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M.Sc. (Bio-Informatics) Third Semester
MBIN-8013: Programming Language in Bio-Informatics – II

Time allowed: 3 Hours

Max. Marks: 60

NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting two questions from each Section.

x-x-x

1. (a) State the role of Perl in Bioinformatics. [8X1.5 = 12]
(b) Write steps to read/translate/compare parts of strings.
(c) Write a Bioperl program to read a protein sequence from a file.
(d) Compare XML and XHTML.
(e) State the elements of XML.
(f) What are valid XML documents?
(g) What is an XML tree?
(h) Explain the usage of XML for biological data.

SECTION – A

2. (a) Explain all the operators in Perl using suitable examples. [6]
(b) Write a note on File handling in Perl with respect to creating, appending, deleting and moving files. [6]
3. (a) Compare internal and external subroutines. Explain both using appropriate examples. [4]
(b) Explain steps to perform read/write from databases in detail. [4]
(c) Explain pattern matching using Perl with suitable examples. [4]
4. (a) Write a Perl program for reading DNA/protein sequences from FASTA files. [6]
(b) Write a Perl program to compute the frequency of nucleotides from DNA sequence using suitable examples. [6]

SECTION – B

5. (a) Explain BioPerl calling BioPerl subroutines in Perl Scripts. [6]
(b) Write short notes on SGML, RSS, MathML and WAP. [6]
6. (a) Write a script to create and display XML file. Make assumptions as required. [6]
(b) What is an XML document? What is its structure? Write steps to create valid XML documents. [6]
7. (a) Write steps to display XML with CSS. [3]
(b) Explain XML parsers. [3]
(c) State the bioinformatics problems solved using Perl and XML. [3]
(d) Write a note on the processing of XML documents using Perl. [3]

x-x-x