Neural Data Science Spring 2022
Homework 4

We will finally bid farewell to "HW1_data.xlsx" after one last analysis.

There is starter code "HW4_starter_code.R" that reads in this data and runs a linear mixed model on it for Trial and Genotype effects (and their interaction).

1) Computing this model throws a singularity warning. What is going wrong in this analysis? What does it mean for the use of Mouse as a random effect?

There is a new data set "HW4_2022_data.xlsx" that indicates object preference time across 4 test trials for 2 groups of 10 mice each. The starter code will read the data in and produce a plot of them.

2) Using lmer, create a linear mixed model with "preference" as the outcome variable, "group" and "trial" and their interaction as fixed effects, and "subject_ID" as a random effect (with a random intercept only), and pass this model to both summary() and anova(). Interpret the output:
- do the control and drug groups differ significantly from one another?
- do you think performance in this task significantly changes across trials?
- if performance differs across trials, does group membership (control vs drug) influence this effect?

You should submit (via Slack DM) your R code (added on to the HW4_starter_code.R file) before the beginning of class **February 23**.