

# M10 Group Work: One Way ANOVA for TAs

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#1. Import libraries and load packages

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

#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. Run a ANOVA

```
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
```

```
one.way <- aov(deformities ~ species, data = UV_deformities)
summary(one.way)
```

```
##              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
```

#5. R2

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

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