

Network Properties for Ranking Predicted miRNA Targets in Breast Cancer.

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Abstract

MicroRNAs control the expression of their target genes by translational repression and transcriptional cleavage. They are involved in various biological processes including development and progression of cancer. To uncover the biological role of miRNAs it is important to identify their target genes. The small number of experimentally validated target genes makes computer prediction methods very important. However, state-of-the-art prediction tools result in a great number of putative targets with an unpredictable number of false positives. In this paper, we propose and evaluate two approaches for ranking the biological relevance of putative targets of miRNAs which are associated with breast cancer.

Involved units

[Microbiome Dynamics](#) [Gianni Panagiotou](#) [Read more](#)

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