Spring 2022

EE550

Computational Biology

Syllabus

Meeting times : Tuesday 13:30, 14:30, 15:30
Text : Paul G. Higgs, Teresa K. Attwood, "Bioinformatics and Molecular Evolution,"
 Wiley-Blackwell, 2005
Instructor : Bilge Karaçalı, PhD
Office : EEE Building Room K1-32
E-mail : bilge@iyte.edu.tr

Summary:
This course will begin with a broad perspective of quantitative and high throughput biology.
Computational methods for pattern detection and clustering will be introduced in the analysis of amino
acid sequences of proteins. Probabilistic models of genetic evolution will be developed along with
sequence alignment and motif detection algorithms. RNA and DNA analysis with microarrays will be
discussed. Dynamic modelling of gene transcription networks will be introduced.

Course Outline:
Week 1: Introduction to computational biology
Week 2: Nucleic acid and protein structure
Week 3: Evolution mechanism through mutations
Week 4: Probabilistic amino acid sequence evolution models
Week 5: Gene and protein databases
Week 6: Sequence alignment
Week 7: Searching sequence databases
Week 8: Inter-species evolutionary relationships via phylogenetic trees
Week 9: Optimality criteria in phylogenetic tree construction
Week 10: Pattern searching in functional protein groups: Sequence motifs
Week 11: Bioinformatics
Week 12: Microarray data analysis
Week 13: Systems biology – Gene transcription networks
Week 14: Regulation of gene transcription

Grading:
Midterm   20%
Final   30%
Homework   20%
Project   30%