

Lesson Plan

Prepared by: Savithri M. Bhat

Duration: 22 Hours

Reviewed by: Sevas Educational Society

S. No.	Topics	Duration
1	Module 1: Introduction to Bioinformatics	1 Hour
2	Applications of Bioinformatics	1 Hour
3	Module 2: Nucleotide and Protein Databases, Introduction	1 Hour
4	Nucleotide databases	1 Hour
5	Protein databases	1 Hour
6	Structural databases	1 Hour
7	Module 3: Sequence Alignment, Introduction	1 Hour
8	Dot Matrix	1 Hour
9	Dynamic Programming & Word Method	1 Hour
10	Multiple sequence alignment, Introduction & Methods	1 Hour
11	Matrix	1 Hour
12	Module 4: Phylogenetic Trees, Introduction	1 Hour
13	Different Methods of Maximum Parsimony	1 Hour
14	UPGMA & NJ Method	1 Hour
15	Applications	1 Hour
16	Problems	1 Hour
17	Module 5: Gene Structure Prediction, Introduction to gene features	1 Hour
18	Various Approaches	1 Hour
19	Module 6: Protein Structure Prediction, Introduction to protein structure	1 Hour
20	Methods of Prediction (Ab Initio, comparative and homology modeling)	1 Hour
21	Project Work & Applied Bioinformatics	2 Hour

Test Books:

1. Bioinformatics, Sequence & Genome Analysis, David W Mount.



2. Bioinformatics-A Practical Guide To The Analysis Of Genes And Proteins -A Baxevanis & B Ouellete.

Software's discussed in this basic course:

1. Rasmol
2. Spdbv
3. ClustalW & ClustalX.
4. Phylip
5. Treeview

Online tools discussed in this basic course:

1. Biological Databases: NCBI, EMBL, DDBJ, SWISS-Prot, PDB etc....
2. Blast, FASTA, ClustalW, Jalview, Emboss tools etc...
3. Literature: Pubmed, PMC etc...
4. Phylodendron
5. Gene prediction tools
6. Protein structure prediction tools.

Concepts discussed in this basic course:

1. Retrieving sequence from databases
2. Collecting biological literature from various sources
3. Performing Sequence Alignment, Needleman Algorithm etc...
4. Dynamic programming, Blast and FASTA algorithms
5. Online Multiple Sequence Alignment.
6. Phylogenetic analysis using Phylip Software
7. Visualization of 3D structure using Rasmol & Spdbv.
8. Viewing Phylogenetic trees using Treeview
9. Gene prediction and protein structure prediction using various online tools.
10. Homology Modeling.

Rules and Regulations:

1. **Teaching Strategy:** This course is called "online correspondence course" i.e. self explanatory materials will be send to your email ID and students can interact with the faculty for one hour per day.
2. The second material will be supplied only after submitting the assignment of first material.
3. Six tests will be conducted on all modules.
Exam type: **Open book**; Duration: **24 Hours**; No. of Questions: **One**.
4. Printed materials will also be supplied through postal service on request.
5. Feedback/Complaints/Suggestions can be send to
E-mail: **info@sbioinformatics.com**
6. Course certificate will be issued only after getting minimum 65 % aggregate.
7. Attested Xerox copies of all certificates with a letter from Head of the department or Faculties or professors or government employees (with their phone number and address) etc....