



Development of Phylogenetic Tree based on Kimura's Method

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Condition: New. Publisher/Verlag: LAP Lambert Academic Publishing | Based on Un-weighted Pair Group method with Arithmetic Mean (UPGMA) and Neighbor Joining (NJ) Scoring Techniques | The research in bioinformatics has accumulated large amount of data. It is the study of Bio-molecules information. Bioinformatics offers different knowledge discovery concepts for molecular biology and has many practical applications. DNA sequence alignment is one of the applications of the bioinformatics. Multiple sequence alignment is used to align the biological sequences along a column. As the process generates distances of multiple alignments among the pairs of different species, phylogenetic tree is being formulated. Multiple sequence alignment arranges the sequences in such a way that evolutionarily equivalent positions across all sequences are matched. Alignment of substitutions made into two categories: Jukes Cantor Method and Kimura's Method. Jukes Cantor Method and Kimura's Method are used in the present work for constructing phylogenetic tree. These trees are based on the two scoring techniques: UPGMA (Un-weighted Pair Group method with Arithmetic Mean) and NJ (Neighbor Joining). Advanced Kimura's method is proposed which supercedes the traditional methods. Web based FASTA sequences are considered as input and the results are compared for all the three models. | Format: Paperback |...



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