1046-92-1896 **Frederick A. Adkins*** (`fadkins@iup.edu`), 212 Stright Hall, Mathematics Department, Indiana, PA 15705. *Modeling MicroRNA Targets via Clustering of mRNA Microarray Data.* Preliminary report.

MicroRNA (miRNA) affect gene expression by either blocking translation or cleaving target mRNA resulting in subsequent degradation. This study investigates models for the role of miRNA in gene expression. Modeling provides a mechanism for possible discovery of new miRNAs and identification of miRNA targets in conjunction with mRNA expression levels. Gene expression mRNA and miRNA data for various disease states are clustered to identify genes that are significantly up or down regulated. For significantly down regulated genes, computational methods are used to identify possible common complementary 20-26 nucleotide sequences that are characteristic of microRNA. Based on weighted sequence alignment, free energy at the target site, and other factors that characterize miRNA, likelihood models can be built to determine likely miRNA and their targets. This method of miRNA target investigation attempts to utilize clustering of levels for gene expression to predict common miRNA targets. Correlation of known miRNA hairpins or computational investigation of possible pri-miRNA hairpins to correspondingly up-regulated mRNA from microarray clustering analysis is used to create models useful for exploration of regulatory networks reflecting cellular activity. (Received September 16, 2008)