

**GANPAT UNIVERSITY****B. Tech. Semester: VI (BM&I) Engineering****Regular Examination April – June 2016****2BM605 Bioinformatics****Time: 3 Hours / As per Scheme****Total Marks: 70**

- Instruction:** 1 This Question paper has two sections. Attempt each section in separate answer book.  
 2 Figures on right indicate marks.  
 3 Be precise and to the point in answering the descriptive questions.

**Section - I**

- Que. – 1** [12]  
 (a) Define: Bioinformatics. Enlist and explain its applications. 6  
 (b) Give the reason behind the complementary bases in DNA structure. 3  
 (c) Differentiate between prokaryotes organism and eukaryotes organism. 3

**OR**

- Que. – 1** [12]  
 (a) What is motif? Write and execute a perl program to find out whether a motif is present in a given DNA sequence or not. 6  
 (b) Explain the conditional statements 'if..elsif..else' and 'unless' in perl with two examples of each. 6

- Que. – 2** [11]  
 (a) What do you understand by central dogma of molecular biology? Explain the process of translation with neat diagram. 6  
 (b) In which organism modification of RNA is required? Explain in detail modification of RNA. 5

**OR**

- Que. – 2** [11]  
 (a) Explain push, pop, unshift operations applied on array with two example of each. 6  
 (b) Write and execute a perl program to read and print the data from the file if and only if the first line of the file is 'agtcagtcagt' and the last line of the file is 'tatatatatatat'. 5

- Que. – 3** [12]  
 (a) Find the optimal local alignment of AAG (sequence #1) and GAAGGC (sequence #2) using Smith-Waterman technique. Use a gap penalty of d= -5. And Use following substitution matrix. 8

	A	C	G	T
A	2	-7	-5	-7
C	-7	2	-7	-5
G	-5	-7	2	-7
T	-7	-5	-7	2

- (b) Explain the following: 4  
 I. scalar@bases;  
 II. sort@bases;  
 III. \$comfort = \$hot cmp \$cold;  
 IV. print "O x 5\n";



## Section – II

- Que. – 4** [12]
- (a) What is protein? Draw the neat diagram of basic structure of amino acid. And explain each part of it in detail. 6
  - (b) Define :  $\Psi$  angle,  $\Phi$  angle,  $\omega$  angle in protein structure. 3
  - (c) Explain the process of protein folding with diagram. 3
- OR**
- Que. – 4** [12]
- (a) Explain with neat diagram cell-based DNA cloning. 6
  - (b) Enlist and explain the types of mutations. 6
- Que. – 5** [11]
- (a) Write a Perl program that reads a file and Writes the data in another file in reversed order. 6
  - (b) Write a subroutine to concatenate three strings of DNA in three different ways. 5
- OR**
- Que. – 5** [11]
- (a) Write a Perl program to determine the frequency of occurrence of each nucleotide occurring in a sequence read from a file. 6
  - (b) Write a perl program that checks for any blank line in a file and displays the message if there is one. 5
- Que. – 6 Write the short note on:** [12]
- (a) Types of protein structure. 6
  - (b) Polymerase chain reaction (PCR). 6

END OF PAPER