

Name :

Roll No. :

Invigilator's Signature :

CS/B.TECH/BT(N)/SEM-5/BT-502/2012-13

2012

BIOINFORMATICS

Time Allotted : 3 Hours

Full Marks : 70

The figures in the margin indicate full marks.

*Candidates are required to give their answers in their own words
as far as practicable.*

GROUP – A

(Multiple Choice Type Questions)

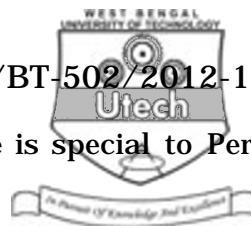
1. Choose the correct alternatives for any *ten* of the following :

10 × 1 = 10

- i) Which of the following is the fastest program to search for similar sequences in databases ?
 - a) BLAST
 - b) FASTA
 - c) Needleman-Wunsch
 - d) Smith-Waterman.
- ii) If you are aligning similar protein from diverged species, which one of the following is a better option ?
 - a) Global alignment
 - b) Local alignment
 - c) Both global and local alignment
 - d) Aligning is not possible.



- iii) Which of the following database is maintained by NCBI ?
- a) EMBL
 - b) PIR-PSD
 - c) Genbank
 - d) Swiss-prot.
- iv) PROWL is used for
- a) protein visualization
 - b) DNA structure prediction
 - c) primary protein structure information
 - d) DNA-protein interaction.
- v) Denovo ligand design is done by
- a) Autodock
 - b) HADDOCK
 - c) LUDI
 - d) VAST.
- vi) Which of the following tool is effective to search homologous sequences in distantly related species ?
- a) Multiple alignment
 - b) Profile
 - c) Pair wise alignment
 - d) None of these.
- vii) Genbank files can be identified uniquely searching using
- a) Text search
 - b) Advanced search
 - c) Specific organism
 - d) Gi number.
- viii) Which of the following is a protein family Database ?
- a) NCBI
 - b) Pfam
 - c) PROSITE
 - d) Both (b) and (c).
- ix) Perl stands for
- a) Pathologically Eclectic Rubbish Lister
 - b) Practical Extraction and Report Language
 - c) Practical Extension and Research Language
 - d) Promoter Extraction and Report Language.



- x) Which of the following loop structure is special to Perl Script ?
- a) While loop b) Do while loop
- c) For loop d) Foreach loop.
- xi) Biologically significant similar sequences have
- a) Higher E-value b) Lower E-value
- c) Lower Raw score d) Lower Bit score.
- xii) Lower k-tuple increases of an algorithm
- a) Specificity b) Sensitivity
- c) Both (a) and (b) d) None of these.

GROUP - B

(Short Answer Type Questions)

Answer any *three* of the following. $3 \times 5 = 15$

2. What is the difference between Bioinformatics & Computational biology ? 2 + 3
3. What do you mean by ORF ? Write down basic steps (in flow charts) of gene prediction. 2 + 3
4. Write a perl program to concatenate two DNA seq (DNA1 = 'AGGCT A' DNA2 = "CAAGCT") using dot operator.
5. What do mean by Multiple sequence alignment (MSA) ? Write down an algorithm for MSA ? You have three protein sequences for ex : Seq 1: MAKYPW, Seq 2 : MKYTW & Seq 3 : MKYVW. Point out Conserved region by aligning three sequences. 1 + 1 + 3
6. Write down Lipinski rule of five for a drug like compound ?



GROUP - C

(Long Answer Type Questions)

Answer any *three* of the following. $3 \times 15 = 45$

7. a) Write a Perl Program to search a Motif from a Sequence stored in the computer.
 b) Write a Perl Script that will count the number of 'A', 'T', 'G', 'C' in a given sequence.
 c) Write a Perl Script to generate a complementary DNA sequence of a given Template sequence.
8. Write short notes on any *three* : $5 + 5 + 5$
 - a) PROFILES
 - b) Smith-Waterman Algorithm
 - c) Hidden Markov Model
 - d) PROSITE
 - e) QSAR.
9. Write the names of structural organization of protein ? What do you mean by protein domain and motif ? Describe Chou-fasman algorithm for the Secondary structure prediction ? Suppose you have downloaded a Human Hypothetical Protein (which has no assigned structure and function) from Uniprot Database. How can you predict structure and function to this protein ? What is PDBsum. $2 + 2 + 5 + 4 + 2$
10. What do you mean by agonist, antagonist and Icm₅₀ ? How can you describe Virtual screening ? What is structure based or rational drug design ? What do you mean by pharmacophore ? Describe first order energy minimization approach ? Give an example of an Molecular Dynamics programme which is widely use for Protein dynamics. $3 + 2 + 3 + 2 + 4 + 1$
11. a) What are the basic principles used in gene prediction algorithm ? Discuss few programs those predict genes from genomic DNA. $3 + 5$
 b) What is consensus sequence ? Explain a Prosite pattern with an Example ? $1 + 3$
 c) Define Secondary database. Give a brief notes on protein family database. $1 + 2$

