circ2CBA: Prediction of circRNA-RBP binding sites combining deep learning and attention mechanism

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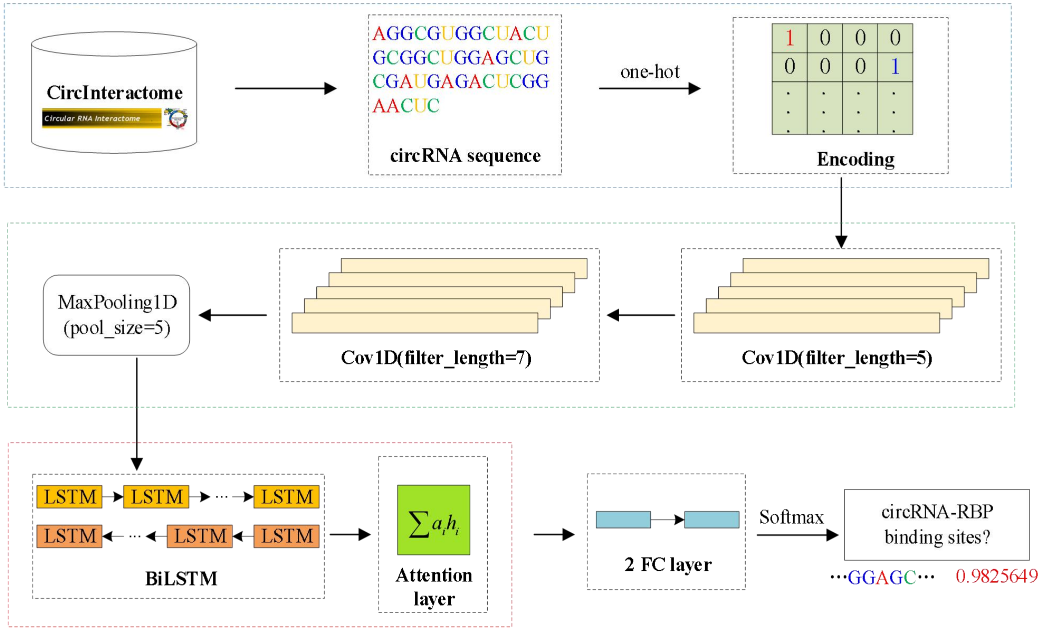
Problems & Ideas

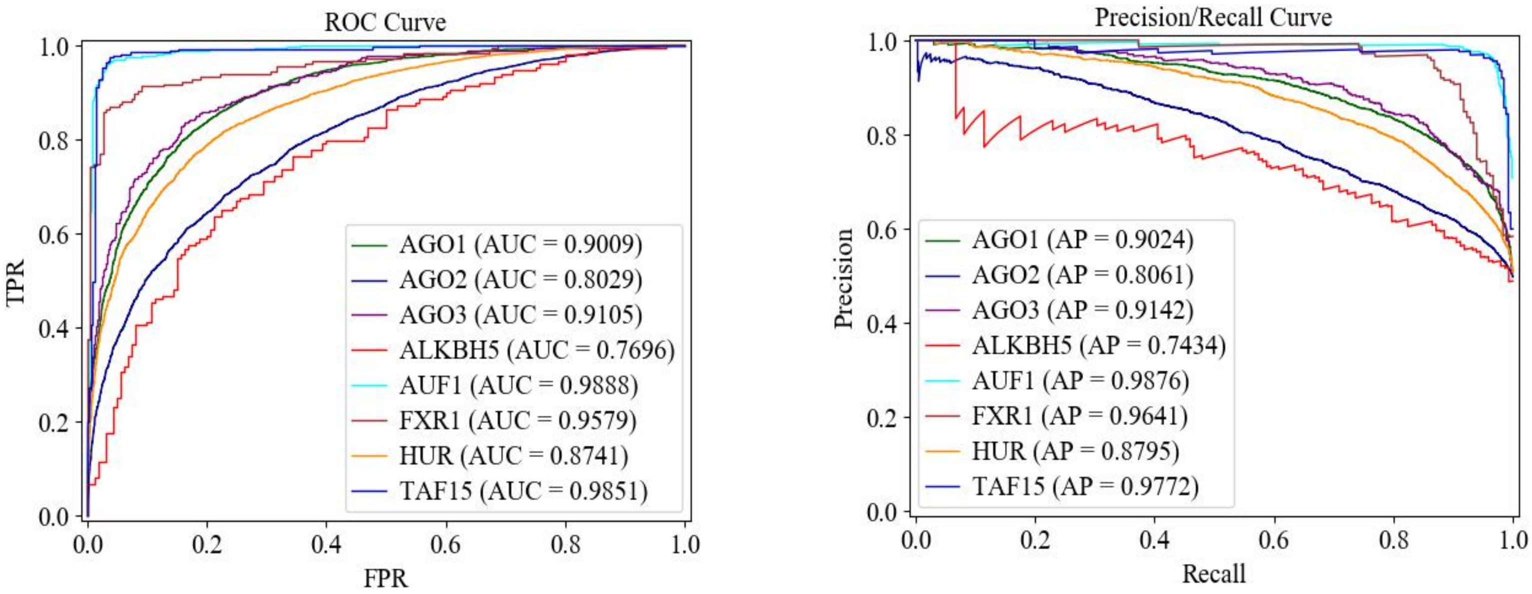
- Problems of conventional binding sites prediction methods:
  - Existing methods can not fully learn and utilize features of circRNA sequences.
  - The performance of existing methods needs to be further improved.
- Ideas: A joint model that considering the context information between sequence nucleotides and the important position weight information of features.



Flowchart of our model. Top: The top part indicates the input data of circ2CBA and the encoding process; Middle: The middle part is to extract latent features from circRNA sequences; Bottom: the bottom part is to learn context information using BiLSTM and to distribute the weight of features using Attention Layer.

Main Contributions

- Contributions:
  - A two-layer CNN that can not only extract features of cricRNA sequences but also get a larger perception domain;
  - A novel joint model that can not only learn the context information from the extracted features but also distribute the weights for the features;
  - A motif analysis to explore the reason for the remarkable performance improvement of our method on some sub-datasets.



The experiment results of circ2CBA on eight sub-datasets. Left: the ROC curve of circ2CBA; Right: the Precision/Recall curve of circ2CBA.