

Name :
Roll No. :
Invigilator's Signature :

**CS/B.Tech/BT(O)/SEM-5/BT-503/2012-13
2012**

BIOINFORMATICS-I

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) PAM is constructed by

a) Lipman

b) Chou-Fasman

c) Dayhoff

d) Waterman.

ii) Which of the following organisms is *not* represented in
Locus Link ?

a) Mouse

b) Fly

c) Human

d) *Escherichia coli*.



iii) Which of the following amino acids is least mutable according to the PAM scoring matrix ?

- a) Alanine
- b) Glutamine
- c) Methionine
- d) Cysteine.

iv) What is the full form of NCBI ?

- a) The National Centre for Biotechnology Information
- b) The National Centre for Biology Information
- c) The National Centre for Botany Information
- d) The National Centre for Biochemistry Information.

v) You have a DNA sequence. You want to know which protein in the main protein database ("nr", the nonredundant database) is most similar to some protein encoded by your DNA. Which program should you use ?

- a) blastn
- b) blastp
- c) blastx
- d) tblastn
- e) tblastx.



vi) PROSITE is a

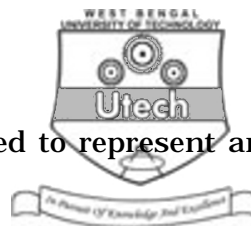
- a) Database of protein motif
- b) Database of promoter region
- c) Database of restriction site
- d) none of these.

vii) The Protein Data Bank (PDB)

- a) functions primarily as the major worldwide repository of macromolecular secondary structures.
- b) contains approximately as many structures as there are protein sequences in SwissProt/TrEMBL
- c) includes data on proteins, DNA-protein complexes as well as carbohydrates
- d) is operated jointly by the NCBI and EBI.

viii) In Perl, the name of the array variable starts with

- a) @
- b) #
- c) \$
- d) %



ix) Which of the following symbols is used to represent an associative array variable ?

- a) @
- b) #
- c) \$
- d) %

x) Any sub-routine defined in Perl should start with

- a) sub_routine
- b) sub
- c) subroutine
- d) none of these.

xi) In Linux, rm command is used

- a) to move files from one location to another
- b) to delete files
- c) to display the current directory
- d) to create a new directory.

GROUP - B

(Short Answer Type Questions)

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

2. What is the scope of bioinformatics ? Why is it a multi-disciplinary field ? What is accession number ? $2 + 2 + 1$

3. What is PERL ? What are the advantages of PERL programming ? What are the importance of Data Bank ?

$1 + 2 + 2$



4. Write down the function of the following terms in Perl with examples : 5 × 1

- a) Split
- b) Join
- c) Reverse
- d) Pop
- e) Push.

5. Write down the commands for the following operation in Vi-editor : 5 × 1

- a) Save the contents from 4th line through 10th line to another file
- b) Remove five right characters from the cursor position
- c) Copy the three lines and paste it to line at the cursor position
- d) Search the word 'biotech' in the file
- e) Go to insert mode at the beginning of the line from end of the line.

6. What is sequence alignment ? What is the utility of it ? 2 + 3



GROUP - C
(Long Answer Type Questions)

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

7. a) What are the difference between PAM and BLOSUM ?
What do you mean by BLOSUM60 ? $3 + 2$
- b) What is the difference between domain and motif ?
What is ORF ? What is the meaning of the expression
E-X(2)-[FHM]-X(4)-{P}-L ? $2 + 1 + 2$
- c) Write a script that will count the number of Adenine,
Thymine, Guanine and Cytosine in your DNA
Sequence. 5
8. What is the difference between local and global alignment ?
When will you apply these ? What is Smith-Waterman
algorithm ? Align these two following sequences by
Needleman-Wunsch Algorithm. Given that the score
for match = 4, mismatch = 1 and gap = - 2.
Seq1 = AGGTCTACGA and Seq2 = AGTCTAG. $3 + 2 + 3 + 7$
9. Write in brief on any *five* of the following : 5×3
- a) PubMed
 - b) Taxonomy browser
 - c) Fasta Format
 - d) OMIM
 - e) Prosite
 - f) Pfam.



10. a) What is subroutine ? Write down the advantage of subroutine ? What is the utility of `my` statement in perl ? Write down the function of any two pattern matching operator. 1 + 3 + 1 + 2
- b) Mention the function of the program `water` in EMBOS. What is the function of promoter in a gene ? What is the objective of gene prediction ? What is GENSCAN ? What is BioPerl ? 1 + 2 + 2 + 1 + 2
11. What is the importance of DOT plot ? Mention the steps of BLAST program in sequence alignment. Mention the relationship between E and P values. Define Masking and mention role of masking in reducing the signal to noise ratio. What does Vi-editor stand for ? Mention briefly the modes of operation of Vi-editor. 2 + 4 + 2 + 1 + 2 + 1 + 3
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