

TwoWay-ANOVA-in-R

```
library(readr)
library(ggplot2)
library(multcompView)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

df <- read_csv("D:/Personal research/suv/suv_anova_tukey/blast_14day.csv", show_col_types = FALSE)

head(df)

## # A tibble: 6 x 4
##   fungi_isolate medium growth days
##   <chr>          <chr>   <dbl> <dbl>
## 1 JFN1          WA       8     14
## 2 KN2           WA      10.8    14
## 3 KN3           WA       9.8     14
## 4 MU4           WA      10.1     14
## 5 VA5           WA       8.5     14
## 6 MA6           WA       8.5     14

# Check the structure
str(df)

## spec_tbl_df [24 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ fungi_isolate: chr [1:24] "JFN1" "KN2" "KN3" "MU4" ...
##  $ medium       : chr [1:24] "WA" "WA" "WA" "WA" ...
##  $ growth       : num [1:24] 8 10.8 9.8 10.1 8.5 8.5 7.6 10.1 9.2 9.5 ...
##  $ days         : num [1:24] 14 14 14 14 14 14 14 14 14 14 ...
##  - attr(*, "spec")=
##    .. cols(
##    ..   fungi_isolate = col_character(),
##    ..   medium = col_character(),
##    ..   growth = col_double(),
##    ..   days = col_double()
##    .. )
##  - attr(*, "problems")=<externalptr>
```

```
#creating a variable as factor for the ANOVA
df$fungi_isolate <- as.factor(df$fungi_isolate)
df$medium <- as.factor(df$medium)
str(df)
```

```
## spec_tbl_df [24 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ fungi_isolate: Factor w/ 6 levels "JFN1","KN2","KN3",...: 1 2 3 5 6 4 1 2 3 5 ...
## $ medium       : Factor w/ 4 levels "OMA","PDA","RPA",...: 4 4 4 4 4 4 2 2 2 2 ...
## $ growth       : num [1:24] 8 10.8 9.8 10.1 8.5 8.5 7.6 10.1 9.2 9.5 ...
## $ days         : num [1:24] 14 14 14 14 14 14 14 14 14 14 ...
## - attr(*, "spec")=
## .. cols(
## ..   fungi_isolate = col_character(),
## ..   medium = col_character(),
## ..   growth = col_double(),
## ..   days = col_double()
## .. )
## - attr(*, "problems")=<externalptr>
```

Analysis of variance

Null hypothesis (H₀) : There is no effects in fungal isolation medium in fungal growth or There is no effects difference in fungal isolates in fungal growth

Alternate Hypothesis (H_a): There is effects in fungal isolation medium in fungal growth or There is effects in fungal isolates in fungal growth

```
anova1 <- aov(growth~fungi_isolate+medium,data=df)
summary(anova1)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fungi_isolate  5 23.337   4.667   298.45 1.85e-14 ***
## medium         3  2.308   0.769    49.19 5.37e-08 ***
## Residuals     15  0.235   0.016
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interpret the results: ANOVA table shows that both factors are statistically significant at 0.05 significance level.

the p-value of fungi_isolate is 85e-14 (significant), which indicates that the fungi_isolate are associated with growth rate. the p-value of medium is 37e-08 (significant), which indicates that the growth medium is associated with with growth rate

ANOVA test, a significant p-value indicates that some of the group means are different, but we don't know which pairs of groups are different.

Tukey Honest Significant Differences Test (Tukey's test) can be used to determine if the mean difference between specific pairs of group are statistically significant.

```
#Comparing means by Tukey's test
TukeyHSD(anova1)
```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = growth ~ fungi_isolate + medium, data = df)
##
## $fungi_isolate
##      diff      lwr      upr      p adj
## KN2-JFN1  2.725  2.4377015  3.0122985 0.0000000
## KN3-JFN1  1.675  1.3877015  1.9622985 0.0000000
## MA6-JFN1  0.575  0.2877015  0.8622985 0.0001209
## MU4-JFN1  2.200  1.9127015  2.4872985 0.0000000
## VA5-JFN1  0.500  0.2127015  0.7872985 0.0005378
## KN3-KN2  -1.050 -1.3372985 -0.7627015 0.0000001
## MA6-KN2  -2.150 -2.4372985 -1.8627015 0.0000000
## MU4-KN2  -0.525 -0.8122985 -0.2377015 0.0003239
## VA5-KN2  -2.225 -2.5122985 -1.9377015 0.0000000
## MA6-KN3  -1.100 -1.3872985 -0.8127015 0.0000000
## MU4-KN3   0.525  0.2377015  0.8122985 0.0003239
## VA5-KN3  -1.175 -1.4622985 -0.8877015 0.0000000
## MU4-MA6   1.625  1.3377015  1.9122985 0.0000000
## VA5-MA6  -0.075 -0.3622985  0.2122985 0.9531471
## VA5-MU4  -1.700 -1.9872985 -1.4127015 0.0000000
##
## $medium
##      diff      lwr      upr      p adj
## PDA-OMA -0.6500000 -0.85809359 -0.44190641 0.0000011
## RPA-OMA  0.1833333 -0.02476025  0.39142692 0.0937780
## WA-OMA  -0.1166667 -0.32476025  0.09142692 0.3996845
## RPA-PDA  0.8333333  0.62523975  1.04142692 0.0000000
## WA-PDA   0.5333333  0.32523975  0.74142692 0.0000122
## WA-RPA  -0.3000000 -0.50809359 -0.09190641 0.0041935

```