**Transcriptomic graph based network analysis of Arabidopsis Thaliana roots in microgravity**

Jairo J. Orozco¹, Vidya Manian¹, and Heeralal Janwa²

¹University of Puerto Rico, Mayaguez, ²University of Puerto Rico, Rio Piedras

**Introduction:** Arabidopsis Thaliana is a model organism that has been grown in the International Space Station (ISS) to understand the molecular and physiological response of these organisms in the space environment. The seedlings were plated and Green Fluorescent Protein (GFP) imaging equipment was used for imaging. Microgravity and radiation are the main environmental stressors in space. The gene information was collected in a gene expression data in real time using Affymetrix and SAGE transcriptome analysis. Our study aims to analyze the effect of microgravity and find the relations between genes by means of graph network analysis.

**Materials and Methods:** The normalized expression data for ground and space flight are used. This data has about 20,000 genes, with fold change, and p-values from the GLDS 7 experiment. The key upregulated and downregulated genes were selected by thresholding the fold change values. The Gene Regulatory Network Boost (GRNBoost) algorithm is used to generate the networks. The algorithm is based on Stochastic Gradient Boosting Machine regression method—the main function of which is to find target genes in the expression data. These target genes are determined from a regression model to predict a target gene's expression profile.

The networks are constructed for upregulated and downregulated genes in ground and flight in ISS. These networks are bipartite directed graphs or bigraphs that are digraphs. The analysis show that these networks have centrally large degrees, called **hub genes** that regulate more target genes called **authority genes**. These target genes are related to biological functions such as cell wall modeling, phosphorylation, and auxin regulation. The statistics computed on these networks show that the upregulated networks for flight vs ground have higher density of 0.168 and 0.159, respectively, and a higher network centralization of 0.663 and 0.649, respectively. The length of paths in all the bigraphs is one, which is also the shortest path. In both the cases one gets a single connected component, with different topological properties, and different behaviors of hub genes and authority genes and strengths.

**Results and Discussion:** The gene regulatory networks for the 4 categories are shown below as directed graphs, where the hub genes are transcription factors that excite or inhibit target genes in the case of up regulation, and down regulation, respectively. With top 500 genes we observe a more nuanced and differentiated outcomes.

![Network Diagrams](image)

**Figure 1.** a) down regulation flight, b) up regulation flight, c) down regulation ground, d) up regulation ground.

**Conclusions:** Even with 100 genes, our analysis of the gene regulatory networks for ground and space ecotypes for the growth of AT show different genes expressed in each ecotype and GRN topological structure and functions. Our novel spectral theoretic techniques are expected to show more refined differentiations with the whole genome, and the genome to phenome analysis is expected to show viability of the plant growth in microgravity.

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