Efficient Reconstruction of DNA Distance Matrices Using an Inverse Problem Approach

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Abstract : We continue to consider one of the cybernetic methods in computational biology related to the study of DNA chains. Namely, we are considering the problem of reconstructing the not fully filled distance matrix of DNA chains. When applied in a programming context, it is revealed that with a modern computer of average capabilities, creating even a small-sized distance matrix for mitochondrial DNA sequences is quite time-consuming with standard algorithms. As the size of the matrix grows larger, the computational effort required increases significantly, potentially spanning several weeks to months of non-stop computer processing. Hence, calculating the distance matrix on conventional computers is hardly feasible, and supercomputers are usually not available. Therefore, we started publishing our variants of the algorithms for calculating the distance between two DNA chains; then, we published algorithms for restoring partially filled matrices, i.e., the inverse problem of matrix processing. In this paper, we propose an algorithm for restoring the distance matrix for DNA chains, and the primary focus is on enhancing the algorithms that shape the greedy function within the branches and boundaries method framework.
Keywords : DNA chains, distance matrix, optimization problem, restoring algorithm, greedy algorithm, heuristics
Conference Title : ICBMS 2024 : International Conference on Biomathematics, Modeling and Simulation
Conference Location : Tokyo, Japan
Conference Dates : February 26-27, 2024