

**JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT**

**TEST -3 EXAMINATION- 2025**

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

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

**MAX. MARKS: 35**

**COURSE NAME: Programming Languages for Bioinformatics**

**COURSE INSTRUCTORS: Dr. Shikha Mittal**

**MAX. TIME: 2 Hours**

**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	a) What is a module in Perl and why is it used? b) Name any two commonly used Perl modules in bioinformatics. c) Write a Perl script using Bio::SeqIO to: <ol style="list-style-type: none"> <li>Read a sequence from a FASTA file.</li> <li>Print the sequence ID and length.</li> <li>Write the sequence in GenBank format</li> </ol>	[CO-2]	(5)
Q2	What is a regular expression? Provide an example to find all ATG codons	[CO-3]	(3)
Q3	Explain the use of lists and dictionaries in Python with examples.	[CO-4, CO-6]	(3)
Q4	Write a Python function to Count the number of times each nucleotide (A, T, G, C) appears in a given DNA sequence.	[CO-4, CO-5]	(4)
Q5	a) Differentiate between scalar and list context in Perl. b) How do arrays differ from hashes in Perl.	[CO-1, CO-3]	(4)
Q6	Create a hash that maps codons to amino acids. Given a DNA sequence, print the amino acid translation	[CO-1]	(3)
Q7	How do you open and read a file in Perl? What are filehandles?	[CO-3]	(4)
Q8	a) <pre>#include &lt;stdio.h&gt; int main() { char seq[] = "ATCG"; printf("%c\n", seq[2]); return 0; }</pre> b) <pre>my \$dna = "ATGC"; my \$rna = \$dna; \$rna =~ tr/T/U/; print "\$rna\n";</pre> c) <pre>my \$seq = "ATGAAGATGCGT";</pre>	[CO-1, CO-2 & CO-3]	(6)

	my @matches = \$seq =~ /ATG/g; print scalar @matches;		
Q9	a) What is the role of split and join functions in Perl? b) What is the purpose of @_ in Perl subroutines? c) Discuss the difference between passing by value and by reference in Perl.	[CO-3]	(3)