

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
END SEMESTER EXAMINATION-2015

B.Tech VIII Semester

COURSE CODE: 15B1WBI834

MAX. MARKS: 45

COURSE NAME: Computational Molecular Evolution

COURSE CREDITS: 03

MAX. TIME: 3 HRS

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are mentioned against each question.

Section A

1. Discuss the computations for number of amino acid replacements between two protein sequences. 1
2. Explain various phases of introns with suitable representations. 2
3. Explain how genome organization is associated with their evolution? 1
4. Which sites are phylogenetically uninformative? 1
5. Explain Saitou and Nei's method with an example. 2
6. Define frameshift mutations and its functional and evolutionary applications. 2

Section B

1. Explain multiregional hypothesis. Also discuss how it is associated with the evolution of human and their migration? 4.5
2. Differentiate between weighted and unweighted parsimony. Explain Fitch procedure for solving a phylogenetic problem through parsimony. 4.5
3. Differentiate between rooted and unrooted trees. Discuss UPGMA method with a suitable example. What are the drawbacks of UPGMA and how we can resolve these drawbacks? 4.5

Section C

1. Describe molecular clock and its usage in the estimation of evolutionary time. Describe relative rate tests and likelihood for molecular clock hypothesis. What are local clocks? 7.5
2. Explain derivation of Jukes and Cantor's two parameter model with 4 scenarios. 7.5
3. What are various theories for intron evolution? Explain each with a suitable example. Also discuss these both theories through a common evolutionary example. Describe various pathways for producing new functions in genes and proteins. 7.5

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