

Exam. Code : 206603

Subject Code : 4623

M.Sc. Bio-Informatics Semester—III

BI-635 : PROGRAMMING IN PERL FOR
BIOINFORMATICS

Time Allowed—3 Hours] [Maximum Marks—75

Note :—Section A is compulsory. Each part is of 1.5 marks. Attempt **one** question from each unit of Section B. Each question is of 12 marks.

SECTION—A

1. Define rapid prototyping.
2. Explain the role of STDIN.
3. What is the usage of binding operator in perl ?
4. Explain pop and push operators.
5. Explain the following statement :
`$string = ~/^agctAGCT/;`
6. What are *metasymbols* in regular expression ?
7. Briefly explain split function with an example.
8. Define *keys* and *values*.
9. Briefly define Bioperl.
10. Explain the *until* statement with suitable example.

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SECTION—B

UNIT—I

1. (a) Why Perl is called flexible language ? Justify your answer with suitable examples. 6
- (b) Write and explain hashes with a suitable programming example. 6
2. (a) Discuss various error messages of perl. Briefly define debugging. 6
- (b) Write a program to read protein sequence data from a file. 6

UNIT—II

3. (a) What do you mean by pattern modifiers ? Explain their usage with suitable example. 6
- (b) Write a program that picks one of four nucleotides and then keeps prompting until you correctly guess the nucleotide it picked. 6
4. Write a detailed note on different loops and conditional structures available in Perl with suitable examples. 12

UNIT—III

5. (a) Write a program to read a DNA sequence from file and determine the frequency of nucleotides. 6
- (b) Write short notes on :
 - (i) Reverse Transcription of RNA to DNA
 - (ii) Join function. 6

6. (a) Write and explain a program to concatenate DNA fragments. 6
- (b) Write a program that switches two bases in DNA string at specified positions. 6

UNIT—IV

7. (a) Write a detailed note on parsing PDB file. 6
- (b) Write and explain a program to generate random DNA sequence. 6
8. (a) Write detailed note on parsing annotations from GenBank file. 6
- (b) Write a detailed note on random number generator with suitable example. 6

UNIT—V

9. (a) Explain different modules available in Bioperl along with their relevance. 6
- (b) Discuss the transforming formats of database. 6
10. (a) Bioperl is useful in manipulation of sequences. Justify the statement. 6
- (b) How one can access local databases with help of Bioperl ? 6