

21/12/17

Exam. Code : 206603

Subject Code : 5149

M.Sc. Bio-Informatics 3rd Semester
PROGRAMMING IN PERL FOR
BIOINFORMATICS

Paper—BI-635

Time Allowed—3 Hours] [Maximum Marks—75

SECTION—A

Note :— Section A is compulsory.

Explain the following in not more than *four* lines each :

1. Linux
2. CPAN
3. Regular expression
4. Loop
5. Concatenating DNA sequence
6. Motifs
7. Random number
8. FASTA format
9. BioPerl
10. Sequence objects. 1.5×10=15

SECTION—B

Note :— Answer *one* question from each unit.

UNIT—1

1. Discuss steps involved in downloading, installation and execution of Perl on Windows Machine.
2. What do you understand by Perl interpreters and script ? Explain features of Perl which make it convenient for bioinformatics.

UNIT—2

3. Discuss file handling in Perl. How do you open, read and write a file ? Explain using example.
4. What are logical operators ? Explain different types of operators in Perl.

UNIT—3

5. Write a program in Perl to read a DNA sequence file and determine frequency of start and stop codon.
6. Write a program to read a DNA file and transcribe it into a RNA sequence. It should determine the frequency of occurrence for AUG, UAA and UGA in the RNA sequence.

UNIT—4

7. Write a program to generate random number.
8. Write a program to separate sequence and annotation from a GenBank file.

UNIT—5

9. Explain how Bioperl can be used for transforming formats of alignment files.
10. What do you understand by Bioperl objects ? Explain location and interface objects.