## I Year M.sc Biotechnology Sem II

Subject: Introduction to Bioinformatics  
Course Code: MS-205  
Faculty: Dr.K.V.Swamy

<table>
<thead>
<tr>
<th>Unit</th>
<th>Topics</th>
<th>No Of Lectures</th>
<th>Lecture Serial No</th>
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</table>
| **Unit-1**  
Introduction to Biological data, Scope of Bioinformatics  
Different areas in Bioinformatics  
Bioinformatics and internet | -1  
-3  
-2 | 1  
4  
6 |
| **Unit-2**  
Biological sequence data bases  
NCBI, EBI, SWISSPROT, PIR | -6 | 12 |
| **Unit-3**  
Sequence alignment and data base search  
BLAST, FASTA, CLUSTALW  
Structural database  
PDB, CSD, NDB | -7  
-4 | 19  
23 |
| **Unit-4**  
Small molecular modeling, properties and Chemical data bases | -2  
-1  
-2 | 25  
26  
28 |
| **Unit-5**  
Basic principles in protein modeling and drug designing  
AUTODOCK, MOE | -3 | 31 |
Reference Books
4) Bioinformatics A practical guide to analysis of genes and protein: BaxevanisA., D & Ouellette B.F.F Wiley
6) Essentials of Biophysics: P. Narayanan, New Age International Publishers,
7) Biophysics :Vasanta Pattabhi, Vikas Publishing
8) Molecular Modeling : Holtje and Folkers G Weinheim New York

Evaluation scheme

<table>
<thead>
<tr>
<th>Sno</th>
<th>Examination</th>
<th>Time</th>
<th>Marks</th>
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<tbody>
<tr>
<td>1</td>
<td>Minor test 1</td>
<td>45 Minutes</td>
<td>15</td>
</tr>
<tr>
<td>2</td>
<td>Minor test 2</td>
<td>45 Minutes</td>
<td>15</td>
</tr>
<tr>
<td>3</td>
<td>Internal &amp; Assignment</td>
<td></td>
<td>40</td>
</tr>
<tr>
<td>4</td>
<td>Final Assessment</td>
<td>2.5 hr</td>
<td>60</td>
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<td>5</td>
<td>Total</td>
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<td>100</td>
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List of practicals
1. Use of internet for accessing Bioinformatics work. Make list of Biological data bases available at NCBI and EMBL
2. Learn use of Pubmed, Go to NCBI site. Open PubMed, Understand data structure in PubMed and Use of PUBMED for sorting Literature, Authors, Abstracts.
3. Find out secondary structure of a protein whose structure is already available at Protein Data Bank (PDB)
5. Predict Secondary structure of a protein using tools available at EXPASY molecular Biology Server and Compare the secondary structure obtained by two methods
6. Calculate Properties of a protein based on its primary structure using tools at EXPASY molecular Biology Server
7 Six frame search of a open Reading Frame (manually as well as using tools at EXPASY molecular Biology Server

8 Translare a gene sequence to amino acid sequence and construct CODON usage table for a given amino acid

9 Align a given sequence with respect to sequences given in SWISS-PROT data base using BLAST algorithm at EXPASY.

10 Build a small molecule using: MOE or ISISDRAW and write down its coordinates in PDB and ECEPP FORMAT

11 Build DNA molecule of a given length, secondary structure and sequence using MOE, Hamog, or Model. Get (Coordinate output in PDB Format. View the molecule using RasMol, RasTop, Qmol or any other molecular graphics soft ware

12 Peptide chain of a given length, secondary structure and sequence using MOE, Hamog, or Model. Get (Coordinate output in PDB Format. View the molecule using RasMol, RasTop, Qmol or any other molecular graphics soft ware Calculate charges on atom center of a small molecule whose coordinates are known

13 Take a PDB file from PDB bank. Plot the Ramachandran map for the same using MOE or MolMol.

14 Calculate potential surface around a given small molecule for which atomic coordinates and charges on atom center are known using MOE or Hamog

15 Find out ligand binding site of a given protein using MOE.

Each practical 4 hours and total 60 hours

Evaluation Scheme:
Examination-Lab
Minor test/Continues assessment 20 marks
Final exam 30 marks
Total 50