Deep Learning-Based Prediction of RNA-Binding Proteins in Antibiotic-Resistant Bacteria

■ Introduction

Antibiotic resistance is a serious global issue. The role of RNA-binding proteins (RBPs) in this area is not well understood. RBPs affect mRNA stability, translation, and stress responses. Thus, they could be key targets for new therapies.

This study will create a deep learning model to predict RBPs in antibiotic-resistant bacteria. We will focus on pathogens like *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. By combining sequence, motif, and structural features, we aim to find new RBPs related to resistance.

■ Research Questions

- How can deep learning model improve the prediction of RBPs in antibiotic-resistant bacteria?
- What sequence and structural features are most indicative of RNA-binding ability?
- Do predicted RBPs have functional roles in antibiotic resistance pathways?
- Can this approach be generalized across multiple bacterial species?

■ Objectives

We aim to create an AI-driven model to predict RBPs. This model will use sequence motifs and structural data to improve performance. The study will also investigate the roles of predicted RBPs in antibiotic resistance. We will build a flexible framework that can adapt to different bacterial species and datasets.

■ Methodology

- We will gather protein sequences from UniProt, PATRIC, and NCBI, using RBP annotations from RBPDB and PRIDB.
- Features such as k-mers, amino acid composition, and short motifs will be extracted. We will also analyze structural properties like RNA-binding potential and disordered regions.
- The model will use a CNN-BiLSTM hybrid, transformer models (ESM-2, ProteinBERT), or graph neural networks (GNNs) to capture both local and global patterns.
- Training will follow an train-validation-test dataset split. We will evaluate performance using accuracy, precision, recall, F1-score, confusion matrix, ROC-AUC curve etc.
- Functional validation will include GO enrichment and KEGG pathway analysis to assess the biological significance of predicted RBPs.

■ Expected Outcomes

This study will produce an AI tool for predicting bacterial RBPs. It will identify new proteins linked to resistance and suggest potential therapeutic targets. The adaptable approach will ensure it can handle new datasets and bacterial strains. This work will enhance our understanding of RNA biology and antibiotic resistance.

■ Conclusion

This research will deepen our knowledge of post-transcriptional regulation in antibiotic-resistant bacteria. By using deep learning to identify RBPs, we may help develop new antimicrobial strategies and RNA-targeted therapies.

■ References

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