GANPAT UNIVERSITY
B. TECH SEM- VI (BM&I) REGULAR EXAMINATION– APRIL-JUNE 2017
2BM605: Bioinformatics

TIME: 3 HRS   **TOTAL MARKS: 60**

Instructions: (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

Q.1   **(10)**
(a) Write the difference between: (i) nucleotide and nucleoside and (ii) prokaryotes organism and   **5**
eukaryotes organism.

(b) Explain in detail modification of RNA.   **5**

OR

Q.1   **(10)**
(a) Define: Bioinformatics. Explain its various applications.   **5**

(b) Describe the process of the DNA transcription with neat diagram.   **5**

Q.2   **(10)**
(a) What is protein? Explain the process of protein folding with diagram.   **5**

(b) What is motif? Explain different types of motif.   **5**

OR

Q.2   **(10)**
(a) Define peptide bond. Enlist the different functions of protein.   **5**

(b) Explain the polymerase chain reaction (PCR) with diagram.   **5**

Q.3   **(10)**
(a) What is sequence alignment? Explain the types of sequence alignment.   **3**

(b) Find the best pair wise global alignment of GAATC and CATAC. Use extended linear gap   **7**
penalty of -4.Use the following substitution matrix.

	A	C	G	T
A	10	-5	0	-5
C	-5	10	-5	0
G	0	-5	10	-5
T	-5	0	-5	10

SECTION: II

(10)

Q.4
(a) What is DNA sequencing? And explain the procedure of DNA sequencing with neat diagram. **5**

(b) How Do Mutations Occur? Explain the types of mutations. **5**

OR

(10)

Q.4
(a) Why gene sequence information and the pattern of gene activity in a cell do not provide a complete and accurate profile of a protein's structure? **3**

(b) Explain various steps involve in proteome analysis. **5**

(c) Define: Genome and proteome. **2**

(10)

Q.5
(a) Write a Perl program to print out the contents of file in reverse order if and only if the first line of the file is 'AGCTAGCT' and the last line of the file is 'TCGATCGA'. **5**

(b) Write a Perl program to determine the percentage of each nucleotide occurring in a sequence read from a file without using foreach loop. **5**

OR

(10)

Q.5
(a) Write a perl program to obtain reverse complement of a DNA strand 'ATTCCCGTAGCTAGCTAGCTACGCTGAT' and display the original strand, reverse strand, complementary strand and reverse complementary strand. **5**

(b) 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. **5**

(10)

Q.6
(a) What is PERL? Why PERL is a preferred language for the bioinformatics applications. Enlist and explain the benefits of using PERL programming language. **5**

(b) Write a Perl program with a subroutine to append ACGT to DNA. Also Illustrate the pitfalls of not using my variables in subroutine. **5**

---END OF PAPER---