Predicting miRNA-drug Interactions via Dual-Channel Network Based on TCN and BiLSTM

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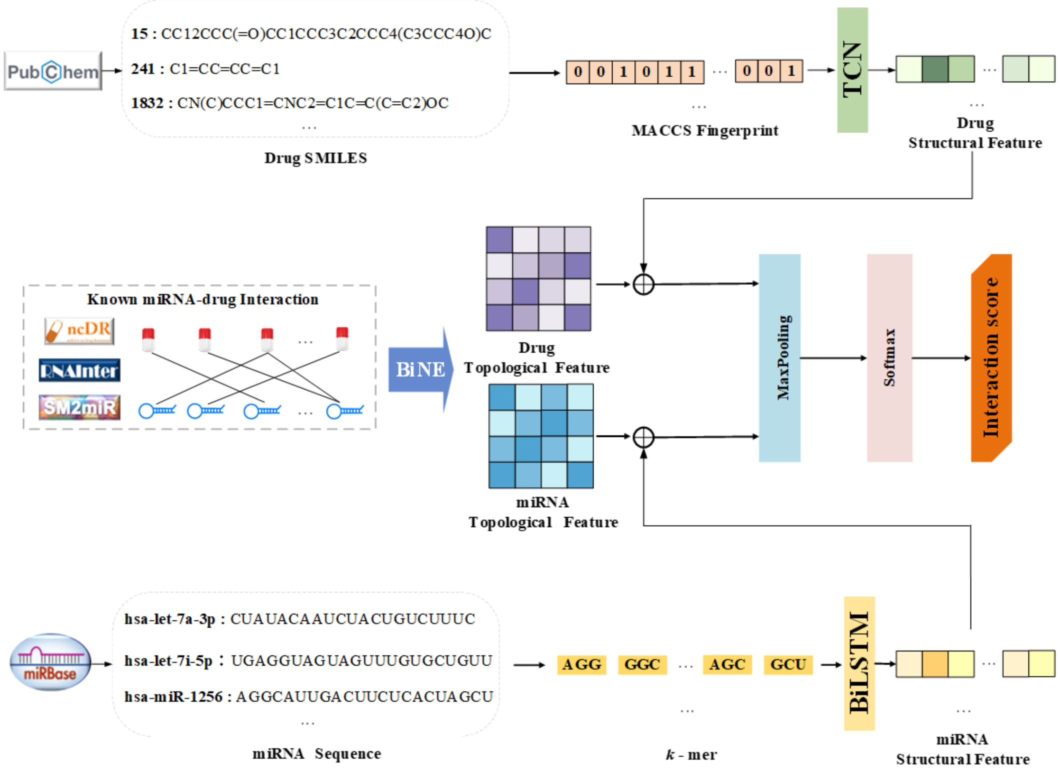
Frontiers of Computer Science, DOI: 10.1007/s11704-024-3862-1

Ideas

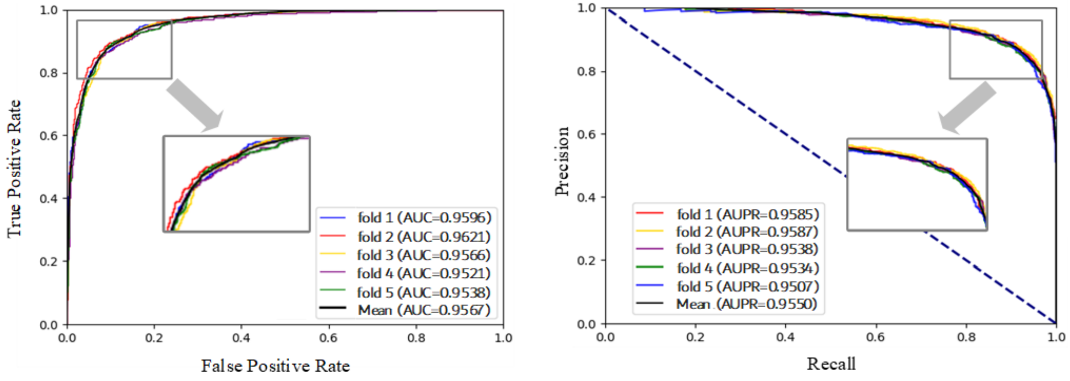
- Idea1: Our model MDIDCN utilizes the graph embedding technique BiNE to acquire the topological characteristics of drugs and miRNAs.
- Idea2: TCN (Temporal Convolutional Network) is utilized to learn the fingerprint features of drugs. Additionally, To learn the *k*-mer features of miRNA, MDIDCN employs BiLSTM (Bidirectional Long Short-Term Memory).
- Idea3: MDIDCN integrates the structural features and topological features separately to represent the fused features of drugs and miRNA. This integration enhances the model's ability to represent features, enabling it to better capture the association relationship between these features.



Flowchart of our model.
Top: The top part is to learn the structural features of drug using TCN;
Bottom: the bottom part is to learn the structural features of miRNA using BiLSTM;
Middle: The middle part is to learn the topological features of miRNA and drug using BiNE, then fuse topological and structural features of drugs and miRNAs respectively to obtain miRNA-drug interaction prediction scores, and potential miRNA-drug pairs are obtained.

Results

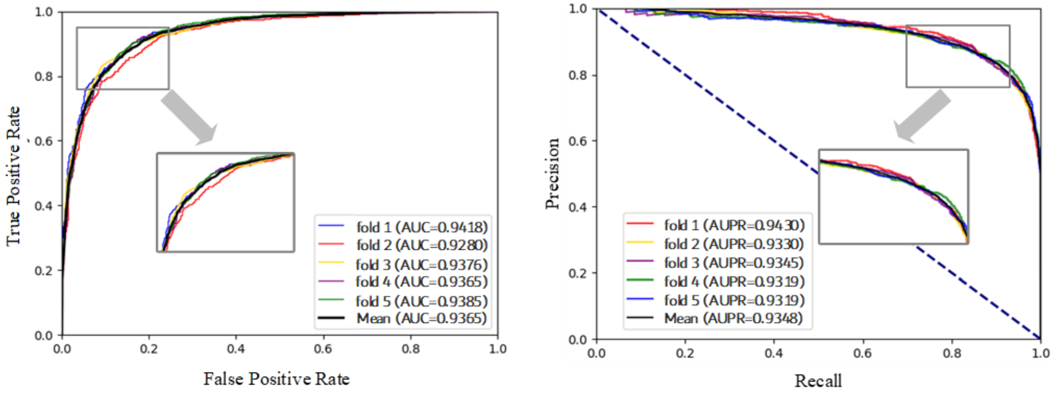
- Below are the ROC and PR curves of the 5-fold cross-validation results on 3 datasets.



(a) (b)

Fig.1 (a)ROC curve of ncDR dataset under 5-fold cross validation.

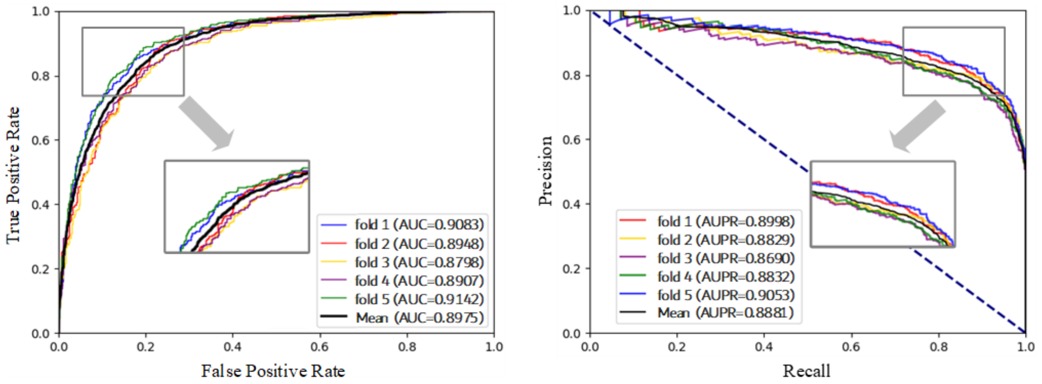
(b)PR curve of ncDR dataset under 5-fold cross validation.



(a) (b)

Fig.2 (a)ROC curve of RNAInter dataset under 5-fold cross validation.

(b)PR curve of RNAInter dataset under 5-fold cross validation.



(a) (b)

Fig.3 (a)ROC curve of SM2miR3 dataset under 5-fold cross validation.

(b)PR curve of SM2miR3 dataset under 5-fold cross validation.