miRACLe: improving the prediction of miRNA-mRNA interactions by a random contact model

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Abstract: The strength of miRNA-mRNA interactions in a biological system depends on both the sequence characteristics and expression patterns of RNAs. Integrating the two features into a random contact model, we propose miRACLe (miRNA Analysis by a Contact modeL) to achieve effective miRNA target prediction at both individual and population levels. Evaluation by a variety of measures shows that fitting a sequence-based algorithm into the framework of miRACLe can improve its predictive power with a significant margin, and the combination of miRACLe and TargetScan consistently outperforms state-of-the-art methods in prediction accuracy, regulatory potential and biological relevance.