Identifying Novel miRNA Targets and Therapeutics Through A Network-Based Computational Pipeline

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miRNAs are small, non-coding RNAs significant in numerous biological processes and disease pathways, proven heavily dysregulated in cancers, with prior literature revealing their potential as key drug targets. However, current experimental and computational approaches identifying disease-associated miRNAs are limited by their inaccuracy and ineffectiveness in rapidly mapping miRNA associations and interactions. This has hindered the vast potential of miRNAs as biomarkers and therapeutic targets in various diseases. The purpose of this study was to overcome the inefficiency of current approaches with the use of a novel multi-omics, deep learning approach to create a rapid method of miRNA target and therapeutic identification. Novel miRNA-target gene interactions were first identified by integrating multi-omics data after which miRNA-disease associations were uncovered through the integration of genetic interactions into a tripartite network. Disease-specific miRNAs were then pinpointed using a network propagation algorithm. Novel associations between miRNAs and therapeutics as well as their regulatory effects were then predicted by utilizing various structural and compositional features in different deep learning models to identify which predicted regulatory effects most accurately. The results were validated on cancers using several metrics, including MCC, F1, ACC scores and ROC curves. With the integration of multi-omics and physicochemical data, the cost and time-ineffectiveness of experimental and computational methods can be overcome for robust, rapid identification of miRNA treatments and targets. This approach can open doors to personalized medicine and facilitate novel drug development through the targeting of pinpointed miRNA mechanisms within disease pathology.

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