

# Revolutionizing Computational Biology with Deep Learning

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**Abstract.** This paper investigates the application of deep learning techniques in computational biology, focusing on their role in analyzing complex biological systems. The research illustrates how deep learning models can uncover hidden patterns in biological data, aiding in areas such as gene expression analysis and protein structure prediction. These advancements highlight the transformative potential of AI in biological research.

**Keywords:** Deep Learning, Computational Biology, Gene Expression, Protein Structure, Biological Systems

## Introduction

The integration of deep learning into computational biology represents a significant leap forward in the analysis of complex biological systems. By employing sophisticated models, researchers can uncover hidden patterns within vast datasets, providing new insights into biological processes. This article examines the application of deep learning techniques in areas such as gene expression analysis and protein structure prediction. The findings demonstrate the transformative potential of AI-driven models in advancing our understanding of biology. As these technologies continue to evolve, they hold the promise of revolutionizing not only research methodologies but also practical applications in medicine and biotechnology.

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## References

1. KUMAR, Nitin; KATARIA, Vipin. Enhanced Sentiment Classification using a Multi-layered Stacked Ensemble Architecture.