

Student Exam No: _____

GANPAT UNIVERSITY
BIOMEDICAL & INSTRUMENTATION ENGINEERING
B.TECH SEM.VI REGULAR EXAMINATION MAY/JUNE-2013
2BM605: BIOINFORMATICS

TOTAL MARKS-70

TIME: 3 HOURS

INSTRUCTION: -1. Answers to the 2 sections must be written in the separate answer books
2. Figures to the right indicate marks.
3. Conventional terms or notation are used.

Section-I

- Que.-1 (a) What is the central dogma of molecular biology? And explain the process of translation. 12
(b) Enlist the enzymes associated with DNA replication. And explain the function of each in brief.
- OR
- Que.-1 (a) Define peptide bond with neat diagram and Draw the neat diagram of basic structure of amino acid. And explain each part of it in detail. 12
(b) What is secondary structure motif? Give any three examples of it. And explain it with neat diagram.
- Que.-2 (a) What is DNA sequencing? And explain the procedure of DNA sequencing with neat diagram. 11
(b) Explain the polymerase chain reaction (PCR) with diagram.
- OR
- Que.-2 (a) Explain with neat diagram cell-based DNA cloning. 11
(b) Enlist the protein function and Explain the process of protein folding with diagram. 12
- Que.-3 (a) Find out the optimal global pair wise alignment of two sequences by dynamic programming. Where the scoring scheme is : $S_{i,j}=2$ (match score),
 $S_{i,j}=-2$ (mismatch score), use linear gap penalty = -1
Sequences are: i) G A A T T C A G T T A, ii) G G A T C G A.
(b) Define: bioinformatics, gene, vector, restriction enzymes.

Section-II

- Que.-4 (a) Explain the following commands with their options and examples:
i) uniq ,ii)cut ,iii)touch. 12
(b) How splice function can be used to add or delete an element from the array?
(c) Explain split and join function with example.

OR

- Que.-4 (a) Explain various methods of changing file permissions in linux. 12
(b) Explain the conditional statements if..elsif..else and unless with examples.
- Que.-5 (a) Write a Perl program to determine the percentage of each nucleotide occurring in a sequence read from a file and Write the results to the same file. 11
(b) Write a Perl program that checks if two strings given as arguments are reverse complements of each other.
- OR
- Que.-5 (a) Write the short note on genome analysis. 11
(b) Write a Perl program that switches two bases in a DNA string at specified positions.
- Que.-6 (a) Write a Perl program to read the contents of two files and Write the contents of both the files in the third file but by arranging the contents alphabetically. 12
(b) Write a Perl program to check whether the given string is a DNA sequence or not. If it is a DNA sequence, display it in both upper case and lower case.

END OF PAPER