JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- APRIL-2023

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

COURSE NAME: Computational Molecular Evolution

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

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

Q.1. Derive one parameter model for the evolution of DNA sequences. Justify that this model can work for all possible cases of nucleotide substitutions. (CO:1-3) [5]

Q.2. Calculate CAI for a gene with 20 codons by assuming the mapping of 10 amino acids *wrt* codons used in encoding gene's product as a protein. Keep in mind that there was a biased-ness in the coon usage. Minimum 1 and max 3 codons were used by any amino acid. (CO:2,3) [5]

Q.3. Elucidate the comparative analysis of codon usage bias while keeping gene expression as the core factor. Additionally, add more parameters to this analysis. (CO:2,3) [3]

Q.4. Discuss the cause and role of mutations in evolutionary process. Explain how frame-shift mutations are being selected in biological sequences and how their role in various diseases could be disseminated? (CO:2-4) [4]

Q.5. Describe various kind of measures for codon usage analysis. Discuss the role of codons in genomics through a case study of an organisms/plants data. Justify the selection of specific codons in various genetic code systems through this analysis. (CO:3-4) [5]

Q.6. Elaborate about the genetic code evolution theories. Analyze two important theories through a comparative discussion about the evolution of genetic code systems with a special emphasis on codon level. (CO:3-4) [3]