

COURSE CODE : 15B11BI421

COURSE NAME: Programming Languages for Bioinformatics

MAX MARKS : 25

MAX. TIME: 1.5 Hrs.

Note: All questions are compulsory. Attempt all questions of a particular section at one place.
Answer each question to the point.

1. Answer the following questions:

(CO1,3) (8 marks)

- What will @sorted consist of –
@sorted = sort (45, 245 , 346) ;
- What will @numbers consist of –
@numbers = sort { \$a <=> \$b } (45, 245, 346) ;
- What is a spaceship operator? Explain with example.
- \$sequence = "AGGGVPLMN";
substr(\$sequence,1,3) = "GGGGG" ;
What will be the value of string in \$sequence ;
- \$chain = join ("-" , split (//, "SYFPEITHI")) ;
What will be the value of \$chain ?
- \$line = "user:600:100:/home/user:/usr/bin/perl";
- @fields = split(/:/, \$line);
What will be the value of \$fields[1] ;
- Write the syntax to get all the keys of a perl hash.

2. Answer the regex questions for the string –

(CO1,3) (5 marks)

\$seq = 'ALA-GLU-ASP-TRP-TRP' ;

What will be the value of \$seq after the following systax.

- \$seq =~ s/(GLU|ASP)/VAL/g ;
- \$seq =~ s/^ALA|TRP\$/g ;
- \$seq =~ s/-/:/g ;
- \$seq =~ s/(TRP)/\1-\1/ ;
- \$seq =~ s/GLU-ASP-TRP// ;

3. What is bioperl? Discuss Bio:Seq and Bio:SeqIO modules with examples. (CO2, 4 marks)

4. How do you handle the files in perl. Write and discuss the syntax of file reading, writing and appending with proper use of error handling. (CO3, 4 marks)

5. Discuss the conditionals in perl. Explain if-elsif-else block with the help of an example. (CO3, 4 marks)