

Some applications of our generalized HITS and link prediction algorithms to gene regulatory networks of *Drosophila melanogaster* flies reared in microgravity

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Gene regulatory networks (GRNs) provide a direct way of representing relationships between genes through a graph object, enabling methods for pathway analysis. These networks are often built from RNA sequencing data, an assay used for measuring gene expression, by which we mean the normalized count of that gene in a group of samples. We construct GRNs using data of the central nervous system of fruit flies (*Drosophila melanogaster*), a model species, reared in microgravity in the International Space Station (ISS).

First, we construct undirected GRNs from our data by measuring the coexpression of differentially expressed genes. Then, we estimate the direction (interpreted as the influence between genes) of the edges in our networks. Finally, we validate our approach by measuring its effectiveness in accurately predicting known regulatory relationships. We then apply specialized implementations of our generalized Hyperlink Induced Topic Search (HITS) algorithm on the resulting network. This yields a stronger method for assessing individual genes' role in gene regulation by distinguishing between hub and authority genes as targets for therapeutics. We also test link prediction approaches to expand our networks and identify potential interactions between genes.

Keywords: gene regulatory networks, HITS, link prediction, hub nodes, hub genes