



**HDR-003-006507**

Seat No. \_\_\_\_\_

**B. Sc. (Bioinformatics) (Sem. I) Examination**

November / December – 2017

**BI-504 : Perl & Bioperl**

**Faculty Code : 003**

**Subject Code : 006507**

Time :  $2\frac{1}{2}$  Hours]

[Total Marks : 70

- Instructions :** (1) All questions are compulsory.  
(2) The right side figure indicates total marks of the question.

**PART - I**

1 Attempt the following: 20

- (1) Perl was first released in \_\_\_\_\_.
- (2) What is Perl?
- (3) Which is the correct syntax for substitute operator?
- (4) How will you convert a string to an array?
- (5) What is Hash?
- (6) If "@var\_def = (B..Y);" then how to print from B-Y values?
- (7) Which regular expression is/are in Perl?
- (8) Is STDOPN is a file handling is or not?
- (9) Which entity is use for "read and write" file in Perl?
- (10) Which operator divides left hand operand by right hand operand and returns remainder?
- (11) Module stands for \_\_\_\_\_ in Perl.
- (12) How will you get size of an array, for array named @arr ?
- (13) Does Perl support mysql, Informix, oracle database?  
(True or False)

- (14) How will you add an element to the beginning of an array?
- (15) In Perl, there are three data types available.  
(True or False)
- (16) What is the output of following program?
- ```
$x = "uvw"; $y = "def";
if ($x ge $y)
{ print "\$x ge \$y is true\n";
}
else {
    print "\$x ge \$y is not true\n";}
```
- (17) Give Perl commands to create a reference for a variable?
- (18) Which statement would translate ORF in 2<sup>nd</sup> reading frame?
- (19) Which Bioperl package would need to represent sequence object?
- (20) \_\_\_\_\_ package is used to run BLAST online with different parameters.

## PART - II

- 2** (a) Explain any **three** : **6**
- (1) Define Perl Identifier.
  - (2) Features of perl.
  - (3) Perl datatypes.
  - (4) For loop statements
  - (5) Substitute operators
  - (6) Give the full form of following File Format
    - (a) PERL
    - (b) CGI

- (b) Explain any **three** : **9**
- (1) Explain scalar variables in Perl.
  - (2) Explain Array with example.
  - (3) Write short note on if statement.
  - (4) Explain Modules in Perl.
  - (5) How BLAST is run locally using Bioperl module?
  - (6) translate() method in Bioperl
- (c) Attempt any **two** : **10**
- (1) List out Precedence of Operator in Perl Explain any one of it with example.
  - (2) Explain Perl regular expression
  - (3) Explain subroutine with array example.
  - (4) How HMM report is parsed using Bioperl?
  - (5) Describe various string manipulation function in Bioperl
- 3** (a) Explain any **three** : **6**
- (1) Explain CGI in Perl.
  - (2) Explain Hash in Perl.
  - (3) Explain Pattern. Matching in Perl.
  - (4) Define foreach loop.
  - (5) RemoteBlast
  - (6) SeqIO
- (b) Explain any **three** : **9**
- (1) Write a Perl script to remove gaps from an input sequence.
  - (2) Explain shift() and unshift() function in Perl.
  - (3) Which Bioinformatics tasks are done using Bioperl?
  - (4) Explain push and pop function with example?
  - (5) Explain File handling in Perl?
  - (6) Explain application of Perl?

(c) Attempt any **two** :

**10**

- (1) Perl Script to calculate frequency of each nucleotide from given user input sequence and display the result.
- (2) How BLAST is run online using Bioperl?
- (3) What are the applications of Perl in Bioinformatics? Explain with examples.
- (4) What is CGI? List of CGI Environmental variables
- (5) Explain Database Connectivity in Perl.

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