

Title of Article : Aligning Multiple Sequences with Genetic Algorithm.

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Abstract: The alignment of biological sequences is a crucial tool in molecular biology and genome analysis. It helps to build a phylogenetic tree of related DNA sequences and also to predict the function and structure of unknown protein sequences by aligning with other sequences whose function and structure is already known. However, finding an optimal multiple sequence alignment takes time and space exponential with the length or number of sequences increases. Genetic Algorithms (GAs) are strategies of random searching that optimize an objective function which is a measure of alignment quality (distance) and has the ability for exploratory search through the solution space and exploitation of current results. In this paper, we view the multiple sequence alignment problems as an optimization problem and present a stochastic approach based on GAs for finding globally optimal multiple alignments in reasonable time, starting from completely unaligned sequences.