

**JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT**

**TEST -2 EXAMINATION- 2025**

**B.Tech-IV Semester (BI)**

**COURSE CODE (CREDITS): 18B11BI414 (3)**

**MAX. MARKS: 25**

**COURSE NAME: Programming Languages for Bioinformatics**

**COURSE INSTRUCTORS: Dr. Shikha Mittal**

**MAX. TIME: 1 Hour 30 Min**

*Note: (a) All questions are compulsory.*

*(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems*

Q.No	Question	CO	Marks
Q1	How do you create and dereference scalar, array, and hash references in Perl? Provide examples.	[CO-2]	(04)
Q2	Write a Perl program to store gene names and their corresponding descriptions in a hash and print the description of a given gene.	[CO-1, CO-3]	(03)
Q3	Write the output of the following questions – a. my @arr = (1, 2, 3, 4); my \$ref = \@arr; push @\$ref, 5; print join(" ", @\$ref), "\n";  b. my \$str = "apple banana cherry"; \$str =~ s/b\w{6}/b/fruit/g; print "\$str\n";	[CO-1, CO-2, CO-3]	(04)
Q4	How do you define and call a subroutine in Perl? Explain with an example.	[CO-2]	(03)
Q5	Write a Perl program that extracts all email addresses from a given text file using a regular expression.	[CO-3]	(03)
Q6	a. How do you sort an array in Perl? Explain sorting in both ascending and descending order. b. How do you delete a key-value pair from a hash in Perl? c. What are metacharacters in Perl regular expressions? Provide examples d. Explain the @_ array in Perl. How is it used to handle function arguments?	[CO-1, CO-2, CO-3]	(08)