



# **Factorial experiment analysis using R Studio**

# 1.7 Factorial ANOVA using R

$LSP = P1 ?$   
*agricolae.*

$LSP = P2$

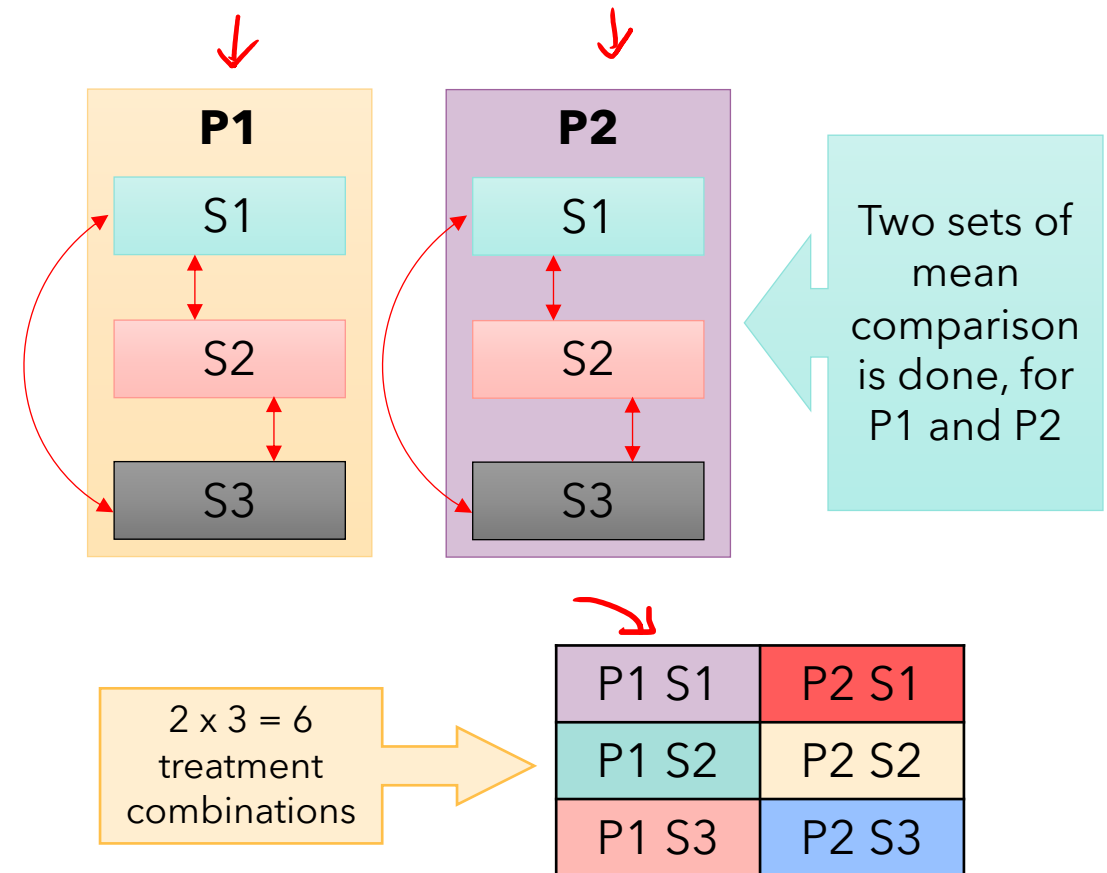
## Significant interaction mean comparison

When the interaction is significant, the mean comparison can be done using either:

- Between levels of one factors separately at each level of another factors.**

For example, the effect of spacing is compared separately in each phosphate. ✓  
Thus, for each phosphate level (P1 and P2), ANOVA and mean comparison are performed to compare between spacing. ✓

- Between treatment combinations.** Create treatment combination of the two factors and run mean comparison as one factor.



# 1.7 Factorial ANOVA using R



## Factorial analysis using AgroR package

# read the data:

```
setwd("D:/GDrive/1.TEACHING/A-2019-20 - SEM 1/R")
```

```
fact_rcbd<-read.csv("fac_rcbd.csv", sep="," , header = T)
```

#ANOVA factorial

```
with(fact_rcbd, FAT2DBC(space, phos, block, yield, quali=c(TRUE, TRUE),  
mcomp="duncan", addmean=F, point="mean_se", ylab="Yield", xlab="Spacing  
(cm)" ))
```

# 1.7 Factorial ANOVA using R



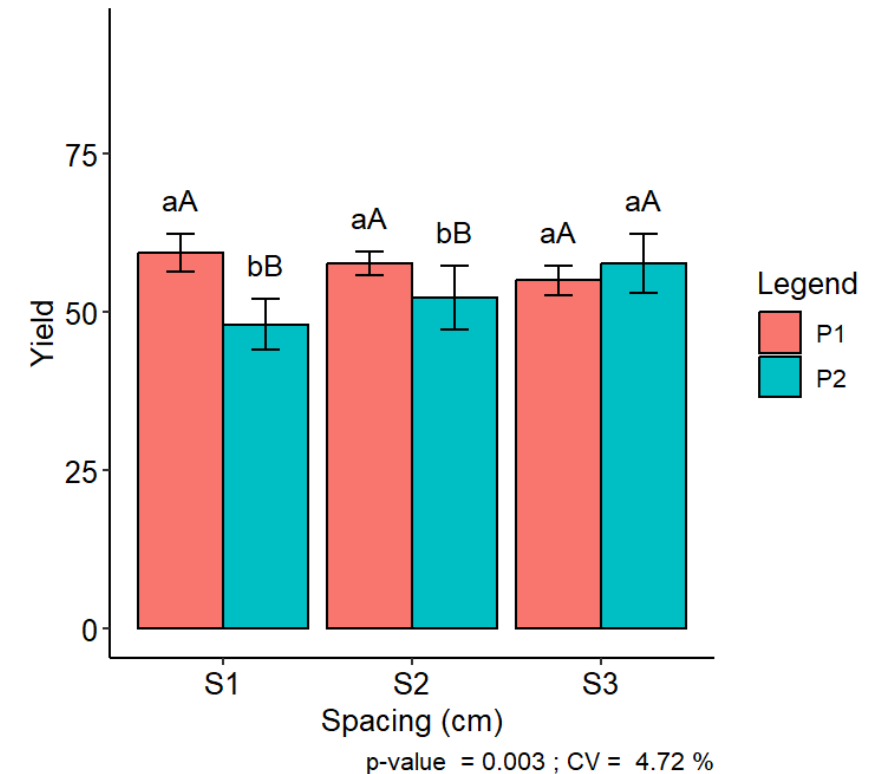
## Factorial analysis using AgroR package

Default factorial RCBD analysis in AgroR will do mean comparison separately for both factors. However, the letter grouping is displayed on the same graph with upper and lower case for each factor mean comparison.

### Final table

	P1	P2
S1	59.3 aA	48.0 bB
S2	57.7 aA	52.3 bB
S3	55.0 aA	57.7 aA

Averages followed by the same lowercase letter in the column and uppercase in the row do not differ by the duncan ( $p < 0.05$ )



# 1.7 Factorial ANOVA using R



Package: agricolae

## Factorial analysis using agricolae package

# read the data:

```
setwd("D:/GDrive/1.TEACHING/A-2019-20 - SEM 1/R")
```

```
fact_rcbd<-read.csv("fac_rcbd.csv", sep="," , header = T)
```

#fit ANOVA (factorial)

```
✓ fit <- lm (y ~ rep + space + phos + space:phos, data = fact_rcbd)
  anova(fit)
```

Red arrows point from the text '#fit ANOVA (factorial)' to the variables 'rep', 'space', 'phos', and 'space:phos' in the R code. A red arrow also points from the text 'anova(fit)' to the 'fit' argument in the 'anova' function.

# 1.7 Factorial ANOVA using R



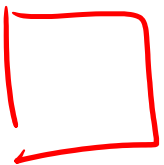
Package: agricolae

## Method 1: Mean comparison between 'space' for each 'phos'

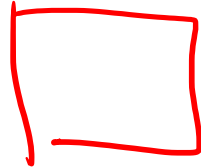
**#Step 1:** create datasets for each phos (phos1, phos2)

✓ `phos1 <- subset(fact_rcbd, phos == "P1")`  
✓ `phos2 <- subset(fact_rcbd, phos == "P2")`

phos 1



phos 2



**#Step 2:** Run ANOVA and mean comparison for each "phos"

```
library (agricolae)
```

```
fitp1 <- lm(y~rep + space, data=phos1)
```

```
anova(fitp1) ✓
```

```
→ (LSD.test(fitp1, "space"))  
↳ code to do LSD in agricolae.
```

```
fitp2 <- lm(y~rep + space, data=phos2)
```

```
anova(fitp2)
```

```
(LSD.test(fitp2, "space"))
```

# 1.7 Factorial ANOVA using R

## Method 2: Mean comparison of treatment combination

Comparison between treatment combinations can be done by (i) creating new column in original dataset file or (ii) by using codes in R.

### i. Test between treatment combination created in Excel file:

```
fit1<- lm (yield ~ block + trt_comb, factorial_data)
anova(fit1)
(lsd_trt<-LSD.test(fit1, "trt_comb"))
```

### ii. Test treatment combination using R codes:

```
library (agricolae)
lsd_trt <- LSD.test(fit, c("phos", "space"), main=" lsd phos x space", console=TRUE)
```