

# R Notebook

```
library(readxl)
```

```
library(dplyr)
```

Load the required library #####

```
##
```

```
## 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
```

```
library(tibble)
```

```
library(flextable)
```

## Importing data —

```
data<-read_excel('data_anova.xlsx',col_names = TRUE)
```

```
## Warning in strptime(x, format, tz = tz): unable to identify current timezone 'U':
```

```
## please set environment variable 'TZ'
```

## Convert categorical variables to factor variables

```
data$Rep = as.factor(data$Rep)
```

```
data$Water = as.factor(data$Water)
```

```
data$Priming = as.factor(data$Priming)
```

```
attach(data)
```

## Analysis of variance in a for loop —

```
for(i in 1:ncol(data[-c(1:3)])) {  
  cols <- names(data)[4:ncol(data)]  
  aov.model <- lapply(X = cols, FUN = function(x)  
    aov(reformulate(termlabels = "Rep + Water*Priming",
```

```

        response = x),
    data = data))

# print df, MS and Pvalue
final = anova(aov.model[[i]])[,c(1,3,5)]

# Getting rownames
rnames = rownames(final)

# Setting column names
colnames(final) = c("DF", "MS", "P-value")
colnames(final)[2] = cols[i]

# Rounding values to 3 decimal place
final = as.data.frame(round(final, digits = 2))

# Assign astericks according to p values
final$sign[final$`P-value` < 0.05] <- "*"
final$sign[final$`P-value` < 0.01] <- "***"
final$sign[final$`P-value` > 0.05] <- "ns"

# Merge MS and significance column together
final[[2]] = paste(final[[2]],
                    ifelse(is.na(final[[4]]), "", final[[4]]))
final = final[-c(3,4)]
anova = writexl::write_xlsx(final,
                             path = paste(cols[i], '-ANOVA.xlsx'))

# Print final ANOVA table ----
file.list <- list.files(pattern='*-ANOVA.xlsx')

df.list <- lapply(X = file.list, FUN = read_excel)

# Combined ANOVA table for all variables
aov.table = rlist::list.cbind(df.list)

# Remove duplicate columns for DF
dup.cols = which(duplicated(names(aov.table)))
aov.table = aov.table[,-dup.cols]

# Names for sources of variation in ANOVA
rownames(aov.table) = rnames
}

```

```

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## Printing ANOVA table

```
table = flextable(data = aov.table %>%
rownames_to_column("SOV"))

bold(table, bold = TRUE, part = "header")
```

```
## Warning: Warning: fonts used in `flextable` are ignored because the `pdflatex`
## engine is used and not `xelatex` or `lualatex`. You can avoid this warning
## by using the `set_flextable_defaults(fonts_ignore=TRUE)` command or use a
## compatible engine by defining `latex_engine: xelatex` in the YAML header of the
## R Markdown document.
```

SOV	DF	Biological yield	Grain per spike	grain weight	Grain yield	Plant height	Spike length	Spikelets
Rep	2	1.93 ns	24.41 ns	79.42 **	0.27 **	0.45 ns	8.71 *	7947.47 **
Water	2	0.2 ns	21.12 ns	3.37 ns	0.2 *	29.93 ns	1.1 ns	266.55 ns
Priming	2	46.74 **	1374.04 **	836.57 **	8.58 **	0.5 ns	40.3 **	14166.35 **
Water:Priming	4	0.18 ns	30.41 ns	7 ns	0.02 ns	15.85 ns	1.44 ns	229.53 ns
Residuals	16	0.7	42.05	5.23	0.03	15.5	1.27	709.58