

Graphics of the Multiple Comparisons with **agricolae**

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1 Graphics of the multiple comparison

The results of a comparison can be graphically seen with the functions `bar.group`, `bar.err` and `diffograph`.

1.1 bar.group

A function to plot horizontal or vertical bar, where the letters of groups of treatments is expressed. The function applies to all functions comparison treatments. Each object must use the group object previously generated by comparative function in indicating that `group = TRUE`.

1.1.1 Example

```
# model <- aov (yield ~ fertilizer, data = field)
# out <- LSD.test (model, "fertilizer", group = TRUE)
# bar.group (out$group)
str(bar.group)
```

```
function (x, horiz = FALSE, ...)
- attr(*, "srcref")= 'srcref' int [1:8] 62 3 64 3 3 3 62 64
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a226517ca8>
```

The Median test with option `group=TRUE` (default) is used in the exercise.

1.1.2 bar.err

A function to plot horizontal or vertical bar, where the variation of the error is expressed in every treatments. The function applies to all functions comparison treatments. Each object must use the means object previously generated by the comparison function, see Figure 1

```
# model <-aov (yield ~ fertilizer, data = field)
# out <-LSD.test (model, "fertilizer", group = TRUE)
# bar.err(out$means)
str(bar.err)
```

```
function (x, variation = c("SE", "SD", "range", "IQR"), horiz = FALSE,
  bar = TRUE, ...)
- attr(*, "srcref")= 'srcref' int [1:8] 69 3 71 3 3 3 69 71
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a2261450f0>
```

variation

SE: Standard error

SD: standard deviation

range: max-min

```
oldpar<-par(mfrow=c(2,2),mar=c(3,3,2,1),cex=0.7)
c1<-colors()[480]; c2=colors()[65]
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
outHSD<- HSD.test(model, "virus",console=TRUE)
```

Study: model ~ "virus"

HSD Test for yield

Mean Square Error: 22.48917

virus, means

	yield	std	r	Min	Max
cc	24.40000	3.609709	3	21.7	28.5
fc	12.86667	2.159475	3	10.6	14.9
ff	36.33333	7.333030	3	28.0	41.8
oo	36.90000	4.300000	3	32.1	40.4

Alpha: 0.05 ; DF Error: 8

Critical Value of Studentized Range: 4.52881

Minimum Significant Difference: 12.39967

Treatments with the same letter are not significantly different.

	yield	groups
oo	36.90000	a
ff	36.33333	ab
cc	24.40000	bc

```
fc 12.86667      c
```

```
bar.err(outhSD$means, variation="range",ylim=c(0,50),col=c1,las=1)
bar.err(outhSD$means, variation="IQR",horiz=TRUE, xlim=c(0,50),col=c2,las=1)
plot(outhSD, variation="range",las=1)
```

Warning in plot.group(outhSD, variation = "range", las = 1): NAs introduced by coercion

```
plot(outhSD, horiz=TRUE, variation="SD",las=1)
```

Warning in plot.group(outhSD, horiz = TRUE, variation = "SD", las = 1): NAs introduced by coercion

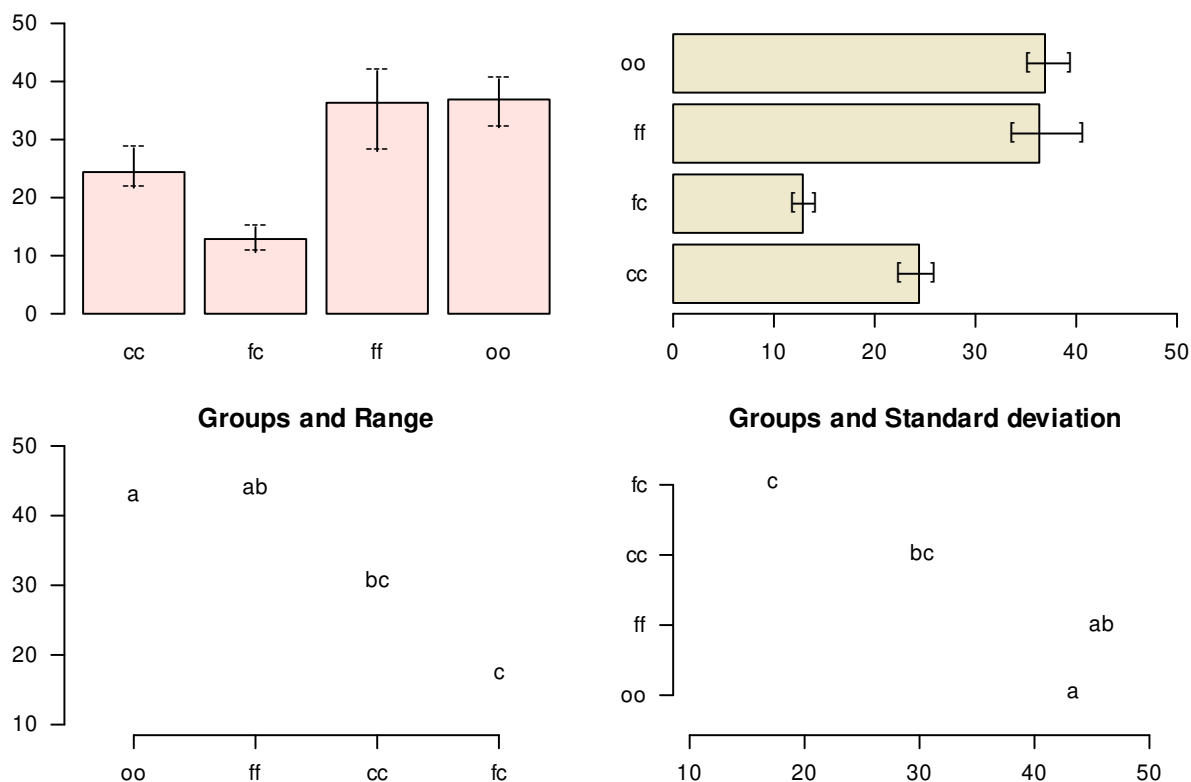


Figure 1: Comparison between treatments

```
par(oldpar)
```

```
oldpar<-par(mfrow=c(2,2),cex=0.7,mar=c(3.5,1.5,3,1))
C1<-bar.err(modelPBIB$means[1:7, ], ylim=c(0,9), col=0, main="C1",
variation="range",border=3,las=2)
C2<-bar.err(modelPBIB$means[8:15,], ylim=c(0,9), col=0, main="C2",
variation="range", border =4,las=2)
# Others graphic
C3<-bar.err(modelPBIB$means[16:22,], ylim=c(0,9), col=0, main="C3",
variation="range",border =2,las=2)
C4<-bar.err(modelPBIB$means[23:30,], ylim=c(0,9), col=0, main="C4",
```

```
variation="range", border =6,las=2)
# Lattice graphics
par(oldpar)
oldpar<-par(mar=c(2.5,2.5,1,0),cex=0.6)
bar.group(modelLattice$group,ylim=c(0,55),density=10,las=1)
par(oldpar)
```

1.2 plot.group

It plot groups and variation of the treatments to compare. It uses the objects generated by a procedure of comparison like LSD (Fisher), duncan, Tukey (HSD), Student Newman Keul (SNK), Scheffe, Waller-Duncan, Ryan, Einot and Gabriel and Welsch (REGW), Kruskal Wallis, Friedman, Median, Waerden and other tests like Durbin, DAU, BIB, PBIB. The variation types are range (maximum and minimum), IQR (interquartile range), SD (standard deviation) and SE (standard error), see Figure 2.

The function: `plot.group()` and their arguments are `x` (output of test), `variation = c("range", "IQR", "SE", "SD")`, `horiz` (TRUE or FALSE), `xlim`, `ylim` and `main` are optional `plot()` parameters and others plot parameters.

```
# model : yield ~ virus
# Important group=TRUE
oldpar<-par(mfrow=c(1,2),mar=c(3,3,1,1),cex=0.8)
x<-duncan.test(model, "virus", group=TRUE)
plot(x,las=1)
```

Warning in `plot.group(x, las = 1)`: NAs introduced by coercion

```
plot(x,variation="IQR",horiz=TRUE,las=1)
```

Warning in `plot.group(x, variation = "IQR", horiz = TRUE, las = 1)`: NAs introduced by coercion

```
par(oldpar)
```

1.3 diffograph

It plots bars of the averages of treatments to compare. It uses the objects generated by a procedure of comparison like LSD (Fisher), duncan, Tukey (HSD), Student Newman Keul (SNK), Scheffe, Ryan, Einot and Gabriel and Welsch (REGW), Kruskal Wallis, Friedman and Waerden (Hsu, 1996) see Figure 3.

```
# function (x, main = NULL, color1 = "red", color2 = "blue",
#   color3 = "black", cex.axis = 0.8, las = 1, pch = 20,
#   bty = "l", cex = 0.8, lwd = 1, xlab = "", ylab = "",
#   ...)
# model : yield ~ virus
# Important group=FALSE
x<-HSD.test(model, "virus", group=FALSE)
diffograph(x,cex.axis=0.9,xlab="Yield",ylab="Yield",cex=0.9)
```

References

Hsu, J. C. (1996). *Multiple Comparisons: Theory and Methods*. Chapman; Hall/CRC.

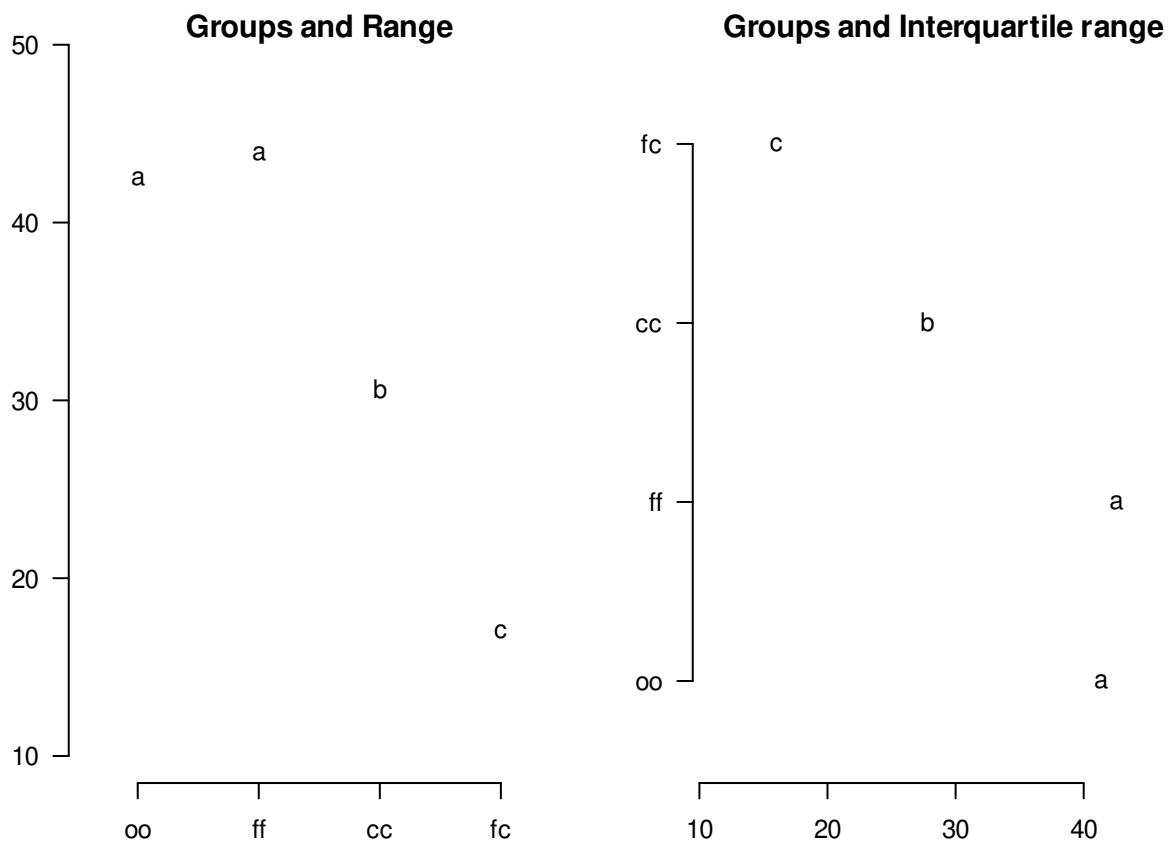


Figure 2: Grouping of treatments and its variation, Duncan method

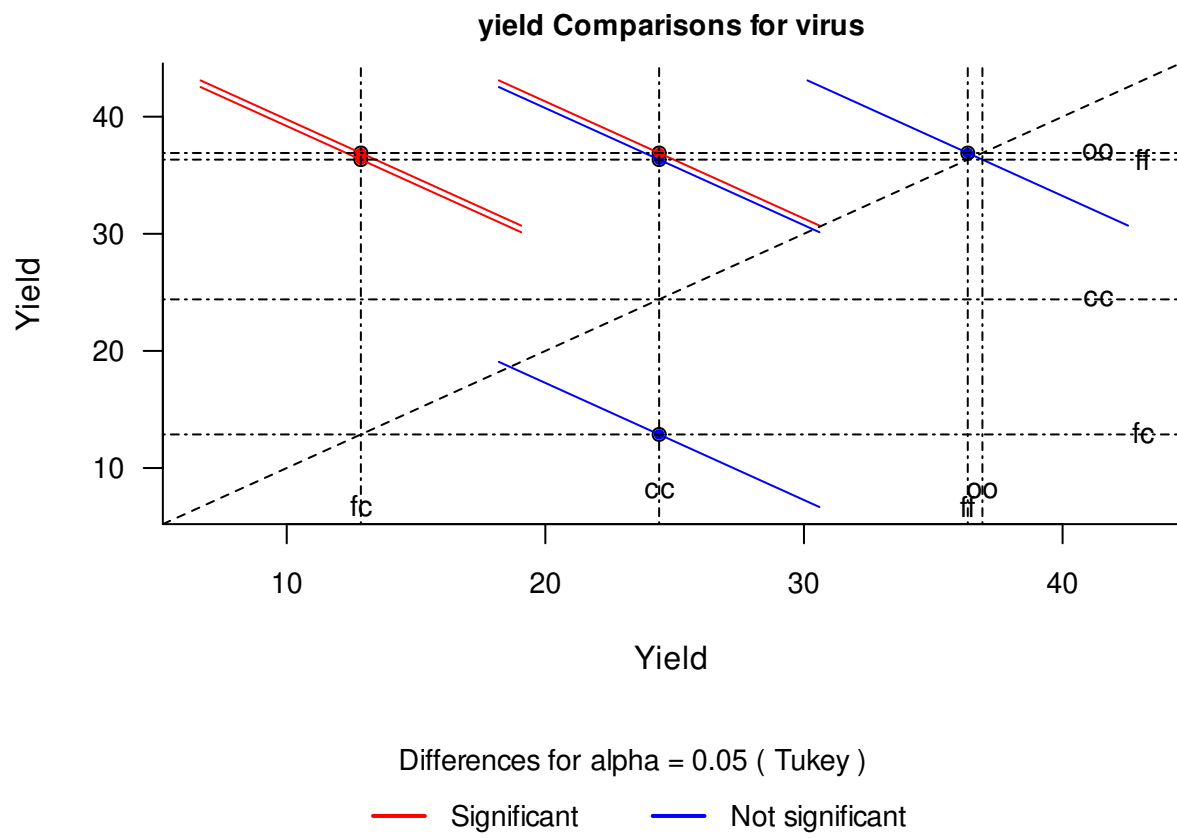


Figure 3: Mean-Mean scatter plot representation of the Tukey method