



A Computational Tool for microRNA–Target Interaction Analysis

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MicroRNAs have shown high potential as disease biomarkers due to their roles in biological processes such as cell differentiation, apoptosis, and tumorigenesis, and their detectability in many body fluids, including blood, saliva, and urine.

In this work, we introduce ShinyMIR, a novel Shiny-based tool designed to address limitations in existing miRNA analysis tools, enabling a robust and insightful analysis for miRNA-based biomarker studies.

ShinyMIR provides an easy-to-use platform for investigating miRNA-disease, miRNA-gene, and over-representation analysis of miRNA-target genes, enhancing current tools by offering more detailed disease-specific information and evidence-based filtering for miRNA-target associations. Additionally, we provide a new miRNA-target tool in which each miRNA is linked to metabolic reactions through its target genes.

The tool was implemented using the R programming language. The whole web-based framework was developed based on the Shiny package from RStudio, and we used information from several public databases to create a relational database developed in SQL to enhance both query performance and storage efficiency.

By offering an intuitive and accessible tool for miRNA analysis, ShinyMIR addresses the growing need for tools that help researchers explore complex biological processes with ease.