JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

BTech-VIII Semester [BI]

COURSE CODE(CREDITS): 18B1WBI831 (3) MAX. MARKS: 25

COURSE NAME: Computational Molecular Evolution

COURSE INSTRUCTOR: Dr. Tiratha Raj Singh MAX. TIME: 1 Hour 30 Minutes

---

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

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

Q.No	Question	CO	Marks
Q1	Define one and two parameter models of nucleotide substitutions. Derive Kimura's one parameter model for these substitutions with an example case.	3	5
Q2	When you compare two DNA sequences of 2000 base pairs, you observe 450 total nucleotide differences. Among these, 250 were transitions and 200 were transversions. Estimate the evolutionary distance using both the models.	3	5
Q3	Elaborate the process of molecular evolution through a genomic journey in your own words. Give examples wherever required to justify the facts.	1,2	4
Q4	What are pseudogenes? How the multi-gene families are associated with pseudogenes? Discuss with an example of a human pseudo gene with its constrained evolutionary timelines.	2,3	3
Q5	What is genetic code? How many types of genetic code systems available? Discuss their importance and applications in the genomic and evolutionary context with a special emphasis on codon redefinition.	3	4
Q6	A gene sequence of length 1000 base pairs undergoes a mutation process where the rate of substitution per site per year is 1.5×10^{-9}. Calculate the expected number of nucleotide substitutions in the gene over 5 million years.	3	2
Q7	A species has a gene that duplicates at a rate of 2×10^{-8} duplications per gene per generation. If the population has 10,000 genes and evolves for 2 million generations, estimate the expected number of gene duplications.	3	2