

**M. SC. BIOINFORMATICS SEM.-II (C.B.C.S.) (2013 COURSE) /
ADVANCED DIPLOMA IN BIOINFORMATICS SEM.-II
(C.B.C.S.) (2013 COURSE) : WINTER - 2017
SUBJECT : PERL AND BIOPERL PROGRAMMING**

Day : Thursday
Date : 09/11/2017

W-2017-1015

Time : 10.00 AM TO 01.00 PM
Max. Marks : 60

N. B. :

- 1) **Q. No. 1 and Q. No.5 are COMPULSORY.** Solve ANY TWO from the remaining questions from each section.
- 2) Figures to the right indicate **FULL** marks.
- 3) Answers to both the sections should be written in the **SEPARATE** answer book.

SECTION-I

Q.1 Answer ANY FIVE of the following questions **(10)**

- a) What are range operators? How will you get size of an array?
- b) What does '\$_' and '\$!' mean?
- c) What's the difference between (\$x++) and (++\$x)?
- d) Name two reasons why subroutines are useful?
- e) What happens when you declare a 'my' local variable with the same name as a global variable?
- f) **BUG BUSTER** ; what's wrong with this program;
Print "enter the word foo :";
chomp (\$input = <STDIN>);
If (\$input = 'foo') {
 Print "thank you\n" ; }
Else {
 Print "that's not the word foo"\n; }

Q.2 Answer the following ; **(10)**

- a) Write a program that accepts any number of lines of any kind of input, ending with a return or Enter. Count and return the number of lines that were entered.
- b) **BUG BUSTER** ;
While () {
 Print "enter a name :";
 Chomp (\$input = < STDIN>);
 If (\$input ne "") {
 \$names ++ ;
 }
 Else {last;}
}

Q.3 Answer the following : **(10)**

- a) Write a string that prompts you for a string and a character and then returns the number of times the character occurs in the string. Use index function.
- b) Write a script to mutate a DNA.

P.T.O.

- Q.4** Answer **Any ONE** of the following : **(10)**
- a)** The elements are copied over from right to left ;
 (\$a , \$b) = (10, 20)
 \$a becomes 10, \$b becomes 20. Investigate what happens when ;
 i) There are more elements on right than on left.
 ii) There are more elements on left than on right.
 iii) There is list on left but a single scalar on right.
 iv) There is a single scalar on left but a list on right.
- b)** Write a subroutine that takes a string as an argument and returns the string in reverse order by words.

SECTION- II

- Q.5** Answer **ANY FIVE** the following : **(10)**
- a)** How do you sort a hash?
b) What does the following function do?
 i) split
 ii) chop
c) What are subroutines?
d) How will you print all the values of a hash?
e) What are qualifiers?
f) BUG BUSTER ;
 Print 'Search for what?';
 Chomp (\$pat = <STDIN>);
 While (<>) {
 While (\$/pat/) {
 \$count ++ }
 }

(10)

- Q.6** Attempt **Any ONE** of the following :
- a)** What is a POD file? Why use POD in your PERL script over some other format like HTML?
b) What does the following hash functions do;
 i) reverse
 ii) sort
 iii) merge

- Q.7** Answer the following : **(10)**
- a)** How will print the sequence of a FASTA file in a single line.
b) Write a script to check whether the sequence is nucleotide of protein.

- Q.8** Answer the following : **(10)**
- a)** What do each of the following pattern do;
 i) /ice\s*cream/
 ii) /\d\d\d/
 iii) /xy|yz+/
 iv) /[\d\s] {2,3}/
- b)** Explain DBI module.

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