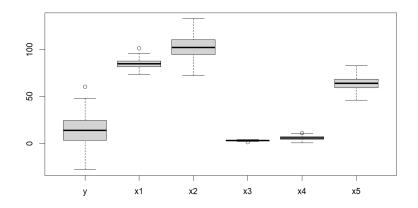
```
> head(mydata)
                          x1
  0.3833838 82.19762 128.38572 2.963222 8.148025
14.8224896 83.84911 117.74896 2.415674 5.945306
                                                                     66.49398
                                                         5.945306 59.39393
  15.5270754 92.79354
                                98.81826 2.682626 5.933339 69.98642
4 -3.3207493 85.35254 108.51833 2.985579 2.967865 72.07055 5 10.0196414 85.64644 97.02792 3.335348 7.580771 65.93392 6 26.9836869 93.57532 96.28504 2.174727 5.578532 65.00873
> names(newdata)
[1] "y"
x5"
                         "x1"
                                                                                                       11
                                             "x2"
                                                                "x3_f_factor" "x4"
> x3_categories <- cut(x3, breaks = category_centers, labels = c("A", "B",
"C", "D"))</pre>
> néwdata <- data.frame(y, x1, x2, x3_categories, x4, x5)</pre>
> head(newdata)
    y X1 x2 x3_categories
0.3833838 82.19762 128.38572 R
                                                               8.148025 66.49398
                                                                5.945306 59.39393
  14.8224896 83.84911 117.74896
  15.5270754 92.79354
                                                               5.933339 69.98642
                                98.81826
4 -3.3207493 85.35254 108.51833
                                                             в 2.967865 72.07055
  10.0196414 85.64644
                                97.02792
                                                             C
                                                                7.580771 65.93392
                                                             B 5.578532 65.00873
6 26.9836869 93.57532
                                96.28504
> unique_values <- unique(newdata$x3_categories)</pre>
  print(unique_values)
[1] B C A D
Levels: A B C D
> print(missing_columns)
character(0)
> #kategorik değişken için frekans analizi yapıyorum
  category_counts <- as.data.frame(table(newdata$x3_categories))</pre>
> ggplot(category_counts, aes(x = Var1, y = Freq)) +
+ geom_bar(stat = "identity") +
+ labs(x = "Kategori", y = "Frekans", title = "x3_categories Kategorik De
ğişkeninin = "kategori" + thoma = "inimal") +
      theme_minimal()
    x3_categories Kategorik Değişkeninin Frekans Dağılımı
                          Kategori
```

summary(category_counts) Var1 Freq

A:1 Min. : 2 B:1 1st Qu.: 5 C:1 Median : 47 D:1 Mean : 50 3rd Qu.: 92 Max. :104

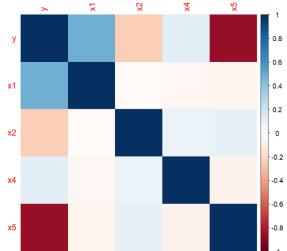
> boxplot(mydata)



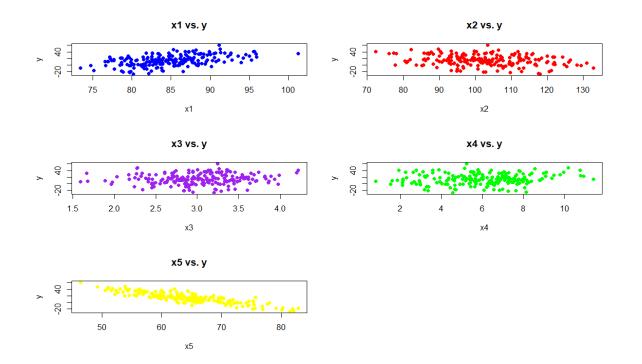
> qqnorm(newdata\$y) > qqline(newdata\$y)

Normal Q-Q Plot Separate of the control of the con

> corrplot(correlation_matrix, method = "color")

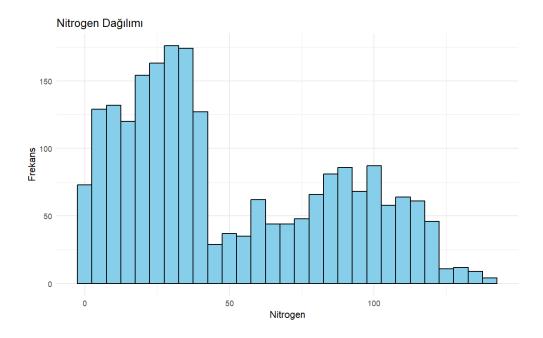


```
> # Bağımsız değişkenlerin grafiğini çizme
> par(mfrow=c(3,2)) # Grafiklerin yan yana yerleştirilmesi için ayar
> plot(x1, y, main = "x1 vs. y", xlab = "x1", ylab = "y", col = "blue", pch = 16)
> plot(x2, y, main = "x2 vs. y", xlab = "x2", ylab = "y", col = "red", pch = 16)
> plot(x3, y, main = "x3 vs. y", xlab = "x3", ylab = "y", col = "purple", p ch = 16)
> plot(x4, y, main = "x4 vs. y", xlab = "x4", ylab = "y", col = "green", pc h = 16)
> plot(x5, y, main = "x5 vs. y", xlab = "x5", ylab = "y", col = "yellow", p ch = 16)
```

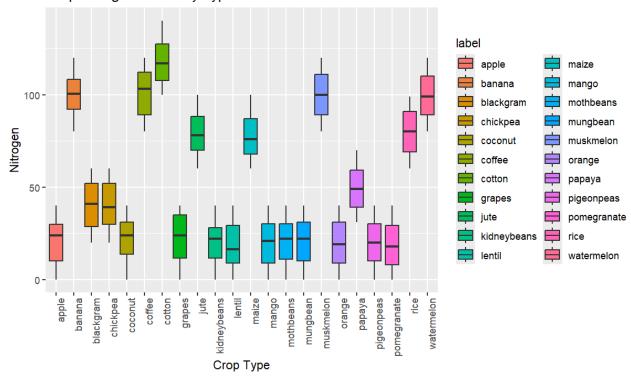


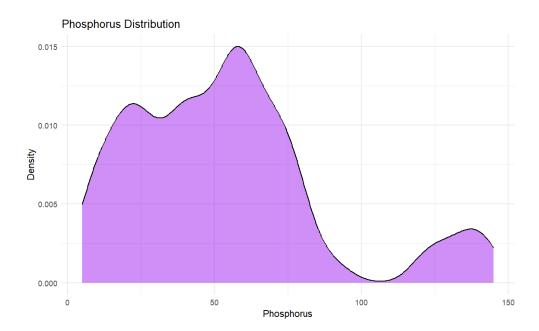
```
data <- read.csv("crop.csv")</pre>
> head(data)
  Nitrogen phosphorus potassium temperature humidity
                                                                ph rainfall labe
   x x.\bar{1}
                     42
                                43
                                      20.87974 82.00274 6.502985 202.9355
1
                                                                               ric
e
2
  NA
      NA
                                      21.77046 80.31964 7.038096 226.6555
         85
                     58
                                41
                                                                               ric
e
  NA
      NA
3
                     55
                                44
                                      23.00446 82.32076 7.840207 263.9642
         60
                                                                               ric
  NA
e
      NA
                                40
                                      26.49110 80.15836 6.980401 242.8640
4
         74
                     35
                                                                               ric
e
5
  NA
      NΑ
        78
                     42
                                42
                                      20.13017 81.60487 7.628473 262.7173
                                                                               ric
e
  NA
      NA
                                      23.05805 83.37012 7.073454 251.0550
6
         69
                     37
                                42
                                                                               ric
e NA
      NA
unique_values <- unique(data$label)</pre>
"chickpea"
                                                    "kidneybeans" "pigeonpeas"
"mothbeans" "mungbean"
[8] "blackgram" "lentil'
"grapes" "watermelon"
[15] "muskmelon" "apple"
"cotton" "jute"
               "mungbean"
ເຫ" "lenti<u>]</u>"
                                    "pomegranate" "banana"
                                                                   "mango"
                                    "orange"
                                                    "papaya"
                                                                   "coconut"
[22] "coffee"
clean_data %>% count(label)
          label
          apple 100
1
2
         banana 100
3
     blackgram 100
4
      chickpea 100
5
       coconut 100
6
7
         coffee 100
         cotton 100
         grapes 100
8
9
           jute 100
10 kidneybeans 100
11
         lentil 100
12
          maize 100
          mango 100
13
14
     mothbeans 100
15
      mungbean 100
16
     muskmelon 100
17
         orange 100
        papaya 100
18
19
    pigeonpeas 100
20 pomegranate 100
21
           rice 100
    watermelon 100
22
```

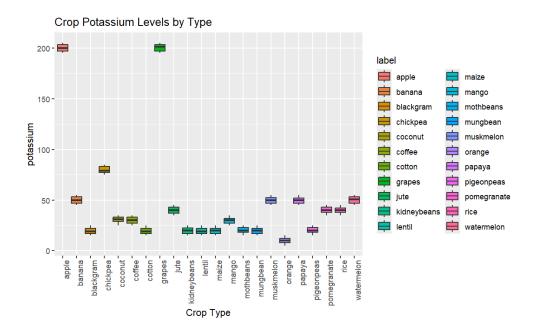
theme_minimal()

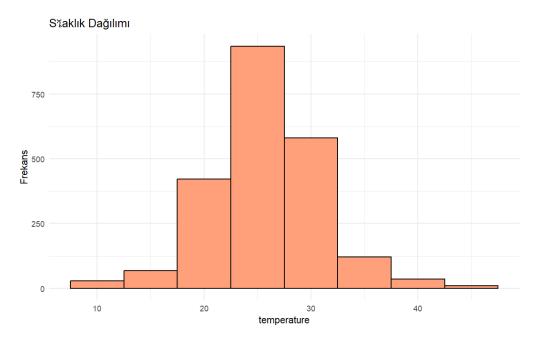


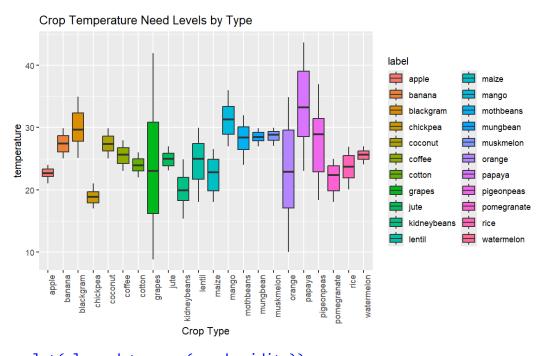
Crop Nitrogen Levels by Type



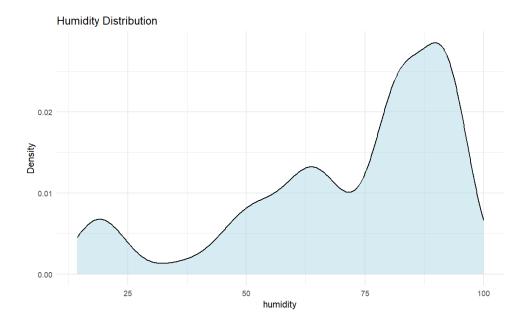


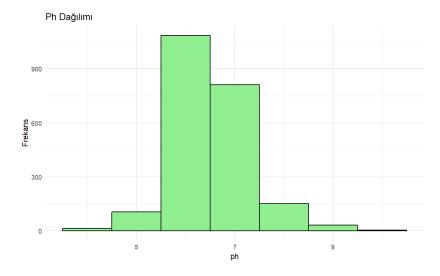




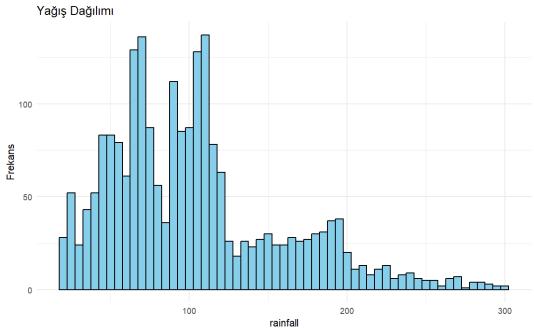


+ theme_minimal()





+ theme_minimal()



> corrplot(correlation_matrix_crop, method = "color")

