

M10 Group Work: One Way ANOVA for TAs

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#1. Import libraries and load packages

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.3.2
```

```
## Warning: package 'ggplot2' was built under R version 4.3.2
```

```
## Warning: package 'tibble' was built under R version 4.3.1
```

```
## Warning: package 'tidyr' was built under R version 4.3.2
```

```
## Warning: package 'readr' was built under R version 4.3.2
```

```
## Warning: package 'purrr' was built under R version 4.3.1
```

```
## Warning: package 'dplyr' was built under R version 4.3.2
```

```
## Warning: package 'stringr' was built under R version 4.3.2
```

```
## Warning: package 'forcats' was built under R version 4.3.2
```

```
## Warning: package 'lubridate' was built under R version 4.3.2
```

```
library(rstatix)
```

```
## Warning: package 'rstatix' was built under R version 4.3.1
```

```
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.3.1
```

```
library(dplyr)
```

```
library(PMCMRplus)
```

```
## Warning: package 'PMCMRplus' was built under R version 4.3.3
```

#2. Importing our data

```
UV_deformities <- read.csv(file = "UV_deformities.csv", header = TRUE)
```

```
#3.Normality
```

```
shapiro.test(UV_deformities$deformities)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: UV_deformities$deformities  
## W = 0.91519, p-value = 0.0001314
```

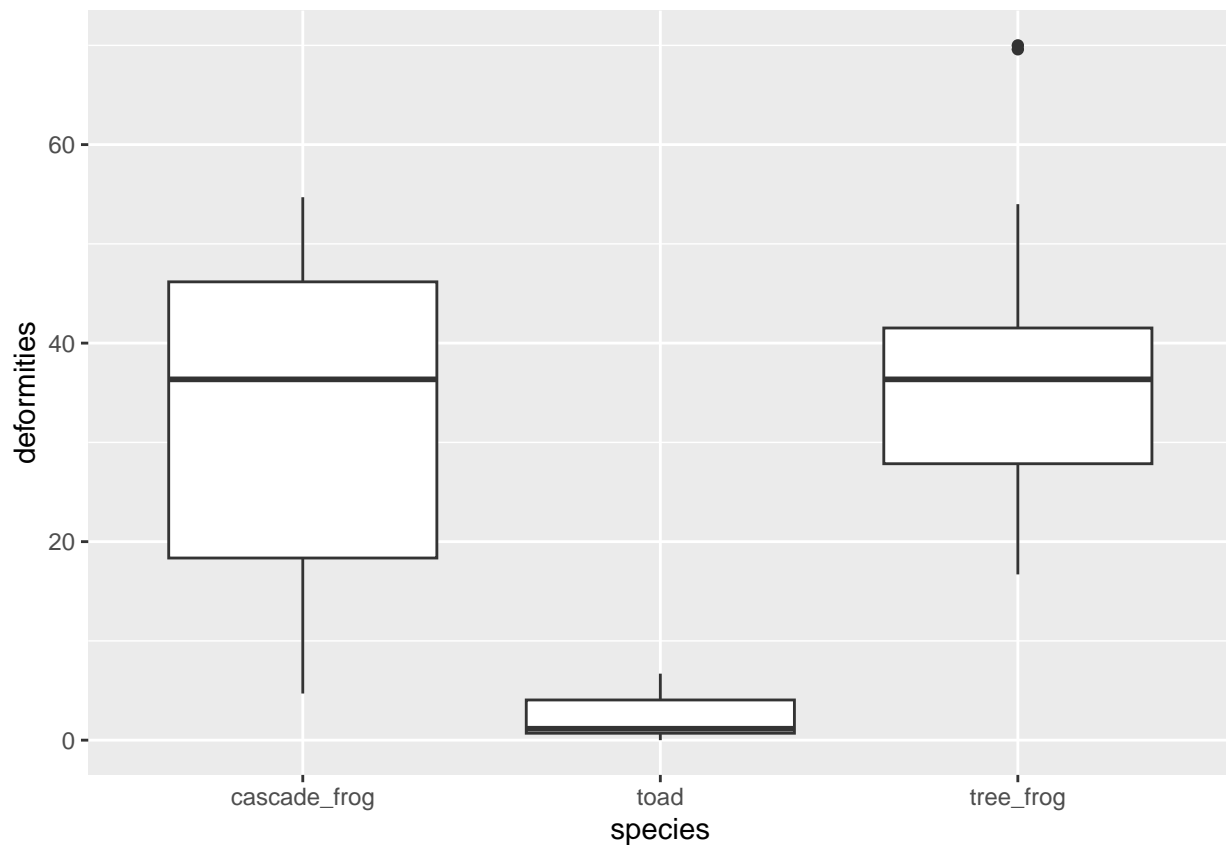
```
#4. #variance
```

```
bartlett.test(deformities ~ species, data = UV_deformities)
```

```
##  
## Bartlett test of homogeneity of variances  
##  
## data: deformities by species  
## Bartlett's K-squared = 60.239, df = 2, p-value = 8.304e-14
```

```
#5. boxplot
```

```
ggplot(UV_deformities) + aes(x = species, y = deformities) +  
  geom_boxplot()
```



#4. Run a kruskal.test # NOT Normal AND NON-Equal Variances

```
kruskal.test(deformities ~ species, data = UV_deformities)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: deformities by species  
## Kruskal-Wallis chi-squared = 46.915, df = 2, p-value = 6.495e-11
```

#All Pairs

```
wilcox_test(deformities ~ species, data = UV_deformities, p.adjust.method = "bonferroni")
```

```
## # A tibble: 3 x 9  
##   .y.      group1 group2  n1  n2 statistic      p  p.adj p.adj.signif  
## * <chr>      <chr>  <chr> <int> <int>      <dbl>  <dbl>  <dbl> <chr>  
## 1 deformities cascade~ toad    24   24    572. 4.54e-9 1.36e-8 ****  
## 2 deformities cascade~ tree_~  24   24    266. 6.65e-1 1.0e+0 ns  
## 3 deformities toad     tree_~  24   24      0 2.95e-9 8.85e-9 ****
```

#Effect Size

```
kruskal_effsize(deformities ~ species, data = UV_deformities)
```

```
## # A tibble: 1 x 5  
##   .y.      n effsize method magnitude  
## * <chr>    <int>  <dbl> <chr>    <ord>  
## 1 deformities    72  0.651 eta2[H] large
```

#5. Another way to find R^2

```
mod <- aov(deformities ~ species, data = UV_deformities)  
summary(mod)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)  
## species      2  18047    9023   65.82 <2e-16 ***  
## Residuals    69   9460     137  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
18047 / (18047+9460)
```

```
## [1] 0.6560875
```

```
summary(lm(deformities ~ species, data = UV_deformities))
```

```
##  
## Call:  
## lm(formula = deformities ~ species, data = UV_deformities)  
##  
## Residuals:
```

```

##      Min      1Q  Median      3Q      Max
## -29.133 -3.704 -0.671   3.559  32.621
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      33.833      2.390  14.156 < 2e-16 ***
## speciestoad     -31.671      3.380  -9.370 6.36e-14 ***
## speciestree_frog   3.546      3.380   1.049   0.298
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.71 on 69 degrees of freedom
## Multiple R-squared:  0.6561, Adjusted R-squared:  0.6461
## F-statistic: 65.82 on 2 and 69 DF,  p-value: < 2.2e-16

```