

## A Similarity/Dissimilarity Measure to Biological Sequence Alignment

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**Abstract :** Analysis of protein sequences is carried out for the purpose to discover their structural and ancestry relationship. Sequence similarity determines similar protein structures, similar function, and homology detection. Biological sequences composed of amino acid residues or nucleotides provide significant information through sequence alignment. In this paper, we present a new similarity/dissimilarity measure to sequence alignment based on the primary structure of a protein. The approach finds the distance between the two given sequences using the novel sequence alignment algorithm and a mathematical model. The algorithm runs at a time complexity of  $O(n^2)$ . A distance matrix is generated to construct a phylogenetic tree of different species. The new similarity/dissimilarity measure outperforms other existing methods.

**Keywords :** alignment, distance, homology, mathematical model, phylogenetic tree

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