

y_maze

2025-05-13

```
# Load dplyr for filtering  
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.2.3
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
## filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
## intersect, setdiff, setequal, union
```

```
df <- read.csv("~/Downloads/Y-Maze.csv")
```

```
head(df)
```

```
##      Time Novel_Arm Genotype   Drug Mouse_ID  
## 1   37.0         0      KI Saline      1  
## 2   23.6         0      KI Saline      2  
## 3  106.8         0      KI Saline      3  
## 4   34.8         0      KI Saline      4  
## 5   79.1         0      KI Saline      5  
## 6  256.5         0      KI Saline      6
```

```
df$Mouse_ID <- factor(df$Mouse_ID)  
df$Drug <- factor(df$Drug)  
df$Genotype <- factor(df$Genotype)  
df$Novel_Arm <- factor(df$Novel_Arm)  
df$Group <- interaction(df$Drug, df$Genotype)  
  
# Get unique groups  
groups <- unique(df$Group)  
  
# Store results  
results <- data.frame(Group = character(), p = numeric(), t = numeric(), df = numeric(),  
                      mean_diff = numeric(), shapiro_p = numeric(), stringsAsFactors = FALSE)  
  
# Loop through each group
```

```

for (g in groups) {
  cat("\n---", g, "---\n")
  sub_df <- subset(df, Group == g)

  # Reshape to wide format
  wide <- reshape(sub_df, idvar = "Mouse_ID", timevar = "Novel_Arm", direction = "wide")

  if (all(c("Time.0", "Time.1") %in% names(wide))) {
    diffs <- wide$Time.1 - wide$Time.0
    shapiro_test <- shapiro.test(diffs)
    #test <- t.test(wide$Time.1, wide$Time.0, paired = TRUE)
    test <- t.test(wide$Time.1, wide$Time.0, paired = TRUE, alternative = "greater")

    cat("Shapiro-Wilk p-value:", round(shapiro_test$p.value, 4), "\n")
    print(test)

    results <- rbind(results, data.frame(
      Group = as.character(g),
      p = test$p.value,
      t = test$statistic,
      df = test$parameter,
      mean_diff = mean(diffs),
      shapiro_p = shapiro_test$p.value
    ))
  } else {
    cat("Skipping group due to insufficient data\n")
  }
}

```

```

##
## --- Saline.KI ---
## Shapiro-Wilk p-value: 0.1503
##
## Paired t-test
##
## data: wide$Time.1 and wide$Time.0
## t = -1.274, df = 10, p-value = 0.8843
## alternative hypothesis: true mean difference is greater than 0
## 95 percent confidence interval:
## -106.1132      Inf
## sample estimates:
## mean difference
##      -43.8
##
##
## --- SKF.KI ---
## Shapiro-Wilk p-value: 0.7427
##
## Paired t-test
##
## data: wide$Time.1 and wide$Time.0
## t = 0.72175, df = 10, p-value = 0.2435
## alternative hypothesis: true mean difference is greater than 0

```

```
## 95 percent confidence interval:
## -45.19828      Inf
## sample estimates:
## mean difference
##      29.90909
##
##
## --- Saline.WT ---
## Shapiro-Wilk p-value: 0.9463
##
## Paired t-test
##
## data: wide$Time.1 and wide$Time.0
## t = 0.89547, df = 10, p-value = 0.1958
## alternative hypothesis: true mean difference is greater than 0
## 95 percent confidence interval:
## -27.54676      Inf
## sample estimates:
## mean difference
##      26.9
##
##
## --- SKF.WT ---
## Shapiro-Wilk p-value: 0.7598
##
## Paired t-test
##
## data: wide$Time.1 and wide$Time.0
## t = 3.002, df = 10, p-value = 0.006649
## alternative hypothesis: true mean difference is greater than 0
## 95 percent confidence interval:
## 35.12992      Inf
## sample estimates:
## mean difference
##      88.65455
```

```
# Adjust p-values
results$adjusted_p <- p.adjust(results$p, method = "holm")

# Print final result table
print(results)
```

```
##      Group      p      t df mean_diff shapiro_p adjusted_p
## t Saline.KI 0.884258993 -1.2739799 10 -43.80000 0.1502967 0.88425899
## t1 SKF.KI 0.243489415 0.7217542 10 29.90909 0.7427031 0.58737477
## t2 Saline.WT 0.195791589 0.8954657 10 26.90000 0.9462970 0.58737477
## t3 SKF.WT 0.006648646 3.0020370 10 88.65455 0.7598357 0.02659458
```

Paired t-tests: Novel Arm Preference

We tested whether mice spent significantly more time in the **novel arm** than in the **familiar arm** within each Drug × Genotype group using **one-sided paired t-tests**.

Hypotheses

Let μ_{novel} be the mean time spent in the novel arm, and μ_{familiar} the mean time in the familiar arm.

- **Null hypothesis:** $H_0 : \mu_{\text{novel}} \leq \mu_{\text{familiar}}$
- **Alternative hypothesis:** $H_1 : \mu_{\text{novel}} > \mu_{\text{familiar}}$

We use `alternative = "greater"` in `t.test()`.

Assumptions

- **Paired measurements:** Each mouse provides both arm 0 and arm 1 observations.
- **Normality of differences:** Checked using the Shapiro–Wilk test.
If $p > 0.05$, the normality assumption holds.
- **Multiple comparisons:** Corrected using the Holm–Bonferroni method.

Results

Overall, only the **SKF + WT** group spent a significantly greater amount of time in the novel arm ($p = 0.0066$, Holm-adjusted $p = 0.0266$).