Marshall University Syllabus

Course Title/Number	IST 444 Bioinformatics/BSC 481 Bioinformatics
Semester/Year	FALL SEMESTER 2014
Days/Time	MWF 10:00-10:50 AM
Location	Morrow Library 222
Instructor	Elizabeth E. Murray, Ph.D.
Office	241G Byrd Biotechnology Science Center (BBSC)
Phone	304-696-3515 Cell Phone # given in Class and is in MU Online
E-Mail	murraye@marshall.edu
Office/Hours	Office hours: T/Th 9-11; M/W 9-10 and by appt. I may be in BBSC 211 (lab) so call or text my cell phone given in class. Please give your name and class time if you text me so I know who you are
University Policies	By enrolling in this course, you agree to the University Policies listed below. Please read the full text of each policy be going to www.marshall.edu/academic-affairs and clicking on "Marshall University Policies." Or, you can access the policies directly by going to http://www.marshall.edu/academic-affairs/?page_id=802
	Academic Dishonesty/ Excused Absence Policy for Undergraduates/ Computing Services Acceptable Use/ Inclement Weather/ Dead Week/ Students with Disabilities/ Academic Forgiveness/ Academic Probation and Suspension/ Academic Rights and Responsibilities of Students/ Affirmative Action/ Sexual Harassment

Course Description: From Catalog

IST 444/BSC 481 Bioinformatics Computer software is used to draw inferences from DNA and protein databases. Students will find patterns and meaning in genomic data through computer-aided analysis of DNA, RNA, and protein. (PR: IST 111 or equivalent

Required Texts, Additional Reading, and Other Materials

1. Optional Text (Available in Kindle from Amazon.com) Bioinformatics for Beginners, Supratim Choudhury, 2014 Elsevier ISBN 9780124104716

2. *NCBI Handbook* http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=handbook.TOC&depth=2

3. Sequence-Evolution-Function: Computational Approaches in Comparative Genomics
   Eugene V. Koonin and Michael Y. Galperin
   http://www.ncbi.nlm.nih.gov/books/bv.fcgi?highlight=sequence,function,*evolution&rid=sef*

4. Introduction to Perl http://www.perl.org/books/beginning-perl/

5. We will make active use of various web sites with extensive Bioinformatics information, and additional handouts and films from instructor

Course Requirements / Due Dates

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1. Quizzes will be given to assess that students are keeping up with the large amount of information in the lectures. There will be 7 quizzes (worth 50 points each) with about 7 objective questions (true/false, multiple choice) and one or two short answer questions. **You will be permitted to drop one quiz.** Quizzes will be given on every other Fridays.. One or two quizzes can be take-home with some problems. Because you can drop up one quiz, there will not be makeup quizzes. If you know you will miss a quiz for a University excused absence in advance, see me and possibly we can work out your taking the quiz early. Quizzes will include information discussed in lecture and in assignments**.** Quiz grades will be returned within a week.

2. Final exam will be based on the quizzes and will occur on date scheduled.

3. Students are assigned a genome of a model organism that will be the focus of a web page they will create. Students will do a series of assignments to learn to use the tools of bioinformatics using their genome as the subject, and these assignments will be posted to the web page. Students will provide instructor with a link to the web page. The Web page will be assessed 4 times during the semester and grade returned within 2 weeks. The web page deadlines are September 26, October 16, October 31 and December 15. The web page will also contain useful information on the relationships between genes of interest and different taxonomic groups.

4. Bioinformatics Project. Students will participate in a hands-on analysis of high throughput DNA sequence data. Students will be work cooperatively to learn Perl script and work with data mining of sequences of the threatened eastern massasauga rattlesnake *(Sistrurus c. catenatus)* to sort next generation sequence data and attempt to determine whether the snakes in the population are males or females. There will also be a guest speaker, Dr. Mike Sovic, who will visit the class and discuss his research on bioinformatics and taxonomic and biogeography. We will be using his dataset and software in this project.

Desired Objectives/Outcomes:

Student Learning Outcomes	How Practiced in this Course	How Assessed in this Course
Students will <u>demonstrate</u> knowledge of the major DNA and protein sequence databases in NCBI and UCSC genome browser.	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest.	Quizzes, Final Exam, Web Page
Students will <u>demonstrate</u> mastery of Entrez, the text-based search and retrieval system used at NCBI for the major databases, including PubMed, Nucleotide and Protein Sequences, Protein Structures, Complete	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest.	Quizzes, Final Exam, Web Page

Genomes, Taxonomy, and others. .		
Students will <u>demonstrate</u> they can enter sequence data into the databases and search for and download data from the databases.	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest, *Sistrurus* project.	Web Page and *Sistrurus* project.
Students will <u>analyze</u> and build taxonomic trees using DNA sequences from their genomes<u>.</u>	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest.	Quizzes, Final Exam, Web Page
Students will <u>demonstrate</u> they can search PubMed and other literature databases for on-line journal articles, abstracts and texts.	In class lectures and internet demonstrations; assigned exercises on gene of interest, *Sistrurus* project.	Web Page and *Sistrurus* project.
Students <u>will</u> <u>evaluate</u> different strategies for high throughput genome sequencing projects and analyze and assemble electronic DNA sequence files using appropriate programs.	In class lectures and internet demonstrations, *Sistrurus* project..	Web Page and *Sistrurus* project..
Students will <u>create</u> a Webpage to hold their Bioinformatics portfolio of output and interpretations of significance of results for a single gene they select with the instructor and <u>demonstrate</u> written, oral and visual communication skills through using appropriate visuals.	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest.	Web Page
Students will <u>demonstrate</u> PERL scripting and <u>design</u> a novel search/sort/compare strategy for a database of sequence files from different individual snakes.	*Sistrurus* project.	*Sistrurus* project,
Students will <u>demonstrate</u> understanding the role of scoring matrices (PAM and BLOSUM) and gaps in protein sequence alignment.	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest, *Sistrurus* project.	Quizzes and final exam, Web Page and *Sistrurus* project.
Students will <u>design</u> and evaluate primer pairs for PCR using software.	In class lectures and internet demonstrations; assigned exercises on gene of interest	Quizzes and final exam, Web Page
Students will collect a set of related DNA sequences and <u>calculate</u> phylogenetic distances and <u>create</u> a tree using software programs. Students will demonstrate understanding of algorithms that	In class lectures and internet demonstrations; assigned exercises on genomes and genes of interest *Sistrurus* project.	Quizzes and final exam, Web Page, *Sistrurus* project

underlie such alignment and tree building programs.		
Students will <u>demonstrate</u> understanding and use of the popular search tools BLAST and FASTA and learn to interpret the significance of the statistics and output from these programs. Students will demonstrate knowledge of homologs and paralogs	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest, *Sistrurus* project.	Quizzes and final exam, Web Page and *Sistrurus* project.
Student will <u>demonstrate</u> understanding of the dynamic programming algorithm and its application, ability to distinguish between global and local alignment algorithms and apply them appropriately, and the significance and applications of the Needleman/Wunsch and Smith/ Waterman algorithms in software packages and apply them appropriately	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest.	Quizzes and final exam, Web Page.
Students will <u>demonstrate</u> knowledge of various methods and strategies of high throughput DNA sequencing and genome assembly and comparisons.	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest, *Sistrurus* project.	Quizzes and final exam, Web Page and *Sistrurus* project.
Students will <u>demonstrate</u> understanding of methods for determining gene expression including microarrays and cDNA high throughput sequencing	In class lectures and internet demonstrations; assigned exercises on genome and genes of interest, *Sistrurus* project.	Quizzes and final exam, Web Page and *Sistrurus* project.

Grading Policy

Evaluation of Learner Outcomes:
Point Breakdown:

Quizzes	300 pts
Final Exam	200 pts
Web Page/Problems	300 pts
Sistrurus project	150 pts
Participation and Attendance	50 pts
Total	1000 pts

Final grade scale:
A = 90-100% Excellent work, goes significantly beyond assignment requirements.
B = 80 89% Good work, meets or exceeds all of the requirements of the assignment.
C = 70 79% Average work, which meets requirements of the assignment.
D = 60 69% Below average work, fails to meet one or more assignment requirements.
F = Below 60% Unacceptable work which fails to meet the minimum standards.

Statement on Academic Dishonesty
All assignments must be the student's own original work. All information and ideas drawn from other sources must be properly acknowledged. Submitting an assignment which is not the student's original and independent work will result in a reduced or failing grade (recorded as a zero) for the assignment. It may result in more serious sanctions, up to and including failure of the course and further sanctions.
If you are ever unsure whether something constitutes academic dishonesty, you should consult with the course instructor before the assignment is graded.
The policy on Academic Dishonesty will be followed in the course as listed in the current Catalog.

Attendance Policy

Attendance: Attendance significant given the interactive nature of this course and the importance of class discussions and computer demonstrations.

Reading Assignments: Students are expected to complete the reading for each class before class starts.

Lateness Policy: This class is preparation for the professional world you will all be entering. You will be expected to turn in assignments on the day you are scheduled. Unless the absence is a University-excused one, late assignments will be penalized one grade a week.

Time	Monday	Tuesday	Wednesday	Thursday	Friday
8					
9	office	office	office	office	
10	IST 444 10-11		IST 444 10-11		IST 444 10-11
11					
12		IST 120		IST 120	Faculty Meeting
1	IST 340	12:30-1:45	IST 340	12:30-1:45	IST 340
2	IST 340		IST 340		IST 340
3	1-2:45		1-2:45		1-2:45
4		IST 120	help 224	IST 120	
5		4-5:15		4-5:15	
6				help 224	

Course Outline: IST 444 Bioinformatics – Fall 2014 – Semester Schedule

Course Outline is a plan and subject to revision

Week 1   8/25 Overview of Bioinformatics, Genomics, Molecular Biology

Week 2   9/1 DNA Cloning, Sequencing and Genomics Projects

Week 3   9/8 PubMed, and NCBI, UCSD Genome Browser

Week 4   9/15 Pairwise Sequence Alignment and algorithms, PAM and BLOSOM matrices.

Week 5   9/22 Multiple Sequence Alignment, Primer design

Week 6   9/29 BLAST, identification of related genes, paralogs and homologs

Week 7   10/6 Gene Expression and ENCODE project

Week 8   10/13 Protein Analysis and Proteomics, Structure and Function

Week 9`   Dr. Murray will be in San Diego for the ASHG meeting. On 10/20, 10/22 you will be assigned two Advanced UCSC Browser tutorials and on 10/24 Guest speaker Dr.Mike Sovic will come to talk about our project

Week 10   10/27 PERL scripting

Week 11   11/3 Phylogenetics and Trees

Week 12   11/10 Molecular Evolution

Week 13   11/17- Genomics and *Sistrurus* project

Week 14   11/25 **THANKSGIVING BREAK** Genomics and *Sistrurus* project.

Week 15   12/1 Genomics and *Sistrurus* project

Week 16   12/ Final Exam