will cover object-oriented programming, introduce analysis of algorithms and sequence alignment methods, and introduce computational environments that are particularly useful in bioinformatics analyses such as R, BioPython, and Web services in bioinformatics. By the end of the class, students will have gained the ability to analyze data within the python interpreter (for example) and write well-documented, well-organized programs. (Fall)

BINF 8112*/ITSC 8112. Bioinformatics Programming II. (3)
Prerequisite: BINF 8111*/ITSC 8111. This is a continuation of Bioinformatics Programming I (BINF 8111). This course is the second semester of Introduction to Bioinformatics Programming I. In this semester, students will practice and refine skills learned in the first semester. New topics introduced will include: programming as part of a team, using sequence analysis algorithms in realistic settings; writing maintainable and re-usable code; Web programming; and graphical user interface development. At the end of the semester, students will be able to evaluate and deploy computer languages, tools, and software engineering techniques in bioinformatics research. (Spring)

BINF 8151*/ITSC 8151/GRAD 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 8171*/ITSC 8171. Business of Biotechnology. (3) This course introduces students to the field of biotechnology and how biotech businesses are created and managed. The 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. (Summer)

BINF 8200*/ITSC 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*/ITSC 8201. Molecular Sequence Analysis. (3)
Prerequisite: BINF 8100*/ITSC 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*/ITSC 8202. Computational Structural Biology. (3)
Prerequisite: BINF 8101*, 8201*/ITSC 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*/ITSC 8203. Genomics. (3)
Prerequisite: BINF 8100*/ITSC 8100 or equivalent. This course 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. Proteomics methods. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

BINF 8204*/ITSC 8204. Mathematical Systems Biology. (3)
Prerequisites: BINF 8200* and 8210*/ITSC 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*/ITSC 8205. Computational Molecular Evolution. (3)
Pre-requisites: BINF 8201*/ITSC 8201 (Molecular Sequence Analysis) and BINF 8200*/ITSC 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*/ITSC 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*/ITSC 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*/ITSC 8310. Advanced Statistics for Genomics. (3)
Prerequisite: BINF 8200*/ITSC 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*/ITSC 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*/ITSC 8312. Computational Comparative Genomics. (3)
Prerequisite: BINF 8201*/ITSC 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*/ITSC 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 8350*/ITSC 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*/ITSC 8380. Programming III. (3)
Prerequisite: BINF 8112 or equivalent. This course emphasizes implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest but may include development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and

"cloud" supercomputers. Students will be expected to complete a significant independent project (Fall).

BINF 8600*/ITSC 8699. 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*/ITSC 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*/ITSC 8911 Research Rotation I (2), BINF 8912*/ITSC 8912 Research Rotation II (2).
Faculty supervised research experience in bioinformatics to supplement regular course offerings.

* Indicates this will be the new course number when the new Bioinformatics and Computational Biology PhD program is approved.

B. JUSTIFICATION.

1. Need for proposed courses.

The field of Bioinformatics and Genomics continues to change rapidly. These proposed modifications to the course curriculum are required to keep our curriculum focused on the most recently developed technology. For example, by changing BINF 6310/8310*/ITSC 8310 from "Analysis of Microarray Data" to "Advanced Statistics for Genomics" we have transitioned that course from focusing on a single technology (microarrays) to theory that is relevant to all genomics technology. Likewise, by changing BINF 6203/8203*/ITSC 8203 from "Genomics, Transcriptomics & Proteomics" to "Genomics" we allow room for the course to include discussion of recently developments in genomics such as metabolomics and epigenetics.

When the original Bioinformatics course curriculum was approved in 2007, we had 5 faculty in our program. We now have 12 faculty, and many of the new courses that we propose, as well as changes to existing courses reflect the skills and abilities of the new members of our department. For example, changing "Numerical Methods in Bioinformatics" to "Numerical Methods and Machine Learning for Bioinformatics" reflects the expertise in machine learning possessed by two of our new faculty (Xiuxia Du and Shannon Schlueter). Likewise our proposed new course "Computational Molecular Evolution" reflects the expertise of Dr. Jessica Schlueter, who was recruited specifically because she brought to our department expertise in this area. Several of the proposed new courses (BINF 6380/8380*/ITSC 8380 Bioinformatics Programming III and BINF 6350/8350*/ITSC 8350 Biotechnology and Genomics Laboratory) have been successfully taught as seminars and their addition to the course catalog therefore formally captures the activities of our faculty.

As our department has continued to grow in terms of both faculty and students, we have gained more experience with our classes and some of the changes we propose reflect this experience. For example, we are finding that two semesters of programming has not been enough time for an in-depth exploration of programming, and we therefore propose to add a third semester (BINF

6380/8380*/ITSC 8380 Bioinformatics Programming III). The Graduate School and us have found that there is a wide variability in our students' abilities to present scientific ideas, and we therefore propose to create a cross-listed course in Professional Communications (BINF 6151/8151*/ITSC 8151/GRAD 6151/8151). Many of our students will pursue careers in the biotechnology industry and we have therefore proposed to add BINF 6171/8171*/ITSC 8171 (The Business of Biotechnology). We have found many of our students wish to pursue independent research projects over the course of a semester, and we therefore propose to create mechanisms (BINF 6880, BINF 8911*/ITSC 8911, BINF 8912*/ITSC 8912) to capture this activity. Finally, we propose minor modifications to the descriptions of a number of courses (BINF 6101/8101*/ITSC 8101, BINF 6111/8111*/ITSC 8111, BINF 6112/8112*/ITSC 8112) in order to more accurately capture their contents now that our faculty have had the opportunity to teach these courses.

2. Prerequisites and corequisites.
   All of the new classes require good standing within our PSM or Ph.D. program or permission of the instructor. In addition, Computational Molecular Evolution (BINF 6205/BINF 8205*/ITSC 8205) requires Statistics for Bioinformatics (BINF 6200/8200*/ITSC 8200) and Molecular Sequence Analysis (BINF 6201/8201*/ITSC 8201). Bioinformatics Programming III (BINF 6380/8380*/ITSC 8380) requires Bioinformatics Programming II (BINF 6112/8112*/ITSC 8112). These requirements are reasonable given the course content.

   While most of the prerequisites for existing courses have not changed, there are some minor changes to prerequisites for some courses reflecting our increased experience as to appropriate student preparation. Therefore, Genomics (BINF 6203/8203*/ITSC 8203) now requires Biological Basis of Bioinformatics (BINF 6100/8100) or equivalent and Computational Comparative Genomics (BINF 6312/8312*/ITSC 8312) now requires Molecular Sequence Analysis (BINF 6201/8201*/ITSC 8201). Finally, Advanced Statistics for Genomics (BINF 6310/8310*/ITSC 8310) now requires Statistics for Bioinformatics (BINF 6200/8200*/ITSC 8200).

3. Justification of course numbering scheme.
   All of the proposed courses are offered with dual 6000/8000 numbers with second digits following the guidelines for course numbers described in the 2005-2007 Graduate Catalog. In addition, we have 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.

C. IMPACT.

1. Students served.

We currently have 20 Ph.D. students and 14 PSM students enrolled in our program. We anticipate another 3 Ph.D. students and 10 PSM students to enroll in the 2010-2011 academic year. Most of the students taking our classes are drawn from students 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.

2. Impact on other courses.

The proposed changes are either new courses taught by our newly-hired faculty or modifications to the descriptions of existing courses.

a. **When and how often the added courses will be taught**
The additional courses will be taught at least once every academic year.

b. **How the content and/or frequency will affect other 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 Ph.D. and PSM programs, we expect eventual enrollment to be 15-20 students in the BINF 6100/8100*/ITSC 8100 and BINF 6200/8200*/ITSC 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.**
Biotechnology and Genomics Laboratory (BINF 6350/8350*/ITSC 8350 in the new course-numbering scheme) has been offered as a special topic previously (with 5 students) by Jennifer Weller. The course was successful and is being offered again this semester (with 10 students enrolled). Bioinformatics Programming III (BINF 6380/8380*/ITSC 8380 in the new course-numbering scheme) is being offered this semester (with 3 enrolled students by Anthony Fodor) and will be offered again in Fall 2010 (by Shannon Schlueter).

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.

D. RESOURCES REQUIRED TO SUPPORT PROPOSAL.

1. 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 plans to recruit at least 1 additional faculty over the next year. 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 6151/8151*/ITSC 8151/GRAD 6151/8151 – Professional Communications (Mays, Sell, Loraine)

BINF 6171/8171*/ITSC 8171 – Business of Biotechnology Course (Jennifer Montague)

BINF 6112/8112*/ITSC 8112 – Bioinformatics Programming III(Fodor, Loraine, S. Schlueter)

BINF 6205/8205*/ITSC 8205 - Computational Molecular Evolution (J. Schlueter)

BINF 6350/8350*/ITSC 8350 – Biotechnology and Genomics Laboratory (Weller)

BINF 6880 – Independent Study (All faculty)

BINF 8911*/ITSC 8911 – Research Rotation I (All faculty)

BINF 8912*/ITSC 8912 – Research Rotation II (All faculty)

2. **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.

3. **Equipment and Supplies.** No new equipment.

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

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

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

E. CONSULTATION WITH THE LIBRARY AND OTHER DEPARTMENTS OR UNITS.

1. **Library consultation:** See Appendix materials

2. **Letters from chairs.** See Appendix materials

F. INITIATION AND CONSIDERATION OF THE PROPOSAL

1. Originating Unit.

This proposal was originated by the department of Bioinformatics and Genomics on January 29, 2009.

2. Other Considering Units.
   The proposal was considered by the College of Computing and Informatics at the 2/16/2010 faculty meeting.

G. ATTACHMENTS:

1. Proposal for BINF 6151/8151*/ITSC 8151/GRAD 6151/8151 – Professional Communications
2. Proposal for BINF 6171/8171*/ITSC 8171 - Business of Biotechnology
3. Proposal for BINF 6205/8205*/ITSC 8205 - Computational Molecular Evolution
4. Proposal for BINF 6350/8350*/ITSC 8350 – Biotechnology and Genomics Laboratory
5. Proposal for BINF 6380/8380*/ITSC 8380 – Bioinformatics Programming III (not yet attached)
6. Proposal for BINF 6880 – Independent Study (not yet attached)
7. Proposal for BINF 8911*/ITSC 8911 – Research Rotation I
8. Proposal for BINF 8912*/ITSC 8912 – Research Rotation II

BINF 6151/BINF 8151*/ ITSC 8151/GRAD 6151/GRAD 8151, PROFESSIONAL COMMUNICATIONS
SYLLABUS – FALL 2010

Instructor: Dr. Lawrence Mays
Office: 311 Bioinformatics
Office Phone: (704) 687-8555
Office Hours: Tuesday and Thursday 2:00pm-3:00pm
Email: lemays@uncc.edu

A. COURSE DESCRIPTION

This course covers: Principles and useful techniques for effective oral presentations, poster presentations, scientific writing, use of references and avoiding plagiarism. 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. BINF 8151*/ITSC 8151/GRAD 8151 students will prepare a CV, job application letter and job talk (1 credit hour).

The course meets in 217 Bioinformatics Bldg on Friday, from 12:30pm to 1:45pm. BINF 6151/GRAD 6151 is for Master's students and BINF 8151*/ITSC 8151/GRAD 8151 is for PhD students.

B. PRE- OR CO-REQUISITES

Prerequisite: Admission to graduate standing and permission of instructor.

C. OBJECTIVES OF THE COURSE

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

- Prepare slides and present an effective oral presentation
- Create and present an effective scientific poster
- Write a coherent, grammatically correct scientific paper with appropriate references
- Organize and run a meeting

D. INSTRUCTIONAL METHOD

The course is presented in a lecture/demonstration format which will include the following elements as appropriate: video recording of presentations with student critiques, interactive demonstrations of methods to be applied in assignments, opportunities for student questions, and discussion.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their ability to utilize the presented material in presentations (20%), a poster (15%), and a scientific paper (35%). A final exam (30%) based on presented material will also be used to evaluate students' performance in the course.

BINF 8151*/ITSC 8151/GRAD 8151 additional requirements: Ph.D. students enrolled in BINF 8151*/ITSC 8151/GRAD 8151 will be required to do write their own CV, write a letter applying for a job (with research and teaching statements) and present an abbreviated job talk. This presentation will count as 20% of the final grade (with the above grading scheme comprising the other 80%).

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 6151/BINF 8151*/ITSC 8151/GRAD 6151/GRAD 8151:

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.

3. GRADING POLICY

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 other class-related work only.

G. TEXTBOOK

- None

Additional reading material may be assigned as needed.

MEETING	TOPIC
8/27	Intro to course; Initial writing sample. Assignments for Oral Presentations.
9/3	Oral presentations: types of talks, content and organization of a talk, visual aids, giving the talk, voice and delivery, Q&A, Oral presentation checklist.
9/10	Individual Presentations: Video and critique.

9/17 Individual Presentations: Video and critique.

9/24 Poster presentations: Function, content, organization, sections of a poster, figures, preparing a poster, presenting a poster, pitfalls, poster checklist.

10/1 Individual Presentations: Poster and presentation; critique.

10/8 Individual Presentations: Poster and presentation; critique.

10/15 Principles of scientific writing: Grammar, technical style, person, voice, tense, common problems.

10/22 Principles of scientific writing: Organization, abstract, figures, tables, discussion, references, Endnote; avoiding plagiarism

10/29 Principles of scientific writing: Individual presentation; critique and revision.

11/5 Principles of scientific writing: Individual presentation; critique and revision.

11/12 Principles of scientific writing: Individual presentation; critique and revision.

11/19 How to run a meeting: Agenda, minutes, Robert’s rules of order, common pitfalls.

11/26 Thanksgiving Break

12/3 Practice Job Talks; Critique of letter of application and CV

12/10-17 EXAM WEEK

BINF 6171/BINF 8171*/ITSC 8171 Business of Biotechnology

Syllabus (2010 Summer I)

Instructor: Dr. Jennifer Montague, jmontag4@uncc.edu

Adjunct Bioinformatics and Genomics Faculty Member

Office Hours: by appointment

Time and Place:

Tuesday and Thursday, 5:30-9:15pm, Bioinformatics 217

Course Website:

TBA

Textbooks Required:

Building Biotechnology by Yali Friedman, Ph.D.; additional handouts to be provided by Dr. Montague

Course Description:

The purpose of "The Business of Biotechnology" course is to introduce students to the field of biotechnology and how biotech businesses are created and managed. The students should be able to define biochemistry 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.

Instructional Methods:

The course will be presented in a lecture format which will include the following elements as appropriate: presentation of concepts, theories and examples in a standard lecture format, interactive demonstrations of methods, and opportunities for student questions and discussion.

Grading Plan:

Students will be evaluated based on their mastering of the concepts and theories taught in the class, and the ability to use them for solving practical problems. The grade is determined as follows:

Exam #1	15%
Exam #2	15%
Exam #3	10%

Project	50%
Attendance	5%
Class Participation	5%
Quickie Quizzes	Extra points

TENTATIVE COURSE OUTLINE

	Subject	
5/24	Introduction, syllabus, expectations	
	Biotechnology as an Industry Overview	
5/26	Molecular Biology	
	Drug Development	
5/31	Tools and Techniques	
	Applications	
6/2	Exam 1	
	Biotech Formation Fundamentals; R&D	
6/7	Finance	
	Marketing	
6/9	Licensing, Alliances, Mergers	
	Managing Biotechnology	
6/14	Exam 2	
	Intellectual Property	
6/16	Regulation	
	Politics and Ethics	
6/21	Putting it all together-building biotech companies	
	Project presentation	
6/23	Career Opportunities	

	Review	
6/28	Exam 3	

Attendance and Participation

Students are expected to punctually attend all scheduled sessions and are responsible for completing work from all class sessions. No make-ups will be provided for missed classroom activities. Enrolled students will receive a grade of zero on days that they miss. Students who miss a class are expected to consult with students who attended to understand testable materials, activities, or assignments that were missed. Students will take one or more exams during the course that will account for the examination component of the student's course grade. Exams may feature a combination of essay/short answer style questions, as well as multiple choice and labeling. Class material, class notes and assigned readings will be very important in providing suitable responses. The participation of all students in classroom discussion of relevant materials is expected as it contributes in a meaningful way to understanding the subject matter.

If you experience difficulty in meeting course expectations, please seek assistance. Some possible sources of assistance include: peers, your professor, and/or other appropriate University academic resources as listed on the University's advising website:

www.advising.uncc.edu/AcademicSupportServices.pdf.

Since much of our learning occurs as a result of classroom activities, classroom participation, defined in terms of students' contributions to a positive learning environment, will constitute a portion of the students' final grades. Students contribute to a positive learning environment by…

- Being an active participant, but not a dominating one.
- Being a good listener and demonstrating respect for others' opinions, even if you disagree.
- Making thoughtful, insightful comments, and not speaking just to be heard.
- Building on others' comments.
- Asking questions, not just giving answers.
- Identifying key assumptions underlying discussion points and arguments.
- Providing constructive and positive comments.

1. **Classroom expectations**. Please read the entire syllabus carefully before continuing in this course. These policies and expectations are intended to create a productive learning atmosphere for all students.

2. **Respectful discussions of ideas.** Each of us brings our unique viewpoint and insights into the classroom. You are expected to listen to someone else's comments and respond to them in a respectful manner. You don't have to agree, but you do need to moderate responses appropriately.

3. **Grades** are on a 10 point scale, where A=90 to 100; B=80-89; C=70-79; U=0-69. There is no curve. The award of a grade of "I" will strictly adhere to The University's catalog guidelines. Grade penalties may be assessed on late assignments. UNC Charlotte's grading policies may be viewed at

   http://www.provost.uncc.edu/Catalogs/2007-2009/acadregs.htm#GRADING_POLICIES.

4. **Communication skills**. Students are expected to demonstrate correct and effective oral and written communication skills including good spelling, grammar and punctuation. Students whose communication and writing skills are deemed by the instructor as inadequate may be required to successfully compete tutoring sessions at the Writing Resources Center in the Department of English. Information on the Writing Resources Center may be found online at http://www.uncc.edu/writing/wrc.html.
5. **Academic integrity.** All students are required to read and abide by the Code of Student Academic Integrity which governs student behavior relating to academic work. 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.

6. **Materials**. All materials submitted as part of course requirements become the property of the instructor. Students desiring to retain copies of their work should make such copies before turning in their materials.

7. **Disability accommodations**. 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. Reasonable and appropriate accommodations will be provided to students presenting a memo from the Office of Disability Services (ODS).

8. **Faculty absence or tardiness**. If I am late in arriving to class, you must wait a full 20 minutes after the start of class before you may leave without being counted absent, or you must follow any written instructions I may give you about my anticipated tardiness.

9. **Sexual harassment.** All students are required to abide by the UNC Charlotte Sexual Harassment Policy (http://www.legal.uncc.edu/policies/ps-61.html) and the policy on Responsible Use of University Computing and Electronic Communication Resources (http://www.legal.uncc.edu/policies/ps-66.html). Sexual harassment, as defined in the UNC Charlotte Sexual Harassment Policy, is prohibited, even when carried out through computers or other electronic communications systems, including course-based chat rooms or message boards.

10. **Communication devices in classroom.** The use of cell phones, beepers, or other communication devices is disruptive, and is therefore prohibited during class.

11. **Computers in the classroom**. Students are permitted to use computers during class for class-related work **only**, if the occasion calls for it. **I prefer students take notes by hand**.

12. **Diversity.** The College of Computing and Informatics strives to create an inclusive academic climate in which the dignity of all individuals is respected and maintained. Therefore, we celebrate diversity that includes, but is not limited to ability/disability, age, culture, ethnicity, gender, language, race, religion, sexual orientation, and socio-economic status.

BINF 6205/BINF 8205*/ITSC 8205 Computational Molecular Evolution

SYLLABUS FALL 2011

Instructor: Jessica Schlueter

Office: Bioinformatics 261

Office Phone: 704-687-8968

Email: jschluet@uncc.edu

COURSE DESCRIPTION

This course will cover major aspects of molecular evolution and phylogenetics with an emphasis on the modeling and computational aspects of the fields. Topics to be covered include: models of nucleotide substitution, models of amino acid and codon substitution, phylogenetics reconstruction, maximum likelihood methods, Bayesian methods, comparison of phylogenetic methods and tests on trees, neutral and adaptive evolution and simulating molecular evolution.

PRE- OR CO-REQUISITES

Prerequisite: Admission to graduate standing, BINF 6201 Molecular Sequence Analysis and BINF 6200 Statistics for Bioinformatics.

OBJECTIVES OF THE COURSE:

- 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.
- An ability to take a data-set and address fundamental questions with respect to genome evolution.

INSTRUCTIONAL METHOD

The instructional method for this course will include: independent reading of a required text, current literature, lecture, weekly assignments, two exams and a final project. Lectures will be based upon the required text and will be supplemented with current literature illustrating the use of the methods and models covered in the course. Weekly assignments will be computational driven and require the students to utilize various software for molecular evolution and phylogenetics. The final project will require the students to take a dataset from either their research or provided from the instructor and perform a series of analyses. For example, taking a set of next-generation sequences from a number of genomes (such as metagenomic sequences), assembling and testing phylogenetic tree methods.

MEANS OF STUDENT EVALUATION

10% student participation

20% weekly homework assignments

40% exams (2 at 20% each)

30% final project

A. SPECIFIC POLICIES REGARDING THE COURSE:

a. University integrity – All students will be required to 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 UNC Charlotte library web site.

b. Attendance – Attendance is required for all classes except in the case of illness or pre-arranged absences with instruction permission. Students who miss class due to illness or by pre-arrangement with the instructor may e-mail any assignments prior to the start of the missed class.

c. Grading policy – Grading policy is as follows:

A: 90–100

B: 80-89

C: 70-79

U: anything below 70

d. Additional requirements – All cell phones must be quieted during class and only answered in the event of an emergency (birth, death, etc.). Students are expected to come to class prepared from reading assignments.

TEXTBOOK

"*Computational Molecular Evolution*" by Ziheng Yang, Oxford University Press.

Additional relevant reading materials include original research papers and review papers.

B. OUTLINE OF COURSE CONTENT

a. Models of nucleotide substitution
    i. Markov models of nucleotide substitution and distance estimation
    ii. Maximum likelihood estimation
    iii. Distance estimations
b. Models of amino acid and codon substitution
    i. Models of amino acid replacement
    ii. Estimation of distance between protein sequences
    iii. Models of codon substitution
    iv. Estimation of synonymous and nonsynonymous rates
c. Phylogenetic reconstruction
    i. Tree concepts
    ii. Exhaustive and heuristic tree search
    iii. Distance methods
    iv. Maximum parsimony
d. Maximum likelihood methods

    i. Likelihood calculation on trees
    ii. Likelihood calculation under complex models
    iii. Reconstruction of ancestral states
    iv. Numerical algorithms for maximum likelihood estimation
    v. Approximations to likelihood
    vi. Model selection and robustness
- e. Bayesian methods
    - i. The Bayesian paradigm
    - ii. Prior
    - iii. Markov chain Monte Carlo
    - iv. Simple moves and their proposal ratios
    - v. Monitoring Markov chains and processing output
    - vi. Bayesian phylogenetics
    - vii. MCMC algorithms under the coalescent model
- f. Comparison of methods and tests on trees
    - i. Statistical performance of tree-reconstruction methods
    - ii. Likelihood
    - iii. Parsimony
    - iv. Testing hypotheses concerning trees
- g. Molecular clock and estimation of species divergence times
    - i. Tests of the molecular clock
    - ii. Likelihood estimation of divergence times
    - iii. Bayesian estimation of divergence times
- h. Neutral and adaptive protein evolution
    - i. The neutral theory and tests of neutrality
    - ii. Lineages undergoing adaptive evolution
    - iii. Amino acid sites undergoing adaptive evolution
    - iv. Adaptive evolution affecting particular sites and lineages
    - v. Adaptively evolving genes
- i. Simulating molecular evolution
    - i. Random number generator
    - ii. Generation of continuous random variables
    - iii. Generation of discrete random variables
    - iv. Simulating molecular evolution

BINF 6350/BINF 8350*/ITSC 8350 Biotechnology and Genomics Laboratory

SYLLABUS SPRING 2011

Instructor: Jennifer Weller

Office: Bioinformatics 353

Office Phone: 704-687-7678

Email: jweller2@uncc.edu

C. COURSE DESCRIPTION

This course will cover laboratory methods used in genomics experiments, based on methods developed in molecular biology and biotechnology. Emphasis will be on generating genome-wide profiles of DNA, RNA and protein in samples. Lectures will cover the concepts and application areas of the methods and instrumentation used to manipulate, purify and characterize the designated classes of biomolecule, the laboratory methods that transform selected elements into commercial products, and bioinformatics tools used throughout in processing and analyzing data for quality assurance, discovery, and validation.

D. PRE- OR CO-REQUISITES

Prerequisite: Admission to graduate standing, and an upper level undergraduate or graduate course in Molecular and Cell Biology, or equivalent knowledge.

E. OBJECTIVES OF THE COURSE:

- A detailed understanding of the wet-lab protocols and instruments used to generate genome-wide profiles.
- A detailed understanding of the bioinformatics tools and processes used as aids to performing genomics experiments.
- A detailed understanding of how methodologies influence outcomes in genomics experiments.

F. INSTRUCTIONAL METHOD

The instructional method for this course will include: independent reading of posted protocols, Web content, journal articles, lecture content, twice weekly laboratory exercises, two exams, and a final project. Lectures will be based upon posted protocols and papers, and will be supplemented with Web material that provides details on protocol steps, instrumentation, and platforms. Weekly assignments will be organization and data entry into lab notebooks, Web-posted write-ups of experiments in progress, five experimental reports, which in some cases will require the students to utilize various software tools for data analysis. The final project will require the students to propose a molecular diagnostic product based upon genomics methods, do market research to determine competing tests and commercial potential, and propose the experimental design required to get regulatory approval.

G. MEANS OF STUDENT EVALUATION

20% Student participation and lab notebooks

25% Experiment write-ups

30% Exams (2 at 15% each)

25% Final project

H. SPECIFIC POLICIES REGARDING THE COURSE:

a. University integrity – All students will be required to 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 UNC Charlotte library web site.

b. Attendance – Attendance is required for all classes except in the case of illness or pre-arranged absences with instruction permission. Students who miss class due to illness or by pre-arrangement with the instructor may e-mail any assignments prior to the start of the missed class.

c. Grading policy – Grading policy is as follows:

    A: 90–100

    B: 80-89

    C: 70-79

    U: anything below 70

d. Additional requirements – All cell phones must be quieted during class and only answered in the event of an emergency (birth, death, etc.). However, those with cameras may be used to document lab data. Students are expected to come to class, especially to labs, prepared from reading assignments.

I. TEXTBOOK

There are no required textbooks, although some are recommended as providing a broader perspective on methods and platforms across the related disciplines.

1. “Molecular Biotechnology: Principles and Applications of Recombinant DNA” by Bernard Glick and Jack Pasternak from ASM Press, edition 3 2003. ISBN 1-55581-224-4.
2. “Molecular Cell Biology” by Lodish, Berk, Zipursky, Matsudaira, Baltimore, Darnell (WH Freeman and Co.) for those not up to date on molecular biology concepts.

3. “Genomics” by Cantor and Smith (John Wiley and Sons, 1999) covers genomics areas well and some chapters will be recommended for further reading.
4. “Biometry” by Sokal and Rohlf (WE Freeman and Co, NY, 1995) for those wanting more detail on statistics.
5. “Physical Biochemistry, Applications to Biochemistry and Molecular Biology” by Freifelder (WH Freeman and Co., NY, 1982).
6. “Modern Experimental Biochemistry” by Boyer (Benjamin/Cummings Publishing Inc., NY, 1993).

J. OUTLINE OF COURSE CONTENT

- a. Basic techniques and tools
  - i. Lab safety, labeling and record keeping, lab notebooks
  - ii. Measurement devices for liquids and solids (micropipettes and balances), precision and accuracy
  - iii. Concentrations, dilutions, mixing, centrifuging
  - iv. Quantification of samples: spectrophotometry and gel electrophoresis
- b. Purification of nucleic acids and proteins
  - i. Cell disruption methods
  - ii. Solvent fractionation methods
  - iii. Column fractionation methods
  - iv. Quality control of fractions
  - v. Stabilization of samples
- c. Nucleic acid characterization: sequencing genomic and mitochondrial DNA
  - i. The polymerase chain reaction
  - ii. Cloning
  - iii. Sequencing basics
  - iv. Next generation sequencing platforms
- d. Nucleic acid characterization: mRNA
  - i. Making cDNA
  - ii. RT-PCR and qPCR
  - iii. The MIQE standards
  - iv. 5’ nuclease assays and multi-channel fluorescent platforms for qPCR
  - v. Microarrays
- e. Nucleic acid characterization: DNA fingerprints and mapping
  - i. Fingerprints based on targeted repeated elements (e.g. microsatellites)
  - ii. Fingerprints based on random PCR primers (RAPDs and AFLPs)
  - iii. Mitochondrial hypervariable region sequence
  - iv. Forensic identification using sequence or fingerprint patterns
  - v. Mapping using sequence or fingerprint patterns
- f. Protein characterization
  - i. Native versus denatured protein purification methods
  - ii. Native gel activity assays
  - iii. One-dimensional gel electrophoresis, and isoelectric focusing
  - iv. Two-dimensional gel electrophoresis
  - v. Affinity purification methods and assays
  - vi. Proteomics platforms
- g. Targeted cell type purification
  - i. Laser Capture Microscopy platforms

ii. Nucleic acid purification and amplification from very small samples
iii. Experimental design for small samples

BINF 6380/ ITSC 8380, PROGRAMMING III
SYLLABUS – FALL 2010

Instructor: Dr. Anthony Fodor

Office: Bioinformatics 361

Office Phone: (704) 687-2092

Office Hours: By appointment

Email: afodor@uncc.edu

H. COURSE DESCRIPTION

This course emphasizes implementation of bioinformatics algorithms in the context of parallel processing. Over the course of the semester students will be required to propose, execute and write-up an independent project in genomics. Students will also be required multiple times over the semester to present papers in the literature and present their progress on their independent project. The grade will be determined based on the student presentations and progress on the independent project over the course of the semester. As appropriate, there may be problem sets, but there will be no exams.

Your independent project can be related to your thesis or dissertation work, but it should stretch you as a programmer and should not be something you have already done or have almost completed. Ideally, it should involve a skill that you do not already have (multi-threading, dynamic programming, suffix trees, graphics manipulation, MPI, graphics card programming, etc.)

I. PRE- OR CO-REQUISITES

Prerequisite: Admission to graduate standing, fluency in a high-level object-oriented programming language (such as C++ or Java) and permission of instructor.

J. OBJECTIVES OF THE COURSE

Having successfully completed this course, the student will have:

- Learned to think in parallel in implementing bioinformatics algorithms
- Worked independently to identify and solve an interesting bioinformatics problem.
- Improved writing and presentation skills through repeated presentations and writing up of independent projects.

K. INSTRUCTIONAL METHOD

The course is presented in a lecture/demonstration format opportunities for student questions and discussion. Approximately every two weeks, students will be responsible for giving their presentations to the rest of the class on their progress on independent projects and papers .

L. MEANS OF STUDENT EVALUATION

Students will be graded on a final project (write-up and presentation) (40%), a mid-term (20%) and final (20%) and homeworks given over the course of the semester (20%).

M. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 6380/ ITSC 8380:

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.

3. GRADING POLICY

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 other class-related work only.

N. TEXTBOOK

Java Concurrency in Practice. Brian Goetz, et al. Addison-Wesley Professional. 2006.

Additional reading material may be assigned as needed.

H. TOPICS TO BE COVERED

Topics to be covered will be determined by student interest and the requirements of independent projects but will likely include:

- Discriminating sequencing error in next-generation pyrosequence datasets.

- Alignment, Clustering and expectation maximization algorithms and their application to next-generation sequencing datasets.
- A brief introduction to suffix tress (including their construction in linear time)
- An introduction to multi-threading in Java with applications to bioinformatics.

New graduate course proposal

1. **Course number / title:** BINF 6880 Independent Study

2. **Course description:** A semester of faculty supervised research experience in bioinformatics to supplement regular course offerings.

3. **Pre- or co-requisites:** Permission of the instructor

4. **Objectives of the course:** The purpose of this course is to broaden students exposure to state-of-the-art technologies currently being utilized within the field of bioinformatics, and to guide them towards recognizing important, outstanding questions in specific scientific domains, and to give them hands-on training in conducting experiments within those domains.
5. **Instructional method:** The course is presented in a one-on-one mentor/mentee format.

6. **Means of student evaluation:** Students will be evaluated on their ability to perform basic tasks independently and to describe their research in a public forum.

7. **Specify policies that apply to this course:**

    a. *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.[1] A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website.[2]

    b. *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.

    c. *Grading policy:* Grades will be assigned on the following scale: A=90-100%, B=80-90%, C=65-80%, and U=0-65%.

    d. *Additional requirements:* Not applicable.

8. **Probable textbooks or resources:** Will vary according to the subject area – discretion of mentor.
9. **Topical outline of course content:** Will vary according to specific topic – discretion of mentor.

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[1] http://www.legal.uncc.edu/policies/ps-105.html
[2] http://library.uncc.edu/display/?dept=instruction&format=open&page=920

New graduate course proposal

1. **Course number / title:** BINF 8911*/ITSC 8911 / Bioinformatics research rotation I

2. **Course description:** A first semester of faculty supervised research experience in bioinformatics to supplement regular course offerings.

3. **Pre- or co-requisites:** Permission of the instructor

4. **Objectives of the course:** The purpose of this course is to broaden students exposure to state-of-the-art technologies currently being utilized within the field of bioinformatics, and to guide them towards recognizing important, outstanding questions in specific scientific domains, and to give them hands-on training in conducting experiments within those domains.
5. **Instructional method:** The course is presented in a one-on-one mentor/mentee format.

6. **Means of student evaluation:** Students will be evaluated on their ability to perform basic tasks independently and to describe their research in a public forum.

7. **Specify policies that apply to this course:**

    a. *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.[3] A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website.[4]

    b. *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.

    c. *Grading policy:* Grades will be assigned on the following scale: A=90-100%, B=80-90%, C=65-80%, and U=0-65%.

    d. *Additional requirements:* Not applicable.

8. **Probable textbooks or resources:** Will vary according to the subject area – discretion of mentor.

9. **Topical outline of course content:** Will vary according to specific topic – discretion of mentor.

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[3] http://www.legal.uncc.edu/policies/ps-105.html

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

New graduate course proposal

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1. **Course number / title:** BINF 8912*/ITSC 8912 / Bioinformatics research rotation II

2. **Course description:** A second semester of faculty supervised research experience in bioinformatics to supplement regular course offerings.

3. **Pre- or co-requisites:** Permission of the instructor

4. **Objectives of the course:** The purpose of this course is to broaden students exposure to state-of-the-art technologies currently being utilized within the field of bioinformatics, and to guide them towards recognizing important, outstanding questions in specific scientific domains, and to give them hands-on training in conducting experiments within those domains.

5. **Instructional method:** The course is presented in a one-on-one mentor/mentee format.

6. **Means of student evaluation:** Students will be evaluated on their ability to perform basic tasks independently and to describe their research in a public forum.

7. **Specify policies that apply to this course:**

   a. *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.[5] A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website.[6]

   b. *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.

   c. *Grading policy:* Grades will be assigned on the following scale: A=90-100%, B=80-90%, C=65-80%, and U=0-65%.

   d. *Additional requirements:* Not applicable.

8. **Probable textbooks or resources:** Will vary according to the subject area – discretion of mentor.

9. **Topical outline of course content:** Will vary according to the subject area – discretion of mentor.

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[5] http://www.legal.uncc.edu/policies/ps-105.html
[6] http://library.uncc.edu/display/?dept=instruction&format=open&page=920