BIOINFORMATICS

01 Introduction to Bioinformatics
Chapter Outline
1. Bioinformatics
2. The Omics Revolution
3. Systems Biology
4. Bioinformatics Applications

Learning Objectives
After completing this chapter, the student will be able to:
- define the terms Bioinformatics, Genomics, Systems Biology
- describe the scope of Bioinformatics
- describe challenges in Bioinformatics

02 Biological Databases (BD)
Chapter Outline
1. Importance of BD
2. Features of BD
3. Primary BD
4. Secondary BD
5. Specialized BD
6. Access to Information

Learning Objectives
After completing this chapter, the student will be able to:
- understand the importance and the features of BD
- define the types and representatives of BD
- be able to search BD and use cross-references

03 Pairwise Sequence Alignment
Chapter Outline
1. Homology and Sequence Similarity
2. Pairwise Sequence Alignment
3. Scoring Matrices
4. Gap Penalties
5. Dot Matrix Plots
6. Dynamic Programming: Needleman–Wunsch and Smith–Waterman

Learning Objectives
After completing this chapter, the student will be able to:
- define homology as well as orthologs and paralogs
- explain how PAM and BLOSUM matrices are derived and contrast their utility
- explain how gap penalties affect the alignment
- interpret dot plots and dynamic programming matrices
- perform pairwise alignments at the EMBL-EBI website

04 Similarity Search on Sequence Databases
Chapter Outline
1. Searching on Aminoacid or Nucleotide Sequence Databases
2. Heuristic Sequence Alignment: FASTA, BLAST
3. Statistical significance of Sequence Alignment

Learning Objectives
After completing this chapter, the student will be able to:
- understand FASTA and BLAST methods
- assess statistical significance
- describe Best Reciprocal Hit BLAST and PSI-BLAST
- perform BLAST searches at the NCBI website

05 Multiple Sequence Alignment (MSA)
Chapter Outline
1. Importance of MSA
2. MSA Scoring
3. Progressive MSA
4. Alternative MSA Approaches
5. Patterns and Regular Expressions
6. Position Specifc Scoring Matrices (PSSMs)
7. Hidden Markov Models (HMMs)
8. MSA Databases

Learning Objectives
After completing this chapter, the student will be able to:
- explain how ClustalW performs MSA
- interpret PROSITE patterns
- define a PSSM
- describe HMMs and explain their advantages for database searching
- perform MSA at the EMBL-EBI website
- search MSA Databases

06 Phylogenetic Analysis
Chapter Outline
1. Phylogenetic Trees
2. Data Types
3. Tree-building Methods
4. Evaluating Trees

Learning Objectives
After completing this chapter, the student will be able to:
- describe the types of phylogenetic trees and their parts
- explain the basis of different approaches to creating phylogenetic trees and evaluating them
- use phylogenetic analysis computational tools

07 Structural Bioinformatics
Chapter Outline
1. Protein Structure

2. Macromolecular Visualization
3. Protein Structure Comparison
4. Protein Structure Prediction

Learning Objectives

After completing this chapter, the student will be able to:

- understand the principles of protein primary, secondary, tertiary, and quaternary structure;
- explain the role of PDB and of structure annotation databases such as SCOP and CATH
- describe approaches to modeling the three-dimensional structure of proteins
- use molecular visualization tools

08 Gene Prediction and Gene Expression

Chapter Outline

1. Prokaryotic vs Eukaryotic Genes
2. Ab Inition and Homology Based Gene Prediction Methods
3. Gene Expression Regulation
4. Transcription Factor Binding Sites
5. DNA Microarrays

Learning Objectives

After completing this chapter, the student will be able to:

- understand the principles of gene prediction methods
- explain the role of Phylogenetic Footprinting
- understand the principles of DNA microarrays
- describe the design of a DNA microarray experiment and the resulting data analysis techniques