SA2 - Alzheimer's Mice

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Analysis for Training Day Errors

2-Way ANOVA

```
anova_training <- aov(Training ~ AD_Status * Treatment, data = data)
summary(anova_training)
```

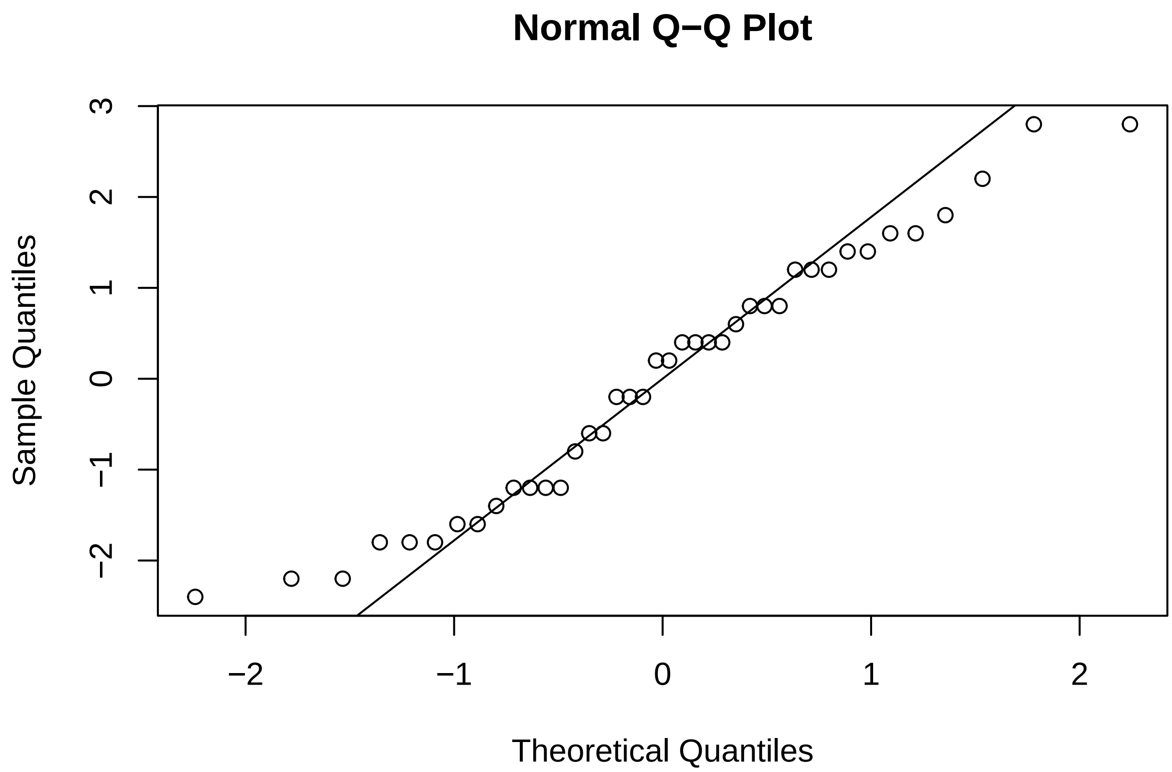
```
##                     Df Sum Sq Mean Sq F value Pr(>F)
## AD_Status            1   3.03   3.025   1.216 0.2784
## Treatment            3  28.28   9.425   3.789 0.0197 *
## AD_Status:Treatment  3   9.08   3.025   1.216 0.3198
## Residuals           32  79.60   2.488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Assumption Check : Normality

```
# Normality check (Shapiro-Wilk test on residuals)
shapiro.test(residuals(anova_training))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(anova_training)
## W = 0.96357, p-value = 0.2214
```

```
qqnorm(residuals(anova_training))
qqline(residuals(anova_training))
```



The Shapiro-Wilk test for Training Day residuals returned a p-value of 0.2214.
Interpretation: Since the p-value is greater than 0.05, the residuals are approximately normal. Therefore, the normality assumption is **met**.

Assumption Check : Homogeneity of Variances

```
# Homogeneity of variances (Levene's test)
leveneTest(Training ~ interaction(AD_Status, Treatment), data = data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  7  0.4346 0.8731
##       32
```

Levene's test for Training Day errors returned an F value of 0.4346 ($p > 0.05$).
Interpretation: Since the p-value is greater than 0.05, the variance across AD_Status × Treatment groups is equal. The homogeneity of variance assumption is **met**.

Post-Hoc Tests

```
# Tukey HSD for main effects and interactions
tukey_training <- TukeyHSD(anova_training)
tukey_training
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Training ~ AD_Status * Treatment, data = data)
##
## $AD_Status
##     diff        lwr      upr     p adj
## 2-1 0.55 -0.4659173 1.565917 0.2783559
##
## $Treatment
##     diff        lwr        upr     p adj
## 2-1  1.5 -0.4110125  3.4110125 0.1664403
## 3-1  0.9 -1.0110125  2.8110125 0.5844498
## 4-1 -0.7 -2.6110125  1.2110125 0.7547388
## 3-2 -0.6 -2.5110125  1.3110125 0.8298123
## 4-2 -2.2 -4.1110125 -0.2889875 0.0190170
## 4-3 -1.6 -3.5110125  0.3110125 0.1269509
##
## $`AD_Status:Treatment`
##                  diff      lwr     upr     p adj
## 2:1-1:1  2.200000e+00 -1.03119 5.43119 0.3751687
## 1:2-1:1  2.600000e+00 -0.63119 5.83119 0.1906395
## 2:2-1:1  2.600000e+00 -0.63119 5.83119 0.1906395
## 1:3-1:1  2.000000e+00 -1.23119 5.23119 0.4943542
## 2:3-1:1  2.000000e+00 -1.23119 5.23119 0.4943542
## 1:4-1:1  4.000000e-01 -2.83119 3.63119 0.9999036
## 2:4-1:1  4.000000e-01 -2.83119 3.63119 0.9999036
## 1:2-2:1  4.000000e-01 -2.83119 3.63119 0.9999036
## 2:2-2:1  4.000000e-01 -2.83119 3.63119 0.9999036
## 1:3-2:1 -2.000000e-01 -3.43119 3.03119 0.9999992
## 2:3-2:1 -2.000000e-01 -3.43119 3.03119 0.9999992
## 1:4-2:1 -1.800000e+00 -5.03119 1.43119 0.6216948
## 2:4-2:1 -1.800000e+00 -5.03119 1.43119 0.6216948
## 2:2-1:2  1.776357e-15 -3.23119 3.23119 1.0000000
## 1:3-1:2 -6.000000e-01 -3.83119 2.63119 0.9986142
## 2:3-1:2 -6.000000e-01 -3.83119 2.63119 0.9986142
## 1:4-1:2 -2.200000e+00 -5.43119 1.03119 0.3751687
## 2:4-1:2 -2.200000e+00 -5.43119 1.03119 0.3751687
## 1:3-2:2 -6.000000e-01 -3.83119 2.63119 0.9986142
## 2:3-2:2 -6.000000e-01 -3.83119 2.63119 0.9986142
## 1:4-2:2 -2.200000e+00 -5.43119 1.03119 0.3751687
## 2:4-2:2 -2.200000e+00 -5.43119 1.03119 0.3751687
## 2:3-1:3  0.000000e+00 -3.23119 3.23119 1.0000000
## 1:4-1:3 -1.600000e+00 -4.83119 1.63119 0.7444909
## 2:4-1:3 -1.600000e+00 -4.83119 1.63119 0.7444909
## 1:4-2:3 -1.600000e+00 -4.83119 1.63119 0.7444909
## 2:4-2:3 -1.600000e+00 -4.83119 1.63119 0.7444909
## 2:4-1:4  1.776357e-15 -3.23119 3.23119 1.0000000
```

```r
emmeans(anova_training, pairwise ~ AD_Status * Treatment, adjust = "tukey")
```

```
## $emmeans
##  AD_Status Treatment emmean    SE df lower.CL upper.CL
##  1         1           13.2 0.705 32     11.8     14.6
```

```
##  2         1           15.4 0.705 32     14.0     16.8
##  1         2           15.8 0.705 32     14.4     17.2
##  2         2           15.8 0.705 32     14.4     17.2
##  1         3           15.2 0.705 32     13.8     16.6
##  2         3           15.2 0.705 32     13.8     16.6
##  1         4           13.6 0.705 32     12.2     15.0
##  2         4           13.6 0.705 32     12.2     15.0
##
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                      estimate    SE df t.ratio
##  AD_Status1 Treatment1 - AD_Status2 Treatment1     -2.2 0.997 32  -2.206
##  AD_Status1 Treatment1 - AD_Status1 Treatment2     -2.6 0.997 32  -2.607
##  AD_Status1 Treatment1 - AD_Status2 Treatment2     -2.6 0.997 32  -2.607
##  AD_Status1 Treatment1 - AD_Status1 Treatment3     -2.0 0.997 32  -2.005
##  AD_Status1 Treatment1 - AD_Status2 Treatment3     -2.0 0.997 32  -2.005
##  AD_Status1 Treatment1 - AD_Status1 Treatment4     -0.4 0.997 32  -0.401
##  AD_Status1 Treatment1 - AD_Status2 Treatment4     -0.4 0.997 32  -0.401
##  AD_Status2 Treatment1 - AD_Status1 Treatment2     -0.4 0.997 32  -0.401
##  AD_Status2 Treatment1 - AD_Status2 Treatment2     -0.4 0.997 32  -0.401
##  AD_Status2 Treatment1 - AD_Status1 Treatment3      0.2 0.997 32   0.201
##  AD_Status2 Treatment1 - AD_Status2 Treatment3      0.2 0.997 32   0.201
##  AD_Status2 Treatment1 - AD_Status1 Treatment4      1.8 0.997 32   1.805
##  AD_Status2 Treatment1 - AD_Status2 Treatment4      1.8 0.997 32   1.805
##  AD_Status1 Treatment2 - AD_Status2 Treatment2      0.0 0.997 32   0.000
##  AD_Status1 Treatment2 - AD_Status1 Treatment3      0.6 0.997 32   0.602
##  AD_Status1 Treatment2 - AD_Status2 Treatment3      0.6 0.997 32   0.602
##  AD_Status1 Treatment2 - AD_Status1 Treatment4      2.2 0.997 32   2.206
##  AD_Status1 Treatment2 - AD_Status2 Treatment4      2.2 0.997 32   2.206
##  AD_Status2 Treatment2 - AD_Status1 Treatment3      0.6 0.997 32   0.602
##  AD_Status2 Treatment2 - AD_Status2 Treatment3      0.6 0.997 32   0.602
##  AD_Status2 Treatment2 - AD_Status1 Treatment4      2.2 0.997 32   2.206
##  AD_Status2 Treatment2 - AD_Status2 Treatment4      2.2 0.997 32   2.206
##  AD_Status1 Treatment3 - AD_Status2 Treatment3      0.0 0.997 32   0.000
##  AD_Status1 Treatment3 - AD_Status1 Treatment4      1.6 0.997 32   1.604
##  AD_Status1 Treatment3 - AD_Status2 Treatment4      1.6 0.997 32   1.604
##  AD_Status2 Treatment3 - AD_Status1 Treatment4      1.6 0.997 32   1.604
##  AD_Status2 Treatment3 - AD_Status2 Treatment4      1.6 0.997 32   1.604
##  AD_Status1 Treatment4 - AD_Status2 Treatment4      0.0 0.997 32   0.000
##  p.value
##   0.3752
##   0.1906
##   0.1906
##   0.4944
##   0.4944
##   0.9999
##   0.9999
##   0.9999
##   0.9999
##   1.0000
##   1.0000
##   0.6217
##   0.6217
```

```
##   1.0000
##   0.9986
##   0.9986
##   0.3752
##   0.3752
##   0.9986
##   0.9986
##   0.3752
##   0.3752
##   1.0000
##   0.7445
##   0.7445
##   0.7445
##   0.7445
##   1.0000
##
## P value adjustment: tukey method for comparing a family of 8 estimates
```

Summary: Training Day

Assumption Checks:

Normality: Shapiro-Wilk test for residuals ($p = 0.2214$) → residuals are approximately normal.

Homogeneity of Variances: Levene's test ($F = 0.4346$, $p > 0.05$) → equal variance across AD × Treatment groups.

ANOVA Results:

The two-way ANOVA tested the effects of AD status, Treatment, and their interaction on Training Day errors.

Significant effects (if any) can be interpreted based on F-values and p-values from the ANOVA table.

Post-Hoc Analysis:

Tukey-adjusted pairwise comparisons revealed which specific AD × Treatment groups differed significantly in Training Day errors.

These comparisons clarify the direction of differences (e.g., which treatment reduced or increased errors in transgenic vs. wild-type mice).

Interpretation:

AD status and drug treatments influence performance during training.

The results highlight potential treatments that improve or impair training performance depending on genotype.

Analysis for Memory Day Errors

2-Way ANOVA

```
anova_memory <- aov(Memory ~ AD_Status * Treatment, data = data)
summary(anova_memory)
```

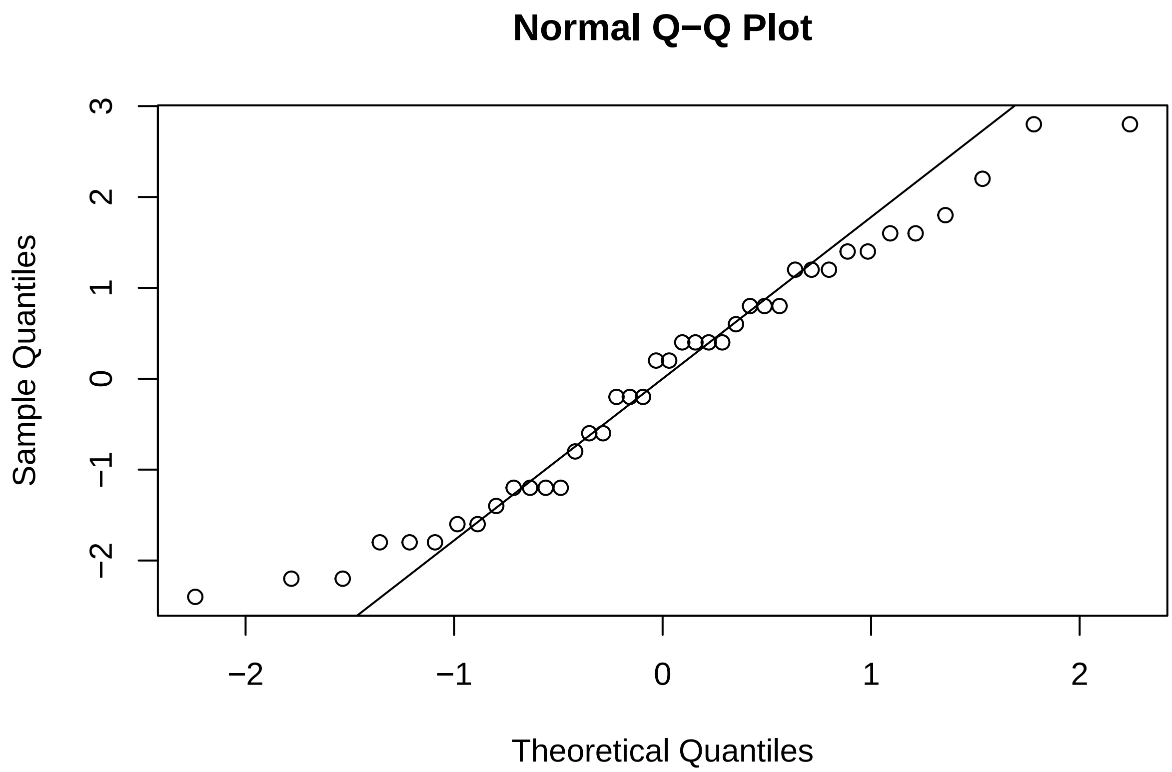
```
##                     Df Sum Sq Mean Sq F value   Pr(>F)    
## AD_Status            1 189.22  189.22  75.313 6.45e-10 ***
## Treatment            3  14.48    4.83   1.920    0.146    
## AD_Status:Treatment  3   8.67    2.89   1.151    0.344    
## Residuals           32  80.40    2.51                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Assumption Checks : Normality

```
# Normality check (Shapiro-Wilk test on residuals)
shapiro.test(residuals(anova_memory))
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  residuals(anova_memory)
## W = 0.96671, p-value = 0.2817
```

```
qqnorm(residuals(anova_training))
qqline(residuals(anova_training))
```



The Shapiro-Wilk test for Memory Day residuals returned a p-value of 0.2817.
Interpretation: Since the p-value is greater than 0.05, the residuals are approximately normal. The normality assumption is **met**.

Assumption Checks : Homogeneity of Variances

```
# Homogeneity of variances (Levene's test)
leveneTest(Memory ~ interaction(AD_Status, Treatment), data = data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  7  0.8275 0.5722
##       32
```

Levene's test for Memory Day errors returned an F value of 0.8275 ($p > 0.05$).
Interpretation: Since the p-value is greater than 0.05, the variance across AD_Status × Treatment groups is equal. The homogeneity of variance assumption is **met**.

Post-Hoc Tests

```
# Tukey HSD for main effects and interactions
tukey_memory <- TukeyHSD(anova_memory)
tukey_memory
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Memory ~ AD_Status * Treatment, data = data)
##
## $AD_Status
##      diff      lwr      upr p adj
## 2-1 -4.35 -5.37101 -3.32899     0
##
## $Treatment
##     diff       lwr       upr     p adj
## 2-1  0.3 -1.620592 2.2205916 0.9740962
## 3-1  0.2 -1.720592 2.1205916 0.9920100
## 4-1 -1.2 -3.120592 0.7205916 0.3439678
## 3-2 -0.1 -2.020592 1.8205916 0.9989766
## 4-2 -1.5 -3.420592 0.4205916 0.1697415
## 4-3 -1.4 -3.320592 0.5205916 0.2185144
##
## $`AD_Status:Treatment`
##         diff        lwr        upr     p adj
## 2:1-1:1 -3.0 -6.2473866  0.2473866 0.0870956
## 1:2-1:1  1.6 -1.6473866  4.8473866 0.7490963
## 2:2-1:1 -4.0 -7.2473866 -0.7526134 0.0076672
## 1:3-1:1  0.8 -2.4473866  4.0473866 0.9920302
## 2:3-1:1 -3.4 -6.6473866 -0.1526134 0.0348894
## 1:4-1:1 -0.4 -3.6473866  2.8473866 0.9999068
## 2:4-1:1 -5.0 -8.2473866 -1.7526134 0.0004930
## 1:2-2:1  4.6  1.3526134  7.8473866 0.0015093
## 2:2-2:1 -1.0 -4.2473866  2.2473866 0.9714894
## 1:3-2:1  3.8  0.5526134  7.0473866 0.0129010
## 2:3-2:1 -0.4 -3.6473866  2.8473866 0.9999068
## 1:4-2:1  2.6 -0.6473866  5.8473866 0.1953308
## 2:4-2:1 -2.0 -5.2473866  1.2473866 0.5006039
## 2:2-1:2 -5.6 -8.8473866 -2.3526134 0.0000898
## 1:3-1:2 -0.8 -4.0473866  2.4473866 0.9920302
## 2:3-1:2 -5.0 -8.2473866 -1.7526134 0.0004930
## 1:4-1:2 -2.0 -5.2473866  1.2473866 0.5006039
## 2:4-1:2 -6.6 -9.8473866 -3.3526134 0.0000052
## 1:3-2:2  4.8  1.5526134  8.0473866 0.0008647
## 2:3-2:2  0.6 -2.6473866  3.8473866 0.9986578
## 1:4-2:2  3.6  0.3526134  6.8473866 0.0213971
## 2:4-2:2 -1.0 -4.2473866  2.2473866 0.9714894
## 2:3-1:3 -4.2 -7.4473866 -0.9526134 0.0045020
## 1:4-1:3 -1.2 -4.4473866  2.0473866 0.9269172
## 2:4-1:3 -5.8 -9.0473866 -2.5526134 0.0000508
## 1:4-2:3  3.0 -0.2473866  6.2473866 0.0870956
## 2:4-2:3 -1.6 -4.8473866  1.6473866 0.7490963
## 2:4-1:4 -4.6 -7.8473866 -1.3526134 0.0015093
```

```r
# Pairwise comparisons for interaction
emmeans(anova_memory, pairwise ~ AD_Status * Treatment, adjust = "tukey")
```

```
## $emmeans
##  AD_Status Treatment emmean    SE df lower.CL upper.CL
```

```
##  1         1           11.6 0.709 32    10.16    13.04
##  2         1            8.6 0.709 32     7.16    10.04
##  1         2           13.2 0.709 32    11.76    14.64
##  2         2            7.6 0.709 32     6.16     9.04
##  1         3           12.4 0.709 32    10.96    13.84
##  2         3            8.2 0.709 32     6.76     9.64
##  1         4           11.2 0.709 32     9.76    12.64
##  2         4            6.6 0.709 32     5.16     8.04
##
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                      estimate SE df t.ratio p.value
##  AD_Status1 Treatment1 - AD_Status2 Treatment1      3.0  1 32   2.993  0.0871
##  AD_Status1 Treatment1 - AD_Status1 Treatment2     -1.6  1 32  -1.596  0.7491
##  AD_Status1 Treatment1 - AD_Status2 Treatment2      4.0  1 32   3.990  0.0077
##  AD_Status1 Treatment1 - AD_Status1 Treatment3     -0.8  1 32  -0.798  0.9920
##  AD_Status1 Treatment1 - AD_Status2 Treatment3      3.4  1 32   3.392  0.0349
##  AD_Status1 Treatment1 - AD_Status1 Treatment4      0.4  1 32   0.399  0.9999
##  AD_Status1 Treatment1 - AD_Status2 Treatment4      5.0  1 32   4.988  0.0005
##  AD_Status2 Treatment1 - AD_Status1 Treatment2     -4.6  1 32  -4.589  0.0015
##  AD_Status2 Treatment1 - AD_Status2 Treatment2      1.0  1 32   0.998  0.9715
##  AD_Status2 Treatment1 - AD_Status1 Treatment3     -3.8  1 32  -3.791  0.0129
##  AD_Status2 Treatment1 - AD_Status2 Treatment3      0.4  1 32   0.399  0.9999
##  AD_Status2 Treatment1 - AD_Status1 Treatment4     -2.6  1 32  -2.594  0.1953
##  AD_Status2 Treatment1 - AD_Status2 Treatment4      2.0  1 32   1.995  0.5006
##  AD_Status1 Treatment2 - AD_Status2 Treatment2      5.6  1 32   5.586  0.0001
##  AD_Status1 Treatment2 - AD_Status1 Treatment3      0.8  1 32   0.798  0.9920
##  AD_Status1 Treatment2 - AD_Status2 Treatment3      5.0  1 32   4.988  0.0005
##  AD_Status1 Treatment2 - AD_Status1 Treatment4      2.0  1 32   1.995  0.5006
##  AD_Status1 Treatment2 - AD_Status2 Treatment4      6.6  1 32   6.584  <.0001
##  AD_Status2 Treatment2 - AD_Status1 Treatment3     -4.8  1 32  -4.788  0.0009
##  AD_Status2 Treatment2 - AD_Status2 Treatment3     -0.6  1 32  -0.599  0.9987
##  AD_Status2 Treatment2 - AD_Status1 Treatment4     -3.6  1 32  -3.591  0.0214
##  AD_Status2 Treatment2 - AD_Status2 Treatment4      1.0  1 32   0.998  0.9715
##  AD_Status1 Treatment3 - AD_Status2 Treatment3      4.2  1 32   4.190  0.0045
##  AD_Status1 Treatment3 - AD_Status1 Treatment4      1.2  1 32   1.197  0.9269
##  AD_Status1 Treatment3 - AD_Status2 Treatment4      5.8  1 32   5.786  0.0001
##  AD_Status2 Treatment3 - AD_Status1 Treatment4     -3.0  1 32  -2.993  0.0871
##  AD_Status2 Treatment3 - AD_Status2 Treatment4      1.6  1 32   1.596  0.7491
##  AD_Status1 Treatment4 - AD_Status2 Treatment4      4.6  1 32   4.589  0.0015
##
## P value adjustment: tukey method for comparing a family of 8 estimates
```

Summary: Memory Day Errors

Assumption Checks

Normality: Shapiro-Wilk test for residuals ($p = 0.2817$) → residuals are approximately normal.

Homogeneity of Variances: Levene's test ($F = 0.8275$, $p > 0.05$) → equal variance across AD × Treatment groups.

ANOVA Results

The two-way ANOVA examined the effects of AD status, Treatment, and their interaction on Memory Day errors.

Significant main or interaction effects indicate whether memory performance is affected by AD status, treatment, or both.

Post-Hoc Analysis

Tukey-adjusted pairwise comparisons identify specific group differences in memory errors.

This reveals which treatments improve or impair memory performance in transgenic vs. wild-type mice.

Interpretation

Both genotype and treatment influence memory performance in mice.

Some drug treatments may alleviate memory deficits in transgenic mice, highlighting their potential therapeutic relevance.