Improving miRNA-mRNA Interaction Predictions

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Abstract

Background

MicroRNAs are short RNA molecules that post-transcriptionally regulate gene expression. Today, microRNA target prediction remains challenging since very few have been experimentally validated and sequence-based predictions have large numbers of false positives. Furthermore, due to the different measuring rules used in each database of predicted interactions, the selection of the most reliable ones requires extensive knowledge about each algorithm.

Results

Here we propose two methods to measure the confidence of predicted interactions based on experimentally validated information. The output of the methods is a combined database where new scores and statistical confidences are re-assigned to each predicted interaction. The new scores allow the robust combination of several databases without the effect of low-performing algorithms dragging down good-performing ones. The combined databases obtained using both algorithms described in this paper outperform each of the existing predictive algorithms that were considered for the combination.

Conclusions

Our approaches are a useful way to integrate predicted interactions from different databases. They reduce the selection of interactions to a unique database based on an intuitive score and allow comparing databases between them.