IJARSCT
International Journal of Advanced Research in Science, Communication and Technology
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
ISSN: 2581-9429
Volume 6, Issue 2, February 2026
Impact Factor: 8.2

A Unified Matrix-Algorithm Framework for DNA Sequencing and Protein Folding Applications

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Abstract: *Bioinformatics relies heavily on mathematical and computational frameworks to analyse large-scale biological data generated by modern sequencing technologies. Among these frameworks, matrix algorithms provide a structured and computationally efficient approach for modelling biological sequences and molecular interactions. In this paper, we propose a unified matrix-algorithm framework that integrates sequence encoding matrices, dynamic programming alignment matrices, and contact/energy matrices for protein folding within a common linear algebraic perspective. Unlike existing studies that treat DNA sequencing and protein folding independently, the proposed framework highlights their shared mathematical structure and analytical consistency. A comparative analysis is presented to demonstrate improved alignment consistency and interpretability of matrix-based methods over conventional heuristic approaches for small and medium-sized biological systems. The study establishes a reproducible mathematical foundation that can be extended to hybrid models combining matrix algorithms with machine learning techniques.*

Keywords*:* Bioinformatics; Linear Algebra; Matrix Algorithms; DNA Sequencing; Protein Folding; Computational Biology

DOI: 10.48175/IJARSCT-31211