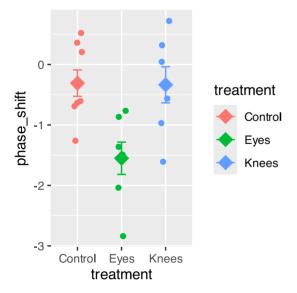
#### Lecture 11 - ANOVA in class

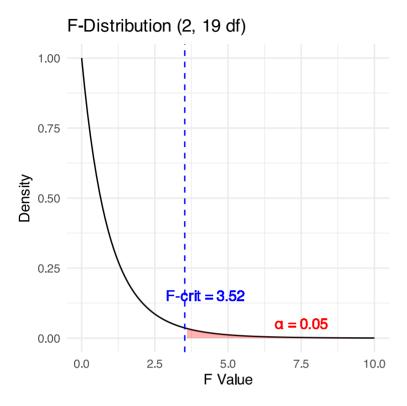
#### Bill Perry

```
# A tibble: 22 \times 2
   treatment phase shift
   <chr>
                   <dbl>
1 Control
                   0.53
2 Control
                    0.36
 3 Control
                    0.2
 4 Control
                   -0.37
 5 Control
                   -0.6
                   -0.64
 6 Control
7 Control
                   -0.68
                   -1.27
8 Control
9 Knees
                   0.73
                    0.31
10 Knees
# i 12 more rows
```

```
# Plot the data
c_plot <- ggplot(c_df, aes(x = treatment, y = phase_shift, color = treatment)) +
    geom_point(position = position_jitter(width=0.1)) +
    stat_summary(fun = mean, geom = "point", size = 5, shape = 18) +
    stat_summary(fun.data = "mean_se", geom = "errorbar", width = 0.2)
c_plot</pre>
```



```
Residuals 9.4153 19
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```



## **ANOVA-Assumptions and Diagnostics**

ANOVA has the same assumptions as the two-sample t-test, but applied to all k groups:

- 1. Random samples from corresponding populations
- 2. **Normality**: Y values are normally distributed in each population
- 3. Homogeneity of variance: variance is the same in all populations
- 4. Independence: observations are independent

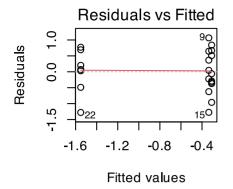
#### Checking assumptions:

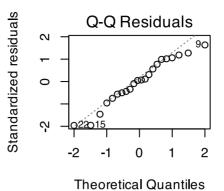
- Normality: Q-Q plots, histogram of residuals, Shapiro-Wilk test
- Homogeneity: plot residuals vs. predicted values or x-values
- Independence: examine experimental design

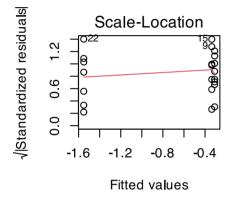
## Lecture 12: ANOVA diagnostics

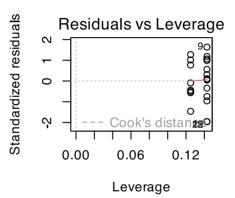
This is the default output of base R

```
# Create diagnostic plots
par(mfrow = c(2, 2))
plot(model_aov)
```









```
par(mfrow = c(1, 1))
```

## **ANOVA Diagnostics**

Levene's test of homogeneity of variance

- Null Hypothesis is that they are homogeneous
- So you want a non significant result here

```
Levene's Test for Homogeneity of Variance (center = median)

Df F value Pr(>F)

group 2 0.1586 0.8545

19
```

## **Lecture 12: ANOVA Diagnostics**

Shapiro-Wilk Normality Test

- Null Hypothesis is that they are normally distributed
- So you want a **non significant** result here

```
Shapiro-Wilk normality test

data: residuals(model_aov)
W = 0.95893, p-value = 0.468
```

## **Lecture 12: ANOVA Post-Hoc Testing**

When ANOVA rejects H<sub>0</sub>, we need to determine which groups differ.

**Example**: Using Tukey's HSD to compare all pairs of treatments in the circadian rhythm data.

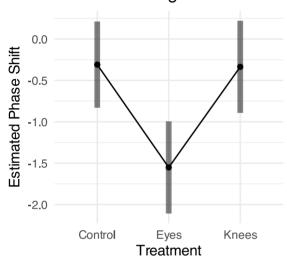
```
contrast
                estimate
                            SE df t.ratio p.value
Control - Eyes 1.243 0.364 19 3.411 0.0088
Control - Knees 0.027 0.364 19 0.074 0.9998
Eyes - Knees -1.216 0.376 19 -3.231 0.0131
P value adjustment: sidak method for 3 tests
emmeans df <- emmeans(model aov, "treatment")</pre>
emmeans df
treatment emmean SE df lower.CL upper.CL
Control -0.309 0.249 19 -0.830 0.212
Eyes -1.551 0.266 19 -2.108 -0.995
Knees -0.336 0.266 19 -0.893 0.221
Confidence level used: 0.95
pairwise comparisons <- pairs(emmeans df, adjust = "sidak")</pre>
pairwise_comparisons
 contrast estimate
                           SE df t.ratio p.value
Control - Eyes 1.243 0.364 19 3.411 0.0088
Control - Knees 0.027 0.364 19 0.074 0.9998
Eyes - Knees -1.216 0.376 19 -3.231 0.0131
P value adjustment: sidak method for 3 tests
# Letters to indicate groups with similar means
letter_groups <- multcomp::cld(emmeans_df, Letters = letters, adjust = "sidak")</pre>
letter groups
treatment emmean
                    SE df lower.CL upper.CL .group
Eyes -1.551 0.266 19 -2.25 -0.855 a
        -0.336 0.266 19 -1.03 0.361
Knees
                                             b
Control -0.309 0.249 19 -0.96 0.343
                                             b
Confidence level used: 0.95
Conf-level adjustment: sidak method for 3 estimates
P value adjustment: sidak method for 3 tests
significance level used: alpha = 0.05
NOTE: If two or more means share the same grouping symbol,
     then we cannot show them to be different.
     But we also did not show them to be the same.
```

#### Can do in one go as well

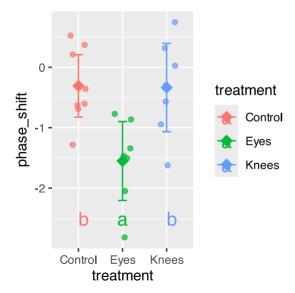
```
treatment emmean
                     SE df lower.CL upper.CL .group
 Eves
           -1.551 0.266 19
                              -2.25
                                       -0.855 a
 Knees
                              -1.03
           -0.336 0.266 19
                                       0.361
                                                b
 Control
           -0.309 0.249 19
                              -0.96
                                        0.343
                                                b
Confidence level used: 0.95
Conf-level adjustment: sidak method for 3 estimates
P value adjustment: sidak method for 3 tests
significance level used: alpha = 0.05
NOTE: If two or more means share the same grouping symbol,
      then we cannot show them to be different.
      But we also did not show them to be the same.
```

## **Lecture 12: ANOVA Post-Hoc Testing**

#### Estimated Marginal Means with



# **Lecture 12: ANOVA Post-Hoc Testing**



# Lecture 12: ANOVA Reporting results

Formal scientific writing example:

"The effect of light treatment on circadian rhythm phase shift was analyzed using a one-way ANOVA. There was a significant effect of treatment on phase shift (F(2, 19) = 7.29, p = 0.004,  $\eta^2$  = 0.43). Post-hoc comparisons using Tukey's HSD test indicated that the mean phase shift for the Eyes treatment (M = -1.55 h, SD = 0.71) was significantly different from both the Control treatment (M = -0.31 h, SD = 0.62) and the Knees treatment (M = -0.34 h, SD = 0.79). However, the Control and Knees treatments did not significantly differ from each other. These results suggest that light exposure to the eyes, but not to the knees, impacts circadian rhythm phase shifts."