University of North Carolina at Charlotte   BINF 10-3-14
New Graduate Course and Curriculum Proposal from Bioinformatics and Genomics
Reduction in Required Credit Hours for Professional Science Masters in Bioinformatics

2014-2015 LONG SIGNATURE SHEET

Proposal Number: **BINF 10-3-14**

Proposal Title: **Reduction in Required Credit Hours for PSM in Bioinformatics**

Originating Department: Bioinformatics and Genomics

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

DATE RECEIVED	DATE CONSIDERED	DATE FORWARDED	ACTION	SIGNATURES
9/28/14	10/3/14	10/3/14	Approved	**DEPARTMENT CHAIR** Lawrence Mays [print name here:]
10/3/14	10/13/14	10/13/14	Approved	**COLLEGE CURRICULUM COMMITTEE CHAIR** Yuliang Zheng [print name here:]
10/13/14	10/17/14	10/31/14	Approved	**COLLEGE FACULTY CHAIR (if applicable)** Srinivas Akella [print name here:]
11/12/2014	11/12/2014		Approved	**COLLEGE DEAN** Yi Deng [print name here:]
			Approved	**GENERAL EDUCATION** (if applicable; for General Education courses) [print name here:]
			Approved	**HONORS COLLEGE** (if applicable; for Honors courses & programs) [print name here:]
			Approved	**UNDERGRADUATE COURSE & CURRICULUM COMMITTEE CHAIR** (for undergraduate content)
11-11-14	12-2-14	12-2-14	Approved	**GRADUATE COUNCIL CHAIR** (for graduate content) ALAN R. FREITAG

Revised 05/06/14
OAA/mjw

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				FACULTY GOVERNANCE ASSISTANT (Faculty Council approval on Consent Calendar)
				FACULTY EXECUTIVE COMMITTEE (if decision is appealed)

LONG FORM
COURSE AND CURRICULUM PROPOSAL

*To: Bioinformatics Graduate Curriculum Committee

From: Cynthia Gibas, Faculty Director, Professional Science Masters in Bioinformatics

Date: September 27, 2014

Re: Reduction in Required Credit Hours for Professional Science Masters in Bioinformatics

The Long Form is used for major curriculum changes. Examples of major changes can include:

Undergraduate: Major changes include new undergraduate degrees, minors, concentrations, certificates, and changes to more than 50% of an existing program (Note: changing the name of an academic department does not automatically change the name(s) of the degree(s). The requests must be <u>approved</u> separately by the Board of Governors.)

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Graduate: Major changes include new graduate courses, major changes to an existing graduate course or major changes to an existing graduate program

Submission of this Long Form indicates review and assessment of the proposed curriculum changes at the department and collegiate level either separately or as part of ongoing assessment efforts.

***Proposals for undergraduate courses and programs should be sent to the Undergraduate Course and Curriculum Committee Chair. Proposals related to both undergraduate and graduate courses, (e.g., courses co-listed at both levels) must be sent to both the Undergraduate Course and Curriculum Committee and the Graduate Council.

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A. PROPOSAL SUMMARY.

1. SUMMARY. The Department of Bioinformatics and Genomics proposes to modify the curriculum requirements of the Professional Science Masters (PSM) in Bioinformatics. Three changes are proposed.

Currently, all PSM in Bioinformatics students are required to take one of two "Gateway Courses", either BINF 6100 (Biological Basis of Bioinformatics) or BINF 6111 (Bioinformatics Programming I), for a total of 3 credit hours. **This requirement will be removed from the program of study.**

Currently, all PSM in Bioinformatics students are required to take BINF 6203 (Genomics). **This requirement will be changed to allow students to choose either BINF 6203 (Genomics) or BINF 6202 (Computational Structural Biology).**

Currently, all PSM in Bioinformatics students are required to take 9 credit hours of advanced elective courses. **This requirement will be reduced to 6 credit hours.**

The result of these changes will be that the total required credit hours for the PSM in Bioinformatics are reduced from 40 to 34.

B. JUSTIFICATION.

1. The main goals of this proposal are to adapt the PSM in Bioinformatics in response to a changing applicant pool, to increase instructional efficiency in preparation for program growth, and to bring the credit requirements for the program more closely in line with other Masters degrees in the College of Computing and Informatics.

2. Currently, students are admitted to the PSM in Bioinformatics with an assumed undergraduate background in either life sciences or computing. They are then advised into one of two Gateway courses based on that background. However, students increasingly enter the program following our own undergraduate minor and early entry programs, or with interdisciplinary undergraduate training from other institutions. Such students have no need of the Gateway courses to make up for deficiencies in their background. Therefore we feel that all students need no longer be required to take one or the other of these courses. The courses will continue to be offered for those students who need them to satisfy prerequisite requirements of Bioinformatics and Genomics core courses.

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Allowing students to choose between BINF 6202 and 6203 will compensate to some extent for the loss of one upper level elective, giving students greater freedom to choose courses based on their interest in the subject matter and on future career goals. Incidentally this change will tend to distribute enrollments more evenly between those two courses, where they are currently strongly skewed towards BINF 6203.

3. No new course numbers are proposed.

4. By reducing the number of elective requirements and the total credit hour requirement of the PSM in Bioinformatics, this proposal makes it possible to plan for growing enrollments. The program has grown from 2 enrolled students in 2009 to 35 enrolled in 2014. Two growing graduate certificate programs also use many of the PSM core courses. Enrollment in some of these courses (such as BINF 6201) has reached nearly 30 students this fall, the maximum that can be accommodated. By reducing the need for electives and the frequency with which lower-enrollment electives are offered, these changes free the department to plan for increased offerings of core required courses as the PSM in Bioinformatics grows.

5. No new course offerings are proposed

C. **IMPACT.** Changes to courses and curricula often have impacts both within the proposing department as well as campus-wide. What effect will this proposal have on existing courses and curricula, students, and other departments/units? Submit an Impact Statement that fully addresses how you have assessed potential impacts and what the impacts of this proposal might be. Consider the following:

1. What group(s) of students will be served by this proposal? (Undergraduate and/or graduate; majors and/or non-majors, others? Explain). Describe how you determine which students will be served.

2. What effect will this proposal have on existing courses and curricula?
   a. No new courses are proposed.
   b. Low-enrollment upper-level electives will be offered every two years rather than annually.
   c. No new courses have been added.
   d. We expect that enrollment in BINF 6100 (Biological Basis of Bioinformatics, BINF 6111 (Bioinformatics Programming I), and BINF 6203 (Genomics) may decrease slightly, while enrollment in BINF 6202 (Computational Structural Biology) will increase, and that enrollments in less-frequently offered elective courses will increase in

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the terms that they are offered.
    e. No other areas of catalog copy will be affected.

III. RESOURCES REQUIRED TO SUPPORT PROPOSAL.
No additional resources are required to support this proposal.

IV. CONSULTATION WITH THE LIBRARY AND OTHER DEPARTMENTS OR UNITS
No new library resources are required to support this proposal. Other departments are not impacted.

V. INITIATION, ATTACHMENTS AND CONSIDERATION OF THE PROPOSAL
    A. ORIGINATING UNIT. This proposal was originated by the Faculty Director of the PSM in Bioinformatics on Sept. 27, approved by the department Graduate Committee on , and discussed and approved by the Department of Bioinformatics and Genomics on .

    B. ATTACHMENTS.

        1. PROPOSED CATALOG COPY:
            a. For a new course or revisions to an existing course, check all the statements that apply:
            ☒   This proposal results in the deletion of an existing course(s) from the degree program.

        2. STUDENT LEARNING OUTCOMES (UNDERGRADUATE & GRADUATE): This curriculum change will not impact the Student Learning Outcomes of the PSM in Bioinformatics.

        3. TEXTBOOK COSTS: ☒ No. This proposal will not increase the number of textbooks that students are required to purchase and may in fact reduce that number for some students.

IMPORTANT NOTE: A Microsoft Word version of the final course and curriculum proposal should be sent to facultygovernance@uncc.edu upon approval by the Undergraduate Course and Curriculum Committee and/or Graduate Council chair.

Bioinformatics and Genomics

- **Ph.D. in Bioinformatics and Computational Biology**
- **M.S. in Bioinformatics**
- **Graduate Certificate in Bioinformatics Applications**
- **Graduate Certificate in Bioinformatics Technology**

Department of Bioinformatics and Genomics
bioinformatics.uncc.edu

Chair
Dr. Lawrence Mays

Program Directors
Dr. Dennis Livesay, Ph.D. Program
Dr. Cynthia Gibas, Professional Science Master's and Graduate Certificate Programs

Graduate Faculty
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Xiuxia Du, Assistant Professor
Anthony Fodor, Associate Professor
Cynthia Gibas, Professor
Jun-tao Guo, Associate Professor
Daniel Janies, Carol Grotnes Belk Distinguished Professor of Bioinformatics and Genomics
Dennis Livesay, Associate Professor
Ann Loraine, Associate Professor
Weijun Luo, Research Assistant Professor
Lawrence Mays, Professor
Jessica Schlueter, Assistant Professor
~~Shannon Schlueter, Assistant Professor~~
Susan Sell, Professor
Wei Sha, Research Assistant Professor
Mindy Shi, Assistant Professor
ZhengChang Su, Associate Professor
Jennifer Weller, Associate Professor

PH.D. IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

The Ph.D. in Bioinformatics and Computational Biology (BCB) is granted for planning, execution, and defense of original research resulting in significant contributions to the discipline's body of knowledge. Moreover, the BCB Ph.D. program also requires didactic coursework to prepare the student for research success. Student progress is primarily assessed by: (a) satisfactory coursework performance, (b) the Qualifying Examination, (c) the Dissertation Proposal, and (d) the Dissertation Defense. Courses and the Qualifying Examination are used to ensure that the student has sufficient breadth of knowledge. The Dissertation Proposal is used to ensure that the scope of dissertation research is important, that the plan is well thought out and that the student has sufficient skills and thoughtfulness needed for success. The Dissertation Defense is used to assess the outcomes of the dissertation research, and whether or not the plan agreed upon by the Dissertation Committee has been appropriately followed.

Didactic Curriculum
In consultation with their Academic Advisor and/or Program Director, students must take an appropriate selection of the following Gateway Courses. For example, an incoming student with a Computer Science background would be expected to take 8100 and 8101, but not 8111. All students must complete the Core Courses prior to taking the Qualifying Examination. Each Ph.D. student must complete two Research Rotations in the first year. Each Research Rotation provides a semester of faculty supervised research experience to supplement regular course offerings. Graduate Research Seminar is taken every semester until the semester following advancement to candidacy. Finally, many additional Elective Courses are available,

but are not explicitly required.

Gateway Courses
BINF 8100 Biological Basis of Bioinformatics (3)
BINF 8101 Energy and Interaction in Biological Modeling (3)
BINF 8111/8111L Bioinformatics Programming I/Bioinformatics Programming I Laboratory (3/0)

Core Courses
BINF 8200/8200L Statistics for Bioinformatics/Statistics for Bioinformatics Laboratory (3/0)
BINF 8112/8112L Bioinformatics Programming II/Bioinformatics Programming II Laboratory (3/0)
BINF 8201/8201L Molecular Sequence Analysis/Molecular Sequence Analysis Laboratory (3/0)
BINF 8202/8202L Computational Structural Biology/Computational Structural Biology Laboratory (3/0)

Research Rotations
BINF 8911 Research Rotation I (2)
BINF 8912 Research Rotation II (2)

Graduate Research Seminar
BINF 8600 Bioinformatics Seminar (1)

Qualifying Examination

Prior to defining a research topic, students are required to pass a Qualifying Examination to demonstrate proficiency in bioinformatics and computational biology, as well as competence in fundamentals common to the field. The Qualifying Examination must be passed prior to the fifth semester of residence. It is composed of both written and oral components that emphasize material covered in the Core Courses listed above.

Dissertation Proposal

Each student must present and defend a Ph.D. Dissertation Research Proposal after passing the Qualifying Examination within ten semesters of entering the Program. The Dissertation Proposal defense will be conducted by the student's Dissertation Committee, and will be open to faculty and students. The proposal must address a significant, original and substantive piece of research. The proposal must include sufficient preliminary data and a timeline such that the Dissertation Committee can assess its feasibility.

Dissertation

Each student must complete a well-designed original research contribution, as agreed upon by the student and Dissertation Committee at the Dissertation Proposal. The Ph.D. Dissertation is a written document describing the research and its results, and their context in the sub-discipline. The Dissertation Defense is a public presentation of the findings of the research, with any novel methods that may have been developed to support the conclusions. The student must present the Dissertation and defend its findings publicly, and in a private session with the Dissertation Committee immediately thereafter.

M.S. IN BIOINFORMATICS

A unique master's degree merging the biological sciences and computer technology, the Professional Science Master's (PSM) program leading to the M.S. in Bioinformatics is an interdisciplinary program at the intersection of the disciplines of Biology, Chemistry, Mathematics and Statistics, Computing and Informatics, and Engineering. It is expected that students entering the program will have completed an undergraduate major in either a life science or a quantitative discipline. The degree requires additional training and demonstrated competence in both life sciences and scientific programming. The PSM program is structured to provide students with the skills and knowledge to develop, evaluate, and deploy bioinformatics and computational biology applications. The program is designed to prepare students for employment in the biotechnology sector, where the need for knowledgeable life scientists with quantitative and computational skills has exploded in the past decade.

Additional Admission Requirements

In addition to the general requirements for admission to the Graduate School, the following are required for study toward the M.S. 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 300 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 M.S. in Bioinformatics degree requires a minimum of 40 34 graduate credit hours, and a minimum of 36 30 credit hours of formal coursework. A minimum of 24 credit hours presented toward an M.S.in Bioinformatics must be from courses numbered 6000 or higher. A maximum of 6 hours of graduate credit may be transferred from other institutions.

Total Hours Required

The PSM program requires 40 34 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 M.S. in Bioinformatics degree, all students will be required to take a general curriculum that includes a two-year sequence of courses as described below:

Core Requirements

Gateway Course

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

Core Bioinformatics Courses

Gateway courses prepare students for the required **Core** courses. All students must take BINF 6101 (Energy and Interaction in Biological Modeling), BINF 6112/6112L (Bioinformatics Programming II/Bioinformatics Programming II Laboratory), BINF 6200/6200L (Statistics for Bioinformatics/Statistics for Bioinformatics Laboratory), BINF 6201/6201L(Molecular Sequence Analysis/Molecular Sequence Analysis Laboratory), BINF 6203/6203L (Genomics/Genomics Laboratory), and BINF 6211/6211L (Design and Implementation of Bioinformatics Databases/Design and Implementation of Bioinformatics Databases Laboratory). All students must also take either BINF 6203/6203L (Genomics/Genomics Laboratory) or BINF 6202/6202L (Computational Structural Biology/Computational Structural Biology Laboratory). A student who has previously taken a course with a syllabus that closely follows one of the course courses may test out of the core requirement by passing a written exam, and may then substitute an advanced elective for the required core course.

The **Gateway** Courses

courses are The department offers two 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 without preparatory coursework in computing or biology may need to to take the **Gateway** course that is appropriate for their background. These courses are not required core courses for all students, but are designed to satisfy core course prerequisites for students who have not encountered the material presented in a previous course. For students entering from computing backgrounds, BINF 6100 (Biological Basis of Bioinformatics), should be chosen, while students entering from biological science backgrounds should choose BINF 6111/6111L (Bioinformatics Programming I/ Bioinformatics Programming I Laboratory).

Professional Preparation Requirement

Students are required to take at least 6 credit hours of electives designed to prepare them to function effectively and ethically in a professional environment. All PSM in Bioinformatics students are required to enroll in BINF 6152 (Program and Professional Orientation) (1credit), BINF 6151 (Professional Communications) (1credit) and BINF 6153 (Career Development) (1credit). The remaining PLUS credits may be chosen from a list of recommended electives, which include BINF 5171 (Business of Biotechnology), BINF 5191 (Biotechnology and the Law), PHIL 6050 (Research Ethics), and ITIS

6362 (Information Technology Ethics, Policy, and Security). Additional elective choices that may fulfill this requirement can be identified by the student and the PSM Executive Committee.

Electives
The remaining 6 credit hours of ~~formal~~ required coursework can be ~~completed in~~satisfied by elective ~~coursework~~courses. The PSM Graduate Coordinator, in conjunction with the Executive Committee. will review the student's plan of study each semester.

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

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

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

Genomic Biology Cluster
BINF 6205 Computational Molecular Evolution (3)
BINF 6350/6350L Biotechnology and Genomics Laboratory/Biotechnology and Genomics Hands on Laboratory (3/0)
BINF 6310/6310L Advanced Statistics for Genomics/Advanced Statistics for Genomics Laboratory (3/0)
BINF 6318 Computational Proteomics and Metabolomics (3)

Modeling and Simulation Cluster
BINF 6202/6202L Computational Structural Biology/Computational Structural Biology Laboratory (3/0)
BINF 6204 Mathematical Systems Biology (3)
BINF 6210 Machine Learning for Bioinformatics (3)
BINF 6311 Biophysical Modeling (3)

Computing and Technology Cluster
BINF 6210 Machine Learning for Bioinformatics (3)
BINF 6310/6310L Advanced Statistics for Genomics/Advanced Statistics for Genomics Laboratory (3/0)
BINF 6380/6380L Advanced Bioinformatics Programming/Advanced Bioinformatics Programming Laboratory (3/0)
BINF 6382/6382L Accelerated Bioinformatics Programming/Accelerated Bioinformatics Programming Laboratory (3/0)

Other Requirements
Bioinformatics Seminar and Internship
In addition to ~~33~~30 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 Principles of Team Science (BINF6399), internal or external internship (BINF 6400) or a faculty-supervised original research project leading to a thesis (BINF 6900).

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

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

GRADUATE CERTIFICATE IN BIOINFORMATICS APPLICATIONS

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

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

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

BINF 6200/6200L Statistics for Bioinformatics/Statistics for Bioinformatics Laboratory (3/0)
BINF 6203/6203L Genomics/Genomics Laboratory (3/0)

And two of the following:
BINF 6201/6201L Molecular Sequence Analysis/Molecular Sequence Analysis Laboratory (3/0)
BINF 6211/6211L Design and Implementation of Bioinformatics Databases/ Design and Implementation of Bioinformatics Databases Laboratory(3/0)
BINF6215 Bioinformatics Pipeline Programming (3)
BINF 6350/6350L Biotechnology and Genomics Laboratory/Biotechnology and Genomics Hands on Laboratory (3/0)

If a student wishes to enter the program having completed coursework that is equivalent to one or more of the core requirements, the requirements may be waived at the discretion of the certificate coordinator. In this case, the required 12 credit hours may be selected from other advanced graduate courses offered by the Department of Bioinformatics and Genomics.

Transfer credit may not be applied toward this certificate.

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

GRADUATE CERTIFICATE IN BIOINFORMATICS TECHNOLOGY

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

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

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

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

If the bachelor's degree is in life sciences:
BINF 6200/6200L Statistics for Bioinformatics/Statistics for Bioinformatics Laboratory (3/0)
BINF 6111/6111L Bioinformatics Programming I/Bioinformatics Programming I Laboratory (3/0)
BINF 6112/6112L Bioinformatics Programming II/Bioinformatics Programming II Laboratory (3/0)
BINF 6203/6203L Genomics/Genomics Laboratory (3/0)

If the bachelor's degree is in computing or mathematics:
BINF 6200/6200L Statistics for Bioinformatics/Statistics for Bioinformatics Laboratory (3/0)
BINF 6100 Biological Basis of Bioinformatics (3)
BINF 6112/6112L Bioinformatics Programming II/Bioinformatics Programming II Laboratory (3/0)
BINF 6203/6203L Genomics/Genomics Laboratory (3/0)

And one of the following courses:
BINF 6201/6201L Molecular Sequence Analysis/Molecular Sequence Analysis Laboratory (3/0)
BINF 6211/6211L Design and Implementation of Bioinformatics Databases/Design and Implementation of Bioinformatics Databases Laboratory (3/0)

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

Transfer credit may not be applied toward this certificate.

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

COURSES IN BIOINFORMATICS (BINF)

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

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

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

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

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

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

BINF 6111L. Bioinformatics Programming I Laboratory. (0) Corequisite: BINF6111. Students will gain hands-on experience in programming to solve bioinformatics problems. *(Fall)*

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

BINF 6112L. Bioinformatics Programming II Laboratory. (0) Corequisite: BINF 6112L or permission of instructor. Students will gain hands-on experience in programming to solve bioinformatics problems *(Spring)*

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

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

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

BINF 6200. Statistics for Bioinformatics. (3) Corequisite: BINF6200L. Prerequisite: Permission of the department. The course grade includes the student's performance in BINF 6200L, which is a required co-requisite. Introduces students to statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. *(Fall)*

BINF 6200L. Statistics for Bioinformatics Laboratory. (0) Corequisite: BINF6200. The aim of this lab course is to introduce R and its application in solving common statistical problems in bioinformatics. Basic relevant concepts from probability, probability distributions, and statistical inference will be introduced and illustrated by examples from bioinformatics applications using R. *(Fall)*

BINF 6201. Molecular Sequence Analysis. (3) Corequisite: BINF6201L**.** Prerequisite: BINF 6100 or equivalent. The course grade includes the student's performance in BINF 6201L, which is a required co-requisite. This course introduces the basic computational methods and open sources software commonly used in molecular sequence analysis. The course covers biological sequence data formats and major public databases, concepts of computer algorithms and complexity, introductions to principle components analysis and data clustering methods, dynamics of genes in populations, evolutionary models of DNA and protein sequences, derivation of amino acid substitution matrices, algorithms for pairwise sequence alignments and multiple sequence alignments, algorithms for fast sequence database search, methods for molecular phylogenetic analysis, hidden Markov models and neural networks for sequence pattern and family recognition, and introductions to genome evolution and omics data analysis. *(Fall)*

BINF 6201L. Molecular Sequence Analysis Laboratory. (0) Corequisite: BINF6201**.** Prerequisite: BINF 6100 or equivalent. This course provides hands-on experience with common software methods for biological sequence data analysis. Topics include: Basic UNIX utilities, principle component analysis, clustering analysis, global and local pair-wise sequence alignments, multiple sequence alignments, sequence database search methods, phylogenetic tree constructions, hidden Markov models and neural networks. *(Fall)*

BINF 6202. Computational Structural Biology. (3) Corequisite: BINF6202L**.** Prerequisites: BINF 6101 and BINF 6201 or their equivalents. The course grade includes the student's performance in BINF 6202L, which is a required co-requisite. 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)*

BINF6202L**. Computational Structural Biology Laboratory. (0)** Corequisite: BINF6202**.** This course will be able to correctly use and apply (a) structural classification databases; (b) software for visualization of biological structures; (c) computational methods to evaluate and compare biological structures; (d) computational methods to align biological structures; and (f) computational methods to predict biological structures from sequence. (*Fall*)

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

BINF 6203L. Genomics Laboratory. (0) Corequisite: BINF 6203. Prerequisite: BINF 6100 or equivalent. This course provides hands-on experience with software methods for genome-scale data analysis. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Functional classification and gene ontologies. Genome evolution and individual variation. Transcriptomic and epigenetic assay design, data acquisition, and data analysis. *(Spring)*

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

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

BINF 6210. Machine Learning for Bioinformatics. (3) Prerequisites: calculus and BINF6200/6200L. The aim of this 3-credit course is to introduce commonly used machine learning methods in the field of bioinformatics. Topics include dimension reduction using principal component analysis, singular value decomposition, and linear discriminant analysis, clustering using k-means, hierarchical, expectation maximization approaches, classification using k-nearest neighbor and support vector machines. To help understand these methods, basic concepts from linear algebra, optimization, and information theory will be explained. Application of these machine learning methods to solving bioinformatics problems will be illustrated using examples from the literature. *(Fall)*

BINF 6211. Design and Implementation of Bioinformatics Databases (3). Co-requisite: BINF 6211L. Pre-requisite: permission of instructor. The course grade includes the student's performance in BINF6211L, which is a required co-requisite**.** This course introduces the fundamentals of database modeling as used in bioinformatics. By the end of the course the student should be able to: understand different types of data models, know how hierarchical and relational models work and give examples that are widely used for biological databases, understand the capabilities of a standard, open source RDBMS, understand the tasks required for data integration and how to use SQL as a research tool. Students will be introduced to XML and XML Schema, and BioOntologies, as widely used data exchange and organization tools in bioinformatics databases. *(Spring)*

BINF 6211L. Design and Implementation of Bioinformatics Databases Laboratory. (0) Co-requisite: BINF6211. Pre-requisite: permission of instructor. Students will practice skills described in the lecture, particularly design principles for the relational model and using SQL. Students will complete projects in which they design, implement, prototype and use a research biological database\. Students will be able to obtain correctly formatted data from public repositories and will know how to use XML, XMLSchema and BioOntologies as tools in the data integration process. Students will learn to use SQL to create, populate and perform complex queries on genomics databases. *(Spring)*

BINF6215. Bioinformatics Pipeline Programming, (3) Prerequisite: BINF 6203. This course covers the concept of pipelines – assemblies of basic bioinformatics tools and data sources to solve complex data processing problems. The pipeline concept will be introduced with simple UNIX command line methods, and then extended to the use of preconfigured commercial and extensible open-source workflow management systems. Reproducibility of analysis, collection of analytic provenance information, and database integration will also be covered. (*On Demand*)

BINF 6310. Advanced Statistics for Genomics. (3) Corequisite: BINF6310L**.** Prerequisite: BINF 6200 or equivalent. The course grade includes the student's performance in BINF6310L, which is a required co-requisite**.** The class covers canonical linear statistics (t-test, ANOVA, PCA) and their non-parametric equivalents. In addition, we will examine the application of Bayesian statistics, Hidden Markov Models and machine learning algorithms to problems in bioinformatics. Students should have fluency in a high-level programming language (PERL, Java, C#, Python or equivalent) and will be expected, in assignments, to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. *(On demand)*

BINF 6310L. Advanced Statistics for Genomics Laboratory. (0) Corequisite: BINF6310**.** Prerequisite: BINF 6200 or equivalent. This is the laboratory class to accompany BINF 6310. This class allows students to gain hands-on experience with using the R programming language. *(On demand)*

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

BINF 6312. Computational Comparative Genomics. (3) Prerequisite: BINF 6201 or equivalent. Introduces computational methods for comparative genomics analysis. Covers the following topics: (a) the architecture of prokaryotic and eukaryotic

genomes; (b) the evolutionary concept in genomics; (c) databases and resources for comparative genomics; (d) principles and methods for sequence analysis; evolution of genomes; (e) comparative gene function annotation; (f) evolution of the central metabolic pathways and regulatory networks; (g) genomes and the protein universe; (h) cis-regulatory binding site prediction; (i) operon and regulon predictions in prokaryotes; and (j) regulatory network mapping and prediction. *(On demand)*

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

BINF 6318. Computational Proteomics and Metabolomics. (3) Prerequisite: BINF 6200 or equivalent. This 3-credit hour course introduces commonly used computational algorithms, software tools, and databases for analyzing mass spectrometry-based proteomics and metabolomics data. Students will learn: 1) how to implement algorithms for processing raw mass spectrometry data and extracting qualitative and quantitative information about proteins and metabolites, 2) how to align multiple datasets, 3) how to perform differential analysis of proteomics and metabolomics datasets, and 4) how to use commonly used protein and metabolite databases. The course also introduces chromatography, mass spectrometry, and isotopic patterns of proteins and metabolites to provide background information for students to understand the nature of mass spectrometry data. *(On demand)*

BINF 6350. **Biotechnology and Genomics Laboratory (3).**Corequisite: BINF6350L**. Prerequisite: A background in molecular biology and biochemistry or the permission of the instructor. The course grade includes the student's performance in BINF6350L, which is a required co-requisite**. This course introduces students to the molecular biological methods by which samples are converted to a state from which sequence information can be produced. When sequence data is produced in a highly parallel fashion across a large fraction of a genome it is the basis of genomics. For historical reasons the sample put on a sequencer is called a library, and the art of genomics lies in library construction. The experimental design and the technical details of library construction will significantly affect the analyses that are appropriate and the conclusions that can be made. Lectures cover the design of experiments, how to critically read the literature to select an appropriate protocol for a variety of experimental purposes, and follow it to transform a sample into high quality sequence data. Quality control and library validation methods will be explained. Topics will include selecting applications tuned to the experiment design to ensure proper data analysis and interpretation
.*(Fall)*

BINF 6350L. **Biotechnology and Genomics Hands on Laboratory (0);** Co-requisite for BINF6350**. Students will gain hands-on experience producing sequencing templates and libraries, discussed in the lecture. The lab introduces students to the practical skills needed to carry out a series of experiments that result in sequence data. The unifying concept will be to characterize allelic variants of selected genes from related organisms. Students will purify nucleic acid and then produce a selected subset of each genome using PCR. Quality control via spectroscopy, gel electrophoresis and quantitative PCR will be performed. Sequencing libraries will be produced and run on the Ion Torrent PGM and the ABI 3130 Genetic Analyzer. The CLCbio Genomics Workbench software for assessing data quality and identifying polymorphisms will be utilized. Students are expected to keep laboratory notebooks that allow all aspects of experiments to be reconstructed. *(Fall)*

BINF 6380. Advanced Bioinformatics Programming. (3) Corequisite: BINF6380L. Prerequisite: BINF 6112 or equivalent or permission of instructor. The course grade includes the student's performance in BINF6380L, which is a required co-requisite. Advanced algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest, but may include assembly of short read fragments from next-generation sequencing platforms, clustering algorithms, machine learning, development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and "cloud" supercomputers. Students are expected to complete a significant independent project. *(On demand)*

BINF 6380L. Advanced Bioinformatics Programming Laboratory. (0) Corequisite: BINF6380**. Prerequisite: BINF 6112 or equivalent. This is the lab component of 6380. The goal of this class is to obtain hands-on experience with multi-threaded programming. *(On demand)*

BINF 6382. Accelerated Bioinformatics Programming. (3) Corequisite: BINF6382L. Prerequisite: BINF 6112 or equivalent or permission of instructor. The course grade includes the student's performance in BINF 6382L, which is a required co-requisite. Computationally intensive algorithms in bioinformatics with an emphasis placed on the implementation

of bioinformatics algorithms in the context of parallel processing using modern hardware processor accelerators such as GPUs and FPGAs. Topics covered depend on instructor expertise and student interest but may include multi-threaded applications and developing for multi-core processors and for large clusters and other "cloud" computers. Students will be expected to complete a significant independent project. *(On demand)*

BINF 6382L. Accelerated Bioinformatics Programming Laboratory. (0) Prerequisite: BINF 6112 or equivalent or permission of instructor. This is the lab component of 6382. The goal of this class is to obtain hands-on experience with accelerated programming in bioinformatics. *(On demand)*

BINF 6399. Principles of Team Science (3) Prerequisite: Department approval. This course will teach students appropriate project design, implementation and management skills needed to function as a small team solving typical problems in Bioinformatics. The students will be given a realistic problem and be required to develop specifications, deliverables, timelines, and costs. Under faculty supervision, the group will assign roles, responsibilities, and deadlines in order to complete the project and then execute the project. At the end of the course, the group will produce a written document with deliverables, and make a formal presentation of the project. (On demand)

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

BINF 6600. Bioinformatics Seminar. (1) Cross-listed as BINF 8600. Prerequisite: Admission to graduate standing in Bioinformatics. Weekly seminars are given by bioinformatics researchers from within the University and across the world. *(Fall, Spring)*

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

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

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

BINF 8010. Topics in Bioinformatics. (3) Prerequisite: permission of department. Topics in bioinformatics and genomics selected to supplement the regular course offerings. A student may register for multiple sections of the course with different topics in the same semester or in different semesters. *(On demand)*

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

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

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

BINF 8111L. Bioinformatics Programming I Laboratory. (0) Corequisite: BINF8111. Students will gain hands-on experience in programming to solve bioinformatics problems. *(Fall)*

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

BINF 8112L. Bioinformatics Programming II Laboratory. (0) Corequisite: BINF 8112L or permission of instructor. Students will gain hands-on experience in programming to solve bioinformatics problems   *(Spring)*

BINF 8151. Professional Communications. (1) Cross-listed as GRAD 8151. Principles and useful techniques for effective oral presentations, poster presentations, scientific writing, use of references and avoiding plagiarism. Students critique and help revise each other's presentations and learn how to avoid common pitfalls. In addition, students learn how to properly organize and run a meeting. Students prepare a CV, job application letter, and job talk. *(Fall)*

BINF 8200. Statistics for Bioinformatics. (3) Corequisite: BINF8200L. Prerequisite: Permission of the department. The course grade includes the student's performance in BINF 8200L, which is a required co-requisite. Introduces students to statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. *(Fall)*

BINF 8200L. Statistics for Bioinformatics Laboratory. (0) Corequisite: BINF8200. The aim of this lab course is to introduce R and its application in solving common statistical problems in bioinformatics. Basic relevant concepts from probability, probability distributions, and statistical inference will be introduced and illustrated by examples from bioinformatics applications using R. *(Fall)*

BINF 8201. Molecular Sequence Analysis. (3) Corequisite: BINF8201L**.** Prerequisite: BINF 8100 or equivalent. The course grade includes the student's performance in BINF 8201L, which is a required co-requisite. This course introduces the basic computational methods and open sources software commonly used in molecular sequence analysis. The course covers biological sequence data formats and major public databases, concepts of computer algorithms and complexity, introductions to principle components analysis and data clustering methods, dynamics of genes in populations, evolutionary models of DNA and protein sequences, derivation of amino acid substitution matrices, algorithms for pairwise sequence alignments and multiple sequence alignments, algorithms for fast sequence database search, methods for molecular phylogenetic analysis, hidden Markov models and neural networks for sequence pattern and family recognition, and introductions to genome evolution and omics data analysis. *(Fall)*

BINF 8201L. Molecular Sequence Analysis Laboratory. (0) Corequisite: BINF8201**.** Prerequisite: BINF 8100 or equivalent. This course provides hands-on experience with common software methods for biological sequence data analysis. Topics include: Basic UNIX utilities, principle component analysis, clustering analysis, global and local pair-wise sequence alignments, multiple sequence alignments, sequence database search methods, phylogenetic tree constructions, hidden Markov models and neural networks. *(Fall)*

BINF 8202. Computational Structural Biology. (3) Corequisite: BINF8202L**.** Prerequisites: BINF 8101 and BINF 8201 or their equivalents. The course grade includes the student's performance in BINF 8202L, which is a required co-requisite. 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)*

BINF8202L. **Computational Structural Biology Laboratory. (0)** Corequisite: BINF8202**.** This course will be able to correctly use and apply (a) structural classification databases; (b) software for visualization of biological structures; (c) computational methods to evaluate and compare biological structures; (d) computational methods to align biological structures; and (f) computational methods to predict biological structures from sequence. (*Fall*)

BINF 8203. Genomics. (3) Prerequisite: BINF 8100 or equivalent. Surveys the application of high-throughput molecular biology and analytical biochemistry methods and data interpretation for those kinds of high volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern genomics technology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: genome sequencing and assembly, annotation, and comparison; genome evolution and individual variation; function

prediction; gene ontologies; transcription assay design, data acquisition, and data analysis; metabolic pathways and databases and their role in genome analysis. *(Spring)*

BINF 8203L. Genomics Laboratory. (0) Co-requisite: BINF 8203. Prerequisite: BINF 8100 or equivalent. This course provides hands-on experience with software methods for genome-scale data analysis. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Functional classification and gene ontologies. Genome evolution and individual   variation. Transcriptomic and epigenetic assay design, data acquisition, and data analysis. *(Spring)*

BINF 8204. Mathematical Systems Biology. (3) Prerequisites: BINF 8200 and BINF 8210 or equivalents. Introduces basic concepts, principles and common methods used in systems biology. 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; and the rules for gene regulation. *(Spring)*

BINF 8205. Computational Molecular Evolution. (3) Prerequisites: BINF 8200 and BINF 8201, or permission of the instructor. Major aspects of molecular evolution and phylogenetics with an emphasis on the modeling and computational aspects of the fields. Topics 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 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. Machine Learning for Bioinformatics. (3) Prerequisites: calculus and BINF8200/8200L. The aim of this 3-credit course is to introduce commonly used machine learning methods in the field of bioinformatics. Topics include dimension reduction using principal component analysis, singular value decomposition, and linear discriminant analysis, clustering using k-means, hierarchical, expectation maximization approaches, classification using k-nearest neighbor and support vector machines. To help understand these methods, basic concepts from linear algebra, optimization, and information theory will be explained. Application of these machine learning methods to solving bioinformatics problems will be illustrated using examples from the literature. *(Fall)*

BINF 8211. Design and Implementation of Bioinformatics Databases. (3) Co-requisite: BINF 8211L. Pre-requisite: permission of instructor. The course grade includes the student's performance in BINF8211L, which is a required co-requisite**.** This course introduces the fundamentals of database modeling as used in bioinformatics. By the end of the course the student should be able to: understand different types of data models, know how hierarchical and relational models work and give examples that are widely used for biological databases, understand the capabilities of a standard, open source RDBMS, understand the tasks required for data integration and how to use SQL as a research tool. Students will be introduced to XML and XML Schema, and BioOntologies, as widely used data exchange and organization tools in bioinformatics databases. *(Spring)*

BINF 8211L. Design and Implementation of Bioinformatics Databases Laboratory. (0) Co-requisite: BINF8211. Pre-requisite: permission of instructor. Students will practice skills described in the lecture, particularly design principles for the relational model and using SQL. Students will complete projects in which they design, implement, prototype and use a research biological database\. Students will be able to obtain correctly formatted data from public repositories and will know how to use XML, XMLSchema and BioOntologies as tools in the data integration process. Students will learn to use SQL to create, populate and perform complex queries on genomics databases. *(Spring)*

BINF 8310. Advanced Statistics for Genomics. (3) Corequisite: BINF8310L**.** Prerequisite: BINF 8200 or equivalent. The course grade includes the student's performance in BINF8310L, which is a required co-requisite**.** The class covers canonical linear statistics (t-test, ANOVA, PCA) and their non-parametric equivalents. In addition, we will examine the application of Bayesian statistics, Hidden Markov Models and machine learning algorithms to problems in bioinformatics. Students should have fluency in a high-level programming language (PERL, Java, C#, Python or equivalent) and will be expected, in assignments, to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. *(On demand)*

BINF 8310L. Advanced Statistics for Genomics Laboratory. (0) Corequisite: BINF8310**.** Prerequisite: BINF 8200 or equivalent. This is the laboratory class to accompany BINF 6310. This class allows students to gain hands-on experience with using the R programming language. *(On demand)*

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

BINF 8312. Computational Comparative Genomics. (3) Prerequisite: BINF 8201 or equivalent. 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; and regulatory network mapping and prediction. *(On demand)*

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

BINF 8318. Computational Proteomics and Metabolomics. (3) Prerequisites: BINF 8200 or equivalent. This 3-credit hour course introduces commonly used computational algorithms, software tools, and databases for analyzing mass spectrometry-based proteomics and metabolomics data. Students will learn: 1) how to implement algorithms for processing raw mass spectrometry data and extracting qualitative and quantitative information about proteins and metabolites, 2) how to align multiple datasets, 3) how to perform differential analysis of proteomics and metabolomics datasets, and 4) how to use commonly used protein and metabolite databases. The course also introduces chromatography, mass spectrometry, and isotopic patterns of proteins and metabolites to provide background information for students to understand the nature of mass spectrometry data.. *(On demand)*

BINF 8350. **Biotechnology and Genomics Laboratory (3).** Co-requisite: BINF8350L**.** Prerequisite: A background in molecular biology and biochemistry or the permission of the instructor. The course grade includes the student's performance in BINF8350L, which is a required co-requisite**.** This course introduces students to the molecular biological methods by which samples are converted to a state from which sequence information can be produced. When sequence data is produced in a highly parallel fashion across a large fraction of a genome it is the basis of genomics. For historical reasons the sample put on a sequencer is called a library, and the art of genomics lies in library construction. The experimental design and the technical details of library construction will significantly affect the analyses that are appropriate and the conclusions that can be made. Lectures cover the design of experiments, how to critically read the literature to select an appropriate protocol for a variety of experimental purposes, and follow it to transform a sample into high quality sequence data. Quality control and library validation methods will be explained. Topics will include selecting applications tuned to the experiment design to ensure proper data analysis and interpretation
.*(Fall)*

BINF 8350. **Biotechnology and Genomics Hands on Laboratory (0);** Co-requisite for BINF8350**.** Students will gain hands-on experience producing sequencing templates and libraries, discussed in the lecture. The lab introduces students to the practical skills needed to carry out a series of experiments that result in sequence data. The unifying concept will be to characterize allelic variants of selected genes from related organisms. Students will purify nucleic acid and then produce a selected subset of each genome using PCR. Quality control via spectroscopy, gel electrophoresis and quantitative PCR will be performed. Sequencing libraries will be produced and run on the Ion Torrent PGM and the ABI 3130 Genetic Analyzer. The CLCbio Genomics Workbench software for assessing data quality and identifying polymorphisms will be utilized. Students are expected to keep laboratory notebooks that allow all aspects of experiments to be reconstructed. *(Fall)*

BINF 8380. Advanced Bioinformatics Programming. (3) Corequisite: BINF8380L. Prerequisite: BINF 8112 or equivalent or permission of instructor. The course grade includes the student's performance in BINF8380L, which is a required co-requisite. Advanced algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics

algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest, but may include assembly of short read fragments from next-generation sequencing platforms, clustering algorithms, machine learning, development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and "cloud" supercomputers. Students are expected to complete a significant independent project. *(On demand)*

BINF 8380L. Advanced Bioinformatics Programming Laboratory. (0) Corequisite: BINF8380**.** Prerequisite: BINF 8112 or equivalent. This is the lab component of 8380. The goal of this class is to obtain hands-on experience with multi-threaded programming. *(On demand)*

BINF 8382. Accelerated Bioinformatics Programming. (3) Corequisite: BINF8382L. Prerequisite: BINF 8112 or equivalent, or permission of instructor. The course grade includes the student's performance in BINF 8382L, which is a required co-requisite. Computationally intensive algorithms in bioinformatics with an emphasis placed on the implementation of bioinformatics algorithms in the context of parallel processing using modern hardware processor accelerators such as GPUs and FPGAs. Topics covered depend on instructor expertise and student interest but may include multi-threaded applications and developing for multi-core processors and for large clusters and other "cloud" computers. Students are expected to complete a significant independent project. *(On demand)*

BINF 8382L. Accelerated Bioinformatics Programming Laboratory. (0) Corequisite: BINF8382. Prerequisite: BINF 8112 or equivalent or permission of instructor. This is the lab component of 8382. The goal of this class is to obtain hands-on experience with accelerated programming in bioinformatics. *(On demand)*

BINF 8600. Bioinformatics Seminar. (1) Cross-listed as BINF 6600. 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. May be repeated for credit. *(Fall, Spring)*

BINF 8601. Bioinformatics Journal Club. (1) Prerequisite: 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. Bioinformatics Research Rotation I. (2) Faculty supervised research experience in bioinformatics to supplement regular course offerings. *(Fall, Spring)*

BINF 8912. Bioinformatics Research Rotation II. (2) Faculty supervised research experience in bioinformatics to supplement regular course offerings. *(Fall, Spring)*

BINF 8991. Doctoral Dissertation Research. (1-9) Individual investigation culminating in the preparation and presentation of a doctoral dissertation. A student may register for multiple sections of this course in the same semester or different semesters. *(Fall, Spring, Summer)*