

MIMR: A web tool for integrated analysis of miRNA and mRNA using Random Walk with Restart

Dayeon Kim¹, and Younhee Ko^{1*}

¹*Division of Biomedical Engineering, Hankuk University of Foreign Studies*

**Corresponding author: younko@hufs.ac.kr*

MicroRNAs (miRNAs) are small non-coding RNAs that intricately regulate target gene products, resulting in the inhibition of gene expression. These miRNAs play an important role in essential biological processes, encompassing immunity, metabolism, and cell death, but there is still much to be discovered about their specific effects on diseases. Recent studies have been focused on the integration of miRNA and mRNA expression to reveal the underlying biological pathways and mechanisms responsible for disease manifestation. The traditional approach focused on identification of miRNAs showing differences in disease condition, and then predicted the targets of these miRNAs based on existing tools such as TargetScan, PicTar, or PITA etc. These approaches mainly consider on the direct interactions between miRNAs and gene, or gene and gene; however, they failed to consider hidden pathological mechanisms indirectly intertwined within the protein network.

In order to address this limitation, we have proposed a novel approach for integrating miRNA and mRNA expression data, applying the Random Walk with Restart (RWR) algorithm. Our method is grounded in the concept that genes associated with the same disease interact more frequently with each other and are closely located within the protein-protein network. We compiled the intersection of target sets of differentially expressed miRNAs and differentially expressed mRNAs in a given disease and these genes were served as seed for RWR algorithm. Our algorithm allows us to explore indirect relationships and influence of seed genes in the network, leading to identify potential disease associated pathways. We developed a web-based application called MIMR, designed to facilitate these procedures for biologists. The proposed method was analyzed and validated with Alzheimer's disease data and found novel biological pathways associated with Alzheimer's disease that were undiscovered by traditional methods. In summary, MIMRs shows a significant potential in elucidating complex and hidden biological pathways associated with diseases.