

**A STUDY OF DNA SIMILARITY ANALYSIS IN EVOLUTIONARY
RELATIONSHIPS USING GRAPH THEORY**

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Since DNA sequences are rapidly increasing in the DNA database, its similarity analysis is one of the major challenges for bio-scientists. During the evolutionary history, there are different kinds of species with a common ancestor, and DNA sequence rearrangements and DNA mutations occur over time. Therefore, it is very important to analyse similarities between DNA sequences. This research work focuses on one of the mathematical structures of DNA sequence to analyse similarities between DNA sequences of evolutionary close species. These species evolved from a common ancestor, and some features, such as conserved regions in DNA sequences, remain from generation to generation. In this study, the graph-based method for DNA similarity analysis was modified. The studied based method with weighted directed graph has an adjacency matrix and representative vector which is applicable for only the conserved regions and DNA variations in considered genomes. The study also checks whether the molecular similarity coefficients are applicable as distance measurements to calculate the similarity between vector representations of DNA sequences. Then the graph spectrum is used as the vector representation of DNA and compare the results of these two vector representations. As an application, the modified method is tested using the 0.9 kb-mitochondrial DNA of evolutionary closed three species: human, gorilla, and orang-utan, by considering different areas in their genomes. The results predict that human and gorilla are very similar in evolution history. The modified method gives the same result with that of based method when the number of nucleotides in the DNA fragments is increased.

Keywords: DNA, Evolutionary, Similarity, Spectrum, Weighted directed graph