## Boxplots Dataset

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## **Data Import**

```
setwd('D:\\ANALYSIS\\All in ONe\\Malini')
malini_control <- read_excel("mkm data-24.8.2022.xlsx")</pre>
head(malini_control)
## # A tibble: 6 x 17
##
     Genoty~1 IRIS ~2 Genot~3 Scode TREAT~4
                                                         Ε
                                                                          WUE leaf_~5
                                                              Gs
                                                                     Ci
##
     <chr>>
              <chr>
                      <chr>
                              <chr> <chr>
                                             dbl>
                                                     <dbl> <dbl> <dbl> <dbl> <
                                                                                <dbl>
## 1 27C1
              IRIS 3~ G1
                              s1
                                    AΤ
                                              25.6 0.0105 0.720
                                                                  297. 0.243
                                                                                 1.5
## 2 27C2
              IRIS 3~ G1
                                    ΑT
                                              22.0 0.00959 0.620
                                                                  301. 0.229
                                                                                 1.57
                              s1
## 3 27C3
              IRIS 3~ G1
                                                                  290. 0.240
                              s1
                                    ΑT
                                              19.5 0.00825 0.488
                                                                                 1.73
                              s1
## 4 27C4
              IRIS 3~ G1
                                    ΑT
                                              17.8 0.00653 0.326
                                                                  268. 0.273
                                                                                 2
## 5 110C1
              IRIS 3~ G2
                                    ΑT
                                              16.5 0.00540 0.354 286. 0.306
                              s1
## 6 110C2
              IRIS 3~ G2
                              s1
                                    ΑT
                                              15.7 0.00602 0.438 303. 0.263
                                                                                 2.07
## # ... with 6 more variables: CE <dbl>, fv_Per_fm <dbl>,
       TotalNoPaniclesPerPlant <dbl>, TotalNoTillersPerPlant <dbl>,
       GrainYieldPlant <dbl>, TDW <dbl>, and abbreviated variable names
       1: Genotypes, 2: 'IRIS ID', 3: Genotype, 4: TREATMENT, 5: leaf_width
## # i Use 'colnames()' to see all variable names
```

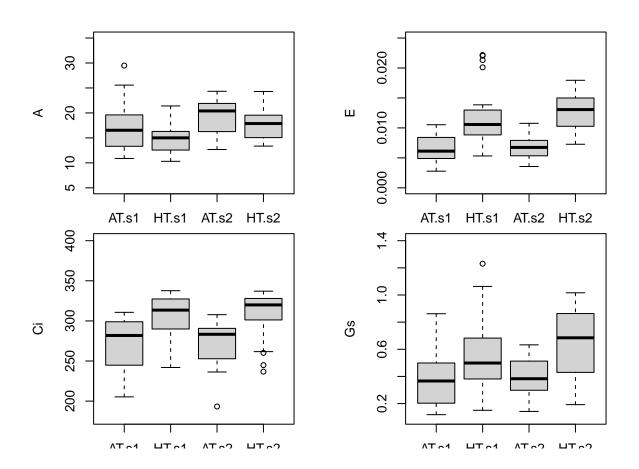
## The Plot

Getteing ANOVA and grouping letters

```
}
dt_tble %>% glimpse()
## Rows: 48
## Columns: 8
## $ Scode
            ## $ TREATMENT <fct> HT, AT, HT, AT, AT, HT, HT, AT, AT, HT, HT, HT, AT, AT, HT, ~
            <dbl> 15.06095449, 16.95384294, 17.54090967, 19.43379812, 0.006223~
## $ emmean
            <dbl> 0.5809206873, 0.5809206873, 0.5809206873, 0.5809206873, 0.00~
## $ SE
## $ df
            ## $ lower.CL
            <dbl> 1.390959e+01, 1.580248e+01, 1.638954e+01, 1.828243e+01, 5.23~
## $ upper.CL
            <dbl> 1.621232e+01, 1.810521e+01, 1.869228e+01, 2.058516e+01, 7.21~
            <chr> "a ", " b ", " b ", " c", "a ", " a ", " b", " b", ~
## $ .group
dt_tble$.group <- gsub(' ', '',dt_tble$.group)</pre>
dt_tble <- dt_tble %>%
      mutate(Var=as_factor(rep(name_vec, each=4))) %>%
      arrange(Var,Scode,TREATMENT)
```

The  $2 \times 2$  boxplot without using ggplot

• Setting initial values for placing letters at right position



## • Final plot

```
layout(mat = matrix(c(1, 2, 3, 4),
                    nrow = 2,
                    ncol = 2),
       heights = c(3.5, 4),
                               # Heights of the two rows
       widths = c(1, 1)
par(mar=c(1.5,6,1,1))
with(malini_control, boxplot(A~TREATMENT+Scode, col= Col_vec, ylim=c(5,35),
                             ylab = parse(text=trait_names['A']), xlab='', las=1,
                             names= c('','','','')
)
)
text(
        x=c(1:nbGroup),
        y=boundaries_A$stats[nrow(boundaries_A$stats),]+7,
        dt_tble[dt_tble$Var=='A','.group']
par(mar=c(3.25,6,1,1))
with(malini_control, boxplot(Ci~TREATMENT+Scode, col= Col_vec, ylim=c(180,400),
                             ylab = parse(text=trait_names['Ci']), xlab='', las=1,
                             names= c(parse(text=paste0('AT', '(italic(S[1]))')),
                                      parse(text=paste0('~HT', '(italic(S[1]))')),
                                      parse(text=paste0('~AT', '(italic(S[2]))')),
                                      parse(text=paste0('~HT', '(italic(S[2]))'))
                             )
)
)
text(
        x=c(1:nbGroup),
        y=boundaries_Ci$stats[nrow(boundaries_Ci$stats),]+30,
        dt_tble[dt_tble$Var=='Ci','.group']
)
par(mar=c(1.5,6,1,1))
with(malini_control, boxplot(E~TREATMENT+Scode, col= Col_vec, ylim=c(0,.025),
                             ylab = parse(text=trait_names['E']), xlab='', las=1,
                             names= c('','','','')
)
)
text(
        x=c(1:nbGroup),
        y=boundaries_E$stats[nrow(boundaries_E$stats),]+.0021,
        dt_tble[dt_tble$Var=='E','.group']
legend("topright", legend = c("AT","HT") ,
       col = Col_vec, bty = "n", pch=20,
       pt.cex = 3, cex = 1, horiz = T, inset = c(0.03, 0.03))
par(mar=c(3.25,6,1,1))
with(malini_control, boxplot(Gs~TREATMENT+Scode, col= Col_vec, ylim=c(.1,1.4),
```

