



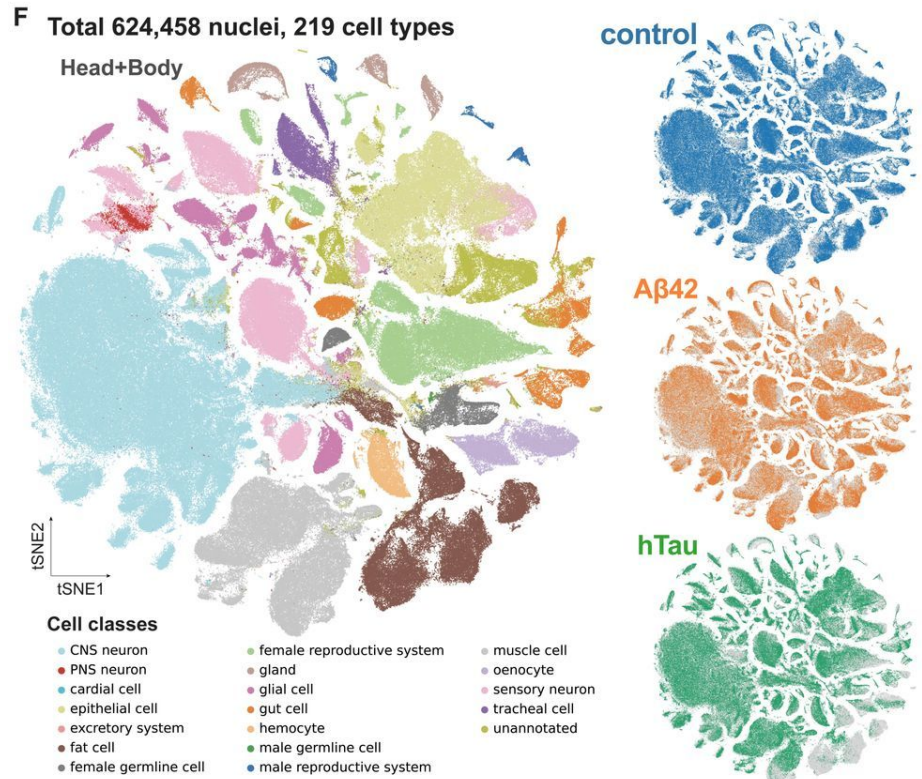
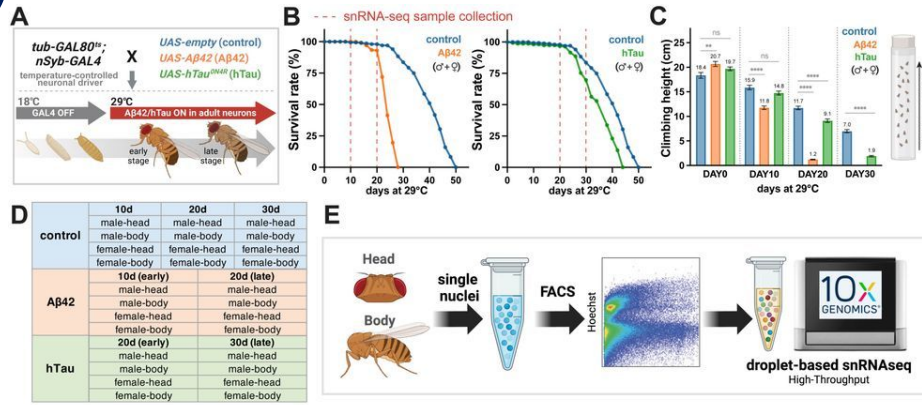
Understanding Sex-Specific Differences in Development of Alzheimer's Disease Through Deep Learning Models

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Background



Single-nuclei gene expression profile

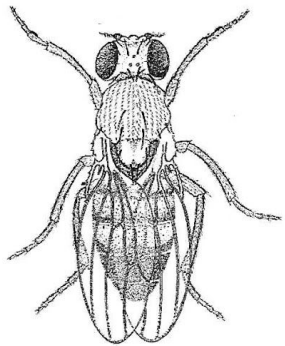
Input

CNN Age Model

Model interpretation (what the model is using to learn)

genoAge of the single cell

Output





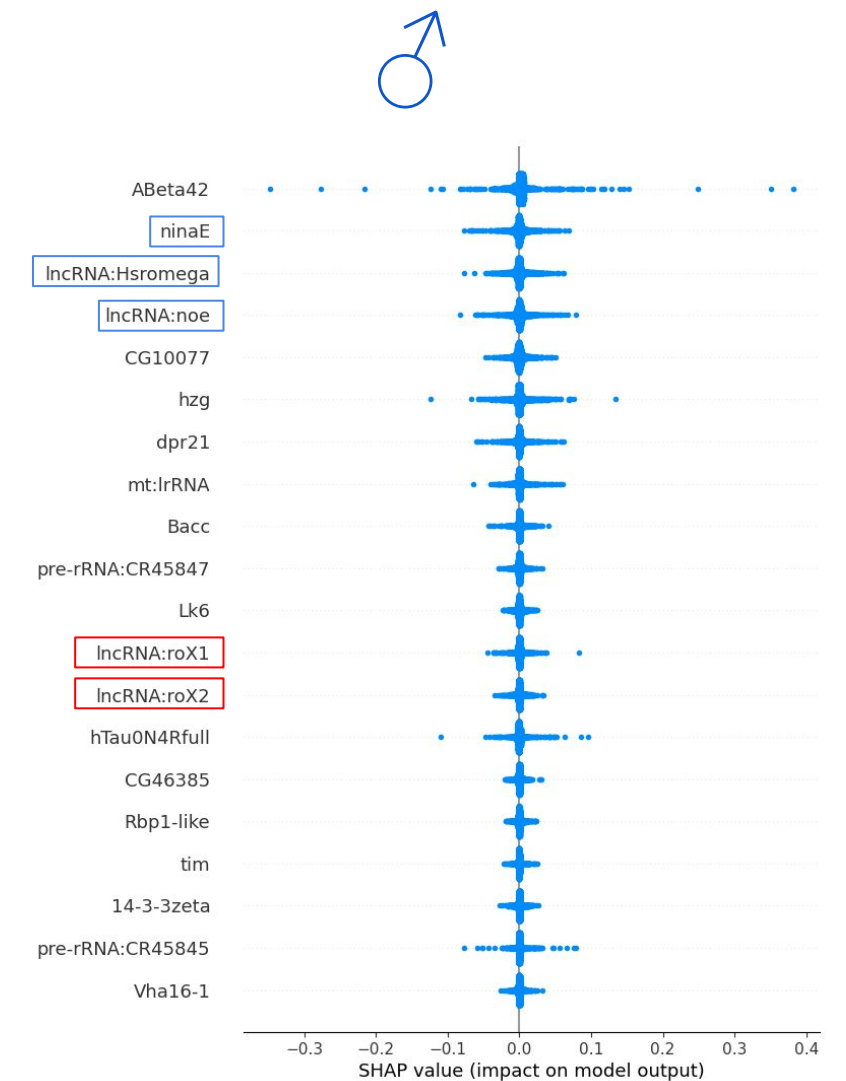
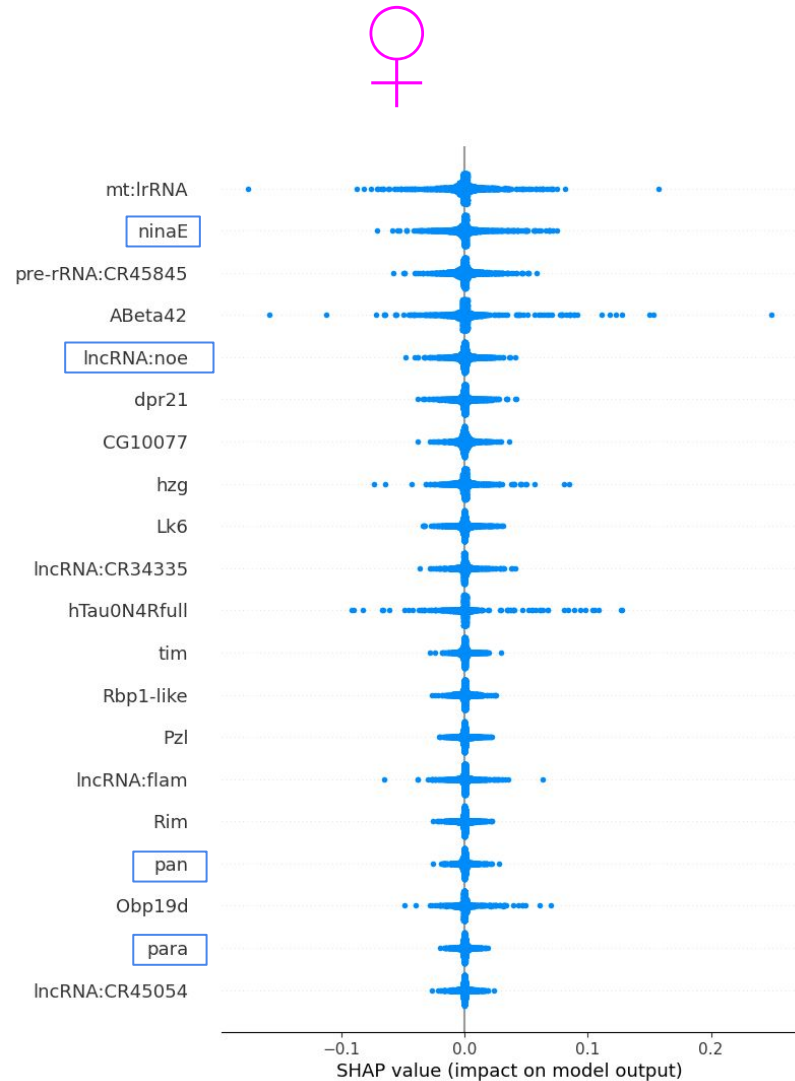
Methods/Results

CNN Model Performance

	Accuracy	Precision	Recall
Male	80.7910%	80.6591%	80.7609%
Female	83.5120%	82.8764%	83.5090%
All	74.1204%	74.3136%	74.1337%

genes observed in previous aging clocks done by lab

genes associated with dosage compensation





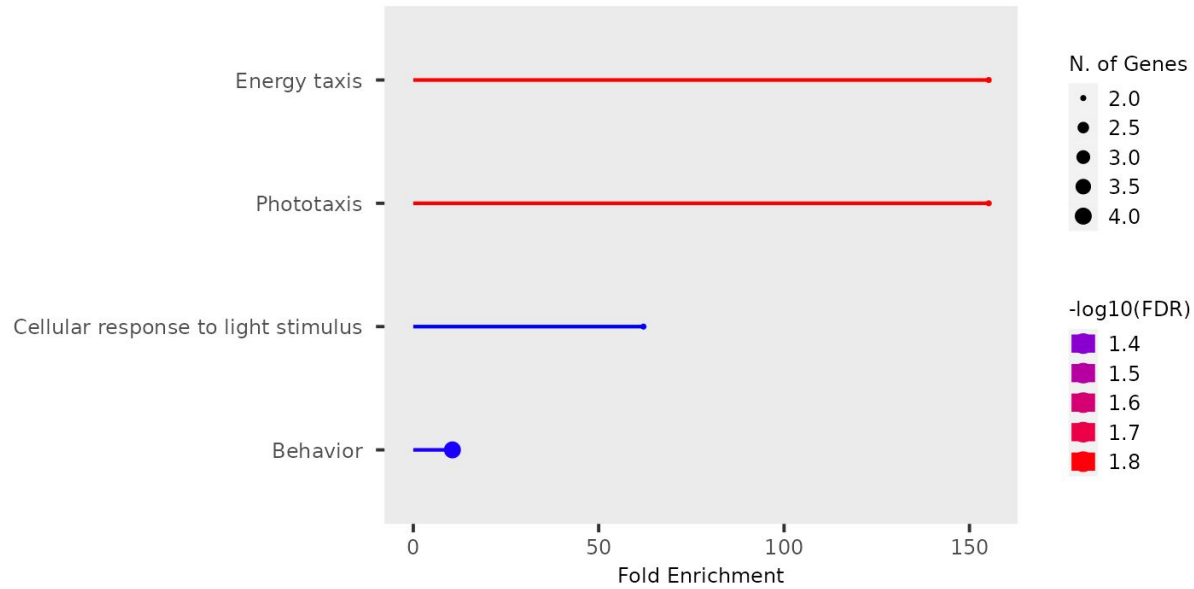
Conclusion and Future Work

- ❖ high accuracy, precision, and recall
- ❖ differences in male and female AD progression
- ❖ dosage compensation genes in males support IISAGE hypothesis surrounding sex-determining pathways and aging
- ❖ potential biomarkers of sex-specific AD pathogenesis



Methods/Results

Male



Female

