DeepCRBP:Improved predicting function of circRNA-RBP binding sites with deep feature learning

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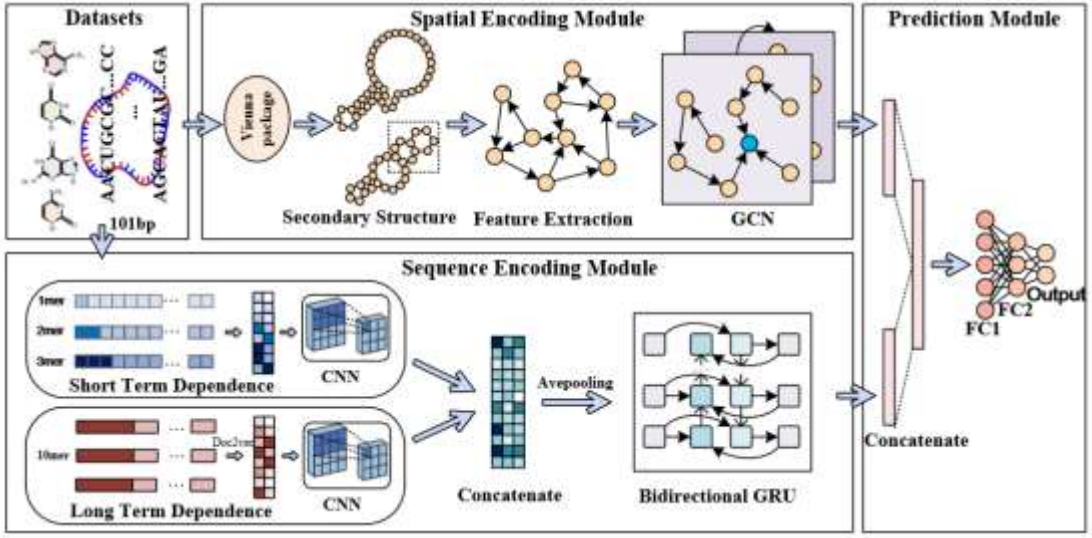
Problems & Ideas

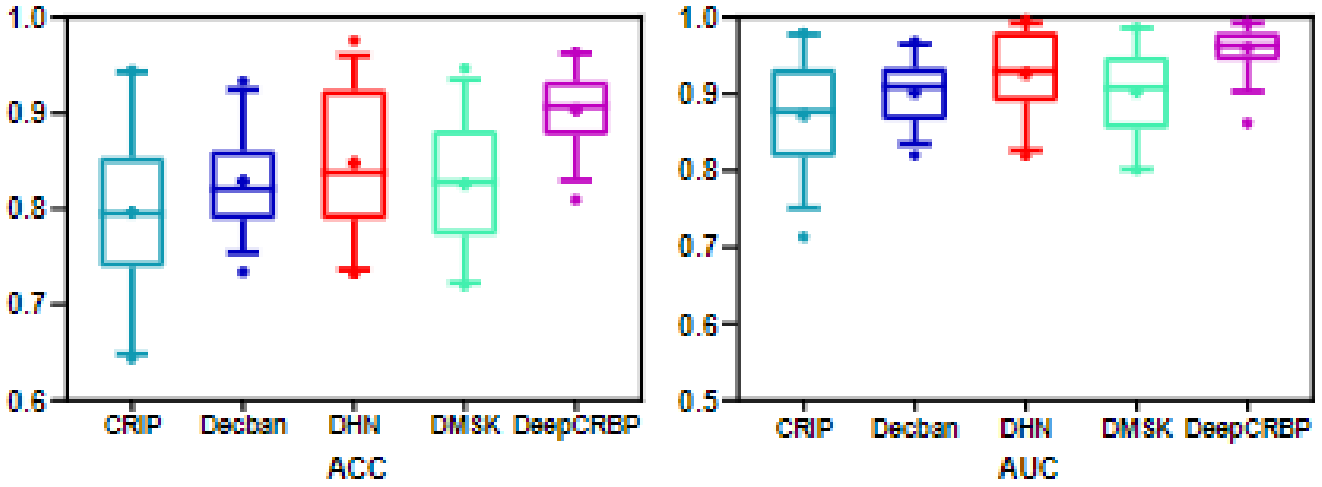
- Problems with existing circRNA feature extraction:
  - The previous works only extract circRNA sequence feature, with a lack of exploiting the essential topological information from the secondary structure.
- Ideas: While using diverse coding schemes to encode the circRNA sequences, molecular maps were collaboratively constructed to represent the secondary structure of the circRNAs to obtain important topological information.



Overview of DeepCRBP. DeepCRBP is composed of spatial encoding module, sequence encoding module and prediction module.

Main Contributions

- Contributions:
  - Spatial encoding module is proposed in which firstly circRNA sequences are transformed to secondary structure represented by molecular graph followed by GCN learning the intrinsic structural feature.
  - In comparison with state-of-the-art methods, experimental results show that Deep CRBP significantly outperforms the state-of-the-art model and shows better model robustness and generalization performance.



The average results of ACC and AUC between DeepCRBP and compared methods on 37 circRNA datasets.