UNC CHARLOTTE
College of Computing and Informatics

Department of Bioinformatics and Genomics
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University of North Carolina at Charlotte BINF 1-7-11

New Undergraduate Course and Curriculum Proposal

Originating Unit: Department of Bioinformatics and Genomics

Title: Course and Curriculum additions and changes in Bioinformatics and Genomics:
Proposal for the development of an undergraduate minor in Bioinformatics and Genomics
Proposals for the development of 12 new BINF designation undergraduate courses
Proposal for renumbering of the existing undergraduate course BINF 4650 to BINF 4450
Proposal for the removal (deletion) of the existing undergraduate course BINF 4201

Catalog Copy:

Bioinformatics and Genomics Minor. Designed to introduce students to the collection, informatics analysis and interpretation of data derived from genomic and biological macromolecular investigations, this minor field of study will provide students with a foundation of understanding and the computing skill necessary to communicate in the increasingly data-centric life sciences. In addition to gaining first-hand experience with current technologies for high-throughput data generation, students will receive training in up-to-date methods for data handling and interpretation while developing an understanding of critical issues in bioinformatics research design, statistical data analysis, and the application of genomics domain knowledge.

Program requirements:

The minor in Bioinformatics and Genomics requires 19 credit hours of coursework consisting of the following required courses.

- BINF 1101: Introduction to Bioinformatics and Genomics
- BINF 2101: Genomic Methods
- BINF 2101L: Genomic Methods Lab
- BINF 2111: Introduction to Bioinformatics Computing
- BINF 2121: Statistics for Bioinformatics
- BINF 3101: Sequence Analysis
- BINF 4600: Bioinformatics Seminar

BINF 1101 Introduction to Bioinformatics and Genomics (3). Designed to introduce students to the genomics perspective in the life sciences, this course combines a general introduction to genomic technologies and the bioinformatics methods used to analyze genome-scale data with a presentation of real world scientific problems where these technologies are having an impact. This course fulfills a general education science requirement. (*Fall*).

BINF 2101 Genomic Methods (3) Prerequisite: BIOL 1101 and 1101L [Principles of Biology I with Lab] or BIOL 2120 [General Biology I] or consent of instructor. Prerequisite or Corequisite: BINF

1101 [Introduction to Bioinformatics]; Corequisite: BINF2101L; Lecture topics are intended to introduce students to core concepts in genomics that allow bench scientists to acquire large datasets in a high-throughput manner as well as address the computational methods used to analyze these data resources. (Spring).

BINF 2101L Genomic Methods Lab (2) Corequisite: BINF 2101 [Genomic Methods]; This is the laboratory component of the genomics methods laboratory course. Labs are intended to give students hands-on experience in setting up and performing experiments with an emphasis on nucleic acid and protein profiling, understanding and trouble-shooting published protocols, and bioinformatically interpreting the data generated. (Spring).

BINF 2111 Introduction to Bioinformatics Computing (4) Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics]. This course introduces fundamentals of programming for bioinformatics (sometimes called “scripting”) using current programming languages and paradigms. This class will introduce both the language and the use of the language within a Unix environment, demonstrating how interpreted languages serve both as a useful tool for writing and testing programs interactively and as a powerful data analysis and processing tool for bioinformatics. (Fall).

BINF 2121: Statistics for Bioinformatics (3) Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics and Genomics]. Prerequisite: Satisfactory completion of either MATH 1103, MATH 1120, MATH 1121, MATH 1241, STAT 1220, STAT 1221, STAT 2122 or permission of instructor based on sufficient demonstration of foundational mathematics concepts. 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 while exploring the use of the R and Bioconductor software for biostatistical analysis. (*Spring*)

BINF 3101 Sequence Analysis (3) Prerequisite or corequisite: BINF 2101 [Molecular Genomics Laboratory Methods and Technologies] or consent of instructor. This course covers the purpose, application, and biological significance of bioinformatics methods that identify sequence similarity, methods that rely on sequence similarity to produce models of biological processes and systems, as well as methods that use sequence characteristics to predict functional features in genomic sequence data. (Fall).

BINF 3111 Bioinformatics Algorithms (4) Prerequisite: ITCS 1212L [Programming I] or equivalent programming experience. Prerequisite or corequisite: BINF 3101 [Sequence Analysis]. This course introduces common algorithms and data structures used in Bioinformatics and Genomics. Consideration is given to the optimization and appropriate use of both through guided laboratory exercises. (Spring).

BINF 3211 Bioinformatics Databases and Data Mining Technologies (3) Prerequisite: BINF 1101 [Introduction to Bioinformatics]. This is a lecture course that incorporates extensive hands-on exercises, some of which will be done in class. Lecture topics are intended to introduce students to core concepts in both database management system theory and implementation and in data modeling for genomics data types. Exercises are intended to give students practical experience in setting up and populating a database, using public data repositories and using standard tools for retrieving data (SQL), and further, using existing tools for data mining and visualization of genomics data types. Emphasis will be placed on standards and emerging practices. (Spring).

BINF 3900 Undergraduate Research (1-3). Prerequisites: BINF 1101 and Permission of the instructor. Enables students in the Bioinformatics and Genomics program to initiate research projects in their respective fields of interest and to interact with faculty in pursuing research experience. May be repeated for credit. (Fall, Spring, Summer).

BINF 4101 Computational Systems Biology (3) Prerequisite: BINF 3101 [Sequence Analysis]. This course will cover the process of reconstructing complex biological networks. Reconstruction of metabolic networks, regulatory networks and signaling networks using bottom-up and top-down approaches will be addressed using collections of historical data as well as departmentally generated data. The principles underlying high-throughput experimental technologies and examples given on how this data is used for network reconstruction, consistency checking, and validation will be covered throughout the semester. (Fall).

BINF 4111 Structural Bioinformatics (3) Prerequisite: BINF 3101 [Sequence Analysis]. This course will cover: (i.) the physical forces that shape biological molecules, assemblies and cells; (ii.) overview of protein and nucleic acid structure; (iii.) experimental methods of structure determination; (iv.) data formats and software for structure visualization; (v.) computational methods to evaluate structure; (vi.) structural classification; (vii.) structure alignment; (viii.) computational algorithms for structure prediction; and (ix.) structural analysis of disease causing mutations. (Spring).

~~**BINF 4201. Introduction to Bioinformatics. (4)** Prerequisites: BIOL 2120 and BIOL 2130 or equivalent. Introduction to biological databases, commonly-used bioinformatics software for molecular sequence and structure analysis, and application of bioinformatics analysis in biological research. (Fall)~~

BINF 4450 Senior Project (3) Prerequisites: senior standing and permission of the department. An individual or group project in the teaching, theory, or application of bioinformatics, genomics, or computational biology under the direction of a faculty member. Projects must be approved by the department before they can be initiated. (On demand)

BINF 4600 Bioinformatics and Genomics Seminar (1) Prerequisite: BINF 3101 [Sequence Analysis] or consent of instructor. This course is a senior level seminar course designed to introduce students to the research being conducted in both the Bioinformatics and Genomics Department here at UNCC as well as through invited speakers from other universities. (Spring).

S Schlueter Jan 2011 UGCC

Undergraduate minor in Bioinformatics and Genomics

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new minor program within the department as part of its developing undergraduate curriculum.

2. Proposed catalog Copy

Bioinformatics and Genomics Minor. Designed to introduce students to the collection, informatics analysis and interpretation of data derived from genomic and biological macromolecular investigations, this minor field of study will provide students with a foundation of understanding and the computing skill necessary to communicate in the increasingly data-centric life sciences. In addition to gaining first-hand experience with current technologies for high-throughput data generation, students will receive training in up-to-date methods for data handling and interpretation while developing an understanding of critical issues in bioinformatics research design, statistical data analysis, and the application of genomics domain knowledge.

Program requirements:

The minor in Bioinformatics and Genomics requires 19 credit hours consisting of the following required courses.

- BINF 1101: Introduction to Bioinformatics and Genomics
- BINF 2101: Genomic Methods
- BINF 2101L: Genomic Methods Lab
- BINF 2111: Introduction to Bioinformatics Computing
- BINF 2121: Statistics for Bioinformatics
- BINF 3101: Sequence Analysis
- BINF 4600: Bioinformatics Seminar

2. Justification

The Department of Bioinformatics and Genomics was created in 2009 to address the intellectual challenges of utilizing mathematic and computational approaches to glean understanding of biological processes. Computing and information technology is a critical necessity in the investigation and application of modern data-centric life sciences. This minor field of study is designed to be equally applicable to students with either information technology or life sciences related major fields of study.

3. Impact

The emerging trends in genomics rely greatly on the creation and analysis of large-scale datasets. There is a growing demand for students that are trained in a cross-disciplinary manner to understand the biological questions as well as the computational skills to address to the questions utilizing these large datasets. This program is the first step in training undergraduates in the areas of Bioinformatics and Genomics from the creation of genomic scale data to the computational analysis and interpretation of the data.

4. Resources Required to Support Proposal

1. Personnel

    The existing faculty members and teaching assistants of the Department of Bioinformatics and Genomics should be able to meet the initial demands of the program. Additional teaching faculty and graduate assistants (needed to support undergraduate laboratory experience) will be determined by program growth.

2. Physical facility

    Existing classroom, computing, and teaching laboratory facilities in the Bioinformatics building are adequate to meet the initial demands of the program.

3. Equipment and Supplies

    Existing laboratory equipment is adequate and necessary supplies will be provided through existing student laboratory fees.

4. Lab/Network Environment

    Students will use existing equipment and infrastructure of the College of Computing and Information Technology.

5. Audio-Visual

    Current facilities are adequate to support this course.

6. Other Resources

    None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

    Library consultation will be undertaken concordant with the proposal and development of constituent courses.

2. Consultation with Other Departments or Units

    Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

    Approved by the Department of Bioinformatics and Genomics on the 7th day of January 2011.

2. Council on General Education (COGE)

This proposal was not submitted to the COGE.

Gibas Jan 2011 UGCC

BINF 1101

Title: Introduction to Bioinformatics and Genomics

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Introduction to Bioinformatics and Genomics as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 1101 Introduction to Bioinformatics and Genomics (3). Designed to introduce students to the genomics perspective in the life sciences, this course combines a general introduction to genomic technologies and the bioinformatics methods used to analyze genome-scale data with a presentation of real world scientific problems where these technologies are having an impact. This course fulfills a general education science requirement. (*Fall*).

2. Justification

This course covers: a case based, introductory survey of the role of bioinformatics and genomics in biomedical and environmental research. The course is designed to introduce students to the genomics perspective in the life sciences, which emerged in the late 20th and early 21st century due to rapid changes in laboratory technology. By making use of popular media reports to show "science in action" and highlight the issues surrounding new technologies, this course will serve as a broad introduction to possible careers in the fields of bioinformatics and genomics.

3. Impact

This course is designed to serve as a core in the undergraduate Bioinformatics and Genomics minor, and an elective for students in related programs (e.g. Biology, Public Health). Having successfully completed this course, the student will be able to:

- Be familiar with the roles of genomics and bioinformatics in current clinical, biological and environmental research
- Read and evaluate articles in the popular media that report on bioinformatics and genomics studies
- Understand and describe the impact of "genome-scale" approaches on the life sciences
- Understand and describe the importance of bioinformatics in genome-scale research
- Understand and describe several commonly-used bioinformatics methods and their uses

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include all faculty members of the Department of Bioinformatics and Genomics

2. Physical facility

Current teaching classrooms in the Bioinformatics building are adequate.

3. Equipment and Supplies

None identified.

4. Lab/Network Environment

None identified.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will be submitted to the COGE.

7. Course Syllabus for BINF 1101

BINF 1101

INTRODUCTION TO BIOINFORMATICS AND GENOMICS

SYLLABUS

A. COURSE DESCRIPTION

This course covers: a case based, introductory survey of the role of bioinformatics and genomics in biomedical and environmental research. The course is designed to introduce students to the genomics perspective in the life sciences, which emerged in the late 20th and early 21st century due to rapid changes in laboratory technology. The course will combine a general introduction to genomic technologies and the bioinformatics methods used to analyze genome-scale data, with a presentation of real world scientific problems where these technologies are having an impact. We will make use of popular media reports to show "science in action" and highlight the issues surrounding new technologies.

B. PRE- OR CO-REQUISITES

Prerequisite: Prerequisites: Admission to undergraduate standing. This course fulfills a general education science requirement.

C. OBJECTIVES OF THE COURSE

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

- Be familiar with the roles of genomics and bioinformatics in current clinical, biological and environmental research
- Read and evaluate articles in the popular media that report on bioinformatics and genomics studies
- Understand and describe the impact of "genome-scale" approaches on the life sciences
- Understand and describe the importance of bioinformatics in genome-scale research
- Understand and describe several commonly-used bioinformatics methods and their uses

D. INSTRUCTIONAL METHOD

The course is presented in a lecture format which will include the following elements as appropriate: presentation of factual material in a standard lecture format, interactive demonstrations of methods to be applied in assignments, and opportunities for student questions, discussion, and presentations by students.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their ability to answer factual questions regarding material presented in the class and assigned texts. Weekly quizzes (50%), three midterm exams (30%), a final exam (10%), and student participation (10%) will be used to evaluate students' performance in the course.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply:

1. UNIVERSITY INTEGRITY

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

2. ATTENDANCE

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency.

3. GRADING POLICY

Grades will be assigned on the following scale:

A=90-100%

B=80-90%

C=70-80%

D=60-70%

F=<60%

4. ADDITIONAL POLICIES.

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

G. PROBABLE TEXTBOOKS OR RESOURCES

- Campbell and Heyer, *Genomics, Proteomics and Bioinformatics*, or similar.

- Textbook will be supplemented with current health and science articles from mainstream news publications.

H. TOPICAL OUTLINE OF COURSE CONTENT

- Unit 1: What do we measure in genomics research? Cells, genomes, genes, proteins, and pathways – a lightning introduction to the machinery of life.
- Unit 2: Why is it important? Genetic variation and human disease. (Ch.1)
- Unit 3: Sequencing genomes (Ch. 2)
- Unit 4: What do we learn from sequencing and comparing genomes? (Ch. 3)
- Unit 5: Genomic variation, disease and the environment. (Ch. 4)
- Unit 6: What do genes do? Measuring gene expression. (Ch. 5-6)
- Unit 7: Gene expression: what do changes mean? Case studies in cancer, human metagenomics, and the environment. (Ch. 6-7)
- Unit 8: The products of genes: measuring proteins. (Ch. 8)
- Unit 9: The whole genome perspective and human health. (Ch. 9)
- Unit 10: Pathways, circuits, and systems biology – what does the genomic approach really mean for health and the environment? (Ch. 10-11)

Weller/J. Schlueter Jan 2011 UGCC

BINF 2101

Title: Genomic Methods

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Genomic Methods as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 2101 Genomic Methods (3) Prerequisite: BIOL 1101 and 1101L [Principles of Biology I with Lab] or BIOL 2120 [General Biology I] or consent of instructor. Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics]; Corequisite: BINF2101L; Lecture topics are intended to introduce students to core concepts in genomics that allow bench scientists to acquire large datasets in a high-throughput manner as well as address the computational methods used to analyze these data resources. (*Spring*).

2. Justification

Genomics methods are key to understanding more complex biological systems. Data generation and data analyses are frequently conducted by individuals trained in only computational or laboratory based skills. Individuals with cross training in bench work, who can design and carry out targeted experiments, and then analyze the resulting data are in high demand. The proposed course provides students with a sound theoretical understanding of the genomic methods and the bioinformatics data analysis tools in conjunction with the laboratory-based component of this course, BINF2101L.

3. Impact

The course is designed to serve as a core in the undergraduate Bioinformatics and Genomics minor, and an elective for students in related programs (e.g. Biology, Public Health). The expected impact of the course is that students will possess bench skills highly desired by industry employers, and it will make those continuing to graduate school very competitive.

4. Resources Required to Support Proposal

1. Personnel

Faculty qualified to teach this course include Dr. Jessica Schlueter and Dr. Jennifer Weller.

2. Physical facility

Current classrooms in the Bioinformatics Building are adequate to support this course.

3. Equipment and Supplies

None identified.

4. Lab/Network Environment

Current computational infrastructure in the Bioinformatics Building and the College of Computing and Informatics is adequate.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments of Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 2101

Course Description: Students will gain an appreciation for the common molecular patterns that give functional coherence to living organisms, as well as the subtle variations that contribute to the wonderfully diverse, colorful and odd complexity of life on this planet. The conceptual path we will follow takes us from DNA sequence to structure, function, organization, genomics, evolution, and complex systems.

Topics Covered: Genomics data generation methods; technical constraints on experimentally derived data; consistency and reproducibility of data; research design; state of the art technologies.

Scope: The Genomic Methods course will cover theory and techniques of molecular biology as they pertain to genomics data generation: PCR, nucleic acid purification and quality assessment, RT-PCR analysis of RNA, and Ion Torrent sequence analysis of DNA. Bioinformatics tools for data assessment and first-level data assessment for analysis preparation will also be used.

Activities: Students will be introduced to experimental design, genomic techniques and bioinformatic analysis following data generation. The role of this course is to introduce the genomics techniques that will be applied in the laboratory course (BINF2101L) and to bioinformatically analyze data generated in the lab course.

Achievements (bases of assessment): At the end of this course students will be able to: 1) interpret the materials and methods section of a current research article in a prominent genomics journal in the domain of gene expression/regulation, 2) actively demonstrate all of the steps used by the authors, from setting up calculations for reactions to defining the timeline for a set of protocols, 3) identify areas in which insufficient data has been provided for another lab to repeat the experiment, 4) describe what quality control steps should be used at critical points in a protocol, 5) critically evaluate the data analysis methods in a publication and explain whether they agree with the findings and, if not, what additional information, experiments, or analyses would need to be done, giving specific examples of programs that will perform the tasks, and demonstrating those tasks. At the end of the semester students will work in groups to organize 15-minutes oral presentations on the results of the class.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

Overview of Course Contents

I. Present the core principles and methods of molecular biology as they are used for genomics research, with particular emphasis on nucleic acids and proteins, and a focus on regulatory control mechanisms. While this is not a Biotechnology course, since such courses generally focus on cloning, we will use many of the standard toolkits of biotechnology, as they are a source of standardized and well-understood reagents and methods.

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

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

Primary concepts that will be presented include:

A. What are the essential feature and properties of nucleic acids and how are they characterized?

B. What are the essential features and properties of proteins and how are they characterized?

C. What are the regulatory elements that affect gene expression and what common mechanisms control gene regulation?

D. What are the accepted standards and tools for data analysis and visualization, interpretation of results, including placing the results in the context of current publications in the research area; what ethical considerations should be taken into account for conducting genomics and bioinformatics research responsibly.

II. Put into context the lab modules, focusing on using the scientific method in designing effective experiments. For each module we will present the theoretical basis for how laboratory methods work and explore what is currently understood about the uses and limitations of commonly available toolkits.

Primary areas to be covered include

A. For each of the main lab modules, what are the theoretical bases for methods used in the lab?

B. For a given experiment, how do the selected methods have to be modified to accomplish the desired goals?

C. For both intermediate and final data sets, what are the available analysis tools, their strengths and their limitations?

Ongoing activities will include: critical reading of current research articles, evaluating them in written papers, and supervised oral arguments about methods and results.

MODULES: For each of the following modules corresponding events will be undertaken in the laboratory component BINF2101L

Basic Molecular Biology Module (5 weeks)

Laboratory and Environmental Safety (presentation by the Biosafety department)

Responsible Conduct of Research * – this is an ongoing project at the University so we will update the modules as they are made available. Initially we will use the CITI module (described below).

Molar and dilution calculations and records (lab notebooks).

Standard measurement methods for solids and liquids; the meaning of precision, accuracy and significant numbers. Using Excel to calculate mean and SD of measurements, significant figures.

The theory behind gel electrophoresis, analysis and image interpretation of results.

Sample Preparation and PCR Module (5 weeks)

Methods of lysing cells, DNA extraction, RNA extraction, cDNA library construction and the underlying concepts found in protocols from various tissue types (human, plant, bacterial, etc.)

The technology of PCR; primer design rules, and reaction condition optimization, with BioMath Calculators, Oligo3 design tools.

RNA quantification module (RT-PCR) (3 weeks)

Define what qPCR is and how to perform qPCR; how to create and use qPCR standards and common references; correct analysis methods (REST).

DNA sequencing module (Sanger and Ion Torrent) (4 weeks)

Concepts behind Sanger sequencing and next generation sequencing technologies, specifically the Ion Torrent.

Analysis and interpretation of data derived from various sequencing platforms discussed.

- Responsible Conduct of Research: CITI on-line module (https://www.citiprogram.org/). NIH modules. Data acquisition, management, sharing and ownership; HIPPA regulations; publication practices and responsible authorship; collaborative science; research misconduct. Two additional core areas, human subjects and research involving animals.

8. Textbook

1. Class material will be provided as selected readings, online resources and through books reserved at the library. No standard text exists targeting genomics, although there are a large number of Biotechnology and Molecular Biology Lab manuals.

2. The following references are recommended:

Molecular Cloning: A Laboratory Manual. 3rd ed. (2001) by Joe Sambrook, CSHL Press.

‘Calculations for Molecular Biology and Biotechnology’ (2003) by FH Stephenson from Academic Press.

‘Molecular Biotechnology: Principles and Applications of Recombinant DNA’ (2005) by Glick, Pasternak and Patten (4th edition), from ASM Press.

‘Biotechnology’ by John E Smith (2009) from Cambridge University Press (5th edition).

3. Policy

  - Class attendance is mandatory

- Class participation in facilitated discussions and posting of work for group assessment are mandatory.

4. Assessment

Students will be assessed by written summaries of published papers, class attendance and participation, presentations, and final paper. The grading distribution will be:

- Written Journal Article Summaries (40%)
- Class attendance and participation (30%)
- Presentation of Experimental Results (10%)
- Final Experiment Summary (20%)

Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=70-80%
D=60-70%
F=<60%

Weller/J. Schlueter Jan 2011 UGCC

BINF 2101L

Title: Genomic Methods Lab

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Genomic Methods Lab as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 2101L Genomic Methods Lab (2) Corequisite: BINF 2101 [Genomic Methods]; This is the laboratory component of the genomics methods laboratory course. Labs are intended to give students hands-on experience in setting up and performing experiments with an emphasis on nucleic acid and protein profiling, understanding and trouble-shooting published protocols, interpreting the data using computational tools. (*Spring*).

2. Justification

Genomics methods are key to understanding more complex biological systems. Data generation and data analyses are frequently conducted by individuals trained in only computational or laboratory based skills. Individuals with cross training in bench work, who can design and carry out targeted experiments, and then analyze the resulting data are in high demand. Lab courses are, by their nature, expensive and genomics instrumentation even more so. We have a rare ability to fill a training niche, using our state of the art experimental lab. The proposed course provides students with the hands-on experience of creating genomics data and understanding the computational challenges with interpreting the results in conjunction with the lecture-based component of this course, BINF2101.

3. Impact

The course is designed to serve as a core in the undergraduate Bioinformatics and Genomics minor, and an elective for students in related programs (e.g. Biology, Public Health). The expected impact of the course is that students will possess bench skills highly desired by industry employers, and it will make those continuing to graduate school very competitive.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include Dr. Jessica Schlueter, Dr. Jennifer Weller as well as Mr. Timm Hamp and Ms. Deepthi Chaturvedi.

2. Physical facility

The lab component will be conducted in the existing laboratory classroom housed in Bioinformatics 246.

3. Equipment and Supplies

Existing laboratory equipment is adequate and necessary supplies will be provided through existing student laboratory fees.

4. Lab/Network Environment

Current computational infrastructure in the Bioinformatics Building and the College of Computing and Informatics is adequate.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 2101L

Course Description: Students will apply the laboratory techniques and computational analysis methods discussed in BINF2101 to generate genomics data in a laboratory setting.

Topics Covered: Genomics data generation methods; technical constraints on experimentally derived data; consistency and reproducibility of data; research design; state of the art technologies.

Scope: The Genomic Methods Laboratory course will apply the techniques of molecular biology as they pertain to genomics data generation: PCR, nucleic acid purification and quality assessment, RT-PCR analysis of RNA, and Ion Torrent sequence analysis of DNA. Bioinformatics tools for data assessment and first-level data assessment for analysis preparation will also be used. These topics will be introduced in BINF2101, the lecture component of this course.

Activities: Students will participate in a semester-long genomics project that will involve the design and production of data of a novel experiment; in practice we will build up a progression of modules of increasing complexity, each of which builds on previous skills and knowledge. We will start with basic assays and tools and progress to the use of state-of-the art platforms and analysis software. While projects will vary from year to year according to the expertise of the instructor, projects will focus on expression analysis and gene sequence variation analysis, using one or more genomics platforms.

Achievements (bases of assessment): At the end of this course students will be able to: 1) clearly interpret and apply a genomics laboratory protocol, including troubleshooting when experiments do not work properly, 2) Describe the steps in basic genomics protocols and the process of designing a protocol 3) keep acceptable laboratory records and convert experimental results into publication-ready formats. At the end of the semester students will work in groups to organize 15-minutes oral presentations on the results of the class.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

Overview of Course Contents

The lab modules have 4 goals: teach the basic general skills of molecular biology, then teaching students to extract nucleic acid and perform gene-specific and genome-wide tests using PCR and sequencing.

Modules will include:

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

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

1. Basic tools and assays for making solutions, harvesting tissue, purifying nucleic acid and demonstrating its integrity.

2. Design of PCR primers and (RT)-PCR of selected DNAs or RNAs; optimization of PCR reactions and validation of PCR products.

3. qPCR analysis of RNAs in the lab; data extraction and primary analysis methods on the computer.

4. Preparation of DNA templates for Sanger sequencing and Ion Torrent sequencing; data extraction and primary analysis methods on the computer.

Ongoing activities will include: keeping lab notebooks and on-line repositories up to date, while periodic activities will include producing summaries of experimental modules and the final experimental outcome.

MODULES: For each of the following modules corresponding lectures will introduce topics and protocols in the lecture component BINF2101

Basic Molecular Biology Module (5 weeks)

Laboratory and Environmental Safety indroduction in the lab, lab bench setup, assignment to teams.

Application of molar and dilution calculations in making solutions and records (lab notebooks).

Using beakers, flasks and graduated cylinders, pipettes and micropipettes. The proper use of a balance and microbalance for solids. Measuring and correcting the pH of a solution. Storage and labeling of solutions and other reagents.

Spectrophotometry: wavelength settings, sample preparation and blanks (creating dilution series, replicate measurements); using Excel to analyze the data.

Gel Electrophoresis , agarose and acrylamide gel formulation (and safety in preparation and proper disposal), use of size standards, staining and image capture.

Sample Preparation and PCR Module (5 weeks)

Lysing (breaking open) cells, safety and integrity procedures; storage and labeling, proper disposal of waste.

Selective extraction of nucleic acids, methods for the estimation of yields and purity.

Making cDNA from RNA; enrichment methods, random and directed priming.

Application of single-gene PCR reactions to amplify gDNA and cDNA, gel electrophoresis to detect products.

RNA quantification module (RT-PCR) (3 weeks)

Carry out RT-PCR experiments with provided standard samples and class sample.

DNA sequencing module (Sanger and Ion Torrent) (4 weeks)

Preparing a template for Sanger sequencing from the cDNA.

Use of the ABI 3130 DNA sequencer and analysis software.

Preparing a template for Ion Torrent sequencing – step 1: fragmentation and quality assessment.

Preparing a template for Ion Torrent sequencing – step 2: emulsification testing and sample running.

Transferring the data set for quality control analysis, assigning quality scores, preparation for assembly.

8. Textbook

1. Class material will be provided as selected readings, online resources and through books reserved at the library. No standard text exists targeting genomics, although there are a large number of Biotechnology and Molecular Biology Lab manuals.

2. The following references are recommended:

Molecular Cloning: A Laboratory Manual. 3rd ed. (2001) by Joe Sambrook, CSHL Press.

'Calculations for Molecular Biology and Biotechnology' (2003) by FH Stephenson from Academic Press.

'Molecular Biotechnology: Principles and Applications of Recombinant DNA' (2005) by Glick, Pasternak and Patten (4th edition), from ASM Press.

'Biotechnology' by John E Smith (2009) from Cambridge University Press (5th edition).

3. Policy

- Lab attendances are mandatory
- Participation in facilitated discussions and posting of work for group assessment are mandatory.

4. Assessment

Students will be assessed through lab notebook (paper and on-line), written summaries of lab module results, quality of results achieved by team, class attendance and participation, and presentations, and final presentation. The grading distribution will be:

- Lab notebook (40%)
- Lab module summaries (20%)
- Class attendance and participation (30%)
- Presentation of Experimental Results (10%)

Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=70-80%
D=60-70%
F=<60%

Loraine Jan 2011 UGCC

BINF 2111

Title: Introduction to Bioinformatics Computing

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Introduction to Bioinformatics Computing as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 2111 Introduction to Bioinformatics Computing (4) Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics and Genomics]. This course introduces fundamentals of programming for bioinformatics (sometimes called “scripting”) using current programming languages and paradigms. This class will introduce both the language and the use of the language within a Unix environment, demonstrating how interpreted languages serve both as a useful tool for writing and testing programs interactively and as a powerful data analysis and processing tool for bioinformatics. (*Fall*).

2. Justification

The high-throughput production of biological datasets demands knowledge of computing skills necessary to process such data in an automated fashion. Interpreted programming languages such as Python, Perl, and Ruby offer their users the ability to quickly prototype and implement common data processing workflows in order to deal with such demand.

3. Impact

The course is designed to serve as a core in the undergraduate Bioinformatics and Genomics minor, and an elective for students in related programs (e.g. Biology, Computer Science, Software Information Systems). The expected impact of the course is that students will possess computing skills required by industry employers.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include Dr. Ann Loraine, Dr. Shannon Schlueter and Dr. Anthony Fodor.

2. Physical facility

A teaching classroom with access to the department server and to the WWW is required, and exists in Bioinformatics 104.

3. Equipment and Supplies

   None identified.

4. Lab/Network Environment

   Students will utilize existing computational infrastructure present in the Bioinformatics building computing labs and data center. No proprietary software is required.

5. Audio-Visual

   Current facilities are adequate to support this course.

6. Other Resources

   None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

   Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

   Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

   Approved by the Department of Bioinformatics and genomics on 7th January 2011

2. Other Considering Units

   Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

   BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 2111

BINF 2111 - Introduction to Bioinformatics Computing

This course introduces fundamentals of programming for bioinformatics (sometimes called "scripting") using python as the teaching language. Python is both a language (syntax and vocabulary) and an application (the python interpreter). Both are key elements of using python. This class will introduce both the language and the use of the language within a Unix environment (MacOS X), demonstrating how the python interpreter serves both as a useful tool for writing and testing programs interactively and a powerful data analysis and processing tool for bioinformatics.

Textbooks:
None required.

Requirements:
This class assumes *no prior experience with programming*.

Activities & Assignments:
The class will feature guided homework and lab assignments and two longer class projects.

Grading: Grades are based on points earned from assignments and projects as shown in the table below. No late assignments will be accepted without prior arrangement.

Assignment	Number	Value	Total
Labs & Homework	14	50	700
Projects	2	150	300
Total			100

Grades will be assigned using the following scale:

Grade	Points
A	900-1000
B	800-899
C	700-799
D	600-699
F	<600

Attendance Policy:
Students must attend each class, except in case of illness or by pre-arrangement with the instructor. Students who miss class due to illness or by pre-arrangement with the instructor may hand in any assignments due in class via email or subversion (starting week 8), and these must be received before the ***start*** of the class period.

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

Schedule and Assignments

Week	**Topics**	**Assignments**
1	Intro to the Unix shell, Emacs	Unix Lab [1]
2	Interactive programming in python (and using an editor) Shell and environment variables in Unix	Emacs Lab [2]
3	Core data types, operator overloading	Numbers & Strings [3]
4	Lists, tuples, and subscripting	Using Lists [4]
5	Dictionaries	Using Dictionaries [5]
6	Flow Control – Looping and Conditional statements	Flow Control [6]
7	Reading files and processing data The "main" method	readFasta.py [7]
8	Version control, Partner code review	Subversion Lab [8] Partner Code Review [9]
From now on, students turn in assignments using subversion.		
9	Regular expressions and the re module Using built-in objects in python – os, sys	Regular expressions [10]
10	Classes and instances of classes – Using match objects	findMotif.py [11]
11	Defining new classes, named arguments	Range.py [12]
12	Keeping your data private, inheritance	Project One: Modeling genes
13	Errors and Exceptions, Unit Testing	Programming Assignment 4: testProject1.py [13]
14	More on main, option parsing (getopt)	Project Two: countReads.py
15	TBA	
16	Partner code review	Partner code review [14]

Du / S/ Schlueter Jan 2011 UGCC

BINF 2121

Title: Statistics for Bioinformatics

1. Proposal Summary and Catalog Copy

1. Summary

   The Department of Bioinformatics & Genomics proposes to add a new course Statistics for Bioinformatics to its undergraduate curriculum.

2. Proposed Catalog Copy

   BINF 2121: Statistics for Bioinformatics (3) Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics and Genomics]. Prerequisite: Satisfactory completion of either MATH 1103, MATH 1120, MATH 1121, MATH 1241, STAT 1220, STAT 1221, STAT 2122 or permission of instructor based on sufficient demonstration of foundational mathematics concepts. 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 while exploring the use of the R and Bioconductor software for biostatistical analysis. (*Spring*)

2. Justification

Biological systems are intrinsically noisy. Fundamentally, biological systems and the processes driving them are “fuzzy” in nature. As a result, any data or observations derived thence will inevitably be equally fuzzy. Due to this inherently noisy nature, the mathematical techniques used to deal with biological datasets must be able to deal with the uncertainty that is invariably present in the data. Statistical methods are the natural solution to this problem. Hence, it is clear that the effective use of bioinformatics necessitates a sound mastery of the underlying mathematical and in particular statistical principles. Complicating this however are the inherent properties and structure of bioinformatics data. These data generally have one to two orders of magnitude fewer replicates among the finite sampling population while consisting of feature spaces two to three orders of magnitude larger than those seen in financial and engineering fields. Additionally the often non-normal distribution of biological datum compel us to introduce foundational statistical principles in a somewhat altered curricular context in order to avoid common mistakes associated with methodology as applied in other disciplines.

3. Impact

The course is designed to serve as a core course for undergraduate students in Bioinformatics. The expected impact of the course is multi-fold: 1) Students will possess theoretical foundations and practical skills for performing statistical analysis with consideration given to the unique properties inherent in biological data. These skills are essential for students to address scientific questions using statistical methods; 2) The course will lay the necessary foundation for students to gain fundamental understanding of many statistical algorithms widely used in bioinformatics (e.g. BLAST); 3) Students will be inclined to think both quantitatively and qualitatively.

4. Resources Required to Support Proposal

1. Personnel

   Faculty and Staff qualified to teach this course include Dr. Xiuxia Du, Dr. Jun-tao Guo, Dr. Shannon Schlueter, and Dr. Anthony Fodor.

2. Physical Facility

   Current classrooms in the Bioinformatics Building are adequate to support this course.

3. Equipment and Supplies

   None identified.

4. Lab/Network Environment

   None identified.

5. Audio-Visual

   Current facilities are adequate to support this course.

6. Other Resources

   None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

   Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

   Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics & Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B.

Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from Department chair Alan Dow. Full support of this course is acknowledged with suggestions for altered Mathematics and/or Statistics prerequisites. We agree with and value the suggestions made regarding sufficient mathematics background and have revised this proposal to coincide with these suggestions.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

2. Council on General Education (COGE)

This proposal was not submitted to the COGE.

7. Course Syllabus for BINF 2121

BINF 2121: Statistics for Bioinformatics

Professor:	Dr. Shannon D. Schlueter	**Office:**	BINF 263
Email:	sschluet@uncc.edu	**Phone:**	704.687.7698

Conditions of enrollment: Prerequisite or Corequisite: BINF 1101 [Introduction to Bioinformatics and Genomics]. Prerequisite: Satisfactory completion of either MATH 1103, MATH 1120, MATH 1121, MATH 1241, STAT 1220, STAT 1221, STAT 2122 or permission of instructor based on sufficient demonstration of foundational mathematics concepts.

Course description: This course will cover 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 while exploring the use of the R and Bioconductor software for biostatistical analysis.

Objectives of the course: The course is designed to serve as a core course for undergraduate students in Bioinformatics. The expected impact of the course is multi-fold: 1) Students will possess theoretical foundations and practical skills for performing statistical analysis with consideration given to the unique properties inherent in biological data. These skills are essential for students to address scientific questions using statistical methods; 2) The course will lay the necessary foundation for students to gain fundamental understanding of many statistical algorithms widely used in bioinformatics (e.g. BLAST); 3) Students will be inclined to think both quantitatively and qualitatively.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

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

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

Cell phones/pagers: Interruptions to class by cell phones or pagers will not be tolerated. If your cell phone rings, immediately get up and leave class to answer it – do not return. If your cell phone rings subsequently – **your most recent exam grade will be reduced by 10%**. Please do not test me on this. On the other hand, if you have a legitimate reason for wanting your phone left on (i.e., sick relative, pregnant wife, etc.) please let me know before class and we will make arrangements accordingly.

Instructional methods: This course will be primarily based on the traditional lecture format. Some of the course material will be presented via PowerPoint presentations, which will be available on the web at the course website.

Grading: 30% mid-term exam; 3**5%** final exam; **25%** homework; and **10%** final presentation. There will be approximately one homework assignment every two weeks. Final grades will be based on 10% increments (i.e., 90-100% = A; 80-89% = B; 70-79% = C; < 70% = U). The final exam will be cumulative.

Late homework: Unless I've granted an extension beforehand, homework is due at the beginning of class on the day listed. Late homework is minus 5% (of the total) per day. Late homework will not be accepted after one week has elapsed.

Attendance: There is no attendance policy. However, note that I will be less willing to help outside of class those students that do not attend.

Getting help: My office hours are "by appointment".

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

Textbook:

The following reference texts are recommended.

- Wayne W. Daniel. Biostatistics: *A foundation for analysis in the health sciences*. Wiley, 2009.
- Bernard Rosner. *Fundamentals of biostatistics*. Thomson Brooks/Cole, 2006.
- Warren J. Ewens and Gregory R. Grant, *Statistical Methods in Bioinformatics. An Introduction* , 2nd Edition, Springer, 2005
- Peter Dalgaard, "*Introductory Statistics with R*", Springer, 2002 3.
- R. Lyman Ott and Michael Longnecker, "*An Introduction to Statistical Methods and Data Analysis*", 5th Edition, Duxbury, 2000

Topical Outline of Course Content:

- Unit 1: Introduction: the concept of probability with regard to bioinformatics
- Unit 2: Probability - set operations and permutation
- Unit 3: R - an introduction to statistical analysis with R
- Unit 4: Conditional Probability - Bayes' Theorem
- Unit 5: Descriptive statistics – Independence, randomness, and distribution
- Unit 6: Exploring non-normally distributed Bioinformatics data
- Unit 7: Statistical Inference – sampling statistics and visual inspection of Bioinformatics data
- Unit 8: Hypothesis testing – ANOVA, t-tests, correlation clustering
- Unit 9: Linear Regression – clustering and classification

- Unit 10: Bioconductor – R programming for Bioinformatics
- Unit 11: Case Study – the statistics of sequence alignment / sequence search
- Unit 12: Case Study – the statistics of microarray / expression analysis
- Unit 13: Case Study – the statistics of proteomics investigation
- Unit 14: Case Study – the statistics of phylogenomics / phylogenetics and evolutionary analysis

Gibas Jan 2011 UGCC

BINF 3101

Title: Sequence Analysis

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Sequence Analysis as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 3101 Sequence Analysis (3) Prerequisite or corequisite: BINF 2101 and BINF2101L [Genomics Methods and Genomic Methods Lab] or consent of instructor. This course covers the purpose, application, and biological significance of bioinformatics methods that identify sequence similarity, methods that rely on sequence similarity to produce models of biological processes and systems, as well as methods that use sequence characteristics to predict functional features in genomic sequence data. (*Fall*).

2. Justification

Genomics methods are required to understand most complex biological systems. The study and investigation of underlying molecular sequences at the genomic and systems level is foundational knowledge in the field of Bioinformatics. The proposed course provides students with a sound theoretical understanding of the biological sequence data and with up-to-date technical experience with methods for its interpretation.

3. Impact

The course is a core element in the undergraduate Bioinformatics and Genomics minor, and an elective for students in related programs. Having successfully completed this course, the student will be able to:

- Understand fundamentals of molecular evolution at the DNA and protein level
- Understand biological significance of sequence similarity
- Understand and apply commonly used molecular sequence analysis methods
- Identify and navigate online sources of molecular sequence data
- Search and collect data from online data sources using sequence similarity-based methods
- Build appropriate input data sets for sequence alignment, phylogenetic analysis
- Understand and define what makes up the genome of an organism
- Know fundamentals of genome and gene structure in eukaryotes and prokaryotes
- Understand fundamentals of *ab initio* gene and feature prediction based on sequence

4. Resources Required to Support Proposal

1. Personnel

   Faculty and Staff qualified to teach this course include all faculty members of the Department of Bioinformatics and Genomics

2. Physical facility

   Current classrooms in the Bioinformatics Building are adequate to support this course.

3. Equipment and Supplies

   None identified.

4. Lab/Network Environment

   None identified.

5. Audio-Visual

   Current facilities are adequate to support this course.

6. Other Resources

   None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

   Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

   Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

   Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

   Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

   BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 3101

BINF 3101

SEQUENCE ANALYSIS

SYLLABUS

A. COURSE DESCRIPTION

This course covers the purpose, application, and biological significance of bioinformatics methods that identify sequence similarity, methods that rely on sequence similarity to produce models of biological processes and systems, as well as methods that use sequence characteristics to predict functional features in genomic sequence data.

B. PRE- OR CO-REQUISITES

Prerequisite or corequisite: BINF 2201 and 2101L (Genomic Methods and Genomic Methods Lab)

C. OBJECTIVES OF THE COURSE

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

- Understand fundamentals of molecular evolution at the DNA and protein level
- Understand biological significance of sequence similarity
- Understand and apply commonly used molecular sequence analysis methods
- Identify and navigate online sources of molecular sequence data
- Search and collect data from online data sources using sequence similarity-based methods
- Build appropriate input data sets for sequence alignment, phylogenetic analysis
- Understand and define what makes up the genome of an organism
- Know fundamentals of genome and gene structure in eukaryotes and prokaryotes
- Understand fundamentals of ab initio gene and feature prediction based on sequence

D. INSTRUCTIONAL METHOD

The course is presented in a lecture format which will include the following elements as appropriate: presentation of factual material in a standard lecture format, interactive demonstrations of methods to be applied in assignments, and opportunities for student questions, discussion, and presentations by students.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their ability to answer factual questions regarding material presented in the class and assigned texts. Weekly quizzes (25%) and homework assignments (25%), three midterm exams (30%), a final exam (10%), and student participation in class discussions and activities (10%) will be used to evaluate students' performance in the course.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 3101:

1. UNIVERSITY INTEGRITY

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

2. ATTENDANCE

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency.

3. GRADING POLICY

Grades will be assigned on the following scale:

A=90-100%

B=80-90%

C=70-80%

D=60-70%

F=<60%

4. ADDITIONAL POLICIES.

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

G. PROBABLE TEXTBOOKS OR RESOURCES

- Zvelebil and Baum, *Understanding Bioinformatics*, or similar.
- This course is a companion course to BINF 3111, Bioinformatics Algorithms. Both courses use the same text which is divided into complementary sections. This course uses the textbook sections that highlight applications.
- Textbook will be supplemented with articles from the biomedical research literature, which illustrate the application and usefulness of sequence analysis methods.

H. TOPICAL OUTLINE OF COURSE CONTENT

- Unit 1: Nucleic acids, the genetic code, and the structure of genes (Ch.1)
- Unit 2: Proteins: sequence to function (Ch.2)
- Unit 3: Introduction to NCBI (Parts of Ch. 3 and supplementary readings)
- Unit 4: Producing Sequence Alignments (Ch. 4.1-4.5)
- Unit 5: Searching Databases by Sequence (Ch. 4.6-4.7)
- Unit 6: Sequence Motifs and Patterns (Ch. 4.8-4.10)
- Unit 7: Molecular evolution and its consequences (Ch. 7.2)
- Unit 8: Reconstructing and interpreting phylogenetic trees (Ch. 7)
- Unit 9: Predicting genes and features in prokaryotic genomes (Ch. 9)
- Unit 10: Predicting genes and features in eukaryotic genomes (Ch. 9)
- Unit 11: Predicting structure from sequence (Ch. 11)
- Unit 12: Sequence/structure/function relationships (Ch. 13-14)

Gibas Jan 2011 UGCC

BINF 3111

Title: Bioinformatics Algorithms

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Bioinformatics Algorithms as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 3111 Bioinformatics Algorithms (4) Prerequisite: ITCS 1212L [Programming I] or equivalent programming experience. Prerequisite or corequisite: BINF 3101 [Sequence Analysis]. This course introduces common algorithms and data structures used in Bioinformatics and Genomics. Consideration is given to the optimization and appropriate use of both through guided computational laboratory exercises. (*Spring*).

2. Justification

The high-throughput production of biological datasets, or genomics, is fast outpacing the capacity of existing systems and personnel to manage it. There is a widely acknowledged need in both the public and private sectors for individuals who understand, can manage and make use of this data correctly. Students with a thorough understanding of the data types and standards common in the bioinformatics domain in addition to knowledge of efficient methods to process such data will be extremely competitive in the global economy. The proposed course provides students with a sound theoretical understanding of the data and with up-to-date technical experience with computing methods currently in use.

3. Impact

The course is designed to serve as a specialization selective in the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs (e.g. Biology, Software Information Systems). Having successfully completed this course, the student will be able to:

- Understand and implement dynamic programming algorithms for sequence comparison
- Understand principles of multiple sequence alignment
- Understand and implement HMM-based profile models of molecular sequence data
- Understand and describe the principal methods used to generate phylogenetic trees from molecular sequence data
- Understand and describe the principal algorithms for tRNA detection, prokaryotic gene detection, and eukaryotic gene detection
- Understand and describe the principal algorithms used in *ab initio* prediction of structures from protein and nucleic acid sequence

4. Resources Required to Support Proposal

1. Personnel

    Faculty and Staff qualified to teach this course include Dr. Xiuxia Du, Dr. Anthony Fodor, Dr. Cynthia Gibas, Dr. Jun-tao Guo, Dr. Dennis Livesay, Dr. Ann Loraine, Dr. Shannon Schlueter and Dr. ZhengChang Su.

2. Physical facility

    A teaching classroom with access to the department server and to the WWW is required, and exists in Bioinformatics 104.

3. Equipment and Supplies

    None identified.

4. Lab/Network Environment

    Students will utilize existing computational infrastructure present in the Bioinformatics building computing labs and data center. No proprietary software is required.

5. Audio-Visual

    Current facilities are adequate to support this course.

6. Other Resources

    None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

    Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

    Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

    Approved by the Department of Bioinformatics and genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 3111

BINF 3111
BIOINFORMATICS ALGORITHMS
SYLLABUS

A. COURSE DESCRIPTION

This course introduces common algorithms used in Bioinformatics and Genomics.

B. PRE- OR CO-REQUISITES

Prerequisite or corequisite: BINF 3101 Sequence Analysis and ITCS 1212L Programming I or equivalent programming experience

C. OBJECTIVES OF THE COURSE

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

- Understand and implement dynamic programming algorithms for sequence comparison
- Understand principles of multiple sequence alignment
- Understand and implement HMM-based profile models of molecular sequence data
- Understand and describe the principal methods used to generate phylogenetic trees from molecular sequence data
- Understand and describe the principal algorithms for tRNA detection, prokaryotic gene detection, and eukaryotic gene detection
- Understand and describe the principal algorithms used in *ab initio* prediction of structures from protein and nucleic acid sequence

D. INSTRUCTIONAL METHOD

The course is presented in a lecture format which will include the following elements as appropriate: presentation of factual material in a standard lecture format, interactive demonstrations of methods to be applied in assignments, and opportunities for student questions, discussion, and presentations by students.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their ability to answer factual questions regarding material presented in the class and assigned texts. Weekly quizzes (25%) and homework assignments (25%), three midterm exams (30%), a final exam (10%), and student participation in class discussions and activities (10%) will be used to evaluate students' performance in the course.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply to students in BINF 3111:

1. UNIVERSITY INTEGRITY

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

2. ATTENDANCE

Attendance at lecture is required, although exceptions will be made for reasons such as illness or family emergency.

3. GRADING POLICY

Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=70-80%
D=60-70%
F=<60%

4. ADDITIONAL POLICIES.

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

G. PROBABLE TEXTBOOKS OR RESOURCES

- Zvelebil and Baum, *Understanding Bioinformatics*, or similar.
- This course is a companion course to BINF 3101, Sequence Analysis. Both courses use the same text which is divided into complementary sections. This course uses the textbook sections that highlight common algorithms and models of data used in sequence analysis.

H. TOPICAL OUTLINE OF COURSE CONTENT

- Unit 1: Introduction: the concept of an algorithm
- Unit 2: Molecular sequence – biology in the abstract
- Unit 3: Dynamic programming and alignment scoring (Ch. 5.1-5.2)
- Unit 4: Indexing and algorithmic approximations (Ch. 5.3)
- Unit 5: Building, searching with, and aligning sequence profiles (Ch. 6.1-6.3)
- Unit 6: Building multiple sequence alignments (Ch. 6.4-6.6)
- Unit 7: Calculating evolutionary distance (Ch. 8.1)
- Unit 8: Generating single phylogenetic trees (Ch. 8.2)
- Unit 9: Generating and evaluating multiple tree topologies (Ch. 8.3-8.4)
- Unit 10: Algorithms for gene detection in prokaryotes (Ch. 10)
- Unit 11: Algorithms for gene detection and gene model building in eukaryotes (Ch. 10.4-10.7)
- Unit 12: Classification of sequence for structure prediction (Ch. 12)
- Unit 13: Further adventures in data classification: introduction to expression (Ch. 15-16)

Weller Jan 2011 UGCC

BINF 3211

Title: Bioinformatics Databases and Data Mining Technologies

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Bioinformatics Databases and Data Mining Technologies as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 3211 Bioinformatics Databases and Data Mining Technologies (3) Prerequisite: BINF 1101 [Introduction to Bioinformatics and Genomics]. This is a lecture course that incorporates extensive computational exercises, some of which will be done in class. Lecture topics are intended to introduce students to core concepts in both database management system theory and implementation and in data modeling for genomics data types. Exercises are intended to give students practical experience in setting up and populating a database, using public data repositories and using standard tools for retrieving data (SQL), and further, using existing tools for data mining and visualization of genomics data types. Emphasis will be placed on standards and emerging practices. (*Spring*).

2. Justification

The high-throughput production of biological datasets is fast outpacing the capacity of existing systems and personnel to manage it. There is a widely acknowledged need in both the public and private sectors for individuals who understand, manage and make use of this data correctly. Students with active database management skills and thorough understanding of the biological data types and standards will be extremely competitive in the global economy. The proposed course provides students with a sound theoretical understanding of the data and with up-to-date technical experience with the methods currently in use. It is expected that students have taken basic biology and computer literacy courses, but they need not have taken molecular biology or database management system courses, or programming courses in order to succeed.

3. Impact

The course is designed to serve as a specialization selective in the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs (e.g. Biology, Software Information Systems). The expected impact of the course is that students will possess computing skills required by industry employers.

4. Resources Required to Support Proposal

1. Personnel

   Faculty and Staff qualified to teach this course include Dr. Shannon Schlueter and Dr. Jennifer Weller.

2. Physical facility

   A teaching classroom with access to the department server and to the WWW is required, and exists in Bioinformatics 104.

3. Equipment and Supplies

   None identified.

4. Lab/Network Environment

   Current computational infrastructure in the Bioinformatics Building and the College of Computing and Informatics is adequate.

5. Audio-Visual

   Current facilities are adequate to support this course.

6. Other Resources

   None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

   Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

   Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

   Approved by the Department of Bioinformatics and genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 3211

Students will gain an understanding of the wealth and diversity of biological data in public databases, how primary measurements are made and results are stored, what common data models and standards exist for public data, how collaboration and sharing are enabled, how to specify datasets for retrieval, and a number of ways for comparing that retrieved data in order to find meaningful patterns of biological significance. The conceptual path will follow DNA sequence and microarray data through logical representations and show how representation needs have led to a variety of common abstraction layers.

Topics covered: Bioinformatics data warehouses; using databases; database structures for bioinformatics research; methods for biological data mining (clustering, classification, machine learning).

Scope: The Bioinformatics Databases and Data Mining Technologies course will cover relational database theory and implementation in modern database management systems; standards for representing genomics data types, including schemas, ontologies and exchange formats for the primary public data sources. Data models that facilitate either statistical or visual analytic outcomes will be highlighted.

Activities: Students will participate in developing a database that integrates data from two primary gene expression measurement technologies that are state-of-the art in genomics in order to develop the practical skills needs to build and use a genomics data repository. We will use data from a model organism from a central repository, and start with understanding what the measurements are and how to assess their quality and proceed to integration of other data through controlled vocabulary and formal ontologies. Students will learn how to read the experimental reports for important details about the data sets, in order to retrieve the desired subsets. Students will learn to formulate SQL queries to retrieve desired subsets of data, prepare the data for the new schema, load that data into the class database, and then perform simple clustering and classification techniques to look for meaningful patterns in subsets of that data.

Achievements: At the end of this course students will be able to explain the data generation methods commonly used for expression data, identify the correct fields in a public repository that house those measurements, and will be able to identify and use the provided access method to retrieve specific subsets of that data. Students will be able to explain the structure of a local relational database schema developed with and by the class for their project; students will be able to determine the source of fields containing controlled vocabularies and ontologies used to interpret the measurements. Students will be able to formulate SQL statements to retrieve data from the relational schema, and will understand common conversions needed to upload that data into a new schema. Students will understand how to prepare retrieved data for a number of basic data mining operations, including applying simple binning, tags and significance boundaries, for clustering, classification and simple machine learning methods, and will understand what, if any, properties, the data must have for the method to be valid. At the end of the semester students will work in groups to organize 15-minute oral presentations on a specific result of one of these methods.

Topics Outline (more or less by week):

Introduction to Scientific Data
Methods of data organization, storage and retrieval
Data mining workbenches and Bioinformatics databases
Genomics data measurement methods and characteristics
Expression genomics data: public data warehouses
The relational model, schemas and RDBMS
Data loading and retrieval: basic SQL
Modern bioinformatics applications of data mining
Exam I
Statistical classification systems
Classification using AI
Data Clustering
Biological Ontologies
Data integration
Feature selection, extraction and anomaly detection
Project presentations
Final exam

8. Textbook

1. Class material will be provided as selected readings, online resources and through books reserved at the library. No standard text exists for this combination of topics.

2. The following references are recommended:

Andreas Baxevanis and Francois Ouellette (2001) "*Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*" 2nd ed. Wiley-INterscience

Peter Rob and Carlos Coronel (2004) "Database Systems: Design, Implementation and Management" (6th ed) from Course Technology.
Kenneth Baclawski and Tianhua Niu (2005) "*Ontologies for Bioinformatics*" from the MIT Press.

Chen and Lonardi (2009) "*Biological Data Mining*" from Chapman and Hall/CRC

Misbet, Elder and Miner (2009) "*Handbook of Statistical Analysis and Data Mining Applications*" from Academic Press.

Theodoridis and Koutroumbas (2008) “*Pattern Recognition*” from Academic Press

Yike Guo and Robert Grossman (ed.s) “*High Performance Data Mining: Scaling Algorithms, Applications and Systems*” from Kluwer Acaddemic Publishers.

3. Policy

- Class and lab attendances are mandatory
- Class participation in facilitated discussions and posting of work for group assessment are mandatory.

4. University Integrity:

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

5. Assessment

Students will be assessed through quizzes, homework, written summaries of published papers, implementation of team projects, class attendance and participation, and presentations, and two exams. The grading distribution will be:

- Quizzes (10%)
- Homework (10%)
- Written Summaries (10%)
- Class attendance and participation (25%)
- Team Project (25%)
- Presentation of project results (10%)
- Two exams (10% each)

Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=70-80%
D=60-70%
F=<60%

J. Schlueter Jan 2011 UGCC

BINF 3900

Title: Undergraduate Research

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course for undergraduate research as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 3900 Undergraduate Research (1-3). Prerequisites: BINF 1101 [Introduction to Bioinformatics and Genomics] and Permission of the instructor. Enables students in the Bioinformatics and Genomics program to initiate research projects in their respective fields of interest and to interact with faculty in pursuing research experience. May be repeated for credit. (*Fall, Spring, Summer*).

2. Justification

This course is designed to allow students in the Bioinformatics and Genomics undergraduate program to participate in research under the guidance of faculty in the department. Students gain a stronger understanding of the concepts covered in traditional lecture courses through the application of those concepts in a research environment. Students also will be more competitive as they pursue future goals (jobs, graduate school, professional school) following research experiences.

3. Impact

This course is designed to serve as a selective in the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs. Students will have (*i.)* participated in ongoing research in a Bioinformatics and Genomics faculty lab; (*ii.)* be able to explain the process of designing and executing an experiment, either computational or laboratory based; and (*iii.)* maintain records of research conducted as well as provide a write- up of the research experience in manuscript format.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include all faculty members of the Department of Bioinformatics and Genomics

2. Physical facility

Current faculty research labs are adequate to support this course.

3. Equipment and Supplies

None identified.

4. Lab/Network Environment

None identified.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 1101

BINF 3900 – UNDERGRADUATE RESEARCH

A. COURSE DESCRIPTION

This course is designed to allow students in the Bioinformatics and Genomics undergraduate program to participate in research under the guidance of faculty in the department. Students gain a stronger understanding of the concepts covered in traditional lecture courses through the application of those concepts in a research environment. This course will require students to identify a faculty member in Bioinformatics and Genomics to participate in on-going research in their research program. Students make participate in research as an integral part of their educational experience in Bioinformatics and Genomics.

B. PRE- OR CO-REQUISITES

Prerequisites: Prerequisites: BINF 1101 and Permission of the instructor.

C. OBJECTIVES OF THE COURSE

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

- Understand the research project in which they are participating and how their portion of the project integrates with the goals of the project overall
- Read and evaluate articles as they relate to their research project
- Explain the process of designing and executing an experiment
- Maintain records of research conducted in the manner expected by the faculty advisor
- Present their work in a manuscript format at the end of the semester.

D. INSTRUCTIONAL METHOD

The course is course in which the students will interact directly with a Bioinformatics and Genomics faculty member to design a research project, execute the project and provide a write-up of the experience. The methods used for instruction are at the discretion of the faculty advisor.

E. MEANS OF STUDENT EVALUATION

Students will be evaluated on their weekly attendance in the research lab, participation in research experience and the written report at the end of the semester. Grades are assigned on the discretion of the advisor.

F. SPECIFY POLICIES THAT APPLY TO THIS COURSE:

The following policies apply:

1. UNIVERSITY INTEGRITY

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

2. ATTENDANCE

Attendance in the research lab is required, although exceptions will be made for reasons such as illness or family emergency.

3. GRADING POLICY

Grades will be assigned on the following scale:

A=90-100%

B=80-90%

C=70-80%

D=60-70%

F=<60%

4. ADDITIONAL POLICIES.

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

G. PROBABLE TEXTBOOKS OR RESOURCES

- Supplemental texts and manuscripts will be provided by the faculty advisor.

H. TOPICAL OUTLINE OF COURSE CONTENT

- This will vary based upon the project and instructor.

S Schlueter Jan 2011 UGCC

BINF 4101

Title: Computational Systems Biology

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Computational Systems Biology as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 4101 Computational Systems Biology (3) Prerequisite: BINF 3101 [Sequence Analysis]. This course will cover the process of reconstructing complex biological networks. Reconstruction of metabolic networks, regulatory networks and signaling networks using bottom-up and top-down approaches will be addressed using collections of historical data as well as departmentally generated data. The principles underlying high-throughput experimental technologies and examples given on how this data is used for network reconstruction, consistency checking, and validation will be covered throughout the semester. (*On demand*).

2. Justification

The field of computational systems biology represents an integration of concepts and ideas from the biological sciences, engineering disciplines, and computer science. Recent advances in biology, including the human genome project and massively parallel approaches to probing biological samples, have created new opportunities to understand biological problems from a systems perspective. Systems modeling and design are well established in engineering disciplines but are relatively new to biology. Advances in computational systems biology require perspective from multiple disciplinary backgrounds with skill in applying principles and tools from engineering and computer science to solve problems in biology and medicine. The proposed course provides students with this skill and experience.

3. Impact

The course is designed to serve as a selective in the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs. Once completed, students will be able to: (*i.*) describe the interrelation of major biological macromolecules; (*ii.*) explain the algorithms and tools primarily employed to infer network/relational structure in biological systems; and (*iii.*) apply said algorithms to derive biological insight.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include Dr Dennis Livesay and Dr Shannon Schlueter.

2. Physical facility

Current classrooms in the Bioinformatics Building are adequate to support this course.

3. Equipment and Supplies

   None identified.

4. Lab/Network Environment

   None identified.

5. Audio-Visual

   Current facilities are adequate to support this course.

6. Other Resources

   None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

   Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

   Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

   Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

   Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

   BIOL:

   Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

   CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 4101

BINF 4101: Computational Systems Biology

Professor:	Dr. Shannon D. Schlueter	**Office:**	BINF 263
Email:	sschluet@uncc.edu	**Phone:**	704.687.7698

Conditions of enrollment: Prerequisite: BINF 3101 [Sequence Analysis].
Course description: This course will cover the process of reconstructing complex biological networks. Reconstruction of metabolic networks, regulatory networks and signaling networks using bottom-up and top-down approaches will be addressed using collections of historical data as well as departmentally generated data. The principles underlying high-throughput experimental technologies and examples given on how this data is used for network reconstruction, consistency checking, and validation will be covered throughout the semester.

Objectives of the course: Once completed, students will be able to: (*i.*) describe the interrelation of major biological macromolecules; (*ii.*) explain the algorithms and tools primarily employed to infer network/relational structure in biological systems; and (*iii.*) apply said algorithms to derive biological insight.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

Cell phones/pagers: Interruptions to class by cell phones or pagers will not be tolerated. If your cell phone rings, immediately get up and leave class to answer it – do not return. If your cell phone rings subsequently – **your most recent exam grade will be reduced by 10%**. Please do not test me on this. On the other hand, if you have a legitimate reason for wanting your phone left on (i.e., sick relative, pregnant wife, etc.) please let me know before class and we will make arrangements accordingly.

Instructional methods: This course will be primarily based on the traditional lecture format. Some of the course material will be presented via PowerPoint presentations, which will be available on the web at the course website.

Grading: As students tend to differ in their preferred learning style so to do they differ in effective assessment methodology, therefore of the three primary assessment mechanisms student grades will be determined by assigning weights (50/30/15%) to the scoring mechanisms in order of individual student performance. Final grades will be based on 10% increments (i.e., 90-100% = A; 80-89% = B; 70-79% = C; < 70% = U).

Late homework: Unless I've granted an extension beforehand, homework is due at the beginning of class on the day listed. Late homework is minus 5% (of the total) per day. Late homework will not be accepted after one week has elapsed.

Attendance: There is no attendance policy. However, note that I will be less willing to help outside of class those students that do not attend.

Getting help: My office hours are by appointment.

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

Textbook: *Biomolecular Networks: Methods and Applications in Systems Biology*; Chen, Wang, and Zhang; Wiley; 1st edition (2009). In addition, my PowerPoint slides will be available from the course website.

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

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

Livesay Jan 2011 UGCC

BINF 4111

Title: Structural Bioinformatics

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Structural Bioinformatics as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 4111 Structural Bioinformatics (3) Prerequisite: BINF 3101 [Sequence Analysis]. This course will cover: (*i.*) the physical forces that shape biological molecules, assemblies and cells; (*ii.*) overview of protein and nucleic acid structure; (*iii.*) experimental methods of structure determination; (*iv.*) data formats and software for structure visualization; (*v.*) computational methods to evaluate structure; (*vi.*) structural classification; (*vii.*) structure alignment; (*viii.*) computational algorithms for structure prediction; and (*ix.*) structural analysis of disease causing mutations. (*Spring*).

2. Justification

The proposed course provides students with a sound theoretical understanding of structural data resources as well as with up-to-date technical experience with computational structural bioinformatics analysis methods.

3. Impact

The course is designed to serve as a selective in the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs. Once completed, students will be able to: (*i.*) describe the major classes of biological macromolecules; (*ii.*) explain the algorithms primarily employed to characterize macromolecule structure; and (*iii.*) apply said algorithms to derive biological insight.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course include Dr Jun-tao Guo and Dr Dennis Livesay.

2. Physical facility

Current classrooms in the Bioinformatics Building are adequate to support this course.

3. Equipment and Supplies

None identified.

4. Lab/Network Environment

None identified.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and Genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 4111

BINF 4111: Structural Bioinformatics

Professor:	Dr. Dennis R. Livesay	**Office:**	BINF 363
Email:	drlivesa@uncc.edu	**Phone:**	704.687.7995

Conditions of enrollment: Prerequisite: BINF 3101 [Sequence Analysis] and a demonstrated proficiency within biochemistry.

Course description: This course will cover: (*i.*) the physical forces that shape biological molecules, assemblies and cells; (*ii.*) overview of protein and nucleic acid structure; (*iii.*) experimental methods of structure determination; (*iv.*) data formats and software for structure visualization; (*v.*) computational methods to evaluate structure; (*vi.*) structural classification; (*vii.*) structure alignment; (*viii.*) computational algorithms for structure prediction; and (*ix.*) structural analysis of disease causing mutations.

Objectives of the course: Once completed, students will be able to: (*i.*) describe the major classes of biological macromolecules; (*ii.*) explain the algorithms primarily employed to characterize macromolecule structure; and (*iii.*) apply said algorithms to derive biological insight.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

Cell phones/pagers: Interruptions to class by cell phones or pagers will not be tolerated. If your cell phone rings, immediately get up and leave class to answer it – do not return. If your cell phone rings subsequently – **your most recent exam grade will be reduced by 10%**. Please do not test me on this. On the other hand, if you have a legitimate reason for wanting your phone left on (i.e., sick relative, pregnant wife, etc.) please let me know before class and we will make arrangements accordingly.

Instructional methods: This course will be primarily based on the traditional lecture format. Some of the course material will be presented via PowerPoint presentations, which will be available on the web at the course website.

Grading: **25%** exam 1; **25%** exam 2; **25%** final exam; **15%** weekly quizzes; and **10%** homework. There will be approximately one homework assignment every two weeks. Final grades will be based on 10% increments (i.e., 90-100% = A; 80-89% = B; 70-79% = C; < 70% = U). The final exam will be cumulative.

Late homework: Unless I've granted an extension beforehand, homework is due at the beginning of class on the day listed. Late homework is minus 5% (of the total) per day. Late homework will not be accepted after one week has elapsed.

Attendance: There is no attendance policy. However, note that I will be less willing to help outside of class those students that do not attend.

Getting help: My office hours are by appointment.

Curricula materials: *Structural Bioinformatics (Methods of Biochemical Analysis)*; Gu and Bourne; Wiley-Blackwell; 2nd edition (2009). In addition, my PowerPoint slides will be available from the course website. Finally, the curricula will include three Scientific American articles (one per exam) covering related topics from a more biological point of view. These articles will be available from the course website.

Calculators: You are free to use any resources that you want on the homework assignments and classroom exercises. However, I will only allow basic scientific calculators during exams. Cell phone calculators, graphing calculators, and other devices with the capability to save information and have additional functionality programmed are not allowed. If you have a question about your device, please see me with it before the first exam.

Course outline:

• Week 1	The physical forces that shape biomacromolecule structure
• Week 2	Biomacromolecule structure
• Weeks 3-4	Experimental structural biology techniques
• Week 4	***Exam 1***
• Week 5	Data formats and structural visualization (software and styles)
• Weeks 6-7	Analysis of protein structures and quality assurance
• Weeks 8-9	Domain identification and protein classification
• Week 9	***Exam 2***

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

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

Weeks 10-11	Protein structure alignment
Weeks 12-13	Structure prediction
Weeks 14-15	Structural analysis of disease causing mutations
Finals Week	***Final exam***

UNC CHARLOTTE

MEMO FORM
COURSE AND CURRICULUM PROPOSAL

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*To: Janet Levy, Undergraduate Course and Curriculum Committee Chair for the University of North Carolina at Charlotte

From: Shannon Schlueter; Assistant Professor of Bioinformatics and Genomics

Date: January 13, 2011

Re: Removal of Deprecated Undergraduate Survey Course BINF 4201 Introduction to Bioinformatics

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SUMMARY:

The Department of Bioinformatics and Genomic proposes to remove from the university registrar and catalog the undergraduate survey course BINF 4201 Introduction to Bioinformatics. As the accompanying proposal to establish a minor in Bioinformatics and Genomics provides a more robust and substantive coverage of the field, the existing introductory survey course BINF 4201 is no longer necessary.

FOR CONSULTATION WITH OTHER DEPARTMENTS:

1. Does the proposed change affect other departments?
   ________Yes __XX____ No

2. If Yes, please list the other departments affected by the proposed change:

   NONE IDENTIFIED

3. Have you consulted with each department listed in question 2 regarding the proposed change?
   ~~________Yes ________No~~

   NONE IDENTIFIED

4. Result(s) of Consultation(s):

RESOURCES: Indicate the additional resources required, if any, to implement and maintain the proposed change:

No resource requirements have been identified as this proposal solely implements the renumbering of an existing course.

PROPOSED CATALOG COPY:

~~**BINF 4201. Introduction to Bioinformatics. (4)** Prerequisites: BIOL 2120 and BIOL 2130 or equivalent. Introduction to biological databases, commonly-used bioinformatics software for molecular sequence and structure analysis, and application of bioinformatics analysis in biological research. (Fall)~~

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

J Schlueter Jan 2011 UGCC

BINF 4600

Title: Bioinformatics and Genomics Seminar

1. Proposal Summary and Catalog Copy

1. Summary

The Department of Bioinformatics and Genomics proposes to add a new course Bioinformatics Seminar as part of its undergraduate curriculum.

2. Proposed catalog Copy

BINF 4600 Bioinformatics and Genomics Seminar (1) Prerequisite: BINF 3101 [Sequence Analysis] or consent of instructor. This course is a senior level seminar course designed to introduce students to the research being conducted in both the Bioinformatics and Genomics Department here at UNCC as well as through invited speakers from other universities. (*Fall, Spring*).

2. Justification

Education in the sciences is not limited to what we learn in the classroom, much of how we continue learning in sciences is through reading of literature and the attendance of seminars presented by the research community. The proposed course will introduce upper-level undergraduate Bioinformatics and Genomics Minors to reading scientific manuscripts, attending seminars on those areas of research. Students graduating with a science major should experience some level of seminar course as part of a well-rounded training.

3. Impact

The course is designed to serve as a part of the undergraduate Bioinformatics and Genomics program, and an elective for students in related programs. The expected impact of the course is that students will possess the skills to interpret and understand Bioinformatics and Genomics research as it is presented in both manuscript and seminar form.

4. Resources Required to Support Proposal

1. Personnel

Faculty and Staff qualified to teach this course are any of the faculty in the Department of Bioinformatics and Genomics.

2. Physical facility

A large seminar room currently available in Bioinformatics room 105.

3. Equipment and Supplies

None identified.

4. Lab/Network Environment

None required.

5. Audio-Visual

Current facilities are adequate to support this course.

6. Other Resources

None identified.

5. Consultation with the Library and Other Departments or Units

1. Library Consultation

Library consultation was completed January 24, 2011. Library holdings were found to be adequate to support the proposed course. Library consultation reports are attached as Appendix A.

2. Consultation with Other Departments or Units

Departments of Computer Science, Software and Information Systems, Biology, Physics and Optical Science, Chemistry, and Mathematics and Statistics consultations will be sought.

6. Initiation and Consideration of the Proposal

1. Originating Unit

Approved by the Department of Bioinformatics and genomics on 7th January 2011.

2. Other Considering Units

Departmental consultations responses are attached as Appendix B. Summations and resultant actions are described below.

BIOL:

Consultation report received January 21, 2011 from interim department chair Cy Knoblauch. Full support of this course as proposed is acknowledged by the Department of Biology.

CHEM:

Consultation request was acknowledged by department chair Bernadette Donovan-Merkert on January 20, 2011. Response to this request is assumed forthcoming.

CS:

Consultation report received February 2, 2011 from department chair William Ribarsky. Full support of this course as proposed is acknowledged.

MATH:

Consultation report received January 25, 2011 from department chair Alan Dow. Full support of this course as proposed is acknowledged.

PHYS:

Consultation report received February 3, 2011 from interim department chair Patrick Moyer. Full support of this course as proposed is acknowledged.

SIS:

Consultation report received January 21, 2011 from department chair Bill Chu. Full support of this course as proposed is acknowledged.

3. Council on General Education (COGE)

This proposal will not be submitted to the COGE.

7. Course Syllabus for BINF 4600

Students will gain an understanding of the various topics and areas covered under Bioinformatics and Genomics. They will learn how the topics covered in their courses are applied to significant biological questions and how the various areas of research overlap and interconnect. This course will also introduce them to the opportunities in Bioinformatics and Genomics Research.

Topics covered: Reading and understanding scientific manuscripts, understanding research presentations.

Activities: Students will attend seminars as part of the Department of Bioinformatics and Genomics seminar series. In preparation for each seminar students will be assigned 2 research publications relating to the research that will be presented. Students will be expected to read these manuscripts and come to the seminar prepared to ask questions. Students will also pick one seminar topic to do a more in-depth summary paper.

Achievements: At the end of this course students will be able to read, dissect and understand scientific publications as they relate to Bioinformatics and Genomics; students will be able to follow a research presentation and based on that presentation ask insightful questions. At the end of the semester students will submit a summary paper that includes an in-depth study of one of the research topics presented during the semester.

Topics Outline: Topics will be dictated by the seminar series and will vary from semester to semester. Broadly the areas covered will include: proteomics, metabolomics, protein structure and function, data visualization, structural and functional genomics, metagenomics, networks, and other topics relating to Bioinformatics and Genomics.

Academic integrity: All students are required to read and abide by the Code of Student Academic Integrity. Violations of the Code of Student Academic Integrity, including plagiarism, will result in disciplinary action as provided in the Code. Definitions and examples of plagiarism are set forth in the Code. The Code is available from the Dean of Students Office or online[1]. A set of links to various resources on plagiarism and how to avoid it is available at the UNCC Library website[2]. Take home message: **DO NOT CHEAT!**

8. Textbook

1. Class material will be provided as selected readings provided through Moodle as pdf's. No standard text exists for this combination of topics.

2. No references are recommended.

3. Policy

- Class and lab attendances are mandatory
- Class participation in the form of asking questions of speakers is mandatory.

4. Assessment

Students will be assessed through written summaries of published papers, class attendance and participation and final summary paper. The grading distribution will be:

- Class attendance and participation (75%)
- Summary paper (25%)

Grades will be assigned on the following scale: A=90-100%, B=80-90%, C=70-80%, D=60-70%, F=<60%

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

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

UNC CHARLOTTE

MEMO FORM
COURSE AND CURRICULUM PROPOSAL

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*To: Janet Levy, Undergraduate Course and Curriculum Committee Chair for the University of North Carolina at Charlotte

From: Shannon Schlueter; Assistant Professor of Bioinformatics and Genomics

Date: January 13, 2011

Re: Renumbering of BINF 4650 Senior Project to BINF 4450

SUMMARY:

The Department of Bioinformatics and Genomic proposes to renumber the existing undergraduate course BINF 4650 Senior Project to BINF 4450 to coincide with university course numbering policy.

FOR CONSULTATION WITH OTHER DEPARTMENTS:

1. Does the proposed change affect other departments?
   ________Yes   __XX____ No

2. If Yes, please list the other departments affected by the proposed change:

   NONE IDENTIFIED

3. Have you consulted with each department listed in question 2 regarding the proposed change?
   ~~________Yes   ________No~~

   NONE IDENTIFIED

4. Result(s) of Consultation(s):

RESOURCES: Indicate the additional resources required, if any, to implement and maintain the proposed change:

No resource requirements have been identified as this proposal solely implements the renumbering of an existing course.

PROPOSED CATALOG COPY:

BINF 4450. Senior Project. (3) Prerequisites: senior standing and permission of the department. An individual or group project in the teaching, theory, or application of bioinformatics, genomics, or computational biology under the direction of a faculty member. Projects must be approved by the department before they can be initiated. (On demand)

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

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 19, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 1101: Introduction to Bioinformatics and Genomics

Summary of Librarian's Evaluation of Holdings:

Please Check One:

Holdings are superior	______
Holdings are adequate	☑
Holdings are adequate only if Dept. purchases additional items.	______
Holdings are inadequate	______

Comments:

This is a proposal for a new undergraduate course. It is designed to introduce students to the genomics perspective in the life sciences, this course combines a general introduction to genomic technologies and the bioinformatics methods used to analyze genome scale data with a presentation of real world scientific problems where these technologies are having an impact.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 1,400 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Introduction to Bioinformatics and Genomics

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Genomics	87	74	22	270
Genomes	47	15	19	291
TOTAL	**243**	**180**	**70**	**1253**

Reese A. Manceaux

Evaluator's Signature

__January 20, 2011__________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 19, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 2101: Genomic Methods & BINF 2101L: Genomic Methods Lab

Summary of Librarian's Evaluation of Holdings:

Please Check One:

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

Comments:

This is a proposal for a new undergraduate course. It is designed to study common molecular patterns that give functional coherence to living organisms, as well as the subtle variations that contribute to the wonderfully diverse, colorful and odd complexity of life on this planet. The conceptual path we will follow takes us from DNA sequence to structure, function, organization, genomics, evolution, and complex systems.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 3,800 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Genomics Methods

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Genomics	87	74	22	270
Genomes	47	15	19	291
DNA	332	136	3	2082
TOTAL	**575**	**316**	**73**	**3335**

Reese A. Manceaux____

Evaluator's Signature

__January 20, 2011____________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 19, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 2111: Introduction to Bioinformatics Computing

Summary of Librarian's Evaluation of Holdings:

Please Check One:

Holdings are superior ______
Holdings are adequate ☑
Holdings are adequate only if Dept. purchases additional items. ______
Holdings are inadequate ______

Comments:

This is a proposal for a new undergraduate course. It introduces fundamentals of programming for bioinformatics using current programming languages and paradigms. This class will introduce both the language and the use of the language within a Unix environment, demonstrating how interpreted languages serve both as a useful tool for writing and testing programs interactively and as a powerful data analysis and processing tool for bioinformatics

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 3,000 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Introduction to Bioinformatics Computing

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Genomics	87	74	22	270
Genomes	47	15	19	291
Parallel Processing Electronic Computers	371	59	12	1493
TOTAL	**614**	**239**	**82**	**2746**

Reese A. Manceaux

Evaluator's Signature

January 20, 2011

Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 21, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 2121: Statistics for Bioinformatics

Summary of Librarian's Evaluation of Holdings:

Please Check One:

Holdings are superior	
Holdings are adequate	☑
Holdings are adequate only if Dept. purchases additional items.	
Holdings are inadequate	

Comments:

This is a proposal for a new undergraduate course. It teaches 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 while exploring the use of the R and Bioconductor software for biostatistical analysis.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 9,000 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Statistics for Bioinformatics

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Stochastic Processes	392	59	18	526
Probability (Probabilities)	738	115	43	2155
Statistical Methods	2200	508	0	2079
Biometry	103	20	18	32
TOTAL	**3542**	**793**	**108**	**5484**

Reese A. Manceaux____

Evaluator's Signature

__**January 21, 2011**____________________________

Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 21, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 3101: Sequence Analysis

Summary of Librarian's Evaluation of Holdings:

Please Check One:

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

Comments:

This is a proposal for a new undergraduate course. It covers the purpose, application, and biological significance of bioinformatics methods that identify sequence similarity, methods that rely on sequence similarity to produce models of biological processes and systems, as well as methods that use sequence characteristics to predict functional features in genomic sequence data.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 4,000 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Revised 10/29/08
OAA jdp

Atkins Library Holdings in Areas Related to Sequence Analysis

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Sequence Analysis (Nucleotide Sequence)	48	8	11	108
Genomics	87	74	22	270
Genomes	47	15	19	291
DNA	332	136	3	2082
TOTAL	**623**	**324**	**84**	**3443**

Reese A. Manceaux____

Evaluator's Signature

__January 21, 2011______________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;
Department of Bioinformatics and Genomics**

From: **Reese Manceaux; J. Murrey Atkins Library
Liaison for Bioinformatics**

Date: **January 21, 2011**

Subject: **Library holdings related to the proposed new course
*BINF 3111: Bioinformatics Algorithms***

Summary of Librarian's Evaluation of Holdings:

Please Check One:

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

Comments:

This is a proposal for a new undergraduate course. It introduced common algorithms and data structures used in Bioinformatics and Genomics.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 9,000 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Bioinformatics Algorithms

Library of Congress Subject Headings	Books	After Year 2001	Journals	Skillport/ Books 24x7
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Computer Algorithms	185	63	7	2028
Data Structures	130	25	2	2354
Computer Programming	650	47	32	3723
TOTAL	**1074**	**226**	**70**	**8797**

Reese A. Manceaux____

Evaluator's Signature

__January 21, 2011______________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 24, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 3211: Bioinformatics Databases and Data Mining Technologies

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Summary of Librarian's Evaluation of Holdings:

Please Check One:

Holdings are superior ______
Holdings are adequate __☑__
Holdings are adequate only if Dept. purchases additional items. ______
Holdings are inadequate ______

Comments:

This is a proposal for a new undergraduate course. It incorporates extensive hands-on exercises, some of which will be done in class. Lecture topics are intended to introduce students to core concepts in both database management system theory and implementation and in data modeling for genomics data types.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 10,000 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Revised 10/29/08
OAA jdp

Atkins Library Holdings in Areas Related to Bioinformatics Databases and Data Mining Technologies

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Data Mining	183	127	6	964
SQL (computer program language)	94	49	0	2172
Computer Programming	650	47	32	3723
Databases (database management)	705	167	22	3284
TOTAL	**1741**	**481**	**89**	**10924**

Reese A. Manceaux

Evaluator's Signature

__January 24, 2011____________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 19, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 3900: Undergraduate Research

Summary of Librarian's Evaluation of Holdings:

Please Check One:

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

Comments:

This is a proposal for a new undergraduate course. It enables students in the program to initiate research projects in their respective fields of interest and to interact with faculty in pursuing research experience. Since the subject area can be so large for this open-ended topic, a holding assessment will not be done. As was shown in other classes are holdings are adequate for this class.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Reese A. Manceaux

Evaluator's Signature

__January 20, 2011______________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 24, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 4101: Computational Systems Biology

Summary of Librarian's Evaluation of Holdings:

Holdings are superior ______
Holdings are adequate __☑__
Holdings are adequate only if Dept. purchases additional items. ______
Holdings are inadequate ______

Comments:

This is a proposal for a new undergraduate course. It will cover the process of reconstructing complex biological networks. Reconstruction of metabolic networks, regulatory networks and signaling networks using bottom-up and top-down approaches will be addressed using collections of historical data as well as departmentally generated data.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of the related subjects retrieved over 1,500 pertinent items.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Computational Systems Biology

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Biology-Mathematical Models (Biological Networks)	35	16	3	673
Biological Control Systems	70	55	4	
TOTAL	**214**	**162**	**36**	**1365**

Reese A. Manceaux

Evaluator's Signature

__January 24, 2011____________________________
Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 24, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 4111: Structural Bioinformatics

Summary of Librarian's Evaluation of Holdings:

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

Comments:

This is a proposal for a new undergraduate course. It will cover 1) the physical forces that shape biological molecules, assemblies and cells; 2) overview of protein and nucleic acid structure; 3) experimental methods of structure determination; 4) data formats and software for structure visualization; 5) computational methods to evaluate structure; 6) structural classification; 7) structure alignment; 8) computational algorithms for structure prediction; and 9) structural analysis of disease causing mutations.

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

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Atkins Library Holdings in Areas Related to Computational Systems Biology

Library of Congress Subject Headings	**Books**	**After Year 2001**	**Journals**	**Skillport/ Books 24x7**
Bioinformatics	74	63	20	368
Computational Biology	35	28	9	324
Biology-Mathematical Models (Biological Networks)	35	16	3	673
Biological Control Systems	70	55	4	
Nucleic Acids	68	14	6	
Organic Compounds	504	90	2	
TOTAL	**786**	**266**	**44**	**1365**

Reese A. Manceaux

Evaluator's Signature

January 24, 2011

Date

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: **Shannon Schlueter;**
Department of Bioinformatics and Genomics

From: **Reese Manceaux; J. Murrey Atkins Library**
Liaison for Bioinformatics

Date: **January 20, 2011**

Subject: **Library holdings related to the proposed new course**
BINF 4600: Bioinformatics and Genomics Seminar

Summary of Librarian's Evaluation of Holdings:

Please Check One:

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

Comments:

This is a proposal for a new undergraduate course. It is designed to introduce students to the research being conducted in both the Bioinformatics and Genomics Department as well as invited speakers. Since the subject area can be so large for this open-ended topic, a holding assessment will not be done. As was shown in other classes are holdings are adequate for this class.

The Library has electronic access to periodicals and other electronic resources (e-books from Skillport/Books 24x7) that support these courses. Skillport, in particular, has an enormous catalog of computer related literature; especially up-to-date programming language books. In addition, the library has many electronic databases such as Springer Link, ACM Digital Library, IEEE Explore, ScienceDirect and Compendex (many with links to full text articles) supporting the overall Computing and Informatics program. The collection, especially if supported by ongoing purchases, is quite adequate to support this program.

Reese A. Manceaux

Evaluator's Signature

__January 20, 2011______________________________
Date

Subject: FW: Bioinformatics and Genomics Minor consultation
Date: Wednesday, February 2, 2011 4:28 PM
From: Mays, Larry <lemays@uncc.edu>
To: Shannon Schlueter <sschluet@uncc.edu>

------ Forwarded Message
From: "Knoblauch, Cy" <knoblauch@uncc.edu>
Date: Fri, 21 Jan 2011 10:23:49 -0500
To: Lawrence Mays <lemays@uncc.edu>
Subject: RE: Bioinformatics and Genomics Minor consultation

Larry

The Biology Department is pleased to support the proposed undergraduate minor in Bioinformatics and Genomics.

Cy

From: Mays, Larry
Sent: Thursday, January 20, 2011 4:19 PM
To: Ribarsky, William; Chu, Bei-Tseng; Donovan-Merkert, Bernadette; Knoblauch, Cy; Johnson, Eric; Dow, Alan
Subject: Bioinformatics and Genomics Minor consultation

Dear Colleagues,
Attached is a large PDF which describes our proposed Bioinformatics and Genomics undergraduate minor, as well as several related courses. I am providing this to you for your consultation since the proposed courses are related to your programs and will likely attract some of your students. Our goal with the minor is to make our program accessible to a wide range of students, from the life sciences to mathematics. I look forward to your comments.
Larry Mays

------ End of Forwarded Message

Subject: FW: Bioinformatics and Genomics Minor consultation
Date: Wednesday, February 2, 2011 4:31 PM
From: Mays, Larry <lemays@uncc.edu>
To: Shannon Schlueter <sschluet@uncc.edu>

------ Forwarded Message
From: Lawrence Mays <lemays@uncc.edu>
Date: Tue, 01 Feb 2011 15:12:28 -0500
To: Bernadette Donovan-Merkert <bdonovan@uncc.edu>
Conversation: Bioinformatics and Genomics Minor consultation
Subject: Re: Bioinformatics and Genomics Minor consultation

Did you ever hear back from them?

On 1/20/11 5:25 PM, "Bernadette Donovan-Merkert" <bdonovan@uncc.edu> wrote:

> Hi Larry,
> I sent the proposal to the Chemistry Department and will provide feedback to you by Wednesday, January 26.
>
> I hope you are doing well!
> Bernadette
>
> Bernadette T. Donovan-Merkert, Ph.D. **|** Professor and Chair of Chemistry
> Acting Director, Nanoscale Science Ph.D. Program
> UNC Charlotte **|** Department of Chemistry
> 9201 University City Blvd. **|** Charlotte, NC 28223
> Phone: 704-687-4436 **|** Fax: 704-687-3151
> bdonovan@uncc.edu **|** http://www.chemistry.uncc.edu <http://www.chemistry.uncc.edu/>
>
> ---
>
> **From:** Mays, Larry
> **Sent:** Thu 1/20/2011 4:18 PM
> **To:** Ribarsky, William; Chu, Bei-Tseng; Donovan-Merkert, Bernadette; Knoblauch, Cy; Johnson, Eric; Dow, Alan
> **Subject:** Bioinformatics and Genomics Minor consultation

Dear Colleagues,
Attached is a large PDF which describes our proposed Bioinformatics and Genomics undergraduate minor, as well as several related courses. I am providing this to you for your consultation since the proposed courses are related to your programs and will likely attract some of your students. Our goal with the minor is to make our program accessible to a wide range of students, from the life sciences to mathematics. I look forward to your comments.
Larry Mays

------ End of Forwarded Message

Subject: FW: BiG UG proposal
Date: Wednesday, February 2, 2011 4:27 PM
From: Mays, Larry <lemays@uncc.edu>
To: Shannon Schlueter <sschluet@uncc.edu>

------ Forwarded Message
From: "Ribarsky, William" <ribarsky@uncc.edu>
Date: Wed, 2 Feb 2011 12:54:38 -0500
To: Lawrence Mays <lemays@uncc.edu>
Subject: RE: BiG UG proposal

Larry,
Sorry for the delay. The CS Department approves the proposal. There may be a couple of comments still coming from the UG Committee, but I expect those to be minor.
Bill

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

From: Mays, Larry
Sent: Tue 2/1/2011 3:13 PM
To: Ribarsky, William
Subject: BiG UG proposal

Bill,
I need to get that UG minor proposal in pretty soon if we are going to have this for Fall. How is your consultation process going?
L

------ End of Forwarded Message

Subject: FW: Bioinformatics and Genomics Minor consultation
Date: Wednesday, February 2, 2011 4:29 PM
From: Mays, Larry <lemays@uncc.edu>
To: Shannon Schlueter <sschluet@uncc.edu>

------ Forwarded Message
From: ALAN DOW <adow@uncc.edu>
Date: Tue, 25 Jan 2011 14:33:33 -0500
To: Lawrence Mays <lemays@uncc.edu>
Cc: Alan Dow <adow@uncc.edu>
Subject: Re: Bioinformatics and Genomics Minor consultation

Hi Larry,

Thanks for sending the proposal. It looks excellent, well designed and a real added value for any student completing it. It has my full support.

The course that is most closely connected to the Department of Mathematics and Statistics is the course
BINF 2121 Statistics for Bioinformatics

I have a suggestion and a question regarding this course.

the suggestion (after consulting with statistics instructors) is that you consider removing Math 1100 from the list of sufficient prerequisites. As a matter of probably requiring a decent level of mathematical problem solving ability, this course alone may not be enough. I would also bring to your attention that Engineering Technology students typically take Math 1121 -- a calculus course specially designed for them, and you could consider adding that. It's about the same level as Math 1120 but includes trigonometry. Math 1103 (PreCalculus) might be sufficient also.

The question concerns degree credit exclusions with Stat 1220, 1221, 1222. I suppose the intention is that a student who has taken one of those courses would be allowed to take BINF 2121 for credit. I am fine with that. Many computer science students will have taken instead Stat 2122, again, I suppose that the course content and objectives have enough difference to allow credit to be given for both courses. We do not use statistics software in Stat 2122.

As I am writing this, I am concluding that the outcome will be no exclusions between any STAT course and BINF 2121. Which then makes me wonder if you might want to allow a student who has complete a course like Stat 1220, Stat 1221 (many Biology majors take this one), Stat 2122 also to be a sufficient prerequisite. I just think that Math 1100 alone would be a mistake.

On Thu, 2011-01-20 at 16:18 -0500, Lawrence Mays wrote:

> Dear Colleagues,
> Attached is a large PDF which describes our proposed Bioinformatics and Genomics undergraduate minor, as well as several related courses. I am providing this to you for your consultation since the proposed courses are related to your programs and will likely attract some of your students. Our goal with the minor is to make our program accessible to a wide range of students, from the life sciences to mathematics. I look forward to your comments.
> Larry Mays

--

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

adow@uncc.edu | http://www.math.uncc.edu

------ End of Forwarded Message

Subject: **FW: Bioinformatics and Genomics Minor consultation**
Date: Thursday, February 3, 2011 4:02 PM
From: Shannon D Schlueter <sschluet@uncc.edu>

Larry,
Thank you for the proposal and for the opportunity to respond. The program looks enticing for our students from the perspective of some interesting elective courses and even a potential minor for our more bio-oriented majors. In particular, the Introduction to Bioinformatics and Genomics, and Structural Bioinformatics courses will likely be taken by some of our students. Thank you again for the opportunity to review this and provide you with feedback. Good luck.
Kind regards,
Pat

Patrick J. Moyer
Associate Professor & Interim Chair
Department of Physics and Optical Science
The University of North Carolina at Charlotte
Charlotte, NC 28223
pjmoyer@uncc.edu <mailto:pjmoyer@uncc.edu>
704-687-8148 phone
704-687-8197 fax

From: Mays, Larry
Sent: Wednesday, January 26, 2011 8:27 AM
To: Moyer, Patrick
Subject: FW: Bioinformatics and Genomics Minor consultation

Dear Pat,
Attached is a large PDF which describes our proposed Bioinformatics and Genomics undergraduate minor, as well as several related courses. I am providing this to you for your consultation since the proposed courses are related to your programs and will likely attract some of your students. Our goal with the minor is to make our program accessible to a wide range of students, from the life sciences to mathematics. I look forward to your comments.
Larry Mays

------ End of Forwarded Message

------ End of Forwarded Message

Subject: FW: Bioinformatics and Genomics Minor consultation
Date: Wednesday, February 2, 2011 4:29 PM
From: Mays, Larry <lemays@uncc.edu>
To: Shannon Schlueter <sschluet@uncc.edu>

------ Forwarded Message
From: Bill Chu <billchu@uncc.edu>
Date: Fri, 21 Jan 2011 08:48:43 -0500
To: Lawrence Mays <lemays@uncc.edu>
Subject: RE: Bioinformatics and Genomics Minor consultation

You have SIS support.

--Bill

-----Original Message-----
From: Mays, Larry
Sent: Thu 1/20/2011 4:18 PM
To: Ribarsky, William; Chu, Bei-Tseng; Donovan-Merkert, Bernadette; Knoblauch, Cy; Johnson, Eric; Dow, Alan
Subject: Bioinformatics and Genomics Minor consultation

Dear Colleagues,
Attached is a large PDF which describes our proposed Bioinformatics and Genomics undergraduate minor, as well as several related courses. I am providing this to you for your consultation since the proposed courses are related to your programs and will likely attract some of your students. Our goal with the minor is to make our program accessible to a wide range of students, from the life sciences to mathematics. I look forward to your comments.
Larry Mays

------ End of Forwarded Message