Boxplots Dataset

Saurav Singla

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```
library(readxl)
library(tidyverse)
library(emmeans)
library(multcomp)
```

Data Import

```
setwd('D:\\ANALYSIS\\All in ONe\\Malini')
malini_control <- read_excel("mkm data-24.8.2022.xlsx")
head(malini_control)
```

```
## # A tibble: 6 x 17
##   Genoty~1 IRIS ~2 Genot~3 Scode TREAT~4    A       E     Gs    Ci   WUE leaf_~5
##   <chr>    <chr>   <chr>   <chr> <chr>   <dbl>   <dbl>  <dbl> <dbl> <dbl>   <dbl>
## 1 27C1     IRIS 3~ G1      s1    AT       25.6 0.0105   0.720  297. 0.243    1.5
## 2 27C2     IRIS 3~ G1      s1    AT       22.0 0.00959  0.620  301. 0.229   1.57
## 3 27C3     IRIS 3~ G1      s1    AT       19.5 0.00825  0.488  290. 0.240   1.73
## 4 27C4     IRIS 3~ G1      s1    AT       17.8 0.00653  0.326  268. 0.273      2
## 5 110C1    IRIS 3~ G2      s1    AT       16.5 0.00540  0.354  286. 0.306      2
## 6 110C2    IRIS 3~ G2      s1    AT       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 <- data.frame()
list_aov <- NULL
name_vec <- names(malini_control)[6:17]
for (ii in name_vec) {
        mal_aov <- with(malini_control,
                    aov(as.formula(paste0(ii,'~Scode+TREATMENT')
                              )
                       )
```

```r
                         )
        list_aov[[ii]]<-summary(mal_aov)

        mean_tab <- emmeans(mal_aov, c('Scode','TREATMENT'))
        cldmean <- cld(mean_tab, Letters = letters)
        dt_tble <- rbind(dt_tble,cldmean)
}

dt_tble %>% glimpse()
```

```
## Rows: 48
## Columns: 8
## $ Scode     <fct> s1, s1, s2, s2, s1, s2, s1, s2, s1, s2, s1, s2, s1, s2, s1, ~
## $ TREATMENT <fct> HT, AT, HT, AT, AT, AT, HT, HT, AT, AT, HT, HT, AT, AT, HT, ~
## $ emmean    <dbl> 15.06095449, 16.95384294, 17.54090967, 19.43379812, 0.006223~
## $ SE        <dbl> 0.5809206873, 0.5809206873, 0.5809206873, 0.5809206873, 0.00~
## $ df        <dbl> 109, 109, 109, 109, 109, 109, 109, 109, 109, 109, 109, 109, ~
## $ 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~
## $ .group    <chr> " a ", " b ", " b ", "  c", " a ", " a ", " b", "  b", ~
```

```r
dt_tble$.group <- gsub(' ', '',dt_tble$.group)
dt_tble <- dt_tble %>%
        mutate(Var=as_factor(rep(name_vec, each=4))) %>%
        arrange(Var,Scode,TREATMENT)
```

The 2 × 2 boxplot without using ggplot

- Setting initial values for placing letters at right position

```r
trait_names <- c(
        `A` ='Photo(`mu`~mol~m^{-1}~s^{-2})',
        `E` ="Transpiration~(mol~m^{-1}~s^{-2})",
        `Gs`="Stomatal~Conductance(~mol~m^{-1}~s^{-2})",
        `Ci`="Internal~CO[2]",
        `WUE`="WUE",
        `leaf_width`="Leaf~Width~(cm)",
        `CE`="Carboxylation~Efficiency~(A/Ci)",
        `fv_Per_fm`="PS~II~efficiency",
        `TotalNoPaniclesPerPlant`="Total~No.~of~panicles/plant",
        `TotalNoTillersPerPlant` ="Total~No.~of~tillers/plant",
        `GrainYieldPlant` = "Grain~Yield/Plant",
        `TDW`="TDW" )

Col_vec=c(rgb(0.1,0.1,0.7) , rgb(0.8,0.1,0.3))
nbGroup <- with(malini_control, nlevels(fct_cross(Scode, TREATMENT)))

#### P2 plot ####
layout(mat = matrix(c(1, 2, 3, 4),
                    nrow = 2,
                    ncol = 2),
       heights = c(3.5, 4),     # Heights of the two rows
```

```r
        widths = c(1, 1))
par(mar=c(1.5,6,1,1))
boundaries_A <- with(malini_control,
                      boxplot(A~TREATMENT+Scode, ylim=c(5,35) ) )
boundaries_Ci <- with(malini_control,
                      boxplot(Ci~TREATMENT+Scode, ylim=c(180,400)))
boundaries_E <- with(malini_control,
                      boxplot(E~TREATMENT+Scode, ylim=c(0,.025) ) )
boundaries_Gs <- with(malini_control,
                      boxplot(Gs~TREATMENT+Scode, ylim=c(.1,1.4)))
```

- Final plot

```r
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('','','','')
)
)
```

```r
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),
                             ylab = parse(text=trait_names['Gs']), 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_Gs$stats[nrow(boundaries_Gs$stats),]+.3,
        dt_tble[dt_tble$Var=='Gs','.group']
)
```