Identification of human microRNA-disease association via low-rank approximation-based link propagation and multiple kernel learning

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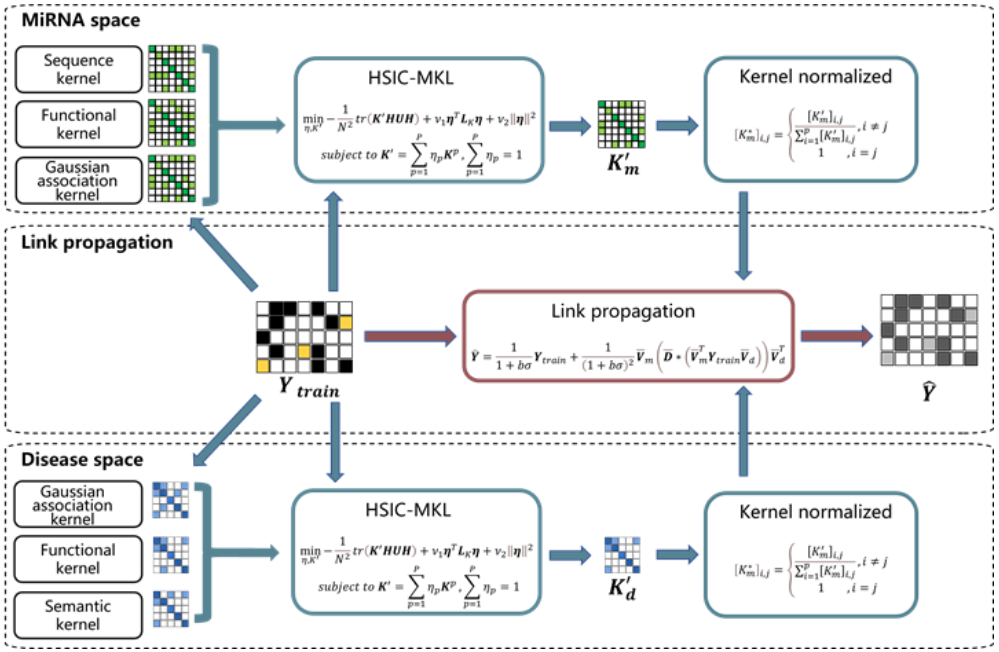
Problems & Ideas

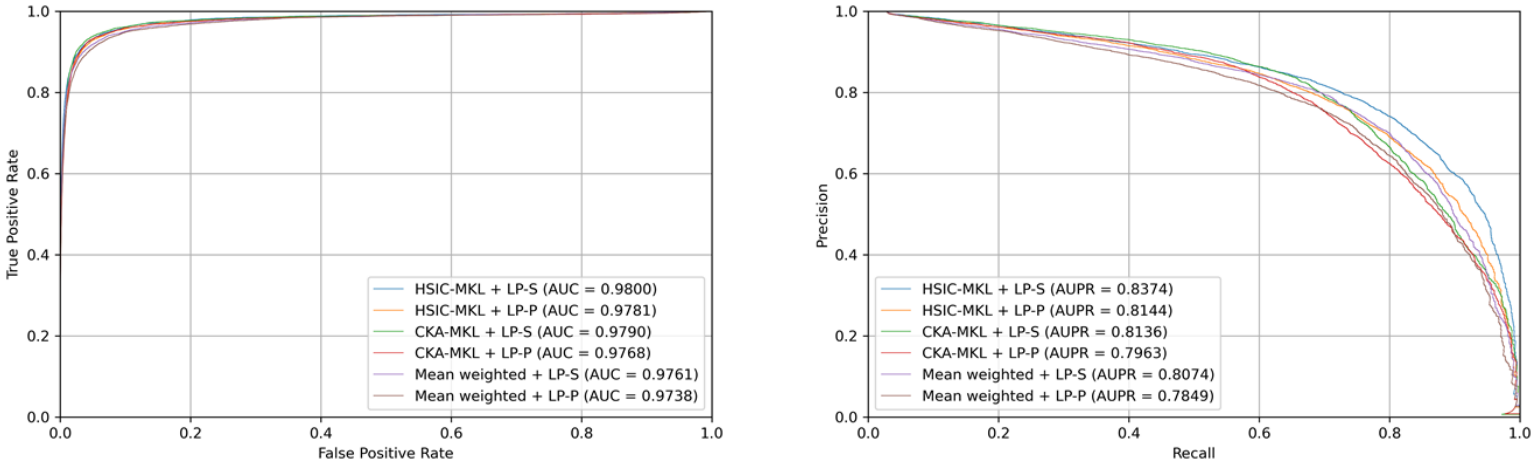
- Problems of predicting microRNA and disease associations:
  - Traditional biological experiments are time-consuming and costly
  - Existing machine learning methods have high time and space complexity, and the prediction effect can be further improved.
- Ideas: A model for predicting microRNA and disease associations using multiple kernel learning and link propagation



Schematic diagram of our proposed method.

Main Contributions

- Contributions:
  - HSIC-MKL is used to effectively fuse the similarity kernels of miRNA space and disease space;
  - The low-rank approximation-based link propagation is used, which significantly reduces the computational cost while maintaining good accuracy;
  - Experiments show that our model achieves excellent results and outperforms current techniques.



The performance (AUC and AUPR) of different models under 5-CV. Left: The AUC of different models under 5-CV; Right: The AUPR of different models under 5-CV