

# The Genetic Basis of Exploratory Behaviors in Mice

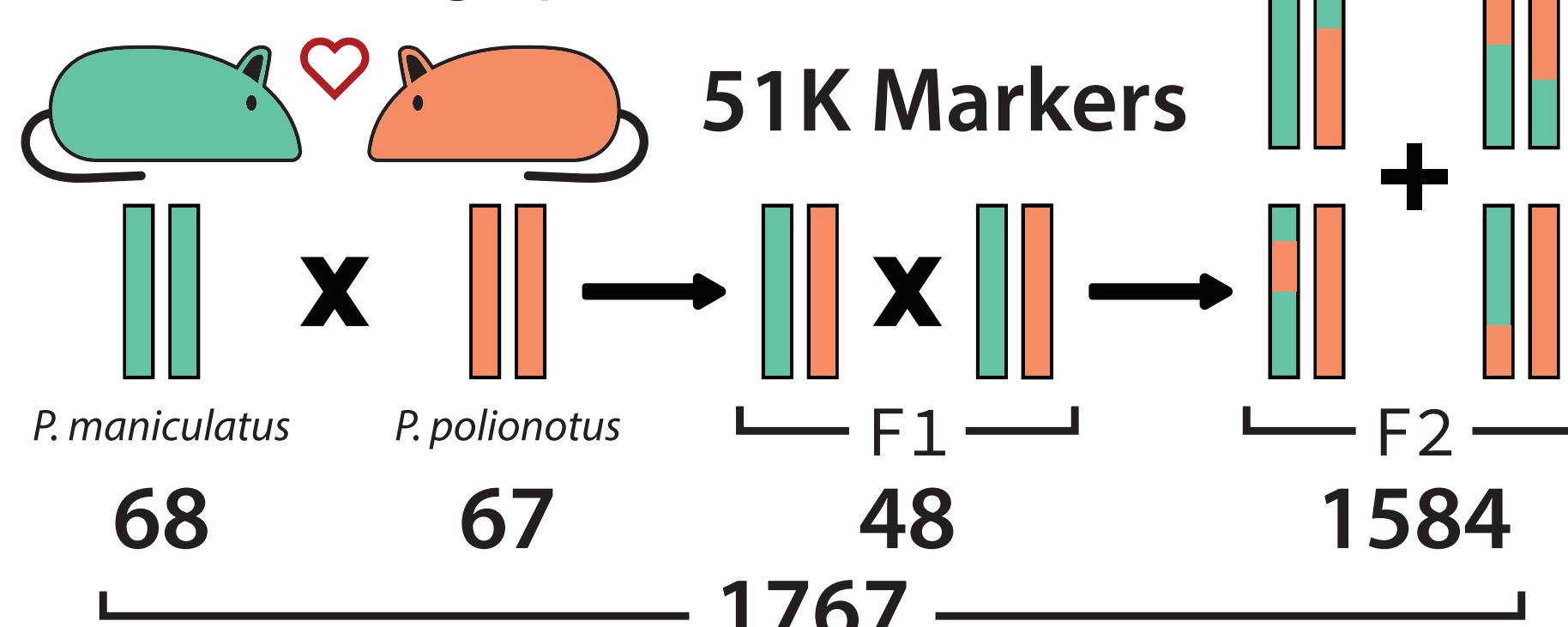
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### Introduction

Animals vary in their exploratory behaviors. This project examines the connections between animal behaviors and their genetic bases using both behavioral data of mice exploring an environment and genetic variation throughout their genomes.

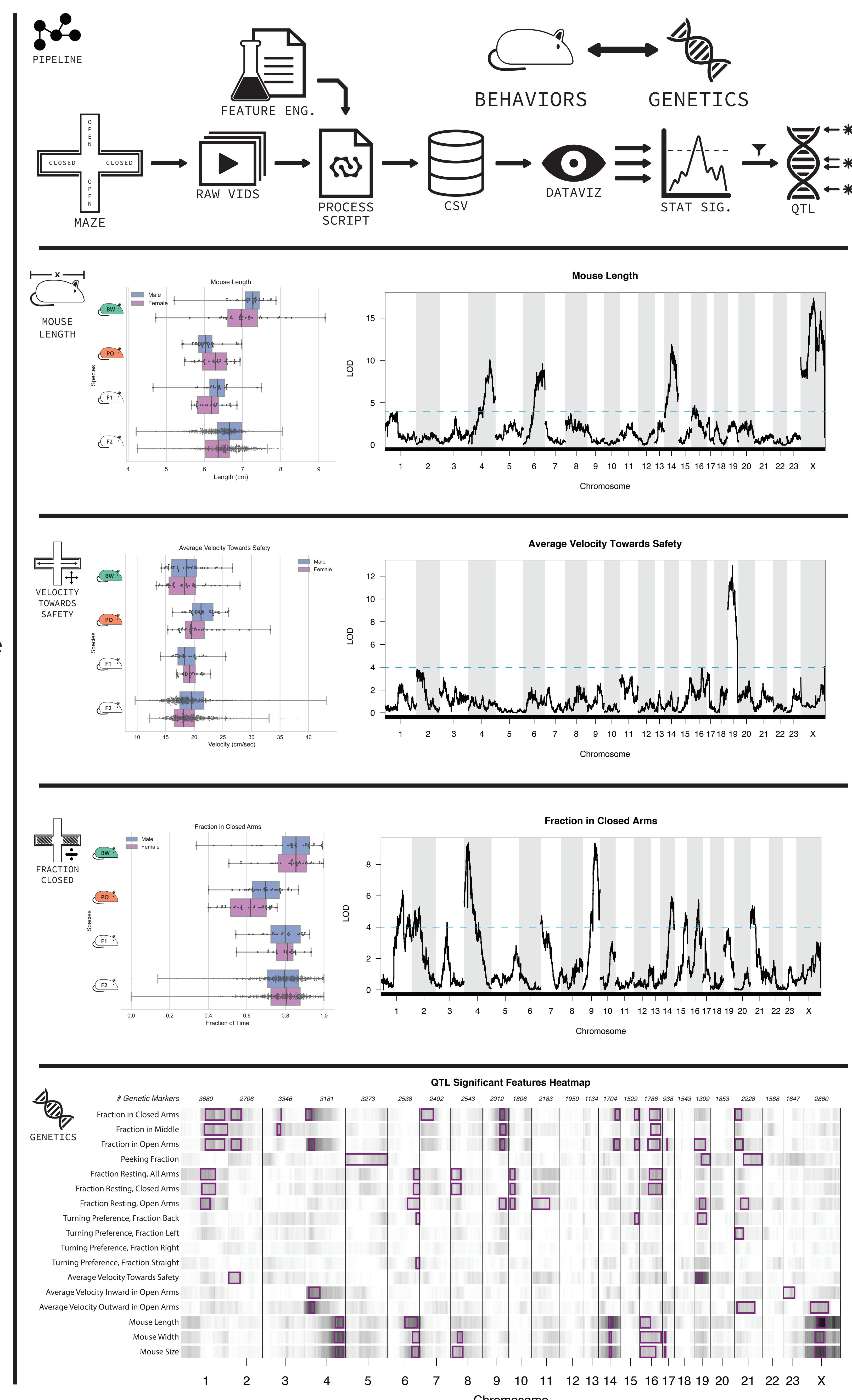
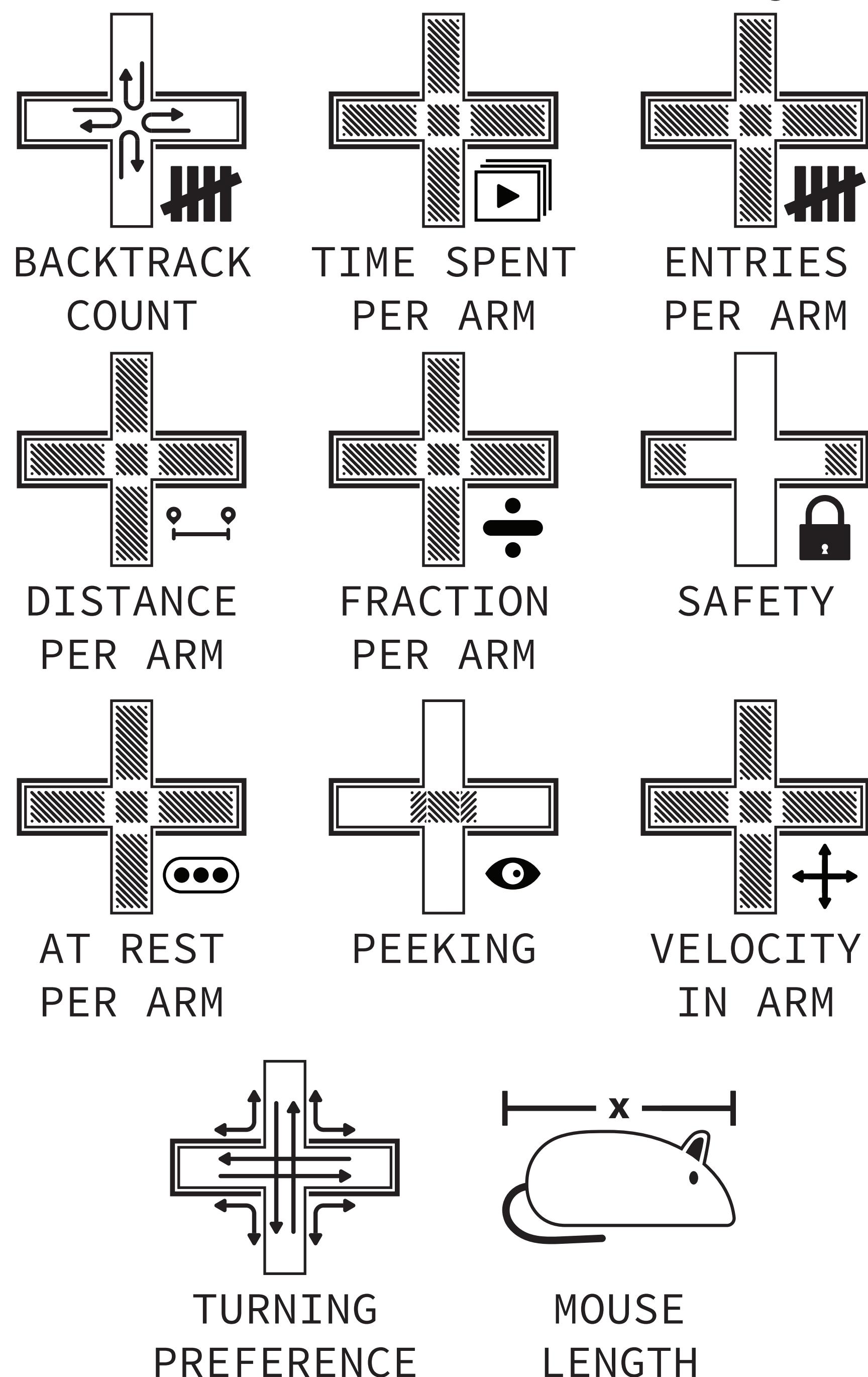
### Background

We use data from *Peromyscus polionotus* (PO) and *Peromyscus maniculatus* (BW) mice—two species with differing exploratory behaviors—and their first and second generation hybrid offspring (BWPOF1 and BWPOF2). The mice explore an elevated plus maze, which simulates differences in exploratory behavior using open and closed arms.



### Feature Engineering

To look at as many behavioral patterns as possible, we created over 200 features across several categories:



### Pipeline

- Analyze behavioral data to extract informative features
- Visualize features and filter for statistical significance between species using two-way ANOVA
- Use quantitative trait loci (QTL) to understand connection to genetics

### Results

The quantitative trait loci (QTL) plots show the LOD scores (logarithm of the odds), which measure the correlation between an observed behavior and a genetic region. We chose a LOD score of four as the threshold for significance.

- **Mouse Length** is a different feature from the rest, as it is a morphology not a behavior. Because of this, we expect many genes heavily influence it. The QTL plot shows multiple peaks far above the threshold, suggesting regions in chromosomes 4, 6, 14, and X are highly correlated with this morphology.

- **Average Velocity Towards Safety** describes the average velocity of a mouse only inside the closed arms running away from the center of the maze. We see that chromosome 19 is highly linked to this behavior. It is interesting to observe a QTL that is linked so strongly and narrowly to a behavior adverse to exploring (running back toward safety).

- **Fraction in Closed Arms** is the fraction of time a mouse spends in the closed arms. The QTL plot indicates many chromosomes influence how long mice spend in these locations. Interestingly, chromosome 19, which was linked to how quickly mice move into safety, is not highly correlated with this feature. This suggests there could be a genetic difference between running into a closed space and spending time in a closed space.

### Next Steps

- Determine which genetic version (BW or PO) at significant QTL regions promotes the observed behaviors
- Explore connection between behaviors and genetics split by sexes
- Perform permutations for each feature to more accurately determine statistical significance

### References

- A Guide to QTL Mapping with R/qtl (<http://www.rqtl.org/book/>)
- Genetic contributions to behavioural diversity at the gene–environment interface (<https://www.nature.com/articles/nrg3065>)
- Selected icons from Noun Project (<http://nounproject.com/zachbogart>)