

Analyzing Sex-specific Aging Differences using Machine Learning



I'm Mikayla Walsh and I am a rising Junior at Brown University. I spent this past summer working in Professor Singh's lab at Brown.



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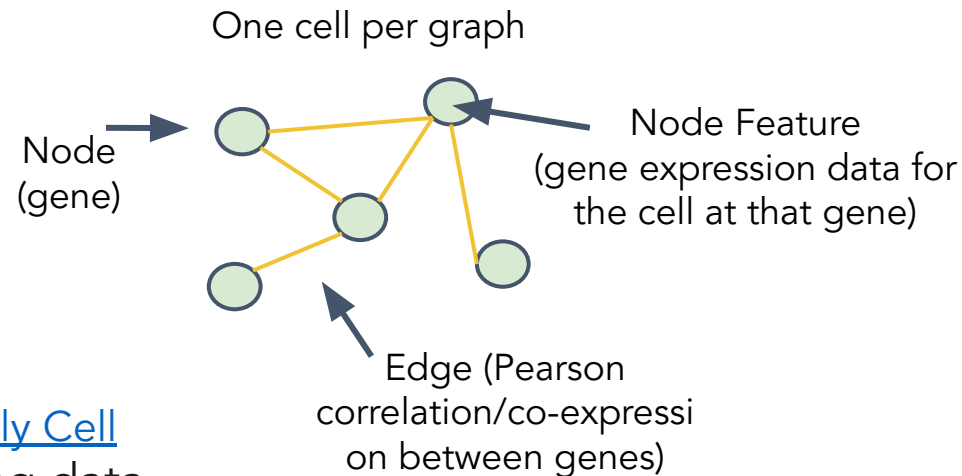
Background

Goal: We wanted to see if we could use a Graph Neural Network to predict either the age or sex of a cell given the gene expression data of the cell. We were hopeful that this would indicate whether or not these genes played a role in determining aging, and if so, which ones are the most important.

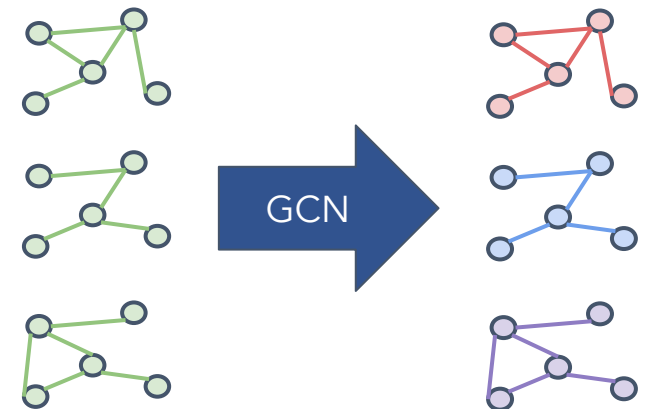
Motivation: We used the paper [Single-cell classification using graph convolutional networks](#) as motivation to base our project off of.



The dataset we used was the [Aging Fly Cell Atlas](#). This dataset consists of RNA-seq data for 289,981 *Drosophila melanogaster*, or fruit fly, head cells and 15,992 genes.



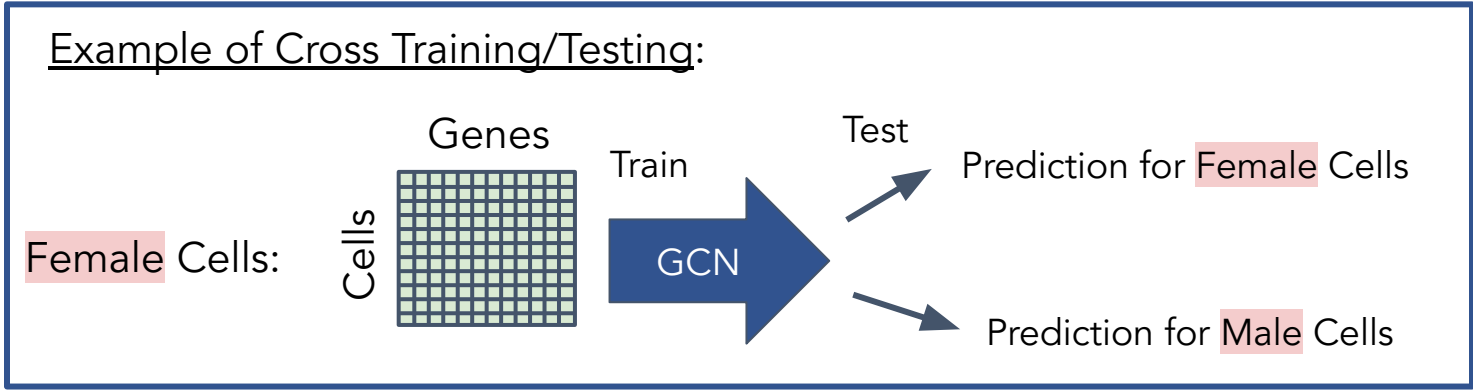
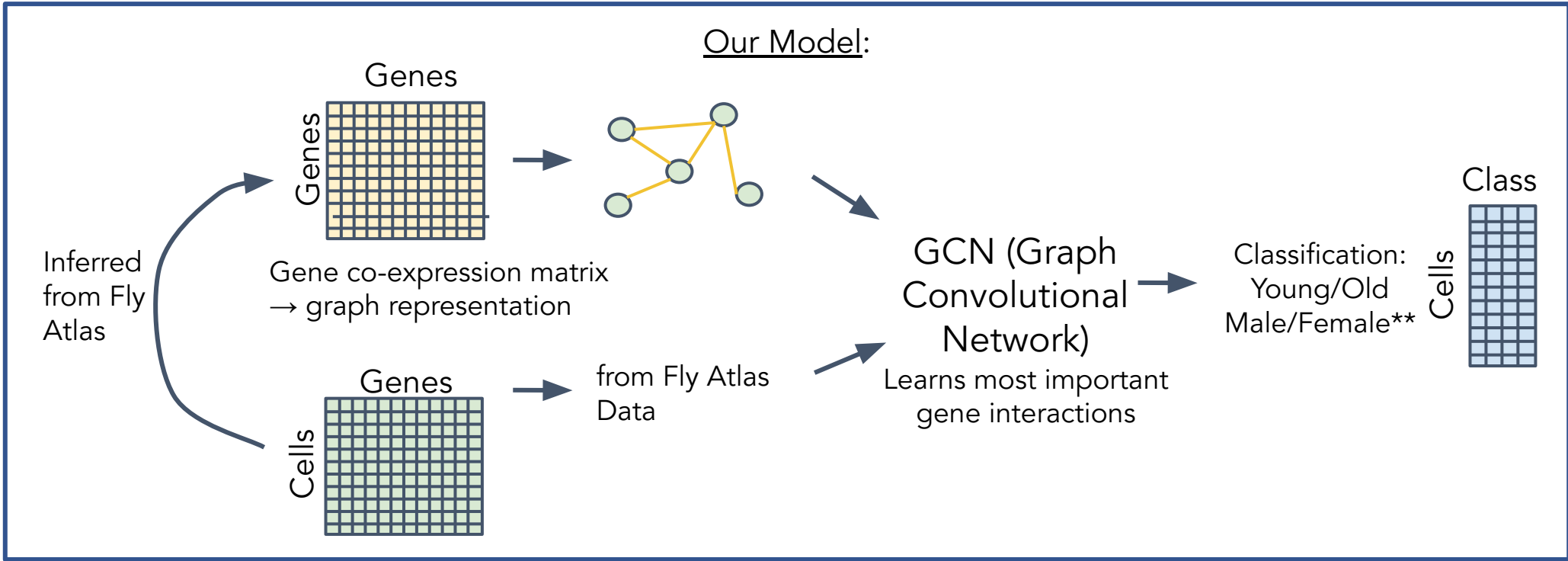
Graph Classification:





Methods

Note: Low quality cells and genes (meaning those with low expression or minimal data) are filtered out before testing in order to optimize results.

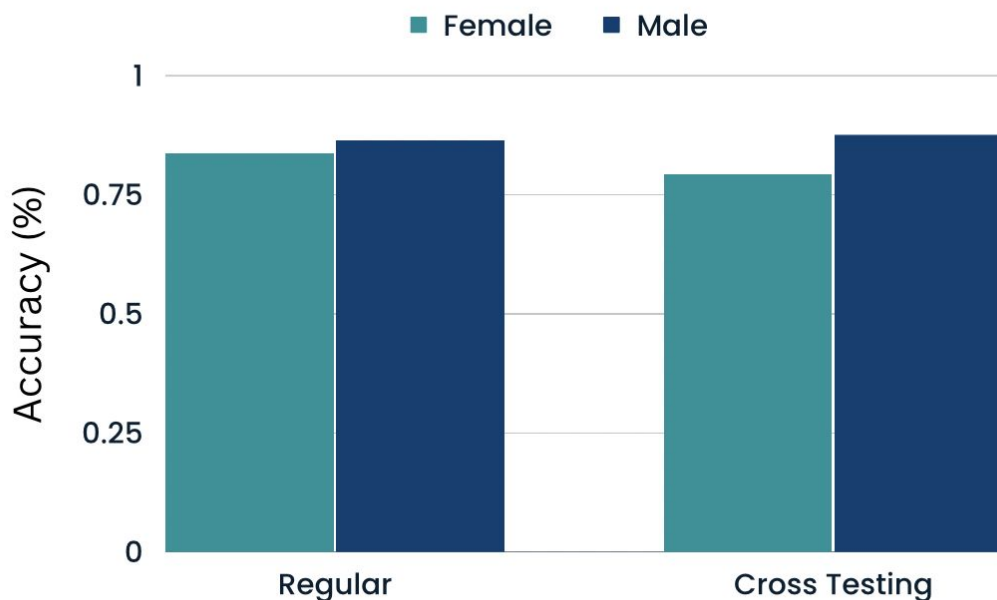


**Female/male cells are any cells labeled female/male respectfully in the dataset. Young cells are any cells labeled age 5 days old. Old cells are any labeled 70 days old.

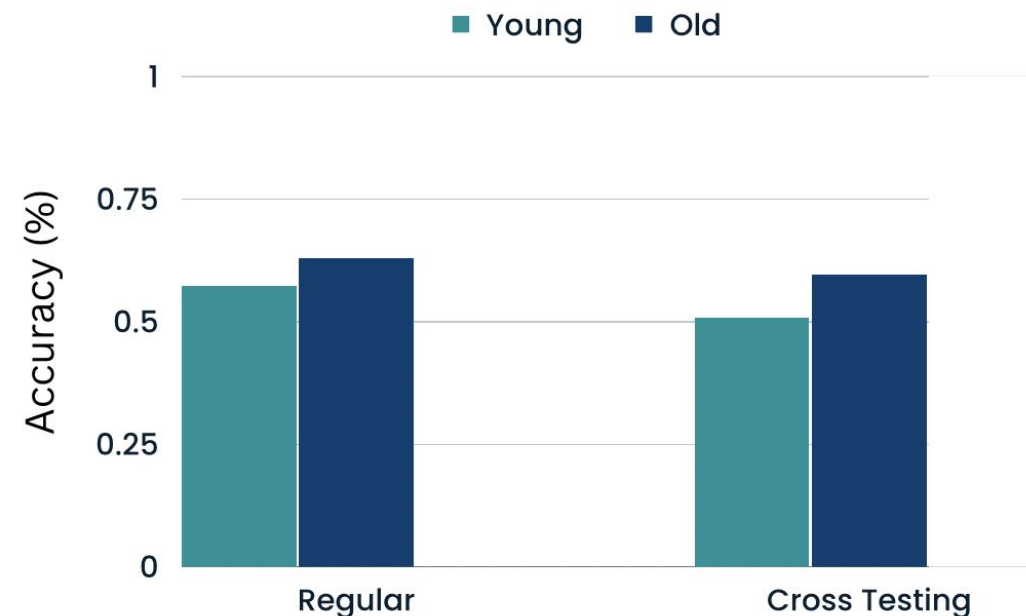


Conclusion

Age Prediction Results



Sex Prediction Results



What this could mean:

- Same gene interactions important in predicting age for males and females?
- Cells 5 days old and 70 days old are too different making this task difficult to generalize?
- Key to predicting if a cell is young/old doesn't lie in gene expression/gene interaction data?

Next Steps:

- Determine which gene interactions were most important
- Incorporate more diverse ages for prediction – more generalizable?