MiRNet: A Novel in silico Network-Based Approach to miRNA Drug Target Identification for Next Generation Drug Discovery

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Chronic disease is the leading cause of death in the world. Next generation therapeutics are needed to combat the growing global health crisis of chronic diseases, such as cancers and heart disease. MiRNAs are key biomolecules that powerfully regulate disease pathways, making them promising therapeutic candidates. The current miRNA drug discovery path—in vitro experiments—is time consuming, expensive, and yields hundreds of miRNAs, many of which are disease non-specific. This study created MiRNet, a network-based model to pinpoint disease specific miRNAs. Integrating massive transcriptomic and genomic datasets, MiRNet is a comprehensive miRNA-disease bipartite network model. A novel network diffusion algorithm utilizing Markov random walks and an unsupervised learning framework for community detection were developed to prioritize miRNA drug targets. MiRNet successfully pinpointed 1-2 key miRNAs per disease. Examples include miR-155 for leukemia and miR-567 for ovarian cancer. Of the total 190 miRNAs identified, 47 were for cancers, 46 for cardiovascular diseases, 69 for endocrine diseases, and 28 for psychiatric diseases. MiRNet's miRNA predictions were evaluated on 3 select diseases where differential miRNA expression data was available: breast cancer (97.6% accuracy, 4.6% false positive rate), leukemia (97.3% Acc, 7.6% FPR), lymphoma (97.1% Acc, 7.3% FPR). The first of its kind in the published literature, MiRNet addresses the greatest barrier to widespread use of miRNA therapeutics: drug target identification. MiRNet provides a paradigm shift towards quicker, cheaper miRNA target discovery and clinical translation.

Awards Won:
Intel ISEF Best of Category Award of $5,000
First Award of $5,000
National Anti-Vivisection Society: Third Award of $2,500