## Checking ANOVA Assumptions in R

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#### Loading required packages

```
library(readxl)
library(tidyverse)
library(ExpDes)
library(agricolae)
library(afex)
library(performance)
library(performance)
```

#### Importing data

### Generating the ANOVA

```
## Analysis of Variance Table

## Response: yield

## Df Sum Sq Mean Sq F value Pr(>F)

## FERT 5 1.3555 0.271107 19.567 1.04e-06 ***

## Residuals 18 0.2494 0.013856

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

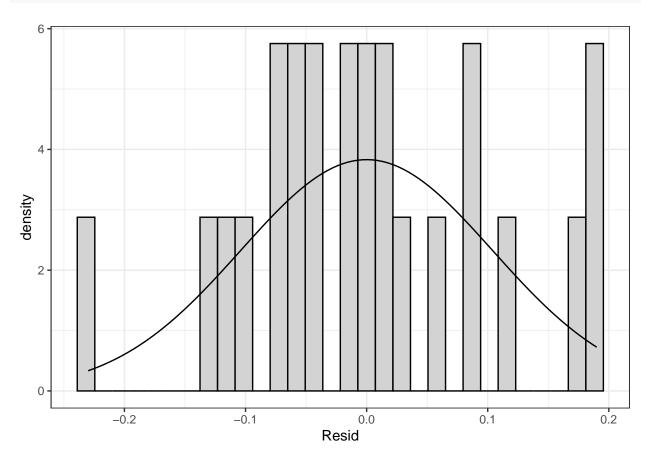
We generate the residuals and add tot he data frame.

```
crop_yield <- crop_yield |>
  mutate(Resid = crop_aov$residuals)
```

#### Checking normality

First, we generate the relative frequency histogram of the residuals to visualize the distribution of the residuals. We add on top of this plot the theoretical normal density curve to determine if the emperical density looks similar to the theoretical density.

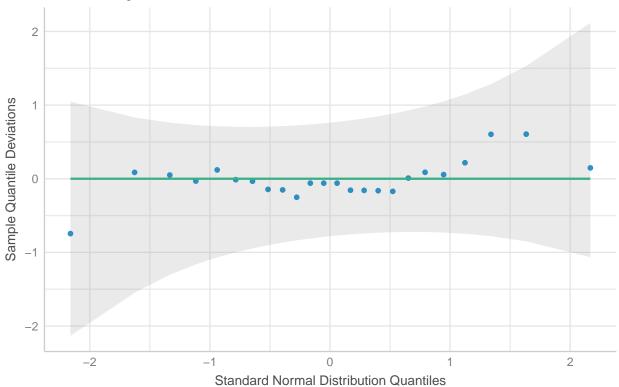
```
ggplot(crop_yield, aes(Resid)) +
  geom_histogram(aes(y = ..density..), fill='lightgray', col='black') +
  stat_function(fun = dnorm, args = list(mean=mean(crop_yield$Resid), sd=sd(crop_yield$Resid))) +theme_'
```



An alternative function for generating a QQ plot is given below.

#### plot(check\_normality(crop\_aov))

# Normality of Residuals Dots should fall along the line



We use the Shapiro-Wilk test to formally test if the residuals are normally distributed or not.

```
with(crop_yield,shapiro.test(Resid))
```

```
##
## Shapiro-Wilk normality test
##
## data: Resid
## W = 0.96856, p-value = 0.6316
```

Alternatively, we can use the *check\_normality()* function in the **performance** package

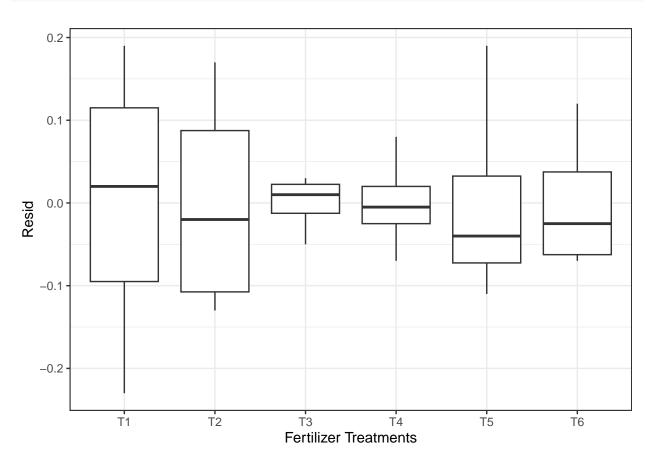
```
check_normality(crop_aov)
```

```
## OK: residuals appear as normally distributed (p = 0.632).
```

#### Checking homogeneity of variance assumption

```
ggplot(crop_yield, aes(x = trt, y = Resid)) +
  geom_boxplot() +
```

```
labs(x = "Fertilizer Treatments") +
theme_bw()
```



```
##
## Bartlett test of homogeneity of variances
##
## data: Resid by FERT
## Bartlett's K-squared = 7.4869, df = 5, p-value = 0.1869
```

```
## Levene's Test for Homogeneity of Variance (center = mean)
## Df F value Pr(>F)
## group 5 2.5367 0.06613 .
## 18
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
##
## Fligner-Killeen test of homogeneity of variances
##
## data: Resid by FERT
## Fligner-Killeen:med chi-squared = 9.6845, df = 5, p-value = 0.08468
```

- If the assumption of homogeneous variances is violated, once can apply data transformation on the response, run ANOVA, and test again the new residuals
- Alternatively, one can run the *oneway.test()* function in the **stats** package. This is only applicable for one way classification data such as that from CRD experiments. We call this as **Welch's ANOVA**.

#### Testing for the assumption of independence

## F = 10.394, num df = 5.0000, denom df = 7.9358, p-value = 0.002484

## data: yield and FERT

```
crop_yield$resid_lag1 <- lag(crop_yield$Resid)
head(crop_yield)</pre>
```

```
## # A tibble: 6 x 6
##
    trt fertilizer yield FERT
                                  Resid resid_lag1
             <dbl> <dbl> <fct>
                                             <dbl>
##
    <chr>
                                  <dbl>
## 1 T1
                   0 4.89 0
                                 0.190
                                           NA
## 2 T1
                   0 4.79 0
                                 0.0900
                                            0.190
## 3 T1
                   0 4.65 0
                                -0.0500
                                            0.0900
## 4 T1
                   0 4.47 0
                                -0.23
                                           -0.0500
## 5 T2
                  50 5.08 50
                                 0.0600
                                           -0.23
## 6 T2
                  50 5.19 50
                                 0.170
                                            0.0600
```

```
cor.test(crop_yield$Resid, crop_yield$resid_lag1)
```

```
##
## Pearson's product-moment correlation
##
## data: crop_yield$Resid and crop_yield$resid_lag1
## t = -0.51752, df = 21, p-value = 0.6102
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
## -0.501236 0.314532
## sample estimates:
##
         cor
## -0.1122195
car::durbinWatsonTest(crop_aov)
## lag Autocorrelation D-W Statistic p-value
##
   1
            -0.1046512
                             2.044908 0.302
## Alternative hypothesis: rho != 0
  • Therefore the assumption is valid!
Generate the table of means
crop_yield.ur <- read_excel("chap4demouequalreps.xlsx")</pre>
```

```
head(crop_yield.ur)
## # A tibble: 6 x 3
## trt fertilizer yield
## <chr> <dbl> <dbl>
               0 4.89
## 1 T1
## 2 T1
                0 4.79
                 0 4.65
## 3 T1
## 4 T2
                50 5.08
## 5 T2
                50 5.19
## 6 T2
               50 4.89
crop_yield.ur |>
 dplyr::group_by(trt) |>
 dplyr::summarize(MEAN = round(mean(yield),2),
                 SD = round(sd(yield),4),
                 n = length(yield))
## # A tibble: 6 x 4
## trt MEAN
    <chr> <dbl> <dbl> <int>
##
## 1 T1 4.78 0.121
## 2 T2
         5.02 0.141
## 3 T3 5.22 0.0361
       5.38 0.0616
5.36 0.132
## 4 T4
                         4
## 5 T5
                         4
```

```
crop.aov1 <- with(crop_yield.ur, aov(yield ~ trt))
anova(crop.aov1)</pre>
```

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## 6 T6 5.28 0.107