

## **Intra-miR-ExploreR, a Novel Bioinformatics Platform for Integrated Discovery of MiRNA:mRNA Gene Regulatory Networks**

**Authors :** Surajit Bhattacharya, Daniel Veltri, Atit A. Patel, Daniel N. Cox

**Abstract :** miRNAs have emerged as key post-transcriptional regulators of gene expression, however identification of biologically-relevant target genes for this epigenetic regulatory mechanism remains a significant challenge. To address this knowledge gap, we have developed a novel tool in R, Intra-miR-ExploreR, that facilitates integrated discovery of miRNA targets by incorporating target databases and novel target prediction algorithms, using statistical methods including Pearson and Distance Correlation on microarray data, to arrive at high confidence intragenic miRNA target predictions. We have explored the efficacy of this tool using *Drosophila melanogaster* as a model organism for bioinformatics analyses and functional validation. A number of putative targets were obtained which were also validated using qRT-PCR analysis. Additional features of the tool include downloadable text files containing GO analysis from DAVID and Pubmed links of literature related to gene sets. Moreover, we are constructing interaction maps of intragenic miRNAs, using both micro array and RNA-seq data, focusing on neural tissues to uncover regulatory codes via which these molecules regulate gene expression to direct cellular development.

**Keywords :** miRNA, miRNA:mRNA target prediction, statistical methods, miRNA:mRNA interaction network

**Conference Title :** ICBCSB 2015 : International Conference on Bioinformatics, Computational and Systems Biology

**Conference Location :** New York, United States

**Conference Dates :** June 04-05, 2015