The Prediction of miRNAs Target Genes Associated with Rheumatoid Arthritis by Using Novel Prediction Algorithm Called Targetscore

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ABSTRACT miRNAs as a biomarker of the immune system, have become an important role in disease biology. MRNAs as the downstream part of miRNAs, could be regulated by miRNAs. It is useful to understand the biological functions of miRNAs by identifying the target genes. In present work, the gene expression profiles of RA and normal groups were extracted from Gene Expression Omnibus (GEO). Furthermore, a novel probabilistic scoring algorithm called targetScore was developed to improve the prediction of miRNAs targets after differentially expressed genes (DEGs) screening. Targets as the transformed fold-changes have been weighted by the Bayesian posteriors. Eventually, targets with larger taregtScore value were selected and the interaction between miRNAs and mRNAs was shown. Optimal targets were detected by integrating the different miRNAs associated with RA, noting that the same target in different miRNAs has the similar tagretScore value, suggesting targetScore achieved significantly higher accuracy.