Exemplo análise (DIC)

aula 02

Um estudo foi desenvolvido com quatro genótipos e cinco repetições, seguindo um delineamento inteiramente casualizado, tendo-se observado o peso das espigas de cada parcela (10 m^2). # Planejamento do experimento

Usando a biblioteca agricolae

```
# Instalando
# install.packages("agricolae",
#                   dependencies = TRUE)
# Habilitando as funções
library(agricolae)
```

```
## Warning: package 'agricolae' was built under R version 4.0.5
```

```
trt <- LETTERS[1:4]
delineamento <- design.crd(trt,
                           r = 5,
                           serie = 0)
delineamento
```

```
## $parameters
## $parameters$design
## [1] "crd"
##
## $parameters$trt
## [1] "A" "B" "C" "D"
##
## $parameters$r
## [1] 5 5 5 5
##
## $parameters$serie
## [1] 0
##
## $parameters$seed
## [1] -197686410
##
## $parameters$kinds
## [1] "Super-Duper"
##
## $parameters[[7]]
## [1] TRUE
##
##
## $book
##    plots r trt
## 1      1 1   D
```

```
## 2         2 1   A
## 3         3 1   B
## 4         4 2   B
## 5         5 2   A
## 6         6 2   D
## 7         7 1   C
## 8         8 2   C
## 9         9 3   C
## 10       10 4   C
## 11       11 5   C
## 12       12 3   D
## 13       13 3   A
## 14       14 3   B
## 15       15 4   B
## 16       16 4   D
## 17       17 5   B
## 18       18 4   A
## 19       19 5   A
## 20       20 5   D
```

```r
# Graficamente
# install.packages("agricolaeplotr",
#                   dependencies = TRUE)
library(agricolaeplotr)
```

```
## Warning: package 'agricolaeplotr' was built under R version 4.0.5
```

```r
plot_design_crd(delineamento,
                ncols = 4,
                nrows = 5)
```
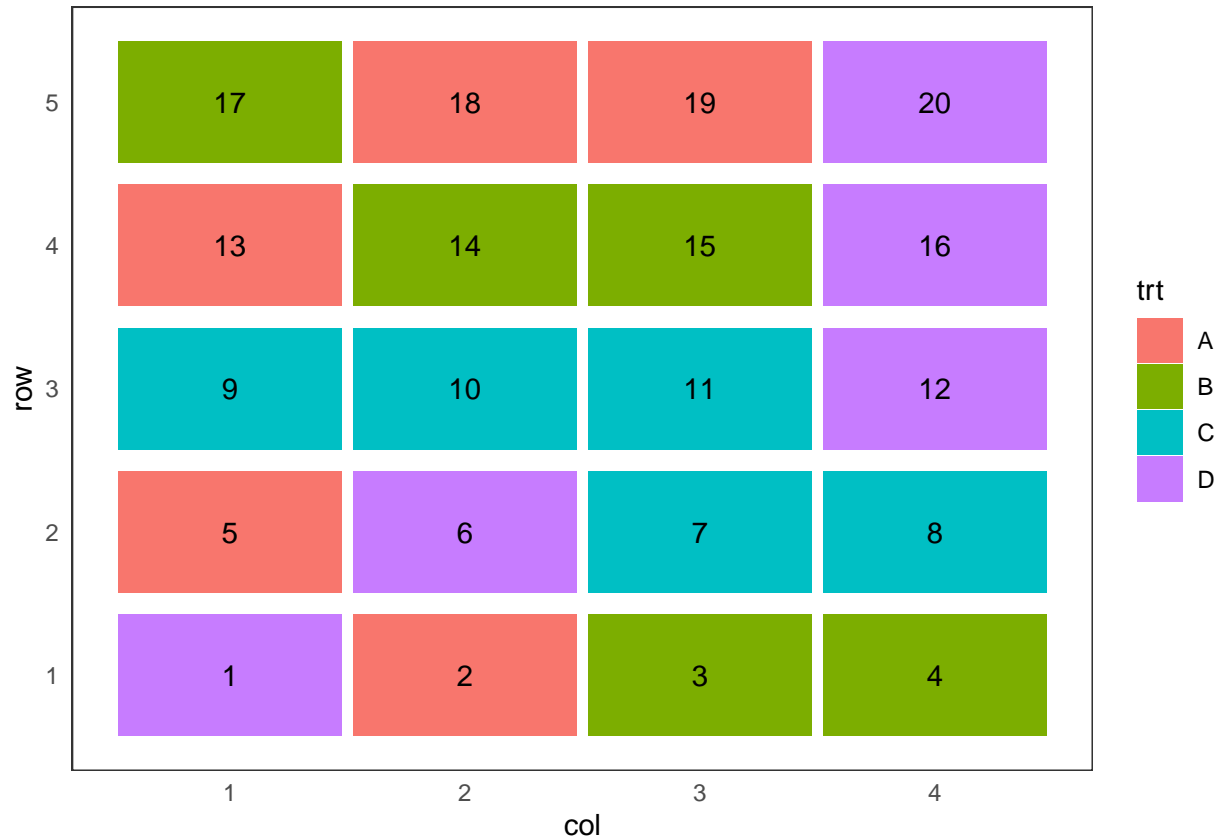
Análise dos dados

```r
dados <- data.frame(
  Genotipo = rep(c(1:4), each = 5),
  prod = c(25, 26, 20, 23, 21,
           31, 25, 28, 27, 24,
           22, 26, 28, 25, 29,
           33, 29, 31, 34, 28))

# install.packages("tidyverse", dependencies = TRUE)
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.5

## -- Attaching packages -------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.6      v purrr   0.3.4
## v tibble  3.1.6      v dplyr   1.0.8
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1

## Warning: package 'ggplot2' was built under R version 4.0.4

## Warning: package 'tibble' was built under R version 4.0.5

## Warning: package 'tidyr' was built under R version 4.0.5
```

```
## Warning: package 'readr' was built under R version 4.0.5

## Warning: package 'dplyr' was built under R version 4.0.5

## Warning: package 'forcats' was built under R version 4.0.5

## -- Conflicts ----------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

#Verificando a estrutura dos dados

```
glimpse(dados)
```

```
## Rows: 20
## Columns: 2
## $ Genotipo <int> 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 3, 3, 3, 3, 3, 4, 4, 4, 4, 4
## $ prod     <dbl> 25, 26, 20, 23, 21, 31, 25, 28, 27, 24, 22, 26, 28, 25, 29, 3~
```

```
dados <- dados %>%
  mutate(Genotipo = factor(Genotipo))
```

Estatísticas descritivas

```
# #' ## Geral

(Resumo <- dados %>%
    summarise(n = length(prod),
              Media = mean(prod),
              Var = var(prod),
              Desvio = sd(prod),
              CV = 100*sd(prod)/mean(prod)))
```

```
##    n Media     Var   Desvio       CV
## 1 20 26.75 14.51316 3.809614 14.24155
```

Por nível de Genótipo

```
(Resumo_Gen <- dados %>%
    group_by(Genotipo) %>%
    summarise(n = length(prod),
              Media = mean(prod),
              Var = var(prod),
              Desvio = sd(prod),
              CV = 100*sd(prod)/mean(prod)))
```
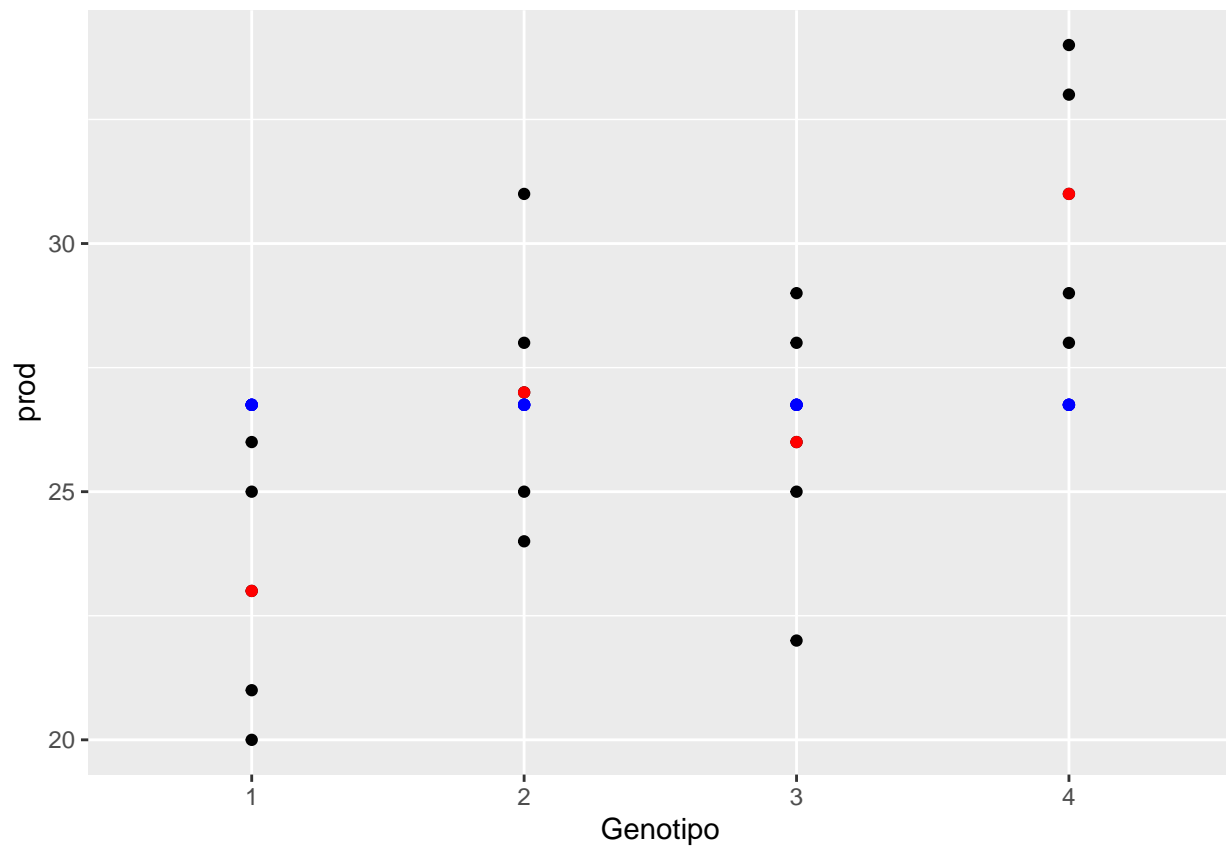
```
## # A tibble: 4 x 6
##   Genotipo     n Media   Var Desvio    CV
##   <fct>    <int> <dbl> <dbl>  <dbl> <dbl>
## 1 1            5    23   6.5   2.55 11.1
## 2 2            5    27   7.5   2.74 10.1
## 3 3            5    26   7.5   2.74 10.5
## 4 4            5    31   6.5   2.55  8.22
```

Graficamente

```
library(ggplot2)
ggplot(dados,
       aes(x = Genotipo,
           y = prod)) +
  geom_point() +
  geom_point(stat = "summary",
             fun = mean,
             color = "red") +
  geom_point(aes(x = Genotipo,
                 y = mean(prod)),
             color = "blue")
```


#ANOVA

Hipóteses

$H_0 : \tau_i = 0, \forall i = 1, \ldots, 5$ *versus* $H_1 : \tau_i \neq 0,$ para algum i

ou

$H_0 : \mu_1 = \mu_2 = \ldots = \mu_5 = \mu$ *versus* $H_1 :$ Pelo menos um contraste de médias difere de zero

Usando a função aov()

```
modelo.aov <- aov(prod ~ Genotipo,
                  data = dados)
summary(modelo.aov)
```

```
##             Df Sum Sq Mean Sq F value  Pr(>F)
## Genotipo     3  163.8   54.58   7.798 0.00198 **
## Residuals   16  112.0    7.00
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

F tabelado

```
qf(0.95, 3, 16)
```

```
## [1] 3.238872
```

Nível descritivo

```
1-pf(7.798, 3, 16)
```

```
## [1] 0.001975152
```