BIRLA INSTITUTE OF TECHNOLOGY & SCIENCE, PILANI
BITS PILANI – DUBAI CAMPUS, DIAC
FIRST SEMESTER 2011 – 2012
EA C414 INTRODUCTION TO BIOINFORMATICS
COMPREHENSIVE EXAMINATION (CLOSED BOOK)

Duration: 3hours **Date: 11.12.2011**
Weightage: 40% **Max. Marks: 40**

Note: a) Answer Part-A and Part-B in separate answer books, b) answer all questions c) answer to the point and d) draw schematic diagram if required.

PART-A

1. Briefly describe on fluorescent in situ hybridization and somatic cell hybrids. [2.0]
2. Explain the different levels of organization of protein structure and draw suitable diagram. Justify your understanding to protein structure prediction. [3.0]
3. How the human genome and other genomes will lead to improvements in the health of mankind? Explain any three examples in detail. [2.0]
4. Differentiate between X-ray crystallography and NMR derived data and applications in protein structure prediction. [2.0]
5. What is gene ontology and how the proteins are classified based on gene ontology? Explain. [2.0]
6. What are expression and proteomics databases? Mention any four applications. [2.0]
7. How the protein stability and folding mechanisms studied? Mention different parameters to be considered for the stable structure of a protein. [2.0]
8. What are the different applications of hydrophobicity profile determination in protein structure prediction? Explain with suitable diagrams. [2.0]
9. Write a short note on the following: [3.0]
   a. DNA microarray
   b. Mass spectrometry
   c. Systems biology

PART-B

1. Briefly describe on open access and its applications in bioinformatics data analysis? [3.0]
2. Explain the different programming languages, tools and methods used and its applications in bioinformatics for the following: [3.0]
   a. Databases
   b. Protein structure prediction
   c. DNA sequence analysis
3. a) Briefly describe the steps followed for dot matrix method of pair wise sequence alignment. [2.0]
   b) What is the advantage of NW method for sequence alignment over dot matrix method? [2.0]
4. a) What is the objective of PSI-BLAST program? [2.0]
   b) Show the schematic diagram or flowchart for the PSI-BLAST program. [2.0]
5. What is the phylogenetic tree and mention the applications? [3.0]
6. Briefly describe the clustering method and the Cladistic method for phylogenetic tree construction. [3.0]

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TEST-II (OPEN BOOK)

Duration: 50 min. **Date: 18.12.2011**
Weightage: 20% **Max. Marks: 20**

Note: a) Answer all questions b) answer to the point and c) draw schematic diagram if required.

1. Briefly define BLAST parameters for identifying protein sequences from Genbank? Consider the Genbank entry of name A00115, title "sequence from patient A00115" and sequence "GATCATCGGTTCCAATTCGCAT" [4.0]
   (a) Write down the sequence in FASTA format
   (b) How will you get the protein sequence from nucleotide sequence?
2. How mutations effect the protein function and protein evolution? How will you identify protein stability and folding of α-helices, β-sheets and 3D conformation of proteins in terms biophysical data, bond angles, entropy and enthalpy? Justify with a suitable example. [5.0]
3. What will you do when there is no useful template is available for protein structure prediction? Explain in brief about energy minimization. [5.0]
4. Using the dot matrix method align the pair of nucleotide sequences shown below. [3.0]

   TAGGATCGT
   TAAGCT
   Assuming +1 for match and -1 for gap, find out the alignment score.
5. How the open access articles of bioinformatics importance is applicable with respect to gene ontology? Explain with respect to current development in biotechnology, drug discovery and development. [3.0]

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TEST ~~QUIZ~~-I (CLOSED BOOK)

Duration: 50 min. **Date: 23.10.2011**
Weightage: 25% **Max. Marks: 25**

Note: a) Answer all questions b) answer to the point and c) draw schematic diagram if required.

1. How hereditary information is stored, passed on and implemented in biological systems. [1.5]
2. Write a short note on: [1.5]
   a. Linkage or gene map
   b. Banding patterns of chromosomes
   c. DNA sequences
3. Write a short note on: [3.0]
   a. Contig or contiguous clone map
   b. Sequence tagged site (STS)
   c. Expressed sequence tag (EST)
4. Differentiate between the genomes of prokaryotes and eukaryotes based on physical and functional aspects. Give the best studied model organisms for each. [2.0]
5. Write a short note on genome databases and genome browsers with an example of each. Give a brief account of user available avenues of each. [2.0]
6. How the following databases are useful in bioinformatics based proteomics research and mention the information and data which you will retrieve for analysis. [4.0]
   a. SWISS-PROT
   b. TrEMBL
   c. PROSITE
   d. ENZYME DB
7. Write a short note on the protein information resource (PIR) and associated databases. Give examples. [2.0]
8. Explain in detail on databases of structures with respect to PDB, information contained in the PDB entry and links associated with the PDB. [2.5]
9. Differentiate between the NMR and X-ray crystallography data with rescpect to bioinformatics. [1.5]
10. How the genes are classified with resepect to Gene Ontology project and briefly explain on each category. [4.0]
11. What are the applications of bioinformatics and biomolecular modeling in molecular biology and how important in global expression analysis, biomedical research and systems biology? [1.0]

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QUIZ-I (CLOSED BOOK)

Duration: 20 min. **Date: 26.9.2011** **Max. Marks: 8**

Name:

ID No:

Note: Answer to the point

1. Define the terms (a) Genotype and (b) Phenotype. [1.0]

2. What is microevolution and macroevolution? Mention the role of bioinformatics. [1.0]

3. Mention any two bioinformatics database and its applications. [1.0]

4. What are the programming languages and software programmes most commonly used for bioinformatics related tools for data analysis. [1.0]

5. What is phylogenetic analysis and mention its applications and mention any one software for phylogenetic analysis. [1.5]

6. Mention classification protein structures based on different levels of organization and give any two example of protein structure data banks/ data basse. [1.5]

7. What is protein structure prediction and mention a general method followed for such analysis. [1.0]