

GANPAT UNIVERSITY
B.TECH SEM VI BIOMEDICAL & INSTRUMENTATION ENGINEERING
REGULAR EXAMINATION April - June 2015
2BM605 BIOINFORMATICS

Time: 3 Hours

Total Marks-70

Instructions:-

1. All the questions are compulsory.
2. Answer of each section must be written in separate answer books.
3. Figure to the right indicate marks.
4. Assume data, if needed.

SECTION: I

Que. 01

- a) What are the advantages of using Perl? Why Perl is more suitable for Bioinformatics applications?
- b) Describe how to read data from a single line and multi line files in Perl with the help of suitable example.

[12]

OR

Que. 01

- a) Write a Perl program to obtain reverse complementary of a DNA strand. Display the original strand, reverse strand, complementary strand and reverse complementary strand.
- b) Write a Subroutine in Perl to append AGCT to given DNA sequence. DNA Sequence: 'AGCTAGCTAGCT'.

[12]

Que. 02

- a) Write a Perl program to print the contents of file if and only if the first line of the file is 'AAAACCCC' and the last line of file is 'GGGGTTTT'.
- b) Write a Perl program to read the data from two files and print the contents of the first followed by the contents of the second.

[11]

OR

Que. 02

- a) Write a Perl program to search a data file for the motif of interest. Ask the user for filename he wants to check in. Also ask for the motif he wants to check for. The program should be executed only when the password entered by the user is correct.
- b) Explain the use of foreach loop with the help of suitable example.

[11]

Que. 03

- a) Write a Perl program to count the number of Glycine amino acid molecules present in a protein sequence read from a file. Triplet codes for Glycine amino acid are GGA, GGC, GGG and GGU.
- b) Give the output of following Perl program.

```
@birds = ("pigeon", "sparrow", "parrot", "cuckoo", "crow");
@numbers = (22, 32, 42, 52, 62);
@union = ("penguin", 45, 22.7, "cock", 3.14);
print "$birds[0]\n";
print "$numbers[1]\n";
print "$union[$#union]\n";
```

[12]

SECTION: II

Que. 04

[12]

- a) Define following terms.
- | | |
|------------------------|--------------------------|
| 1. Molecular Biology | 4. Computational Biology |
| 2. Bioinformatics | 5. Gene |
| 3. Medical Informatics | 6. Genome |
- b) Draw and explain the structure of RNA. What is the role of RNA in the process of protein synthesis

OR

Que. 04

[12]

- a) Which enzymes take parts in the process of DNA replication and transcription process? Explain the significant of each.
- b) Explain the structure and function of Messenger RNA, Transfer RNA and Ribosomal RNA.

Que. 05

[11]

- a) What is Central Dogma of molecular biology? Briefly explain the process of DNA replication with the help of suitable diagram.
- b) Give the difference between Point Mutation and Frame-shift Mutation with the help of example.

OR

Que. 05

[11]

- a) Explain the process of translation in eukaryotes with the help of suitable diagram.
- b) What is Cloning? Explain the process of Polymerase Chain Reaction with its advantages and disadvantages.

Que. 06

[12]

- a) What is the significant of Sequence Alignment? Give the difference between Local alignment and Global Alignment.
- b) Compute the optimal global alignment for the following two DNA sequences, using Needleman and Wunsch algorithm. Take Match score = +1, Mismatch score = -1 and Gap penalty = -2.
DNA Sequence 1 = AGGT
DNA Sequence 2 = AGCGT

-----END OF PAPER-----