M. Sc. Bioinformatics Sem.-II (C.B.C.S.) (2013 Course) / Advanced Diploma in Bioinformatics Sem.-II (C.B.C.S.) (2013 Course) :
WINTER - 2018
SUBJECT: PERL AND BIOPERL PROGRAMMING

Day	:	Tuesday	Time :	02.00 PM TO 05.00 PM
Date	:	30/10/2018	**W-2018-1259**	Max. Marks: 60

N. B.:

1) **Q. No. 1** and **Q. No. 5** are **COMPULSORY**. Out of remaining attempt **ANY TWO** questions from each sections.
2) Figures to the right indicate **FULL** marks.
3) Answer to the both sections should be written in **SEPARATE** answer books.

SECTION-I

Q.1 Answer the following (10)
1) What is perl?
2) Enlist the datatypes of perl
3) What is string?
4) Define : Interpolation
5) Enlist file test operators.

Q.2 Answer the following (**ANY TWO**) (10)
1) Explain with examples Operators in regular expression?
2) What will be the result when following operator is evaluated?
14+6*3-10/2
3) What does command 'use strict' and 'use warnings' do and why should we use it?

Q.3 Differentiate between (**ANY TWO**) (10)
1) C programming and perl programming
2) While and do while loop
3) Arrays and scalars.

Q.4 Write a subroutine to print following output using loop (10)
(BIOINFORMATICS, each word in next line).

OR

w.a.p. to copy the content of one file into another file.

SECTION-II

Q.5 Answer the following (10)
1) What is CGI?
2) Use of bioperl module?
3) What are access modifiers?
4) What is POD?
5) Define class.

Q.6 Answer the following (**ANY TWO**) (10)
1) What is regular expression? Explain regular expression variables with example.
2) What is hash? Explain its functions with example.
3) Write a program to print values and keys from hash.

Q.7 Explain object oriented programming concept in detail. (10)
OR
What are perl modules? Explain its use with one example.

Q.8 Write a short note on (**ANY TWO**) (10)
1) Packages in perl
2) Autoloads
3) Complex data structures.

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