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A Novel Approach for Predicting MicroRNA-Disease Associations by Unbalanced Bi-random

Walk on Heterogeneous network

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Abstract: MicroRNAs (miRNAs) play a critical role by regulating their targets in post-transcriptional level. Identification of potential miRNA-disease associations will aid in deciphering the pathogenesis of human polygenic diseases. Several computational models have been developed to uncover novel miRNA-disease associations based on the predicted target genes. However, due to the insufficient number of experimentally validated miRNA-target interactions as well as the relatively high false-positive and false-negative rates of predicted target genes, it is still challenging for these prediction models to obtain remarkable performances. The purpose of this study is to prioritize miRNA candidates for diseases. We first construct a heterogeneous network, which consists of a disease similarity network, a miRNA functional similarity network and a known miRNA-disease association network. Then, an unbalanced bi-random walk-based algorithm on the heterogeneous network (BRWH) is adopted to discover potential associations by exploiting bipartite subgraphs. Based on 5-fold cross validation, the proposed network-based method achieves AUC values ranging from 0.782 to 0.907 for the 22 human diseases and an average AUC of almost 0.846. The experiments indicated that BRWH can achieve better performances compared with several popular methods. In addition, case studies of some common diseases further demonstrated the superior performance of our proposed method on prioritizing disease-related miRNA candidates.

Keywords: Disease semantic similarity; Disease miRNA prediction; miRNA-disease association; miRNA similarity; Heterogeneous network

1. Introduction

MicroRNAs (miRNAs) are a class of endogenous single-stranded non-coding RNAs (~22 nt) that play critical roles in post-transcriptional level and various biological processes [1-3]. Increasing evidence has demonstrated that

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