Case Study : Balanced Incomplete Block Design - example 2

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CASE STUDY PRESENTATION

The design involves 6 varieties of wheat crop in a BIBD with 10 blocks of 3 plots each.

PREPARATION OF THE WORKING INTERFACE IN R

```
### I. Set working directory  ####
# On RStudio: tab 'Session'-> Set Working Directory -> Choose Directory.
# Choose the directory containing the datafile and the associated R script.

### II. Possibly, installation of new R packages needed for the analysis on RStudio:
# Click on the 'Packages' tab in the bottom-right window of R Studio interface->'Install Packages'
# Comment #1: R package installation requires a connection to internet
# Comment #2: Once packages have been installed,
# no need to re-install them again when you close-open again RStudio.

### III. Initialisation of the working space
# To erase all graphs
graphics.off()
# To erase objects from the working space - Clean up of the memory
rm(list = ls())


# this is a trick to detect which folder contains the R script and the data
main_dir <- dirname(rstudioapi::getSourceEditorContext()$path)
setwd(main_dir)
```

LOADING REQUIRED METHODS FOR ANALYSIS

```
library(agricolae)
library(emmeans)
```

ANALYSIS OF THE CASE STUDY

```
## Load the data and examine
BIBD2 <- read.table('BIBD2.txt', sep = ' ', header = TRUE)
str(BIBD2)
```

```
## 'data.frame':    30 obs. of  3 variables:
```

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```
##  $ block  : int  1 2 3 4 5 1 2 6 7 8 ...
##  $ variety: int  1 1 1 1 1 2 2 2 2 2 ...
##  $ y      : int  69 77 72 63 70 54 65 65 57 59 ...
```

```
BIBD2$block <- factor(BIBD2$block)
BIBD2$variety <- factor(BIBD2$variety)
str(BIBD2)
```

```
## 'data.frame':    30 obs. of  3 variables:
##  $ block  : Factor w/ 10 levels "1","2","3","4",..: 1 2 3 4 5 1 2 6 7 8 ...
##  $ variety: Factor w/ 6 levels "1","2","3","4",..: 1 1 1 1 1 2 2 2 2 2 ...
##  $ y      : int  69 77 72 63 70 54 65 65 57 59 ...
```

```
## Draw at the white board. What are the characteristics of this design ?

BIBD2
```

```
##    block variety  y
## 1      1       1 69
## 2      2       1 77
## 3      3       1 72
## 4      4       1 63
## 5      5       1 70
## 6      1       2 54
## 7      2       2 65
## 8      6       2 65
## 9      7       2 57
## 10     8       2 59
## 11     1       3 50
## 12     3       3 45
## 13     6       3 68
## 14     9       3 75
## 15    10       3 59
## 16     2       4 38
## 17     4       4 60
## 18     7       4 60
## 19     9       4 62
## 20    10       4 55
## 21     3       5 54
## 22     5       5 65
## 23     7       5 62
## 24     8       5 65
## 25     9       5 61
## 26     4       6 39
## 27     5       6 54
## 28     6       6 67
## 29     8       6 63
## 30    10       6 56
```

```
BIBD2[order(BIBD2$block), ]
```

```
##    block variety  y
## 1      1       1 69
## 6      1       2 54
## 11     1       3 50
## 2      2       1 77
## 7      2       2 65
## 16     2       4 38
## 3      3       1 72
## 12     3       3 45
## 21     3       5 54
```

```
## 4      4       1 63
## 17     4       4 60
## 26     4       6 39
## 5      5       1 70
## 22     5       5 65
## 27     5       6 54
## 8      6       2 65
## 13     6       3 68
## 28     6       6 67
## 9      7       2 57
## 18     7       4 60
## 23     7       5 62
## 10     8       2 59
## 24     8       5 65
## 29     8       6 63
## 14     9       3 75
## 19     9       4 62
## 25     9       5 61
## 15    10       3 59
## 20    10       4 55
## 30    10       6 56
```

```
##################
##################   generate the same BIBD using agricolae
##################

## function to create BIBD
str(design.bib)
```

```
## function (trt, k, r = NULL, serie = 2, seed = 0, kinds = "Super-Duper",
##     maxRep = 20, randomization = TRUE)
```

```
# function (trt, k, r = NULL, serie = 2, seed = 0, kinds = "Super-Duper",
#           maxRep = 20, randomization = TRUE)

trt <- c("V1", "V2", "V3", "V4", 'V5', 'V6' )  # treatments
k <- 3   # size of blocks

## generate the exp. design. Remember the properties of a BIBD
outdesign <- design.bib(trt, k, seed = 3264, serie = 2)
```

```
##
## Parameters BIB
## ==============
## Lambda     : 2
## treatmeans : 6
## Block size : 3
## Blocks     : 10
## Replication: 5
##
## Efficiency factor 0.8
##
## <<< Book >>>
```

```
print(outdesign$parameters)
```

```
## $design
## [1] "bib"
##
## $trt
## [1] "V1" "V2" "V3" "V4" "V5" "V6"
```

```
##
## $k
## [1] 3
##
## $serie
## [1] 2
##
## $seed
## [1] 3264
##
## $kinds
## [1] "Super-Duper"
```

```
book <- outdesign$book
plots <- as.numeric( book[,1] )
matrix(plots, byrow = TRUE, ncol = k)
```

```
##       [,1] [,2] [,3]
##  [1,]  101  102  103
##  [2,]  201  202  203
##  [3,]  301  302  303
##  [4,]  401  402  403
##  [5,]  501  502  503
##  [6,]  601  602  603
##  [7,]  701  702  703
##  [8,]  801  802  803
##  [9,]  901  902  903
## [10,] 1001 1002 1003
```

```
print(outdesign$sketch)
```

```
##       [,1] [,2] [,3]
##  [1,] "V4" "V5" "V3"
##  [2,] "V2" "V6" "V4"
##  [3,] "V5" "V2" "V3"
##  [4,] "V3" "V6" "V1"
##  [5,] "V6" "V1" "V5"
##  [6,] "V5" "V6" "V4"
##  [7,] "V4" "V2" "V1"
##  [8,] "V3" "V6" "V2"
##  [9,] "V1" "V2" "V5"
## [10,] "V3" "V4" "V1"
```

```
# write in hard disk
# write.csv(book,"book.csv", row.names=FALSE)
# file.show("book.csv")
##################


##################
##################   Analysis of the BIBD using agricolae
##################

Analysis <- BIB.test(block = BIBD2$block,
         trt = BIBD2$variety,
         y = BIBD2$y,
         test = c("tukey"),
         alpha = 0.05, group = TRUE,  # compute groups of means
         console = TRUE)
```

```
##
```

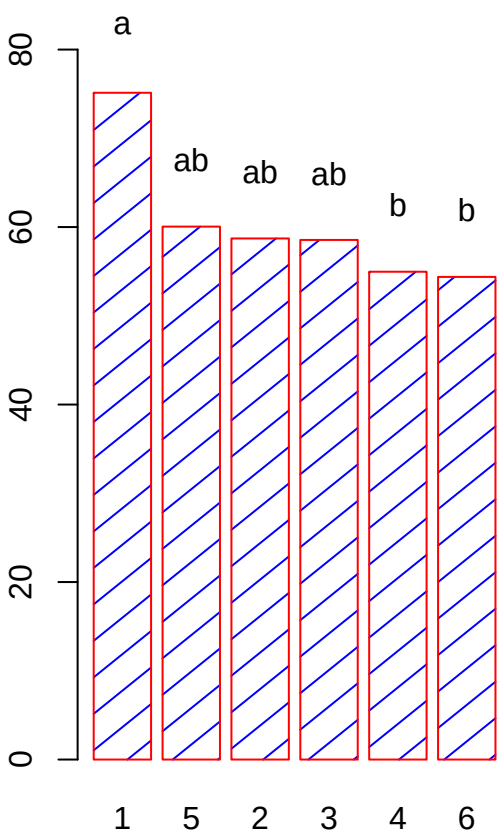
```
## ANALYSIS BIB:  BIBD2$y
## Class level information
##
## Block:  1 2 3 4 5 6 7 8 9 10
## Trt  :  1 2 3 4 5 6
##
## Number of observations:  30
##
## Analysis of Variance Table
##
## Response: BIBD2$y
##             Df  Sum Sq Mean Sq F value  Pr(>F)
## block.unadj  9  466.97  51.885  0.9019 0.54712
## trt.adj      5 1156.44 231.289  4.0206 0.01629 *
## Residuals   15  862.89  57.526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## coefficient of variation: 12.6 %
## BIBD2$y Means: 60.3
##
## BIBD2$variety,  statistics
##
##   BIBD2$y mean.adj       SE r       std Min Max
## 1    70.2 75.13333 3.728552 5  5.069517  63  77
## 2    60.0 58.71667 3.728552 5  4.898979  54  65
## 3    59.4 58.55000 3.728552 5 12.381438  45  75
## 4    55.0 54.96667 3.728552 5  9.848858  38  62
## 5    61.4 60.05000 3.728552 5  4.505552  54  65
## 6    55.8 54.38333 3.728552 5 10.756393  39  67
##
## Tukey
## Alpha      : 0.05
## Std.err    : 3.792292
## HSD        : 17.42458
## Parameters BIB
## Lambda     : 2
## treatmeans : 6
## Block size : 3
## Blocks     : 10
## Replication: 5
##
## Efficiency factor 0.8
##
## <<< Book >>>
##
## Comparison between treatments means
##       Difference pvalue sig.
## 1 - 2 16.4166667 0.0705    .
## 1 - 3 16.5833333 0.0666    .
## 1 - 4 20.1666667 0.0191    *
## 1 - 5 15.0833333 0.1096
## 1 - 6 20.7500000 0.0155    *
## 2 - 3  0.1666667 1.0000
## 2 - 4  3.7500000 0.9792
## 2 - 5 -1.3333333 0.9998
## 2 - 6  4.3333333 0.9616
## 3 - 4  3.5833333 0.9829
## 3 - 5 -1.5000000 0.9997
```

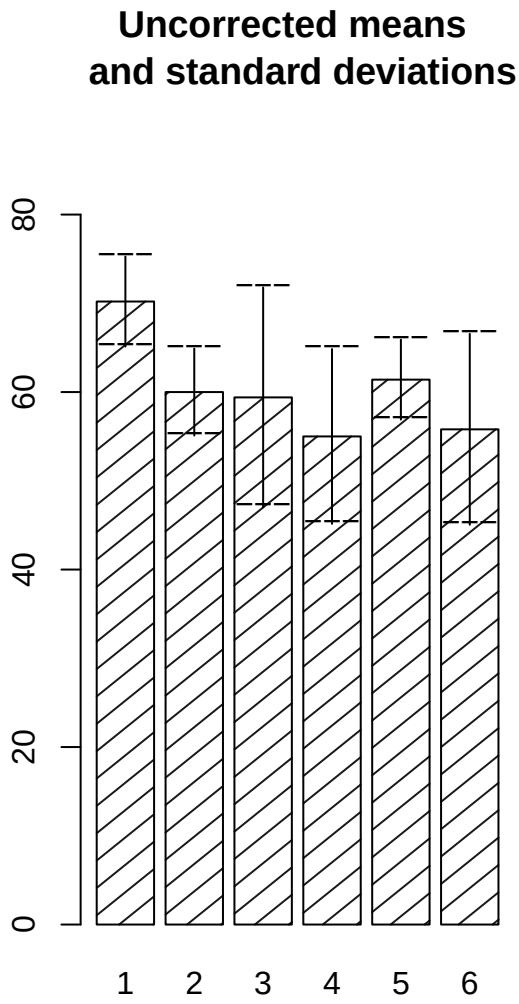
```
## 3 - 6  4.1666667 0.9674
## 4 - 5 -5.0833333 0.9273
## 4 - 6  0.5833333 1.0000
## 5 - 6  5.6666667 0.8908
##
## Treatments with the same letter are not significantly different.
##
##    BIBD2$y groups
## 1 75.13333      a
## 5 60.05000     ab
## 2 58.71667     ab
## 3 58.55000     ab
## 4 54.96667      b
## 6 54.38333      b
```

```
## use of agricolae::bar.group() function
x11()
par(mfrow=c(1,2), cex = 1)  ## two graphics within the same figure

bar.group(Analysis$groups,
          col = "blue", border = "red", density = 6,
         ylim = c(0, 90),
         main = 'Adjusted means'
          )

bar.err(Analysis$means, variation = "SD",
        col = 'grey10', density = 8,
        ylim = c(0,90),
        main = "Uncorrected means \n and standard deviations" )
```






```
##################
##################   Analysis of the BIBD by hand'
##################

## Because not all treatmnents are tested in all block, the SS of block and
## treatment are NOT independant

## ANOVA for treatment adjusted for block effect, block unadjusted
Ana1a <- aov(y ~ block + variety, data = BIBD2)
summary(Ana1a)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## block        9  467.0   51.89   0.902 0.5471
## variety      5 1156.4  231.29   4.021 0.0163 *
## Residuals   15  862.9   57.53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## marginal means ie adjusted means
emmeans(Ana1a, ~ variety)
```

```
##  variety emmean   SE df lower.CL upper.CL
##  1         75.1 3.73 15     67.2     83.1
##  2         58.7 3.73 15     50.8     66.7
##  3         58.5 3.73 15     50.6     66.5
##  4         55.0 3.73 15     47.0     62.9
##  5         60.0 3.73 15     52.1     68.0
##  6         54.4 3.73 15     46.4     62.3
```

```
##
## Results are averaged over the levels of: block
## Confidence level used: 0.95
```

```
## ANOVA for blocks adjusted for treatment effect, treatment unadjusted
## ** NOT really useful **
Ana1b <- aov(y ~ variety + block, data = BIBD2)
summary(Ana1b)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## variety      5  742.3  148.46   2.581 0.0708 .
## block        9  881.1   97.90   1.702 0.1742
## Residuals   15  862.9   57.53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## marginal means ie adjusted means
emmeans(Ana1b, ~ variety)
```

```
##  variety emmean   SE df lower.CL upper.CL
##  1         75.1 3.73 15     67.2     83.1
##  2         58.7 3.73 15     50.8     66.7
##  3         58.5 3.73 15     50.6     66.5
##  4         55.0 3.73 15     47.0     62.9
##  5         60.0 3.73 15     52.1     68.0
##  6         54.4 3.73 15     46.4     62.3
##
## Results are averaged over the levels of: block
## Confidence level used: 0.95
```