

Analysis of the Effect of Beverage Consumption on Gene Expression in Blood

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Short Abstract — This study examines the changes over time in lymphocyte gene expression after exposure to different beverages. We construct a dynamic Bayesian network showing, which genes are most-likely regulating which other genes in response to the beverage treatment.

Keywords — Gene Network, Gene Expression, Environmental Stimuli, Dynamic Bayesian Network

I. PURPOSE

THIS investigation examines the influence of various beverages water, grape juice, wine, and dilute ethyl alcohol on gene activity in the peripheral blood system over the course of several hours. We use a dynamic Bayesian network inference tool called Banjo [1] to develop a network showing how changes in the activity of certain genes affect the activity of others at later time points.

II. BACKGROUND

Our data were obtained from NCBI GEO (Gene Expression Omnibus) [2] and were originally collected by Baty *et al.* as part of [3]. Baty's study included 6 participants over the course of 4 trials over several days. Each was exposed to one of the treatment conditions, consuming 250 ml of one of the test beverages. Blood samples were then taken at 0, 1, 2, 4, and 12 hours after beverage consumption. The authors tested four beverages water, grape juice, wine, and ethyl alcohol diluted with water to be the same concentration as the alcohol present in wine. The authors hoped to observe clues to the cardio-protective effects observed in those who consume moderate amounts of red wine. Samples were analyzed with the Affymetrix HGU133A microarray which measured the activity of 22,283 genes.

To make the analysis of this dataset feasible, we used a selection criterion based on the coefficient of variation, a coefficient greater than 0.25, to eliminate genes not showing significant changes over the time course. This approach limits the number of genes being studied to 1920, which vary most across times and treatments.

III. CONCLUSION

Using Banjo we have developed a proposed gene regulatory network made up of the subset of observed genes

that we have included in our model.

REFERENCES

- [1] Hartemink A. (2007) *Banjo: Bayesian Network Inference with Java Objects*. <<http://www.cs.duke.edu/~amink/software/banjo/>> (2008, April 14).
- [2] NCBI: GEO. (2007) *Dataset Record* <http://www.ncbi.nlm.nih.gov/projects/geo/gds/gds_browser.cgi?gds=2767> (2008, April 14).
- [3] Baty et al. (2006) *Analysis with respect to instrumental variables for the exploration of microarray data structures*. *BMC Bioinformatics*. <<http://www.biomedcentral.com/1471-2105/7/422>> (2008, April 14).

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