

Analysis of Variance

Zarrin Sovha Khan

```
library(AgroR)
```

```
treat <- paste("Tr", 1:4)  
sketch(treat, r = 3)
```

```
sketch(treat, r = 3, ID = T)
```

```
##      plots r trat x y  
## 1      1 1 Tr 3 1 1  
## 2      2 1 Tr 2 2 1  
## 3      3 1 Tr 1 3 1  
## 4      4 2 Tr 1 4 1  
## 5      5 2 Tr 3 1 2  
## 6      6 2 Tr 2 2 2  
## 7      7 3 Tr 1 3 2  
## 8      8 1 Tr 4 4 2  
## 9      9 2 Tr 4 1 3  
## 10     10 3 Tr 3 2 3  
## 11     11 3 Tr 2 3 3  
## 12     12 3 Tr 4 4 3
```

```
#Creating design from RCBD
```

```
sketch(treat, r = 3, design = "DBC")
```

```
treat2 <- c("x", "y", "z")
```

```
sketch(treat, treat2, r = 3, design = "FAT2DIC")
```

```
## Conducting ANOVA (CRD)
```

```
library(readxl)
```

```
df <- read_excel("D:/Data Analysis/Assignment/CRD.xls")  
View(df)
```

```
str(df)
```

```
## tibble [28 × 3] (S3: tbl_df/tbl/data.frame)  
## $ Rep : num [1:28] 1 1 1 1 1 1 1 2 2 2 ...  
## $ Treat: num [1:28] 1 2 3 4 5 6 7 1 2 3 ...  
## $ Yield: num [1:28] 4 10 3 7 20 8 14 0 8 3 ...
```

```
head(df)
```

```
## # A tibble: 6 × 3
##   Rep Treat Yield
##   <dbl> <dbl> <dbl>
## 1     1     1     4
## 2     1     2    10
## 3     1     3     3
## 4     1     4     7
## 5     1     5    20
## 6     1     6     8

# Ensure Treat is a factor
df$Treat <- as.factor(df$Treat)

str(df)

## tibble [28 × 3] (S3: tbl_df/tbl/data.frame)
##  $ Rep   : num [1:28] 1 1 1 1 1 1 1 2 2 2 ...
##  $ Treat: Factor w/ 7 levels "1","2","3","4",...: 1 2 3 4 5 6 7 1 2 3 ...
##  $ Yield: num [1:28] 4 10 3 7 20 8 14 0 8 3 ...

library(ggplot2)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following object is masked from 'package:AgroR':
##
##   desc

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

# Define the width.column variable
width.column <- 0.5
# Call the DIC function
DIC(df$Treat, df$Yield,
  theme = theme_light(),
  ylab = expression("Yield" ~ "(tha"^-1~")"),
  sup = 3,
  xlab = "Treat",
  angle = 45,
  dec = 4,
  width.column = 0.5,
  width.bar = 0.2
) +
```

```
geom_col(data = df, aes(x = Treat, y = Yield, fill = Treat), color = 1, width = 0.5)
```

```
##
## -----
## Normality of errors
## -----
##               Method Statistic   p.value
## Shapiro-Wilk normality test(W) 0.9735953 0.6794685

## As the calculated p-value is greater than the 5% significance level,
## hypothesis H0 is not rejected. Therefore, errors can be considered normal

##
## -----
## Homogeneity of Variances
## -----
##               Method Statistic   p.value
## Bartlett test(Bartlett's K-squared) 5.534712 0.4772712

## As the calculated p-value is greater than the 5% significance
## level, hypothesis H0 is not rejected. Therefore, the variances can be
## considered homogeneous

##
## -----
## Independence from errors
## -----
##               Method Statistic   p.value
## Durbin-Watson test(DW) 1.738426 0.3291335

## As the calculated p-value is greater than the 5% significance level,
## hypothesis H0 is not rejected. Therefore, errors can be considered
## independent

##
## -----
## Additional Information
## -----
##
## CV (%) = 12.6
## MStrat/MST = 0.99
## Mean = 9
## Median = 8
## Possible outliers = No discrepant point
##
## -----
## Analysis of Variance
## -----
##               Df Sum Sq   Mean.Sq   F value   Pr(F)
```

```
## Treatment 6 1035 172.500000 134.1667 1.233649e-15
## Residuals 21 27 1.285714

## As the calculated p-value, it is less than the 5% significance level. The
hypothesis H0 of equality of means is rejected. Therefore, at least two
treatments differ

##
##
## -----
## Multiple Comparison Test: Tukey HSD
## -----
## resp groups
## 5 20.75 a
## 7 14.00 b
## 2 9.25 c
## 6 8.00 cd
## 4 6.00 d
## 3 3.25 e
## 1 1.75 e
##
```

```
## NULL

# Load required libraries
library(ggplot2)
library(agricolae)

# Create the data frame
df <- data.frame(
  Rep = rep(1:4, each = 7),
  Treat = as.factor(rep(1:7, times = 4)), # Convert Treat to factor
  Yield = c(4, 10, 3, 7, 20, 8, 14, 0, 8, 3, 6, 22, 9, 12, 2, 10, 4, 5, 21,
8, 16, 1, 9, 6, 6, 20, 7, 14)
)

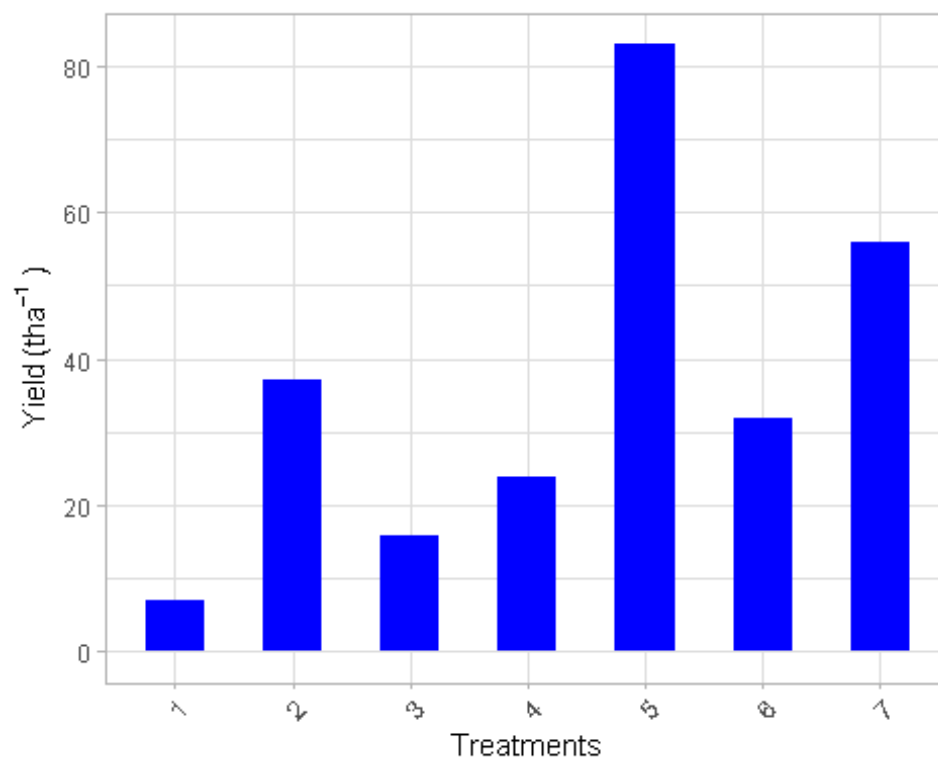
# Custom DIC plot function
DIC <- function(trat, resp, theme = theme_light(), ylab = expression("Yield"~
"(tha"^-1~)"),
  sup = 3, xlab = "Treatments", fill = "blue", angle = 45, dec
= 4,
  width.column = 0.5, width.bar = 0.2) {
  df <- data.frame(trat, resp)
  ggplot(df, aes(x = trat, y = resp)) +
    geom_col(fill = fill, width = width.column) +
    theme +
    labs(x = xlab, y = ylab) +
    theme(axis.text.x = element_text(angle = angle, hjust = 1))
}
```

```

}

# Use the custom DIC plot function
DIC(df$Treat, df$Yield,
  theme = theme_light(),
  ylab = expression("Yield" ~ "(tha"^-1~")"),
  sup = 3,
  xlab = "Treatments",
  fill = "blue", # Specify a valid color
  angle = 45,
  dec = 4,
  width.column = 0.5,
  width.bar = 0.2)

```



```

# Perform single factor CRD ANOVA
anova_result <- aov(Yield ~ Treat, data = df)
summary(anova_result)

##              Df Sum Sq Mean Sq F value    Pr(>F)
## Treat          6 1002.4   167.07    108.8 1.04e-14 ***
## Residuals     21   32.2     1.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

2 Factor CRD

```
# Load required libraries
```

```
library(ggplot2)
```

```
library(agricolae)
```

```
# Create the data frame
```

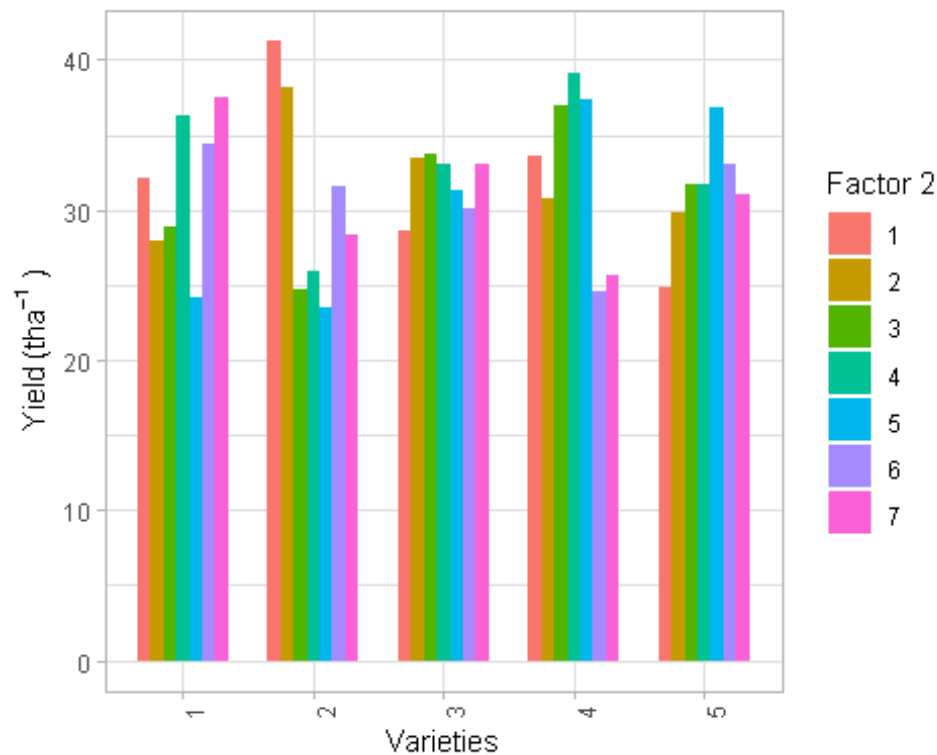
```
df <- data.frame(
  Rep = rep(1, 35),
  Fac1 = as.factor(c(1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 3, 3, 3, 3, 3,
3, 3, 4, 4, 4, 4, 4, 4, 4, 5, 5, 5, 5, 5, 5, 5)),
  Fac2 = as.factor(c(1, 2, 3, 4, 5, 6, 7, 1, 2, 3, 4, 5, 6, 7, 1, 2, 3, 4, 5,
6, 7, 1, 2, 3, 4, 5, 6, 7, 1, 2, 3, 4, 5, 6, 7)),
  Yield = c(32.1, 27.88, 28.91, 36.28, 24.19, 34.44, 37.53, 41.25, 38.19,
24.75, 25.94, 23.44, 31.63, 28.31, 28.66, 33.44, 33.69, 33.08, 31.25, 30.13,
33.02, 33.53, 30.75, 36.97, 39.09, 37.41, 24.63, 25.6, 24.88, 29.84, 31.75,
31.75, 36.77, 33, 31.08)
)
```

```
# Custom FAT2DIC plot function
```

```
FAT2DIC <- function(var1, var2, resp, theme = theme_light(), ylab =
expression("Yield"~ "(tha"^-1~)"),
                    sup = 3, xlab = "Factors", fill = "blue", angle = 45, dec
= 4,
                    width.column = 0.7, width.bar = 0.2, angle.label = 90) {
  df <- data.frame(var1, var2, resp)
  ggplot(df, aes(x = var1, y = resp, fill = var2)) +
    geom_col(position = position_dodge(width = width.column), width =
width.column) +
    theme +
    labs(x = xlab, y = ylab, fill = "Factor 2") +
    theme(axis.text.x = element_text(angle = angle.label, hjust = 1))
}
```

```
# Use the custom FAT2DIC plot function
```

```
FAT2DIC(df$Fac1, df$Fac2, df$Yield,
        theme = theme_light(),
        ylab = expression("Yield"~ "(tha"^-1~)"),
        sup = 3,
        xlab = "Varieties",
        fill = "blue", # Specify a valid color
        angle = 45,
        dec = 4,
        width.column = 0.7,
        width.bar = 0.2,
        angle.label = 90)
```



```
# Perform two-factor CRD ANOVA
anova_result <- aov(Yield ~ Fac1 * Fac2 + Error(Rep), data = df)

## Warning in aov(Yield ~ Fac1 * Fac2 + Error(Rep), data = df): Error() model
is
## singular

summary(anova_result)

##
## Error: Within
##           Df Sum Sq Mean Sq
## Fac1       4   16.3    4.064
## Fac2       6   25.6    4.266
## Fac1:Fac2 24  700.3   29.178
```

Factorial RCBD

```
# Load required libraries
library(ggplot2)
library(dplyr)
library(agricolae)

# Create the data frame
df <- data.frame(
  Rep = rep(1:4, each = 9),
  Fac1 = rep(rep(1:3, each = 3), times = 4),
```

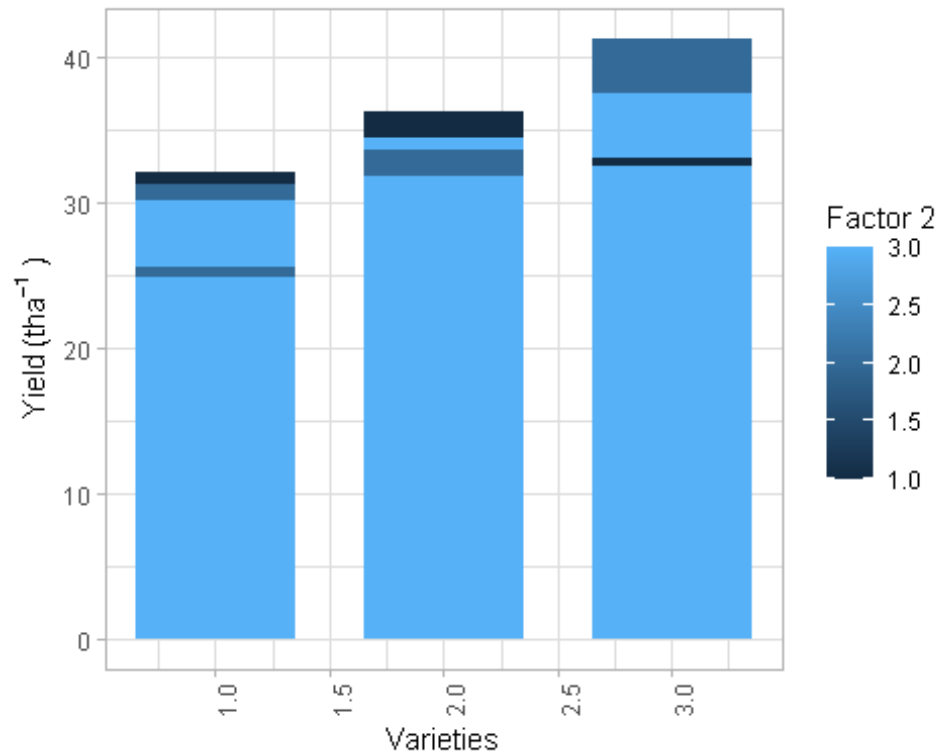
```

Fac2 = rep(1:3, times = 12),
Yield = c(32.1, 27.88, 28.91, 36.28, 24.19, 34.44, 37.53, 41.25, 38.19,
          24.75, 25.94, 23.44, 28.66, 31.63, 28.31, 33.44, 33.69, 33.08,
          30.56, 31.25, 30.13, 33.02, 33.53, 30.75, 36.97, 39.09, 37.41,
          24.63, 25.5, 24.88, 29.84, 31.75, 31.75, 33, 31.08, 32.5)
)

# Custom FAT2DBC plot function
FAT2DBC <- function(var1, var2, rep, resp, theme = theme_light(), ylab =
expression("Yield"~ "(tha"^-1~)"),
                    sup = 3, xlab = "Varieties", fill = "blue", angle = 45,
dec = 4,
                    width.column = 0.7, width.bar = 0.2, angle.label = 90) {
  df <- data.frame(var1, var2, rep, resp)
  ggplot(df, aes(x = var1, y = resp, fill = var2)) +
    geom_col(position = position_dodge(width = width.column), width =
width.column) +
    theme +
    labs(x = xlab, y = ylab, fill = "Factor 2") +
    theme(axis.text.x = element_text(angle = angle.label, hjust = 1))
}

# Use the custom FAT2DBC plot function
FAT2DBC(df$Fac1, df$Fac2, df$Rep, df$Yield,
        theme = theme_light(),
        ylab = expression("Yield"~ "(tha"^-1~)"),
        sup = 3,
        xlab = "Varieties",
        fill = "blue", # Specify a valid color
        angle = 45,
        dec = 4,
        width.column = 0.7,
        width.bar = 0.2,
        angle.label = 90)

```

```
# Perform two-factor RCBD ANOVA
anova_result <- aov(Yield ~ Fac1 * Fac2 + Rep, data = df)
summary(anova_result)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Fac1	1	394.1	394.1	41.525	3.49e-07 ***
Fac2	1	2.0	2.0	0.214	0.647
Rep	1	25.5	25.5	2.687	0.111
Fac1:Fac2	1	1.5	1.5	0.159	0.692
Residuals	31	294.2	9.5		

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RCBD

```
# Load required libraries
library(ggplot2)
library(dplyr)
library(agricolae)

# Create the data frame
df <- data.frame(
  Rep = rep(1:4, each = 9),
  Fac1 = rep(rep(1:3, each = 3), times = 4),
  Fac2 = rep(1:3, times = 12),
  Yield = c(32.1, 27.88, 28.91, 36.28, 24.19, 34.44, 37.53, 41.25, 38.19,
            24.75, 25.94, 23.44, 28.66, 31.63, 28.31, 33.44, 33.69, 33.08,
```

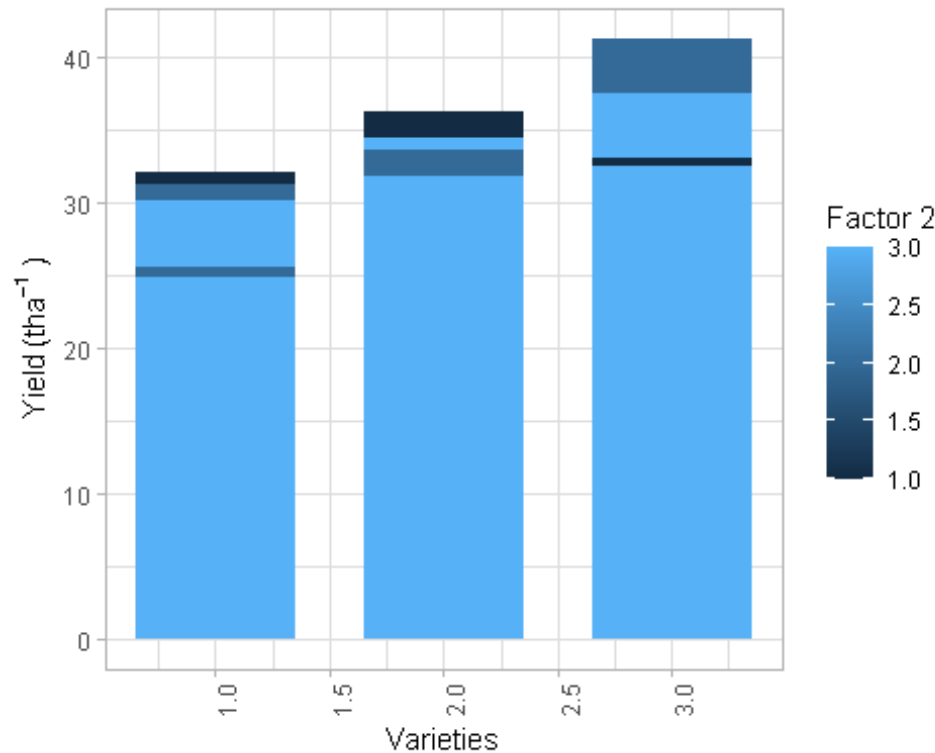
```

30.56, 31.25, 30.13, 33.02, 33.53, 30.75, 36.97, 39.09, 37.41,
24.63, 25.5, 24.88, 29.84, 31.75, 31.75, 33, 31.08, 32.5)
)

# Custom FAT2DBC plot function
FAT2DBC <- function(var1, var2, rep, resp, theme = theme_light(), ylab =
expression("Yield"~ "(tha"^-1~")"),
                    sup = 3, xlab = "Varieties", fill = "blue", angle = 45,
dec = 4,
                    width.column = 0.7, width.bar = 0.2, angle.label = 90) {
  df <- data.frame(var1, var2, rep, resp)
  ggplot(df, aes(x = var1, y = resp, fill = var2)) +
    geom_col(position = position_dodge(width = width.column), width =
width.column) +
    theme +
    labs(x = xlab, y = ylab, fill = "Factor 2") +
    theme(axis.text.x = element_text(angle = angle.label, hjust = 1))
}

# Use the custom FAT2DBC plot function
FAT2DBC(df$Fac1, df$Fac2, df$Rep, df$Yield,
        theme = theme_light(),
        ylab = expression("Yield"~ "(tha"^-1~")"),
        sup = 3,
        xlab = "Varieties",
        fill = "blue", # Specify a valid color
        angle = 45,
        dec = 4,
        width.column = 0.7,
        width.bar = 0.2,
        angle.label = 90)

```



Perform two-factor RCBD ANOVA

```
anova_result <- aov(Yield ~ Fac1 * Fac2 + Rep, data = df)
summary(anova_result)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Fac1       1  394.1   394.1   41.525 3.49e-07 ***
## Fac2       1    2.0     2.0    0.214   0.647
## Rep        1   25.5    25.5    2.687   0.111
## Fac1:Fac2   1    1.5     1.5    0.159   0.692
## Residuals  31   294.2     9.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RCBD Several

Load required libraries

```
library(ggplot2)
library(agricolae)
```

Create the data frame

```
df <- data.frame(
  Varieties = as.factor(c(1, 1, 1, 2, 2, 2, 3, 3, 3, 1, 1, 1, 2, 2, 2, 3, 3,
3, 1, 1, 1, 2, 2, 2, 3, 3, 3, 1, 1, 1, 2, 2, 2, 3, 3, 3)),
  DS = as.factor(c(1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1,
2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3)),
  Replication = as.factor(c(1, 1, 1, 2, 2, 2, 3, 3, 3, 1, 1, 1, 2, 2, 2, 3,
3, 3, 1, 1, 1, 2, 2, 2, 3, 3, 3, 1, 1, 1, 2, 2, 2, 3, 3, 3)),
```

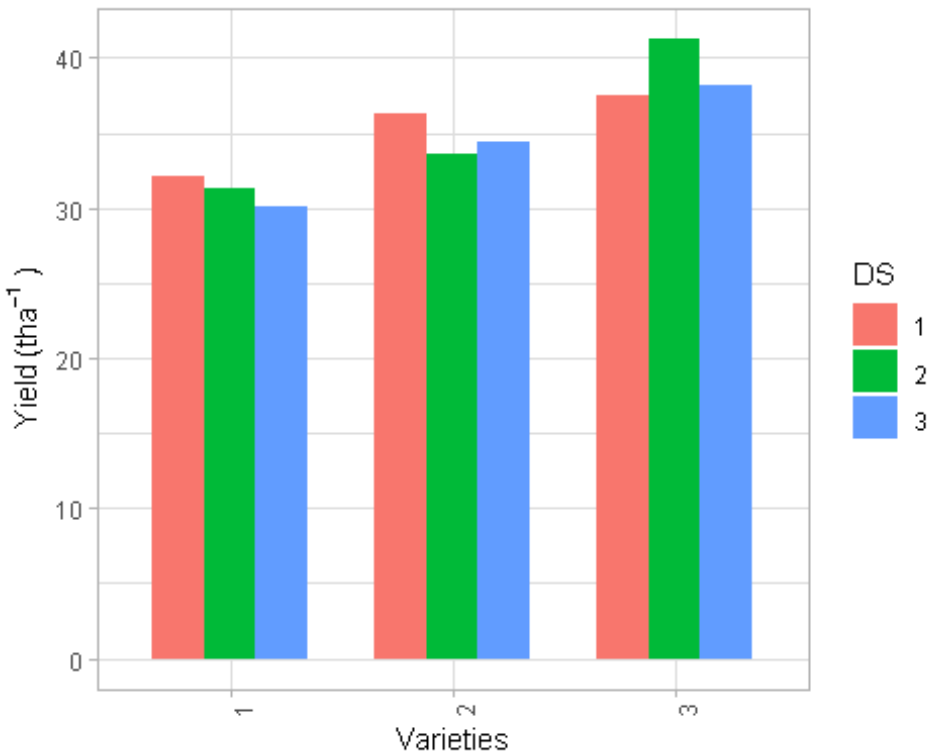
```

Yield = c(32.1, 27.88, 28.91, 36.28, 24.19, 34.44, 37.53, 41.25, 38.19,
24.75, 25.94, 23.44, 28.66, 31.63, 28.31, 33.44, 33.69, 33.08, 30.56, 31.25,
30.13, 33.02, 33.53, 30.75, 36.97, 39.09, 37.41, 24.63, 25.5, 24.88, 29.84,
31.75, 31.75, 33, 31.08, 32.5),
yld_ctrl = c(30.5, 26.5, 27.9, 35.0, 23.8, 34.1, 36.7, 40.2, 37.8, 30.5,
26.5, 27.9, 35.0, 23.8, 34.1, 36.7, 40.2, 37.8, 30.5, 26.5, 27.9, 35.0, 23.8,
34.1, 36.7, 40.2, 37.8, 30.5, 26.5, 27.9, 35.0, 23.8, 34.1, 36.7, 40.2, 37.8)
)

# Custom FAT2RCBD.ad plot function
FAT2RCBD.ad <- function(varieties, ds, replication, yield, yld_ctrl,
                        theme = theme_light(), ylab = expression("Yield"~
"(tha"^-1~")"),
                        sup = 3, xlab = "Varieties", fill = "blue", angle =
45, dec = 4,
                        width.column = 0.7, width.bar = 0.2, angle.label =
90) {
  df <- data.frame(varieties, ds, replication, yield, yld_ctrl)
  ggplot(df, aes(x = varieties, y = yield, fill = ds)) +
    geom_col(position = position_dodge(width = width.column), width =
width.column) +
    theme +
    labs(x = xlab, y = ylab, fill = "DS") +
    theme(axis.text.x = element_text(angle = angle.label, hjust = 1))
}

# Use the custom FAT2RCBD.ad plot function
FAT2RCBD.ad(df$Varieties, df$DS, df$Replication, df$Yield, df$yld_ctrl,
            theme = theme_light(),
            ylab = expression("Yield"~ "(tha"^-1~")"),
            sup = 3,
            xlab = "Varieties",
            fill = "blue", # Specify a valid color
            angle = 45,
            dec = 4,
            width.column = 0.7,
            width.bar = 0.2,
            angle.label = 90)

```



```
# Perform two-factor RCBD ANOVA
```

```
anova_result <- aov(Yield ~ Varieties * DS + Replication, data = df)
summary(anova_result)
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Varieties      2   395.2   197.62   17.164 1.55e-05 ***
## DS              2     2.1     1.03    0.089    0.915
## Varieties:DS    4     9.3     2.32    0.201    0.935
## Residuals     27   310.9    11.51
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
```

Split plot

```
# Load necessary packages
```

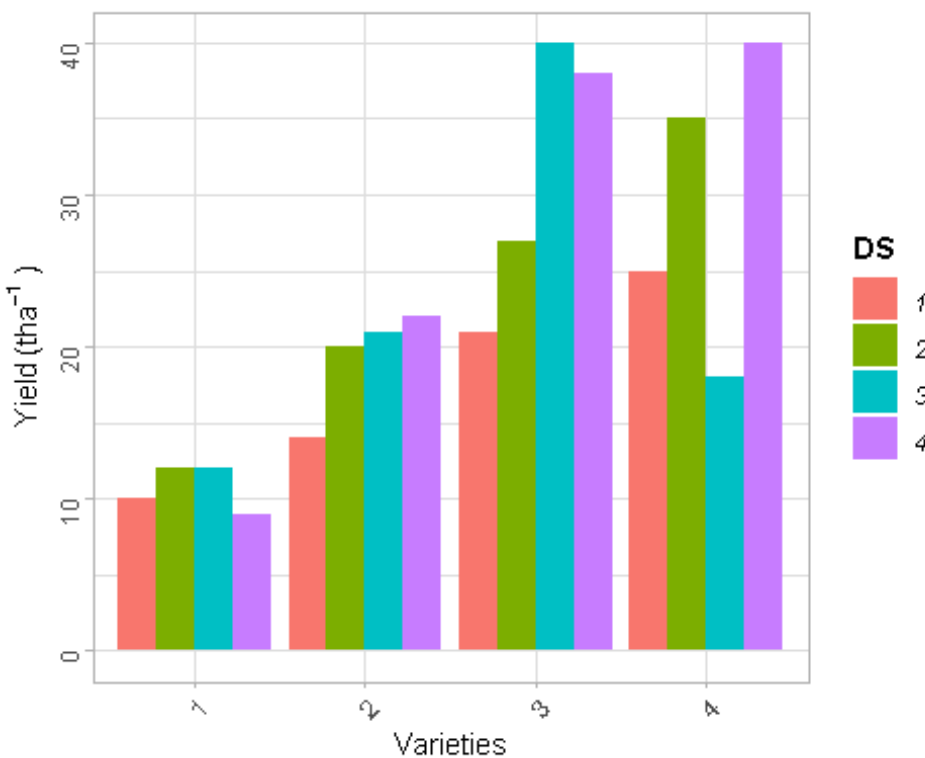
```
library(ggplot2)
library(dplyr)
```

```
# Create the dataframe based on the provided data
```

```
df <- data.frame(
  Replication =
c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3,3,3,
3,3,4,4,4,4,4,4,4,4,4,4),
  Varieties =
c(1,1,1,1,2,2,2,2,3,3,3,3,4,4,4,4,1,1,1,1,2,2,2,2,3,3,3,4,4,1,1,1,1,2,2,2,3,3,
3,3,1,1,1,1,2,2,2,2,3,3,3)),
  DS =
```

```
c(1,2,3,4,1,2,3,4,1,2,3,4,1,2,3,4,1,2,3,4,1,2,3,4,3,1,2,3,4,1,2,3,1,2,
,3,4,1,2,3,4,1,2,3,4,1,2,3),
  yield =
c(5,12,11,6,13,9,13,22,20,4,10,18,25,35,18,40,7,12,10,9,9,16,18,12,21,27,40,1
8,4,10,7,12,8,14,20,19,13,20,26,38,6,11,11,7,10,15,21,15,11,24,29)
)
```

```
ggplot(df, aes(x = factor(Varieties), y = yield, fill = factor(DS))) +
  geom_bar(stat = "identity", position = "dodge") +
  theme_light() +
  labs(y = expression("Yield"~ "(tha"^-1~)"),
       x = "Varieties",
       fill = "DS") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.text.y = element_text(angle = 90),
        legend.title = element_text(face = "bold"),
        legend.text = element_text(face = "italic"))
```



```
# Load necessary packages
library(ggplot2)
library(dplyr)

# Create the dataframe based on the provided data
df <- data.frame(
  Replication =
```

```
ggplot(df, aes(x = factor(MP), y = GY, fill = factor(SP))) +
  geom_bar(stat = "identity", position = "dodge") +
  theme_light() +
  labs(y = expression("Yield" ~ "(tha"-1~")"),
       x = "Varieties",
       fill = "SP") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.text.y = element_text(angle = 90),
        legend.title = element_text(face = "bold"),
        legend.text = element_text(face = "italic"))
```

