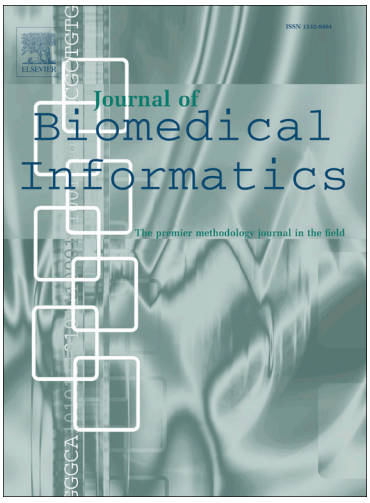

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Predicting microRNA-disease associations using label propagation based on linear neighborhood similarity

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Abstract

Interactions between microRNAs (miRNAs) and diseases can yield important information for uncovering novel prognostic markers. Since experimental determination of disease-miRNA associations is time-consuming and costly, attention has been given to designing efficient and robust computational techniques for identifying undiscovered interactions. In this study, we present a label propagation model with linear neighborhood similarity, called LPLNS, to predict unobserved miRNA-disease associations. Additionally, a preprocessing step is performed to derive new interaction likelihood profiles that will contribute to the prediction since new miRNAs and diseases lack known associations. Our results demonstrate that the LPLNS model based on the known disease-miRNA associations could achieve impressive performance with an AUC of 0.9034. Furthermore, we observed that the LPLNS model based on new interaction likelihood profiles could improve the performance to an AUC of 0.9127. This was better than other comparable methods. In addition, case studies also demonstrated our method's outstanding performance for inferring undiscovered interactions between miRNAs and diseases, especially for novel diseases.

Keywords

disease-related miRNAs; miRNA-disease association; linear neighborhood similarity; label propagation

1. Introduction

MicroRNAs (miRNAs), which are approximately 22-nucleotide non-coding RNAs, are a class of important regulators involved in post-transcriptional regulation of gene expression [1,2]. Functional studies have indicated that miRNAs serve vital roles in multiple cellular processes, including development, differentiation, apoptosis and cell proliferation [3-6]. Not surprisingly,