

TO: Faculty Council Members
FROM: Alan Freitag, Faculty President
DATE: April 28, 2010
RE: Consent Calendar

Attached is the Consent Calendar (See Article V, Section 3.A (3 & 4), J. (3 & 5) and K.3 of the Standing Rules of the Faculty Council.) consisting of these proposals:

- ITIS 10-16-09 Establishment of ITIS 6220 and 8220, Data Privacy
- BINF 1-29-10 Modification of Bioinformatics Track Curriculum

Below are the catalog copy descriptions. If you wish to read the full proposals, they are posted on the Academic Affairs website.

If there are any objections regarding these proposals, they must be registered with the Faculty Governance Administrative Assistant (Clarence Greene, ext. 5719) by **5 PM on May 12, 2010**. If no objections are registered, the proposals will stand approved.

ITIS 10-16-09 Establishment of ITIS 6220 and 8220, Data Privacy

Proposed Catalog Copy

ITIS 6220. Data Privacy. (3) Prerequisites or Corequisites: ITIS 6200, full graduate standing, or permission of department; Topics include privacy concepts, policies, and mechanisms; identity, anonymity, and confidentiality; private data analysis and database sanitization; privacy-preserving data mining techniques including k-anonymity, randomization, and secure function evaluation; privacy issues in social networks, RFID, and healthcare applications. (Fall, Evenings)

ITIS 8220. Data Privacy. (3) Prerequisites or Corequisites: ITIS 6200, full graduate standing, or permission of department; Topics include privacy concepts, policies, and mechanisms; identity, anonymity, and confidentiality; private data analysis and database sanitization; privacy-preserving data mining techniques including k-anonymity, randomization, and secure function evaluation; privacy issues in social networks, RFID, and healthcare applications. (Fall, Evenings)

Proposed Catalog Copy

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 associate 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.