

**P.G. Diploma in Bio - Informatics
Annual Examinations – 2006**

**Paper PBID – 104
Computational Biology**

Time allowed: Three hours

Maximum Marks: 80

1. Attempt all questions from Section I.
2. Attempt any six questions from Section II.
3. Attempt any three questions from Section III

SECTION – I

Marks

Q1. Select the correct answer.

- (i) KDD knowledge discovery in database uses
 - a) Machine Learning
 - b) Visualization technique
 - c) Statistical technique.
 - d) All a,b,c

- (ii) Which factor derives for data mining technique development
 - a) Increase flood of data
 - b) Increase science
 - c) Increase information system
 - d) Increase population

- (iii) Which is the most recent technique and consider as a snapshot of gene activity for the entire genome.
 - a) Microarray
 - b) Gel electrophoresis
 - c) Paper chromatography
 - d) None

- (iv) Who found the helical nature of DNA
 - a) Watson and Crick
 - b) Moris and Boyed
 - c) Zakale and Pearson
 - d) Azel and Tom

- (v) The protein sequence is produced from mRNA by the process
- Transformation
 - Translation
 - Transcription
 - Translitaarton
- (vi) Which codon causes termination in sequence
- UAA
 - UAG
 - UGA
 - All a,b,c
- (vii) Biological motivation for studying sequence similarity is
- Hypothesizing the function of new sequence
 - Researching the effect of multiple sclerosis
 - Both a,b
 - None
- (viii) Which is the oldest method of sequence alignment
- Dotplot
 - Dynamic programming
 - K-tuple method
 - None of the above
- (ix) The program based on Dotplot method is downloaded from EBI-ftp server
- Dotter
 - MAXDOT
 - FRTDOT
 - EBIDOT
- (x) ORF stands for
- Open reading frame
 - Open reading factor
 - Outer reading frame
 - Open reading face
- (xi) Profile scan software is used for
- To find out the structural & sequence motif in protein.
 - To find out the structural & sequence motif in RNA

- c) To find out the structural & sequence motif in DNA
- d) To draw phylogenetic tree

(xii) Protein Domain database is

- a) BLOCKS
- b) PRINTS
- c) PRODOM
- d) PROSITE

(xiii) Genbank database is hosted at which site

- a) NCBI
- b) EBI
- c) PDB
- d) PIR

(xiv) BLAST stands for

- a) basic local alignment search tool
- b) baysian local alignment search tool
- c) basic local alignment search technique
- d) basic local alignment string tool

(xv) The program used for Homology search against database

- a) BLAST
- b) FASTA
- c) Both a,b
- d) None

(xvi) The query protein sequence the word length used in BLAST software is

- a) 4
- b) 3
- c) 5
- d) 11

(xvii) Which Program is heuristic program

- a) BLAST
- b) FASTA
- c) Clustal - w
- d) AL a,b,c

(xviii) Select the software used in ab-initio gene prediction

- a) Gene mark
- b) Genscan
- c) GRAILEXP
- d) ESP

(xix) NJ method was given by

- a) Saitou and Nei
- b) Zakale et al
- c) Michel & Devis
- d) Nedlemen & Wunch

(xx) UPGMA method for drawing tree is basically

- a) Distance method
- b) Matrix method
- c) Character method
- d) None

SECTION – II

5X6=30

Q2. Attempt any six of the following

- a) What is the evolutionary basis for sequence alignment?
- b) Discuss the type of tree style.
- c) List the five programs used for secondary structure prediction and folding classes in protein sequence.
- d) Write down the blast algorithm.
- e) What is the Dotplot method, discuss with an example.
- f) Elaborate the type of ftp server used in bioinformatics.
- g) Discuss the basic feature of SEQUIN software.

SECTION – III

10X3=30

Attempt any three questions of the following

Q3. Find out the optimal sequence alignment by using dynamic programming method globally for the given sequences.

Seq 1 TTGGTGGCCTTG

Seq 2 GGTTCCTGCATG

If $S_{ij} = 1$ (Match)

$S_{ij} = 0$ (Mismatch)

$W = 0$ (Gap Penalty)

Q4. Draw the phylogenetic tree by using UPGMA or FM Method/Algorithm of the given distance matrix

	Gene 1	Gene 2	Gene 3	Gene 4
Gene 1	-			
Gene 2	-	8		
Gene 3	-	-	10	
Gene 4	-	-	14	12
				16
				18
				-

Q5. What is the data mining? Discuss its need and method in detail.

- Q6. a) What are the tasks of computational Biology?
b) Write down the basic feature of clustral-w software.