Izmir Institute of Technology

MBG 305 – Applied Bioinformatics

Instructor	Jens Allmer E-Mail: bioinformatics@allmer.de Web: http://bioinformatics.allmer.de	
Text Books	Claverie, Notredame, Bioinformatics for Dummies, 0-470-08985-7 Attwood, Parry-Smith, Introduction to bioinformatics, 0-582-32788-1	
Description	The course will cover some of the databases available in biology such as NCBI and SwissProt. It will also demystify BLAST, FASTA and other search algorithms currently employed in research. Finally, many tools which can be employed in projects will be explained in varying detail. Among these are multiple sequence alignment, building of pylogenetic trees, predicting secondary information about genes and proteins. Prediction of sub cellular localization of proteins, gene structure prediction, and discovery of putative functional domains of proteins are among the information that may be predicted. The course will only scratch on the surface of a large number of tools that are very helpful in daily biological research. For each of these tools the confidence that can be put into the result is discussed in detail.	
Outline	17-Sep	Course Introduction Exact Pattern Matching
	9-Okt 10-Okt	Substitution Matrices BLAST and FASTA
	16-Okt 17-Okt	Pairwise Sequence Alignment Sequence Databases
	23-Okt 24-Okt	Nucleotide Sequences Storage and Retrieval
	6-Nov 7-Nov	Review Midterm
	14-Nov 15-Nov	Multiple Sequence Alignment
	20-Nov 21-Nov	More Multiple Sequence Alignments Trees (Dendrograms/ Phylogenetic)
	27-Nov 28-Nov	Protein Sequences Pattern Discovery
	4-Dec 5-Dec	Protein Sequences Predictions (Structure, Topology, …)
	18-Dec 19-Dec	2D Structures (RNA/ Protein) 3D Structures (Protein)
	25-Dec 26-Dec	Student Presentations
	2-Jan	Review
GRADING	Homework	20
	Project (inc. Presentation)	30
	Midterm	20
	Final	30
Office Hours	Tuesday	13:00 – 15:00