DA2

```
library("magrittr") # for piping %>%
head(iris, 3)
```

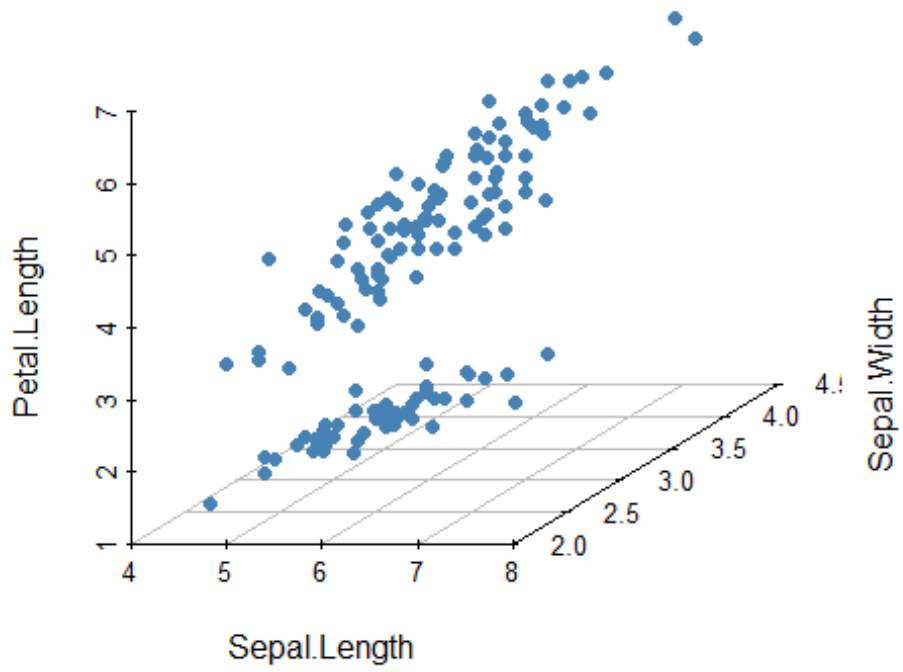
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
```

```
library(scatterplot3d)
scatterplot3d(
  iris[,1:3], pch = 19, color = "steelblue",
   grid = TRUE, box = FALSE,
   mar = c(3, 3, 0.5, 3)
  )
library(GGally)
```

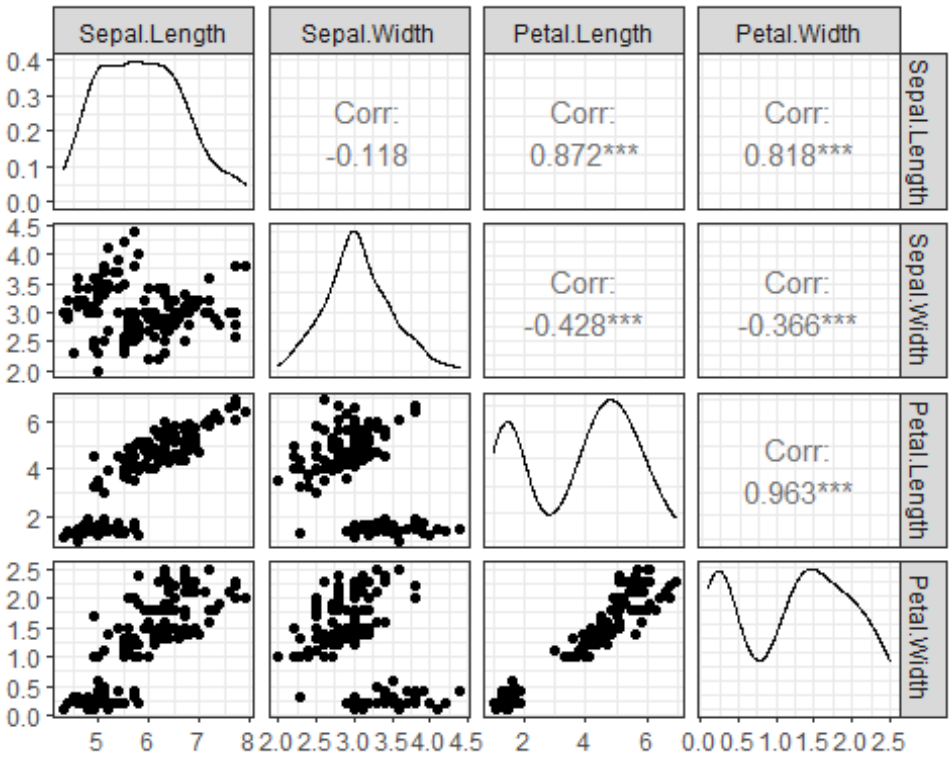
```
## Warning: package 'GGally' was built under R version 4.1.3
```

```
## Loading required package: ggplot2
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```



```
library(ggplot2)
ggpairs(iris[,-5])+ theme_bw()
```




```
p <- ggpairs(iris, aes(color = Species))+ theme_bw()
# Change color manually.
# Loop through each plot changing relevant scales
for(i in 1:p$nrow) {
  for(j in 1:p$ncol){
    p[i,j] <- p[i,j] +
        scale_fill_manual(values=c("#00AFBB", "#E7B800", "#FC4E07")) +
        scale_color_manual(values=c("#00AFBB", "#E7B800", "#FC4E07"))
  }
}
p
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

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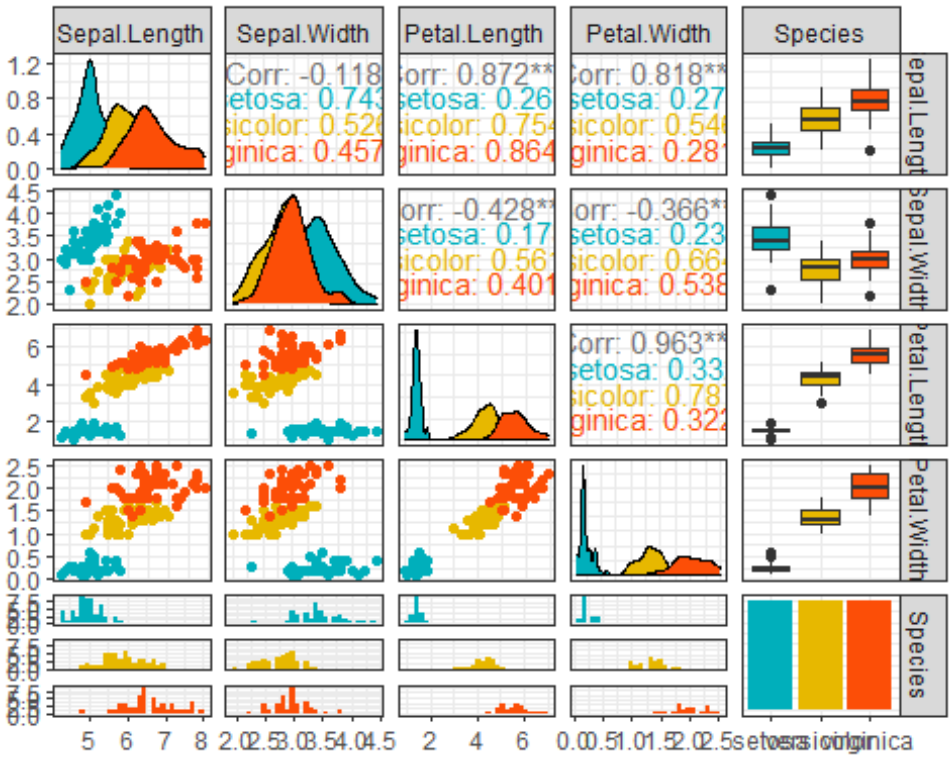
```




```
# install.packages("PerformanceAnalytics")
library("PerformanceAnalytics")

## Warning: package 'PerformanceAnalytics' was built under R version 4.1.3

## Loading required package: xts

## Loading required package: zoo

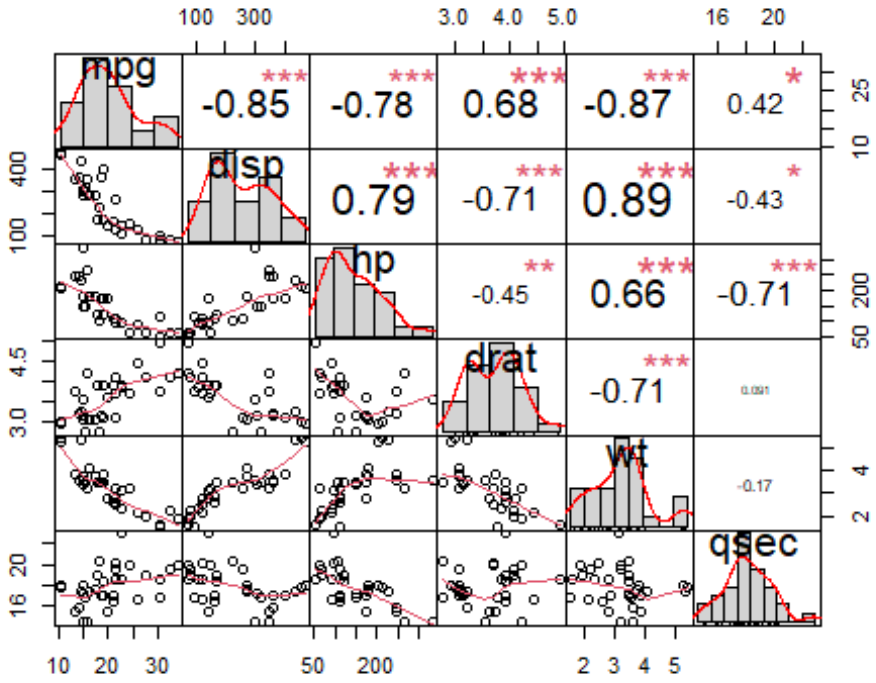
##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric

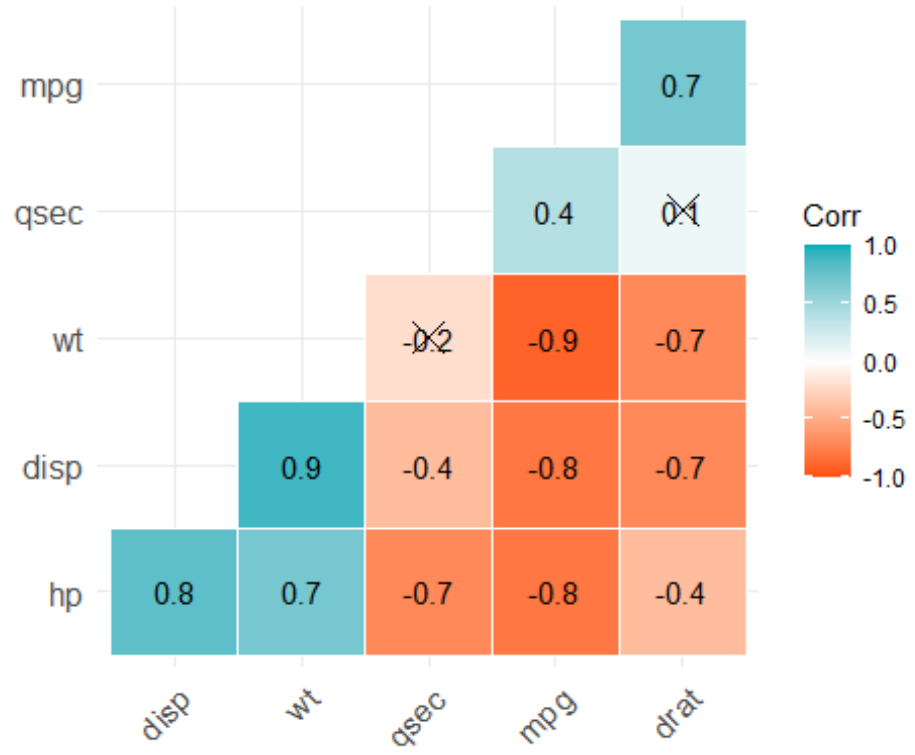
##
## Attaching package: 'PerformanceAnalytics'

## The following object is masked from 'package:graphics':
##
##     legend

my_data <- mtcars[, c(1,3,4,5,6,7)]
chart.Correlation(my_data, histogram=TRUE, pch=19)
```




```
library("ggcorrplot")
# Compute a correlation matrix
my_data <- mtcars[, c(1,3,4,5,6,7)]
corr <- round(cor(my_data), 1)
# Visualize
ggcorrplot(corr, p.mat = cor_pmat(my_data),
           hc.order = TRUE, type = "lower",
           color = c("#FC4E07", "white", "#00AFBB"),
           outline.col = "white", lab = TRUE)
```

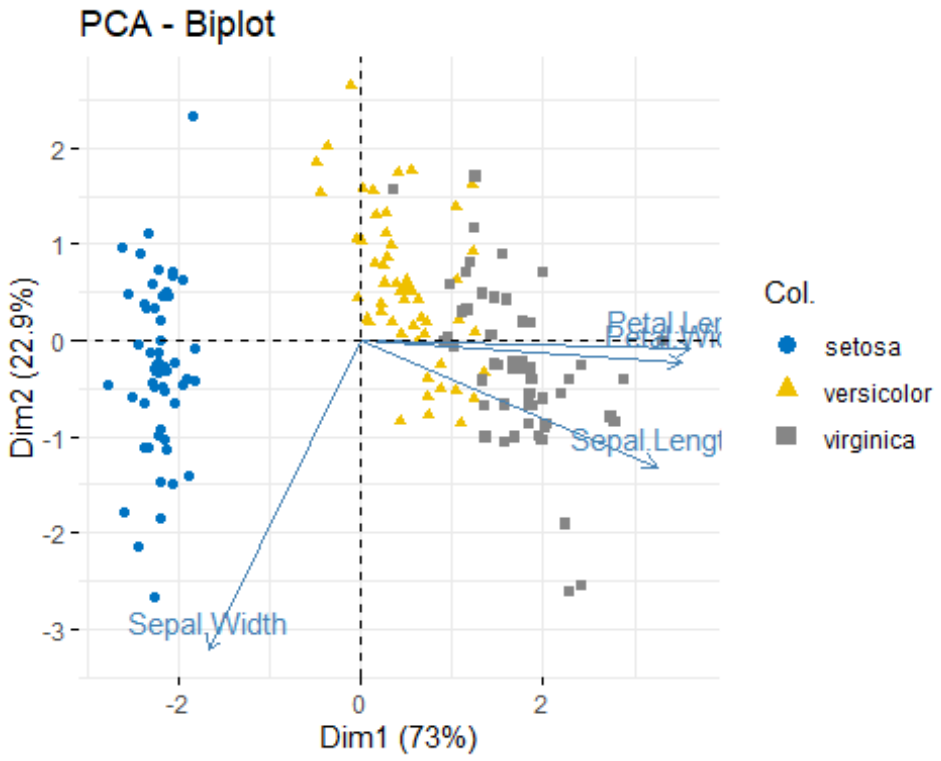



```
library("factoextra")

## Warning: package 'factoextra' was built under R version 4.1.3

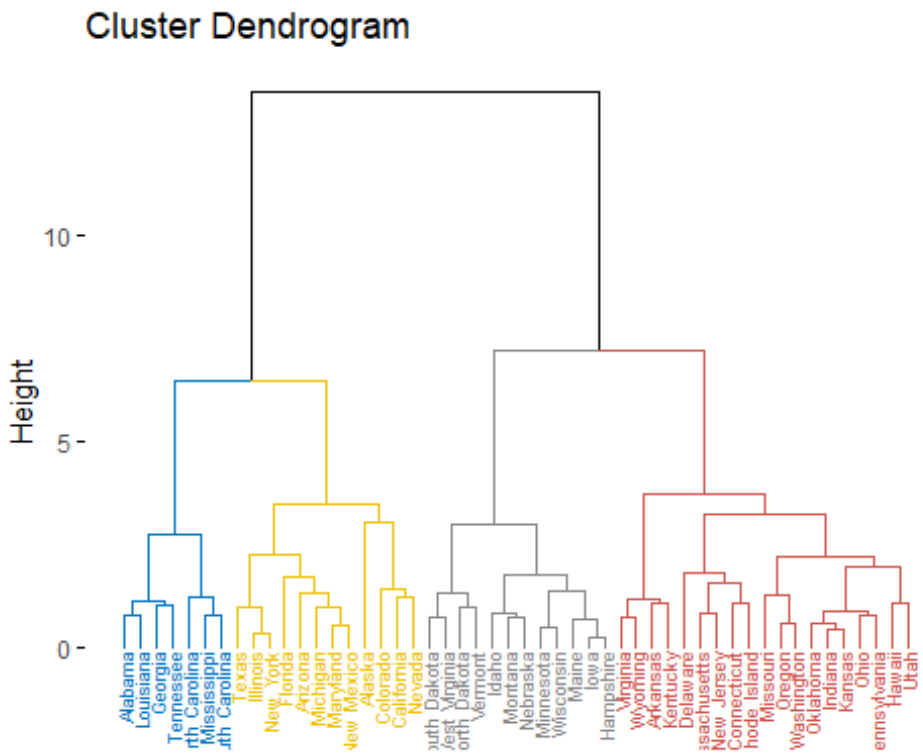
## Welcome! Want to learn more? See two factoextra-related books at
https://goo.gl/ve3WBa

my_data <- iris[, -5] # Remove the grouping variable
res.pca <- prcomp(my_data, scale = TRUE)
fviz_pca_biplot(res.pca, col.ind = iris$Species,
                palette = "jco", geom = "point")
```




```
library(factoextra)
USArrests %>%
  scale() %>%                          # Scale the data
  dist() %>%                           # Compute distance matrix
  hclust(method = "ward.D2") %>%       # Hierarchical clustering
  fviz_dend(cex = 0.5, k = 4, palette = "jco") # Visualize and cut
```

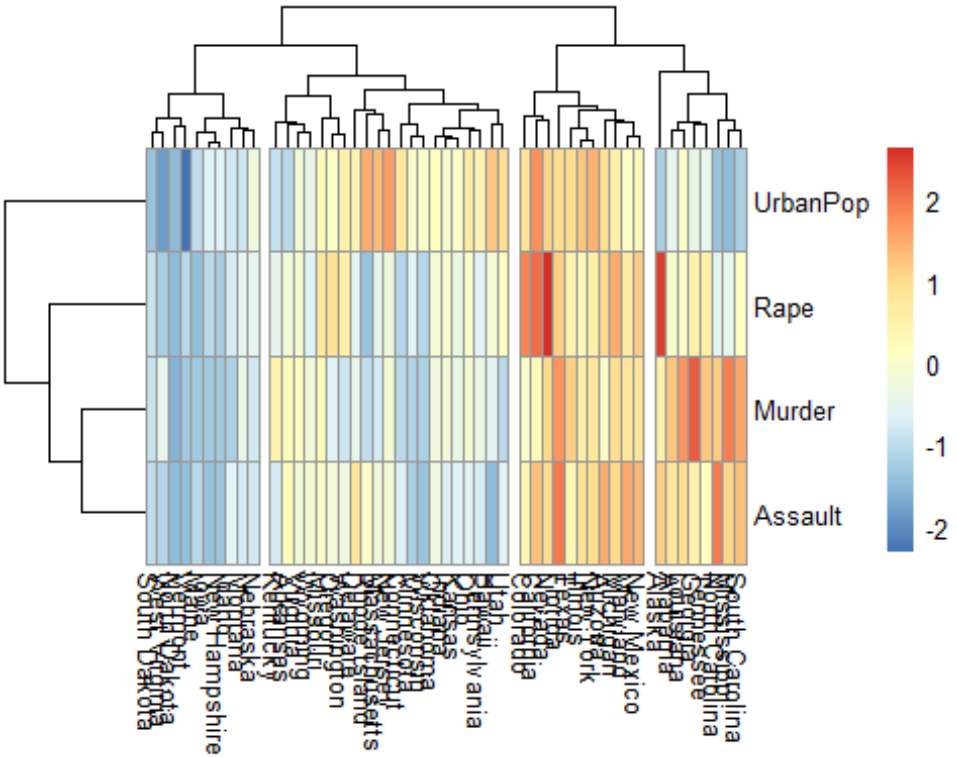
```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use
`guides(<scale> =
## "none")` instead.
```




```
                                          # into 4 groups
library(pheatmap)

## Warning: package 'pheatmap' was built under R version 4.1.3

USArrests %>%
  scale() %>%                    # Scale variables
  t() %>%                        # Transpose
  pheatmap(cutree_cols = 4)      # Create the heatmap
```


UrbanPop
Rape
Murder
Assault
2
1
0
-1
-2