M10 Group Work: One Way ANOVA for TAs

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2024-04-03 19:56:33

#1. Import libraries and load packages

```
library(tidyverse)
library(rstatix)
library(readxl)
library(dplyr)
library(PMCMRplus)
```

#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
```
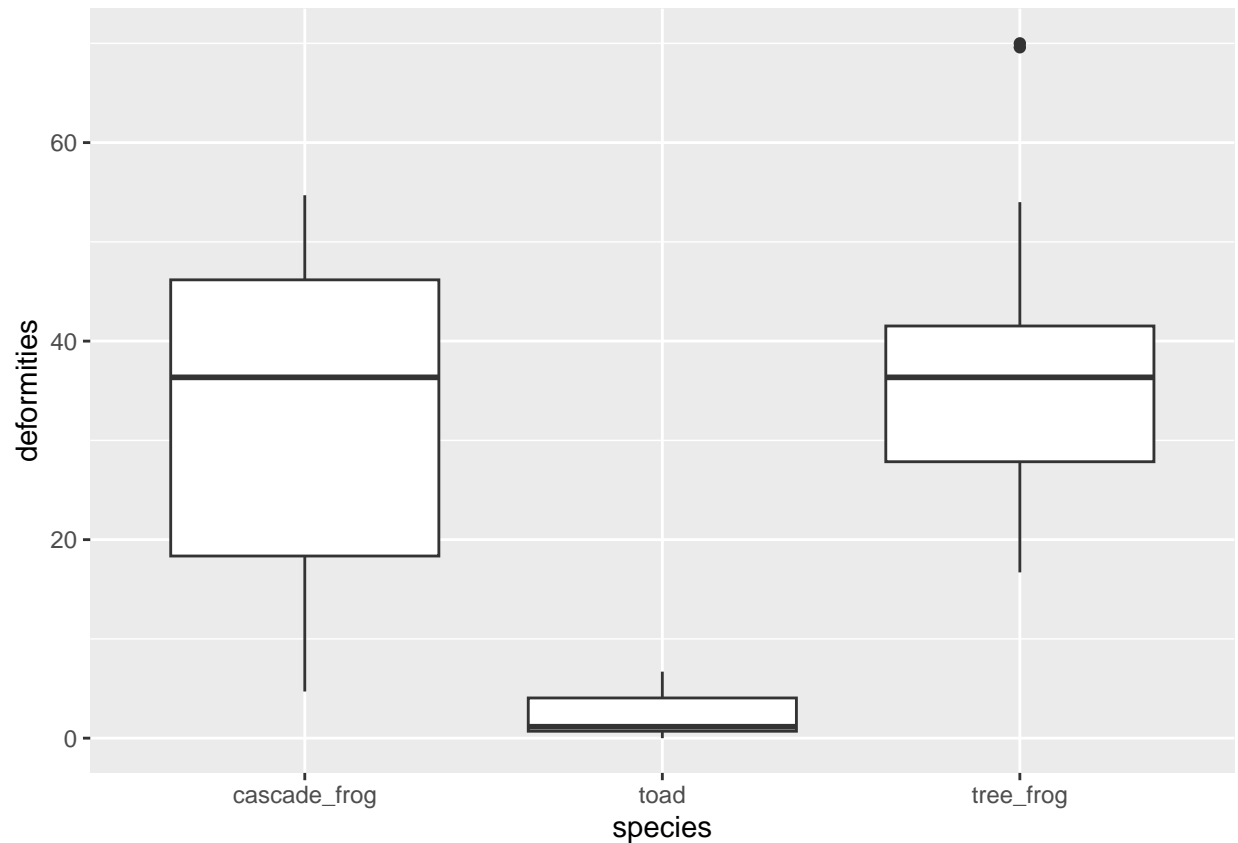
#4. #variance

```
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   e+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
```

2

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