Biochemistry & Molecular Biology Graduate Program

BMB 6206 Bioinformatics tools on the WEB

2 Credit Hours

**Location:**  First part: Research Building 6, 5th floor, small conference room **5.416A**

**Textbook:** References provided by each lecturer depending on the topic

**Course Director:**  Werner Braun

**Lecturers:** Werner Braun, PhD, Professor, Biochemistry and Molecular Biology,

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**Course Description:** The course BMB 6206 is a 15 week course with one 2h class every week. The course introduces the students to fundamental concepts of data representations, data formats and software tools for search, retrieval and analysis of amino acid and nucleotide sequences of genes and proteins, including recent developments of tools in systems biology and Next Generation Sequencing. Specific data bases discussed are gene and protein sequence databases, the Protein Data Bank of 3D protein structures and the SCOP and CATH databases of protein folds. The software tools include the BLAST, FASTA and Clustal W programs, computational methods for secondary and tertiary structure prediction of

 proteins, and methods for the analysis and validation of 3D structures.

**Course Schedule: Part 1**

**Class 1** Overview of Computational Biology and Bioinformatics

Thu, Jan 14 Probabilities and probabilistic models

10:00-noon Bayes theorem

WB Basics of sequence alignment, Substitution matrices

**Class 2** Theory and procedures of dynamic programming,

Tue, Jan 19 Needleman-Wunsch algorithm

2:00-4:00 Significance of scores

WB

**Class 3** Practical aspects of sequence alignment

Tue, Jan 26 FASTA, BLAST, CLUSTAL\_W, DALI, PCPMer

2:00-4:00 PROSITE patterns

WB

**Class 4** Motif and profile search

Tue, Feb 02 Markov chains and hidden Markov models

2:00-4:00

WB

**Class 5**

**Tue, Feb 09 UNIX OS system, Files and Directories, UNIX shell script**

2:00-4:00

SN

**Class 6** Retrieval and Visualization of Protein structures, the PDB

Thu, Feb.11 data bank, PYMOL software tool

10:00-noon

SN

**Class 7** Protein fold classifications, the SCOP and CATH data base

Tue, Feb.16

2:00-4:00

WB

**Class 8** Basics of Homology Modeling

Tue, Feb 23 Secondary and tertiary structure prediction

2:00-4:00 Fold recognition methods

SN

**Class 9** Assessment of 3D structure prediction by CASP

Tue, Mar 01 Quality assessment tools for 3D models

2:00-4:00

WB

**Class 10** Protein-Protein Interactions, Prediction of T-cell and B-cell epitopes,

Tue, Mar 08 Progress in computational vaccinology

2:00-4:00

WB