

2071
B.Sc. (Hons) Bio-Informatics
Sixth Semester
BIN-6001: Introduction to Perl Programming

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 Unit.

x-x-x

I. Answer the following:-

- a) What is the difference between *for* and *for each* construct in Perl?
- b) Differentiate between `chop()` and `chomp()` function.
- c) Explain `grep()` function.
- d) Enlist file test operators.
- e) Expand the term PERL and CPAN.
- f) What are Boundary Characters? (6x2)

UNIT - I

- II. a) Compare features of PERL with C and JAVA.
b) What are Scalar Data and Scalar variable? Discuss various Data types in PERL. (6,6)
- III. a) What are Control Statements in Perl? Explain with examples iterative constructs.
b) Discuss array functions available in PERL with example. (6,6)
- IV. a) Explain the concept of defining and calling subroutines.
b) What are associative arrays? Explain keys, values and each associative array function. (6,6)

UNIT - II

- V. a) Explain pattern matching operators with examples.
b) Write note on Quantifiers. (6,6)
- VI. a) Explain the use of modifiers.
b) Write program to demonstrate the use of `substr`, `index` and `rindex` functions. (6,6)

P.T.O.

(2)

- VII. a) Write a perl script to read the content of a nucleotide sequence text file, count the total number of A,T,G,C and store the result into a new text file.
- b) Write a note on CGI. (8,4)