Improved Modeling and Analysis of Gene Expression

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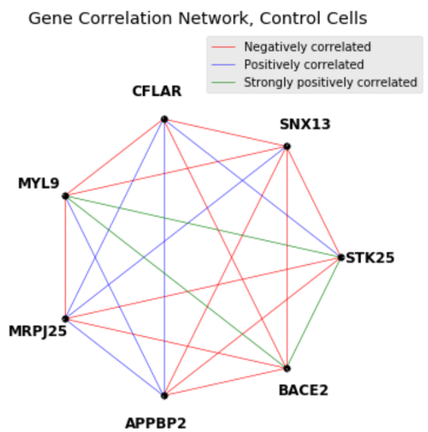
Goals

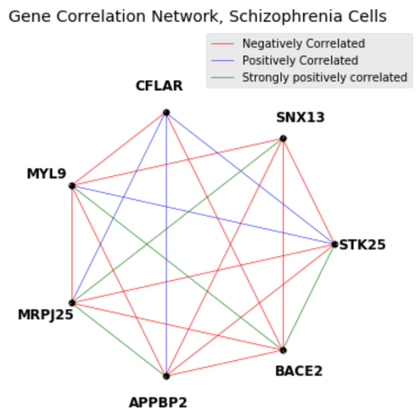
Differential gene extraction: develop methods to extract biologically significant genes that might not be detected by current methods

- *Zeroth order:* develop improved hypothesis testing
- *First order:* find which linear regulatory relationships between genes differ significantly in different conditions

Methods

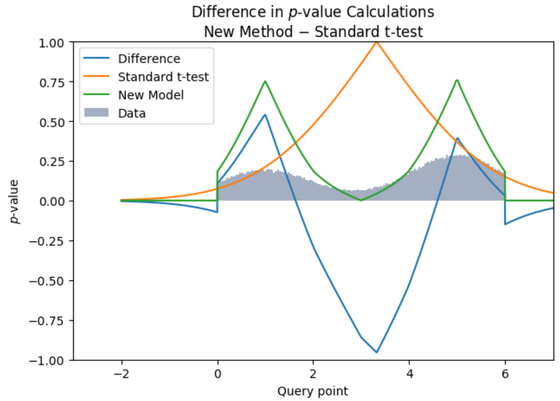
1. Implement mixture model including normal and truncated distributions.
2. Implement model selection algorithm and improved measure of significance
3. Perform correlational analysis to determine differentially expressed genes in two disease states: Control and Schizophrenia





Results

- Significant (p = 0.05) genes discovered through correlational analysis:
  - ACLY, FOXJ3, MPZL1 [3], STXBP1
- New model detects significant values in synthetic dataset which are not detected by standard t-test



Difference in calculated p-value on bimodal data.

Conclusion and Future Work

- This model uses hypothesis testing and correlational analysis to better detect significant gene expression levels.
- Next steps: test zeroth order model on real data; apply more refined network algorithms to model relationships between genes

References

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[2] James W. Jawitz. Moments of truncated continuous univariate distributions}, Advances in Water Resources, Volume 27, Issue 3, 2004, Pages 269-281, ISSN 0309-1708, https://doi.org/10.1016/j.advwatres.2003.12.002.

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