BIRLA INSTITUTE OF TECHNOLOGY & SCIENCE, PILANI- DUBAI CAMPUS
DUBAI INTERNAITONAL ACADEMIC CITY
SECOND SEMESTER 2011 – 2012
EA C414 INTRODUCTION TO BIOINFORMATICS
COMPREHENSIVE EXAMINATION (CLOSED BOOK)

Duration: 3hours **Date: 3.6.2012**
Weightage: 40% **Max. Marks: 40**

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

1. a. How the use of DNA sequences to determine the phylogenetic relationships of living things is achieved? [1.0]

   b. Mention the sequential procedure for the phylogenetic analysis. [2.0]

   c. Draw the outcomes of phylogenetic analysis using schematic diagrams. [2.0]

2. a. How the protein structure prediction and engineering is carried out? [1.0]

   b.Mention the different stages of protein structure prediction protocol using bioinformatics software and tools. [2.0]

   c. How the Critical Assessment of Structure Prediction (CASP) is used to protein structure prediction? [2.0]

3. Outline the information derived out of the genome sequences of a prokaryotic and an eukaryotic genome. [3.0]

4. Describe the different programming languages and tools used in bioinformatics with respect to (a) traditional programming languages, (b) Scripting languages, (c) programs for specialized molecular biology, (d) Java-computing over the web and (e) Applications in DNA sequence analysis. [5.0]

5. Briefly explain on the following with suitable examples:
   a. The Dotplot. [2.0]

   b. Sequence alignment and the applications in sequence alignment. [3.0]

6. The accuracy and precision of protein structure determination is important in biological applications. Brief on the following in above applications:
   a. Nuclear Magnetic resonance (NMR) [2.0]

   b. X-ray crystallography [2.0]

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7. What are the different parameters which describe the allowed mainchain conformations in protein stability and folding in the Sasisekharan-Ramakrishnan Plot? Explain with respect to conformational angles of polypeptides, side chains, protein physic-chemical properties, protein stability, folding and clustering of residues in the α- and β-regions and the exceptions occurring in glycine residues. Draw suitable diagrams. [5.0]

8. What are the applications of hydrophobicity profile in bioinformatics? Explain with any two examples. Draw suitable diagrams. [3.0]

9. a. How the DNA microarrays, Mass spectrometry help in understanding the global transcriptome analysis and expression profiling? [3.0]

   b. How the information derived is applied in systems biology? [2.0]

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SECOND SEMESTER 2011 – 2012
EA C414 INTRODUCTION TO BIOINFORMATICS
TEST-II (OPEN BOOK)

Duration: 50 min. **Date: 18.4.2012**
Weightage: 20% **Max. Marks: 20**

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

1. Using the dot matrix method align the pair of nucleotide sequences shown below. [4.0]

   CGTGACTA
   CGACTGTA
   Assuming +1 for match and -1 for gap, find out the alignment score

	C	G	T	G	A	C	T	A
C								
G								
A								
C								
T								
G								
T								
A								

2. Which of the following protein sequences has the highest information content and why? [2.0]
   a. TGCADESWQRFIYKLHM
   b. TGCADCATGDSWSDEW
   c. TGGSSTTTGGSSSTTGG

3. What are the different BLAST parameters are required for identifying protein sequences from Genbank? Consider the Genbank entry of name A00115, title "sequence from patient A00115" and sequence "GATCATCGGTTCCAATTCGCAT" [3.0]
   (a) Mention the sequence in FASTA format for BLAST search
   (b) What are the different possibilities of getting the protein sequence from nucleotide sequence?

4. Mutations affect the protein functions and also evolve through protein evolution. Explain with suitable examples. [3.0]

5. What are the different methods available and parameters required to study protein stability and protein folding? Justify with a suitable example. [4.0]

6. How the *ab initio* method for protein structure determination is carried out in the absence of a suitable homology structure is not available for a protein sequence? Explain with energy minimization techniques involved. [4.0]

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FIRST SEMESTER 2011 – 2012
EA C414 INTRODUCTION TO BIOINFORMATICS
TEST-I (CLOSED BOOK)

Duration: 50 min. **Date: 29.2.2012**
Weightage: 25% **Max. Marks: 25**

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

1. Define the terms (a) Genotype and (b) Phenotype. [2.0]
2. How hereditary information is stored, passed on and implemented in biological systems and provide a schematic diagram? [2.0]
3. Write a short note on: [3.0]
   a. Contig or contiguous clone map
   b. Expressed sequence tag (EST)
4. Name any four programming language used in bioinformatics. [2.0]
5. What is phylogeny and briefly discuss on SINES and LINES? [2.0]
6. Differentiate between the genomes of prokaryotes and eukaryotes based on physical and functional aspects. Give the best studied model organisms for each. [3.0]
7. 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]
8. Briefly discuss on different levels of organization of protein structures with respect to protein structure prediction and engineering. [4.0]
9. What are the applications of bioinformatics and biomolecular modeling in molecular biology and how important in global expression analysis by using Mass Spectrometry and DNA Microarrays? [3.0]
10. What are the different approaches used to identify the protein coding regions in DNA? Briefly discuss. [2.0]

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SECOND SEMESTER 2011 – 2012

Course Code: EA C414 **FOURH YEAR (ALL)** Date: 22.13.12

Course Title: Introduction to Bioinformatics **QUIZ 1** Max Marks: 08

Duration : 20 minutes Weightage: 8%

Name: . . . . . ID No: . . . . . Sec / Prog: . . . . . .

Instructions: (if any) Closed book- Answer all the Questions. "amino_acid_tbl" is shown on last page.

1. The logical structure (or interrelationships among data) is called as _____ **[1M]**

2. Briefly explain the join operation in relational database and the need for WHERE clause **[2M]**

3. Explain what is positional formatting in organizing data in a file. Compare it with the XML approach ? **[1M]**

4. What is the role feature table in a nucleotide db file, Give any 2 examples?. **[1M]**

P.T.O

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5. Following is a snippet of a nucleotide db file. What interpretation can be derived from it.? **[1M]**

```
FT   CDS             1..676
FT                   /product="ATPA7"
FT                   /protein_id="AAG47427.1"
FT                   /translation="IVYQP……"
SQ   Sequence 675 BP;
     attgttatc……
//
```

6. For the table "amino_acid_tbl" shown, give the SQL statement for the following queries. **[2M]**
   a) List the name, 3 letter code, and Distal Group of all amino acids which has volume is between 150 & 200?

   b) Find the name of all amino acids belonging to the Distal Group Amide?