

## Clustering of hypergraphs using microRNA and mRNA expression data from TCGA

Yongsheng Bai, Henjin Chi, and Cheng Zhao\*, Indiana State University

MicroRNA (miRNA) is a short RNA that can regulate gene expression at the post transcriptional level (Shahab et al., 2011). Aberration of miRNA expressions could affect their targeting mRNAs involved in cancer-related signaling pathways (Jansson & Lund, 2012). Using microRNA and mRNA expression data from TCGA, we form vertex-weighted r-uniform hypergraphs with miRNAs as the vertex set and the vertex weights calculated from the connection between miRNA and mRNA. We generated a number of vertex-weighted r-uniform hypergraphs, and detect the clusters in the r-uniform hypergraphs by employing a continuous characterization of the maximum vertex-weighted clique in hypergraphs.

Keywords: Vertex-weighted hypergraphs, Cliques and Clusters in Hypergraphs, Polynomial Optimization.