BINF 6203/BINF 8203, GENOMICS
SYLLABUS

A. COURSE DESCRIPTION
This course is a survey of the application and interpretation of high-throughput molecular biology methods used to produce high-volume biological data. The relationship between biological research objectives, modern biotechnology methods, and bioinformatics solutions is emphasized. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Functional classification and gene ontologies. Genome evolution and individual variation. Transcriptomic and epigenetic assay design, data acquisition, and data analysis. (3 credit hours)

B. PRE- OR CO-REQUISITES
Corequisite: BINF 6203L. Prerequisite: BINF 6100/ITSC 8100 or equivalent.

C. OBJECTIVES OF THE COURSE
Having successfully completed this course, the student will be able to:
• Understand and describe modern high-throughput molecular biology methods used to produce high-volume biological data
• Recognize appropriate biological applications for high-throughput data collection, and distinguish between hypothesis-testing and discovery applications
• Understand and apply appropriate experimental design strategies for high-throughput experiments
• Understand and apply methods for direct analysis of signal collected in such experiments, and reduction of raw data to an interpretable form
• Understand and apply computational biology methods for interpretation of data from high-throughput experiments

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, to correctly solve problems using methods presented in the class, and to participate productively in critical discussion of course material. Two midterm exams (60%), and a final exam (30%) will be used to evaluate students’ performance in the course. Classroom participation via discussion and a presentation on an individual project will count for 10% of the grade.

ITSC 8203 additional requirements. Ph.D. students enrolled in ITSC 8203 will be required to suggest a genomics-related problem and experimental/analytical design for a research-driven presentation, based on their own scientific interests. They will present their project to the class in the form of a 20-minute platform talk.
F. Specify policies that apply to this course:
The following policies apply to students in BINF 6203/8203:

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

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

3. Grading Policy
Grades will be assigned on the following scale:
A=90-100%
B=80-90%
C=65-80%
U=0-65%

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
Required:
• Brown, S. Next-generation DNA sequencing informatics. 2013, Cold Spring Harbor Laboratory Press.

Additional readings from the current literature will be assigned throughout the course.

H. Topical Outline of Course Content
• Genome Projects: Organization and Objectives
• Genome Sequencing and Annotation
• Comparative Genomics
• SNPs and Variation
• Experimental Design for High Throughput-Experiments
• Gene Expression and the Transcriptome
• Integrative Genomics