Student Exam No._____

GANPAT UNIVERSITY
B. Tech. Semester VIth Biomedical & Instrumentation Engineering
CBCS Regular Examination May 2014
2BM605: Bioinformatics

Time: 3 Hours   Total Marks: 70

Instructions:
1. Answer to the question of section must be written in separate answer books.
2. Figure to the right indicates marks.
3. Conventional terms / notations are used.
4. All the questions are compulsory.

Section - I

Que. – 1 (1) Define DNA Translation. Explain entire process of DNA translation with neat diagram. 06

(2) What is nucleotide? Draw single nucleotide of DNA.Draw and Explain different nitrogen bases of DNA. 06

OR

Que. – 1 (1) Define Prokaryotes. Explain DNA Transcription in Prokaryotes. 05

(2) What is DNA? Explain structure of DNA with neat diagram. 07

Que. – 2 (1) Find the local alignment for the following sequences: ATTCGATCC and ACGAT. Use match score =1, mismatch score=0, gap penalty= - 06

(2) Explain different types of RNA with neat diagram. 05

OR

Que. – 2 (1) What is cloning? Explain Cell based DNA cloning with neat diagram. 07

(2) Explain Peptide bond and Phosphodiester bond with its chemical structure. 04

Que. – 3 (1) Explain basic structure of Amino acid. Explain primary and secondary structures of protein in detail. 07

(2) What is Mutation? How do Mutations occur? Explain point and Frame shift mutations with examples of each. 05

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Section – II

Que. – 4

(1) Write a Perl program to print out the contents of file in alphabetical order if and only if the third line of the file is 'This is DNA' and the last line of the file is 'This is RNA'.   05

(2) Explain grep, cut, cmp commands used in Linux with example.   04

(3) Write a Perl program that checks whether the number of nucleotides in a given sequence is even or odd.   03

OR

Que. – 4

(1) What is PERL? What are the types of variables used in Perl? Give one example of each   05

(2) Write a Perl program to search any given motif in a particular sequence read from a file.   04

(3) Write a subroutine that checks for any blank line in a file and displays the message if there is one. If there are blank lines in the file, remove them and print out the data.   03

Que. – 5

(1) Write a Perl program that checks if two strings given as arguments are reverse complements of each other or not. If they are not, find out the reverse complements of both sequences.   06

(2) Write a PERL program to determine the percentage of each nucleotide occurring in sequences read from a file.   05

OR

Que. – 5

(1) Define array variable. How splice function can be used to add or delete an element from the array? What is the use of split function in PERL? Explain with example.   06

(2) What is the significance of the regular expressions in PERL? Explain different regular expressions in detail.   05

Que. – 6

(1) Define flow control of a program. Explain types of loops in PERL. Explain flow control in PERL using loops with example of each.   06

(2) Write a short note in LINUX operating system. Explain wild cards in Linux with example.   03

(3) Write a Perl program to read the data from two files and print the data in such a way that lines of both files are printed alternately i.e. first line from one file and second line from another file and so on.   03

END OF PAPER