Biochemistry & Molecular Biology Graduate Program
Spring 2008

HBCG 6206 Bioinformatics on the WW Web, 2 Credit Hours
Term: January 3 - April 18, 2008

**Class Times:**
Monday 10:00 am - 11:45 am
Thursday 10:00 am - 11:45 am

**Location:**
Clay Hall Conference room 2.130

**Textbook:**
Gibas, Jambeck: Developing Bioinformatics Computer Skills O’Reilly & Assoc., Inc. Sebastopol, CA
Durbin, Eddy, Krogh, Mitchison: Biological sequence analysis Cambridge University Press

**Course Director:**
Werner Braun, PhD, Professor, Biochemistry and Molecular Biology, 202 Clay Hall, webraun@UTMB.EDU, (409) 747-6810

**Course Description:**
This course introduces molecular biologists to software tools on the World Wide Web for search, retrieval and analysis of amino acid and nucleotide sequences. The software includes BLAST, FASTA and Clustal W. The course also covers secondary and tertiary structure prediction of proteins, homology or comparative modeling and methods for the analysis and validation of structures. 3-D modeling based on experimental & theoretical constraints will be explained with special reference to software including MASIA, EXDIS, DIAMOD & FANTOM. Two sessions will be given per week. The first session will describe the scientific concepts behind the tools and the computational procedures. The second session will be an “I day” where students will learn to use these tools through hands on sessions on modern graphic workstations. The goals are to provide a critical appreciation of bioinformatics tools and enable the student to apply them to his/her research.

**Grades:**
Grades will be calculated based on the performance of the following:

- Five home work problems (80%)
- Class participation (20%)
- *Evaluation Form

The grading may be subject to change at the discretion of the co-directors, but final course grades will be determined using the GSBS grading scale:

- 90-100 = A
- 80-89 = B
70-79 = C
69 or below = F

***Student end of course evaluations are required for all A/B/C/F-graded GSBS courses. Students are required to fill out the evaluations to receive a grade in the course. If the specified evaluation form is not received, an “I” Incomplete grade will be reported to the Office of Enrollment Services. If the course requirements are not completed within 30 days, the grade automatically converts to an “F” Failure grade. The evaluations are anonymous and will be available to course directors only after grades are assigned.

Examinations/Evaluations:
No final examinations. The grades are based on the quality of the home work exercises.

Excused Absences:
Since the course is highly interactive, attendance and participation are required. Students can be excused from graded assignments without penalty to their grade if an excused letter is obtained from Dr. Lillian Chan, Director of BMB Graduate Program or Dr. Wayne Bolen, Director of BSCB Educational Track, in advance. If absences are excused, appropriate make-up work will be provided for students at the discretion of the co-directors.

Important Dates:
No GSBS classes
Monday, January 21 President's Day
Monday, February 18 Martin Luther King Day

Last Day to Drop/Add Course
Tuesday, January 22

Course Schedule:
There will be two lectures per week. Each lecture meeting will be 2 hr. The practical exercises towards the end of the course are 3h. Additional meetings with the mentors can be arranged on an individual basis.

W. Braun
Jan 7, 2008 Overview of Computational Biology and Bioinformatics Probabilities and probabilistic models Bayes theorem Basics of sequence alignment, Substitution matrices

W. Braun/D. Power
Jan. 10, 2008 Selection of Student projects UNIX OS system, Files and Directories, UNIX shell
Scripts Communication, Perl scripts, Bioperl
W. Braun  
Jan 14, 2008 Molecular Mechanics: Nature of forces Estimation of parameters; calculation of energies

C.H. Schein  
Jan 17, 2008 Practical aspects of sequence alignment FASTA, BLAST, CLUSTAL_W, DALI, PCPMer motif search, PROSITE patterns

W. Braun/N. Oezguen  
Jan 21, 2008 Molecular modeling, Retrieval and Visualization of Protein structures, the PDB data bank

W. Braun  
Jan 24, 2008 Theory and procedures of dynamic programming, Needleman-Wunsch algorithm  
Significance of scores

W. Braun  
Jan 28, 2008 Motif and profile search Markov chains and hidden Markov models

O. Ivanciuc  
Jan 31, 2008 Basics of Homology Modeling, MPACK Fold recognition servers

WB/DP/CHS/OI/NO  
Feb 4, 2008 Practical exercises with fold recognition servers

WB/DP/CHS/OI/NO  
Feb 7, 2008 Practical exercises with Molecular Modeling and Empirical energy calculations

WB/DP/CHS/OI/NO  
Feb 11, 2008 Practical Exercises on 3D modeling

WB/DP/CHS/OI/NO  
Feb 18, 2008 Practical Exercises on 3D modeling