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**Frederick A Adkins\*** (fadkins@iup.edu), Mathematics Department, Indiana University of Pennsylvania, Indiana, PA 15705. *MicroRNA Target Modeling 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 investigation models 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 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 characterizing miRNA binding, likelihood models are used to determine possible miRNA and their targets. This method of miRNA target investigation attempts to utilize clustering of 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 for exploration of regulatory networks reflecting specific cellular activity. (Received September 22, 2011)