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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
B.Tech. BI, BT, BTDD (Semester VIII), Test 3 (May-June 2016)

Course Code: 15B1WBI834 **Max. Marks: 35**
Course Name: Computational Molecular Evolution
Course Credit: 3 **Max. Time: 2:00 Hrs**

Attempt all questions. Carrying of mobile phones will be treated as the case of unfair means.

Q. 1. How we estimate amino acid replacements between two protein sequences. Provide all formulations and generate computations for following two fragments of amino acids: ARNDCPANCP and NDCANP. Make required assumptions for the formulations. [4]

Q.2. Compare out-of-Africa and multiregional hypothesis for human evolution. [3]

Q.3. How we compare rooted and un-rooted trees? Explain any character based method for phylogeny. [4]

Q.4. How we date and measure non-functionalization of genes? How it is associated with gene duplication? [5]

Q.5. Explain following terms with an example and their applications in evolutionary scenario:
(a) Introns theories (b) Exon shuffling (c) C value paradox (d) Overlapping genes
(e) Pseudogenes (f) Retroevolution [1.5*6=9]

Q.6. Explain Kimura's two parameter model with four distinct scenarios. Give derivations for the same for all conditions. [6]

Q.7. Describe positive, negative and neutral selections with their computational parameters. Explain how selection can be advantageous and how it is associated with genetic drift? [4]