DSA 8070 R Session 1: Exploratory Analysis of Multivariate Data

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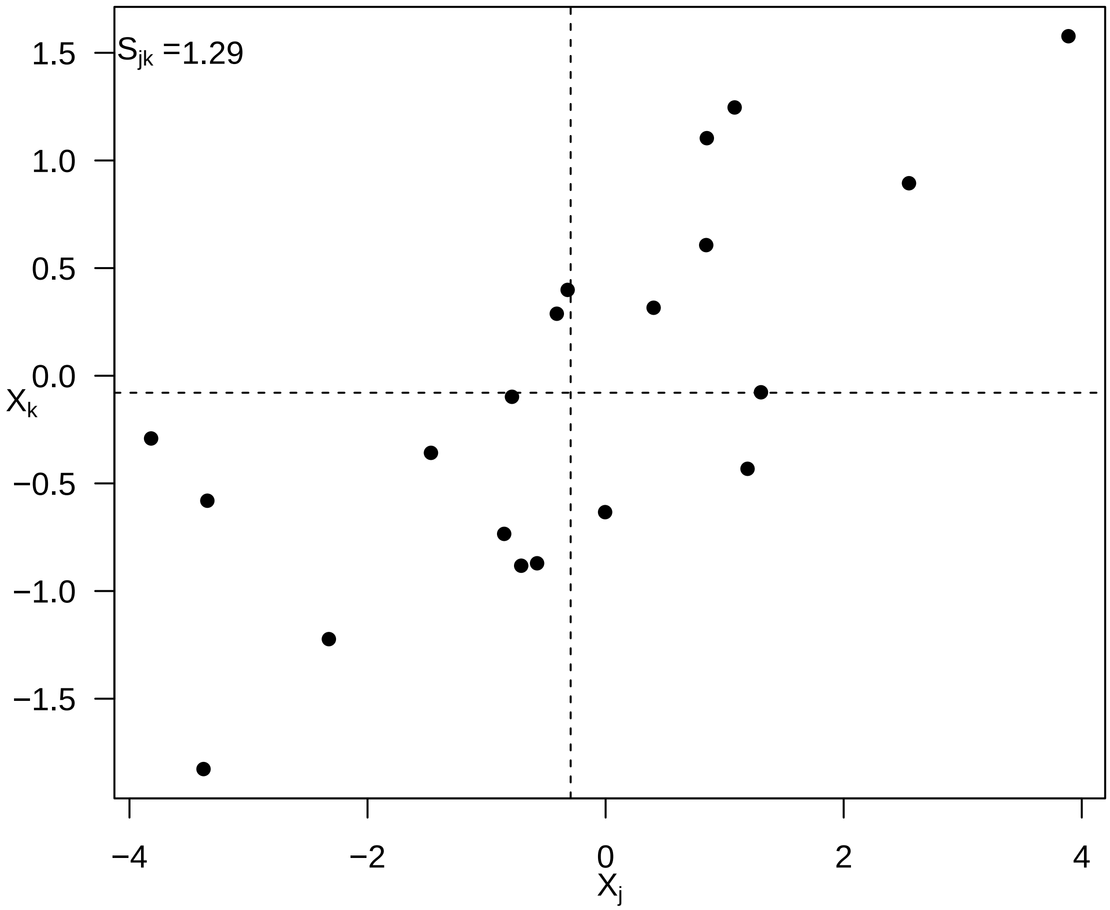
Descriptive Statistics

Sample covariance visualization

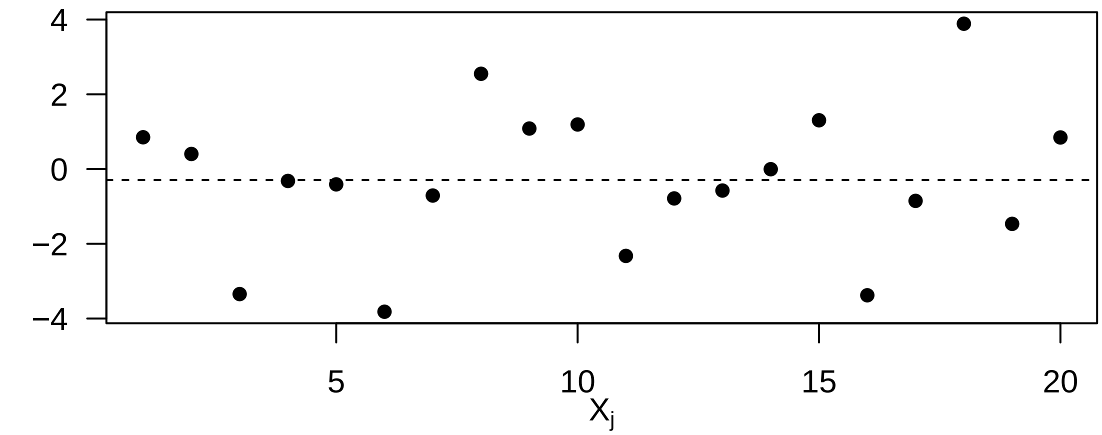
Here, we simulate a bivariate dataset from a bivariate normal distribution with a mean vector of $(0, 0)^T$ and variances of 4 and 1, respectively. Furthermore, the two variables are positively correlated, with a population covariance of 1.4 (resulting in a population correlation of $\frac{1.4}{\sqrt{4}\times\sqrt{1}} = 0.7$). We will use a scatterplot to visualize the covariance.

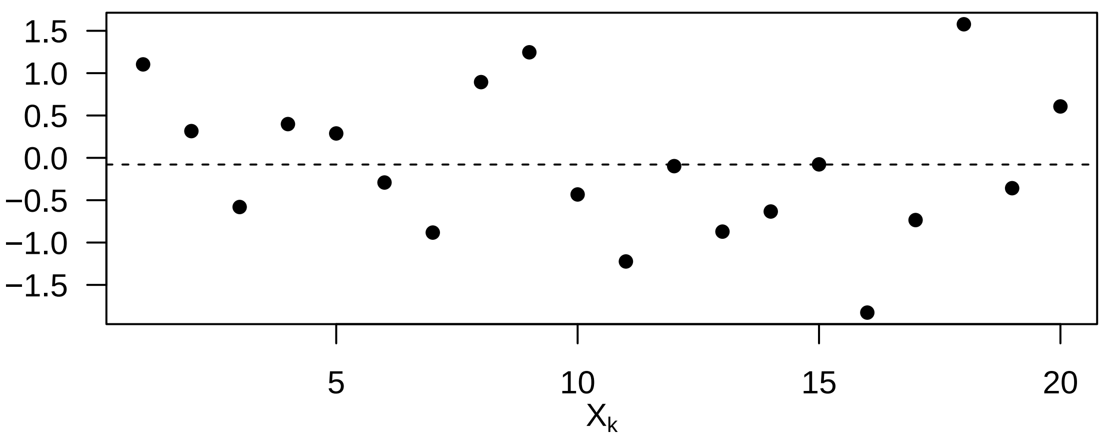
```r
set.seed(123)
library(MASS)
dat <- mvrnorm(n = 20, mu = c(0, 0), Sigma = matrix(c(4, 1.4, 1.4, 1), 2))
n <- dim(dat)[1]
par(mar = c(3.6, 3.6, 0.8, 0.6), las = 1)
plot(dat, pch = 16, las = 1, xlab = "", ylab = "")
mtext(expression(X[j]), 1, line = 2); mtext(expression(X[k]), 2, line = 2)
text(-3.8, 1.5, expression(paste(S[jk], " = ")))
text(-3.3, 1.5, round(cov(dat[, 1], dat[, 2]), 2))
abline(h = mean(dat[, 2]), lty = 2); abline(v = mean(dat[, 1]), lty = 2)
```



We can also create two side-by-side run plots (i.e., plot data by order) to visualize the co-movement.

```
par(mfrow = c(2, 1), mar = c(3.6, 3.6, 0.8, 0.6), las = 1)
plot(1:n, dat[, 1], pch = 16, xlab = "", ylab = "")
abline(h = mean(dat[, 1]), lty = 2)
mtext(expression(X[j]), 1, line = 2)
plot(1:n, dat[, 2], pch = 16, xlab = "", ylab = "")
abline(h = mean(dat[, 2]), lty = 2)
mtext(expression(X[k]), 1, line = 2)
```





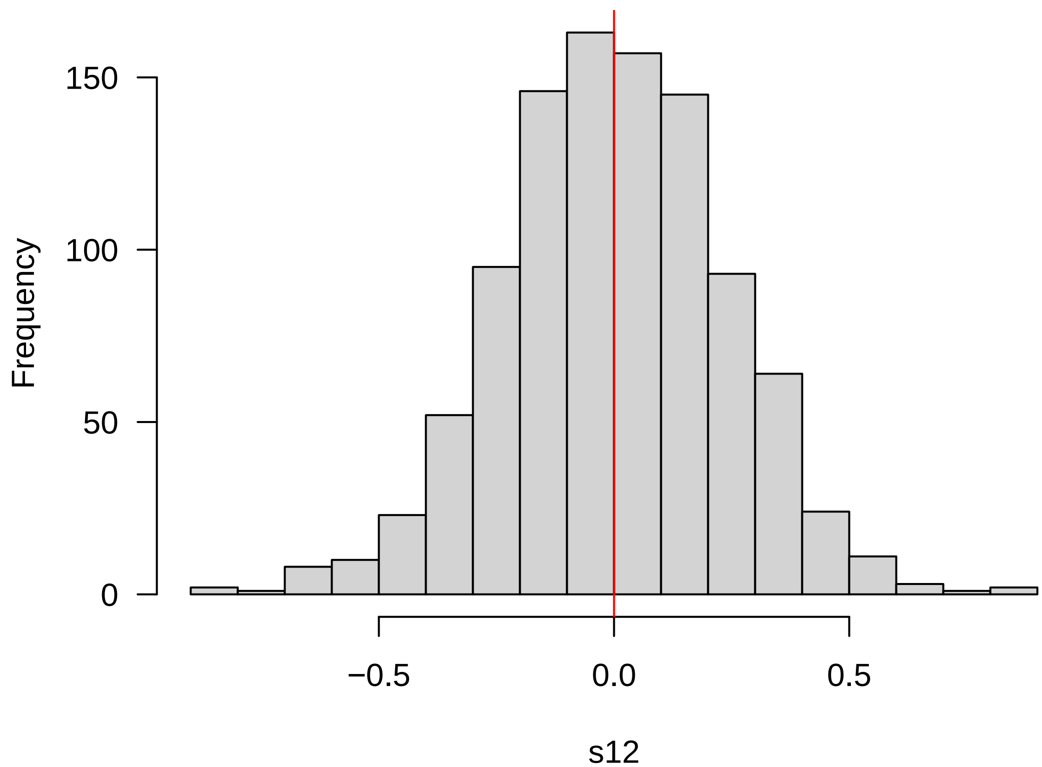
Sample and population covariance

Here, we simulate data with size sample $n = 20$ from a bivariate normal distribution with *population covariance* $\rho_{12} = 0$. For each simulated data set, we calculate the *sample covariance* s_{12} and repeat this process 1,000 times.

The main purpose of this exercise is to demonstrate that one can conduct a *Monte Carlo* experiment to approximate the *sampling distribution* of s_{12} when two variables are independent to each other.

```
dat <- replicate(1000, mvrnorm(n = 20, mu = c(0, 0), Sigma = matrix(c(1, 0, 0, 1), 2)))

s12 <- apply(dat, 3, function(x) cov(x[, 1], x[, 2]))
hist(s12, 20, las = 1, main = "")
abline(v = 0, col = "red")
```



Bivariate Data Example

```
data <- cbind(x1 = c(42, 52, 88, 58, 60), x2 = c(4, 5, 7, 4, 5))
(means <- apply(data, 2, mean))
```

```
## x1 x2
## 60  5
```

```
cov(data)
```

```
##     x1   x2
## x1 294 19.0
## x2  19  1.5
```

```
cor(data)
```

```
##           x1        x2
## x1 1.0000000 0.9047619
## x2 0.9047619 1.0000000
```

Generliazed Variance

The generalized variance is the determinant of the covariance matrix - it reflects the overall spread (volume) of the data in multivariate space.

```r
data(mtcars)
vars <- which(names(mtcars) %in% c("mpg", "disp", "hp", "drat", "wt"))
car <- mtcars[, vars]; S <- cov(car)
(genVar <- det(S))
```

```
## [1] 3951786
```

- With fixed variances, stronger correlations (positive or negative) reduce the generalized variance.
- If variables are uncorrelated, it equals the product of their variances.

```r
set.seed(123)
dat <- mvrnorm(n = 100, mu = c(0, 0), Sigma = matrix(c(4, 1.4, 1.4, 1), 2))
det(cov(dat))
```

```
## [1] 1.585516
```

```r
set.seed(123)
dat1 <- mvrnorm(n = 100, mu = c(0, 0), Sigma = matrix(c(4, 0, 0, 1), 2))
det(cov(dat1))
```

```
## [1] 3.108855
```

Sample vs. Population Population values come from the true covariance matrix; sample values use the sample covariance and vary due to random sampling but converge to the population value as sample size grows.

```r
det(cov(dat))
```

```
## [1] 1.585516
```

```r
det(matrix(c(4, 1.4, 1.4, 1), 2))
```

```
## [1] 2.04
```

```r
det(cov(dat1))
```

```
## [1] 3.108855
```

```r
det(matrix(c(4, 0, 0, 1), 2))
```

```
## [1] 4
```

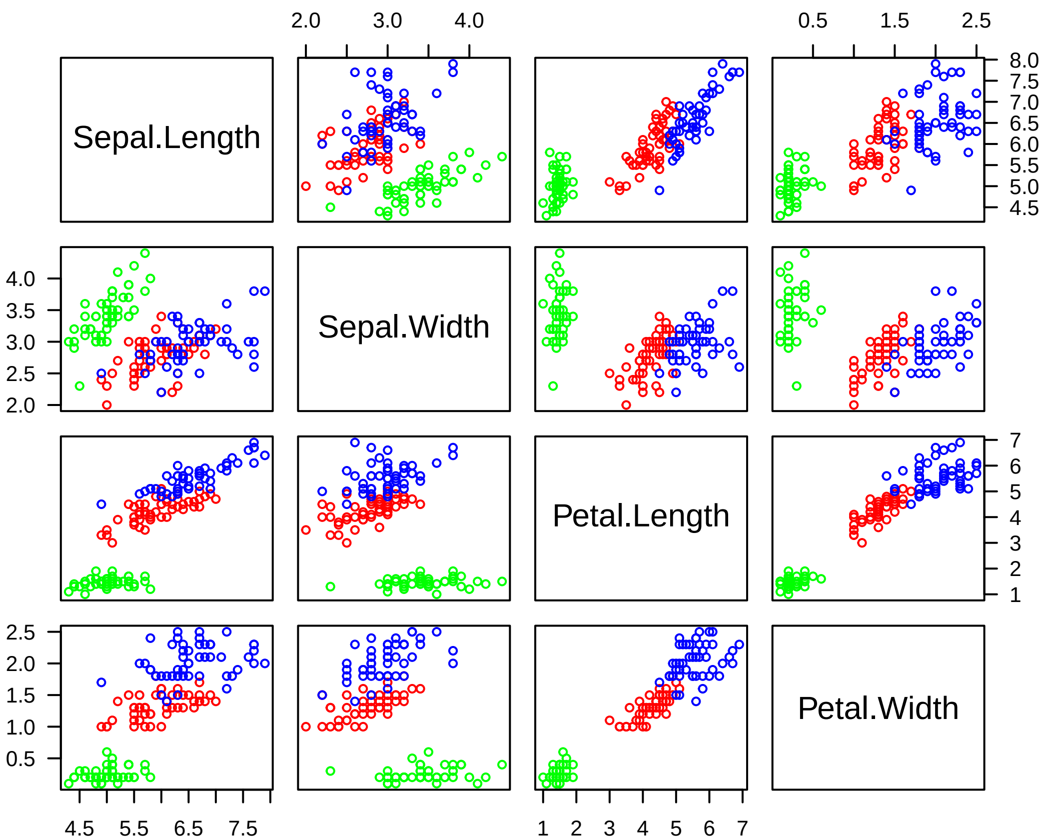
Graphs and Visualization

pairs

```r
head(iris)
```

```
##   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
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

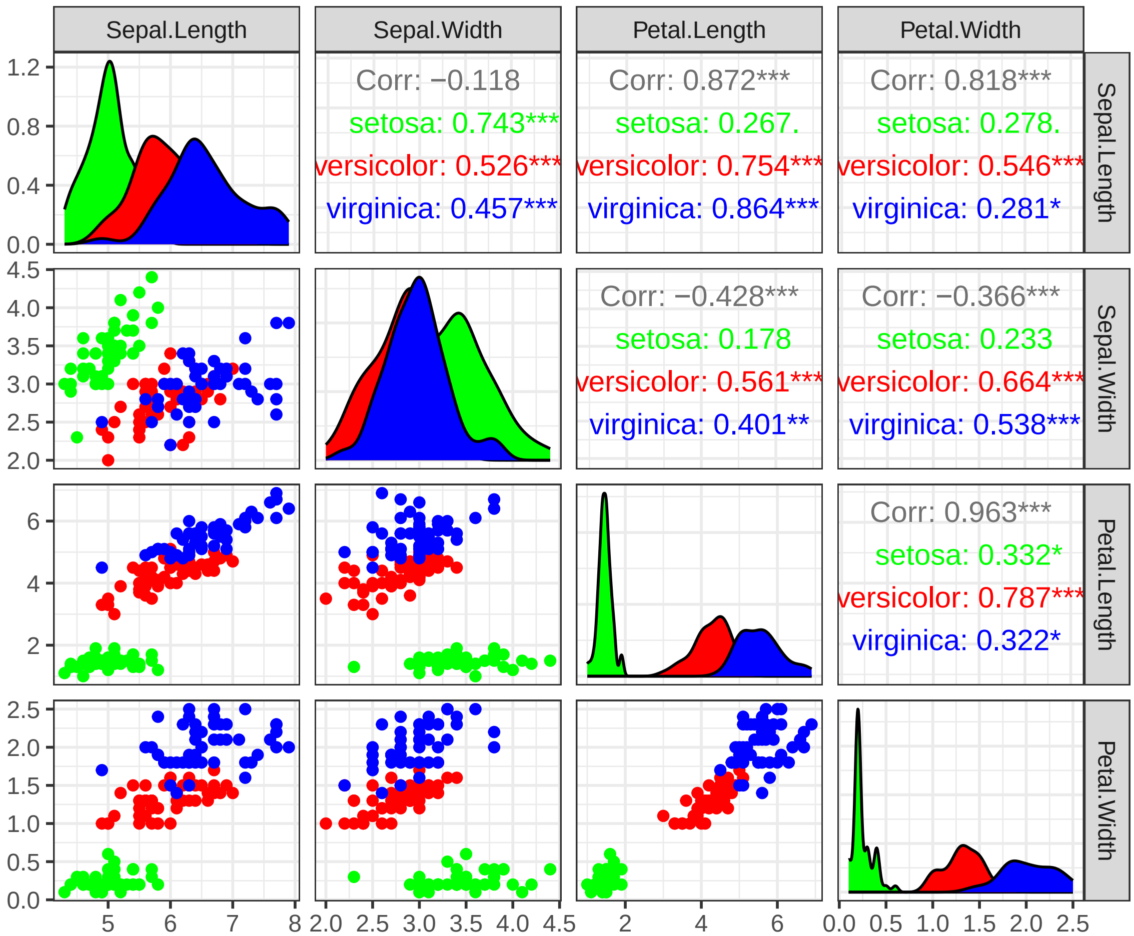
```r
pairs(iris[, -5], las = 1, col = rep(c("green", "red", "blue"), each = 50), cex = 0.8)
```



ggpairs

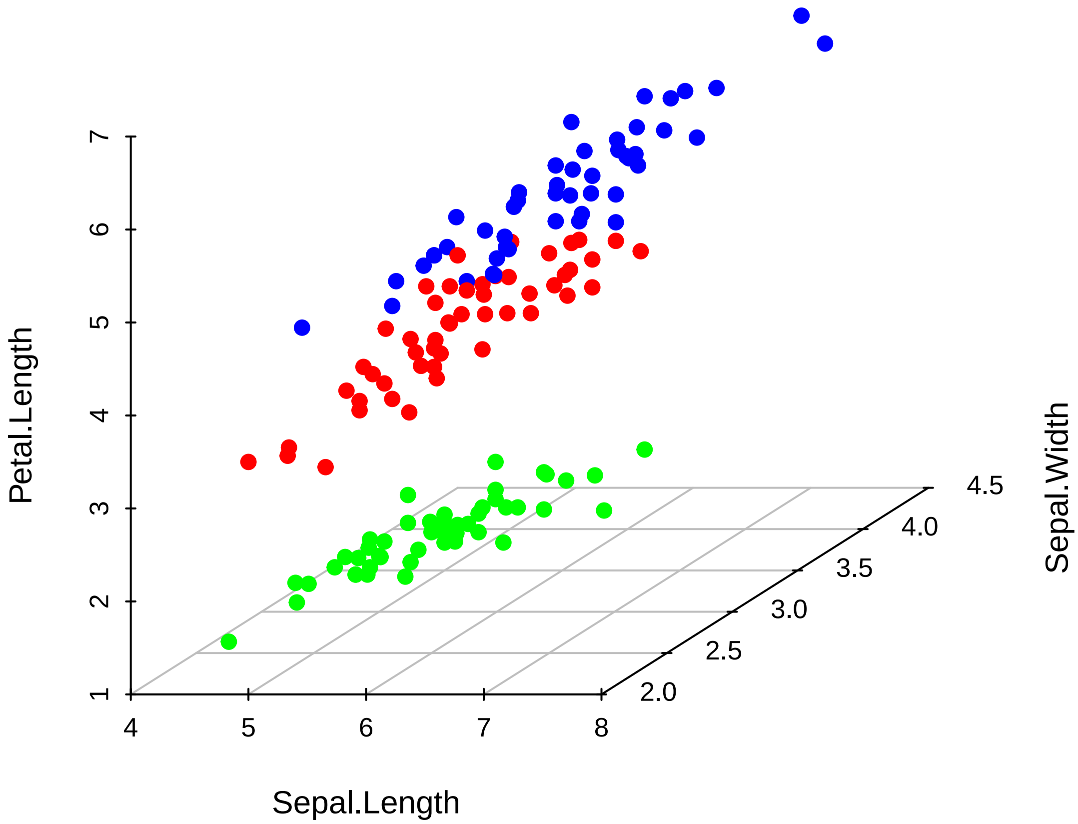
```r
library(GGally)
library(ggplot2)
p <- ggpairs(iris[, -5], aes(color = iris$Species)) + theme_bw()
# Change color manually.
# Loop through each plot changing relevant scales
for(i in 1:p$nrow) {
  for(j in 1:p$ncol){
    p[i, j] <- p[i, j] +
        scale_fill_manual(values = c("green", "red", "blue")) +
```

```
        scale_color_manual(values = c("green", "red", "blue"))
  }
}
p
```



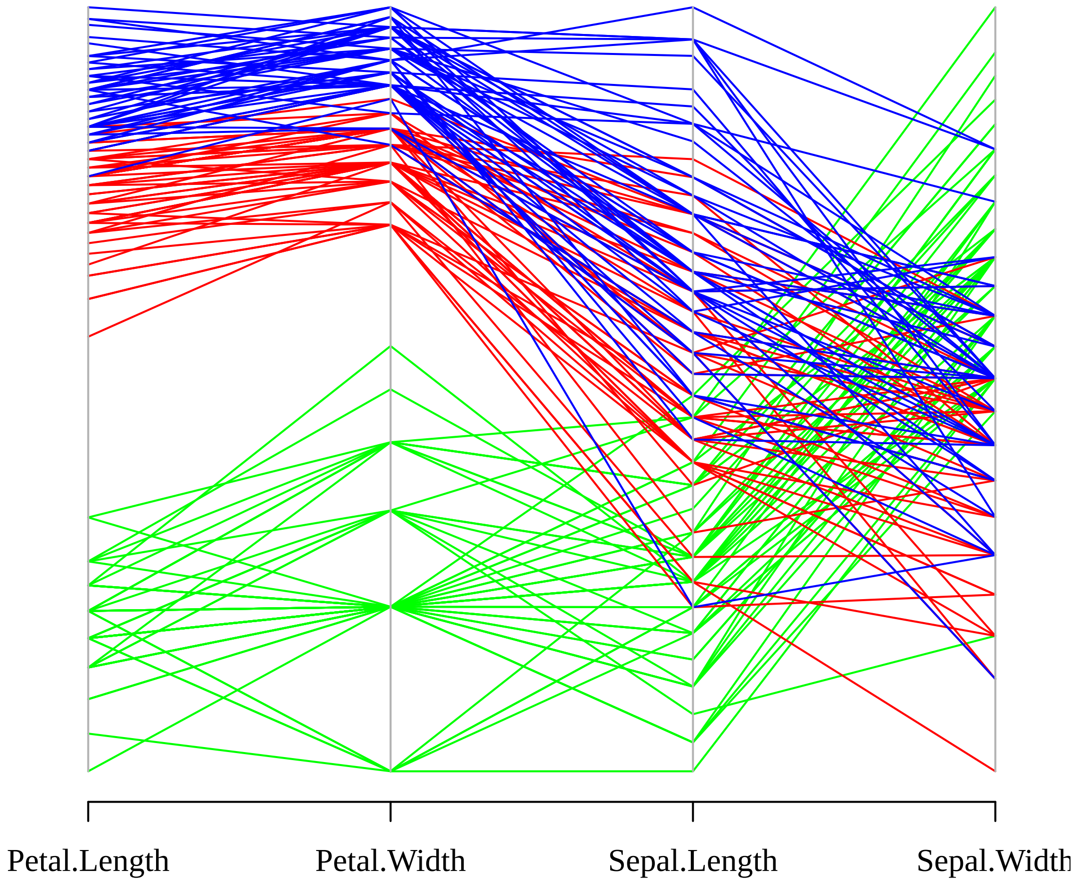
3D Scatter Plot

```
library(scatterplot3d)
scatterplot3d(iris[, 1:3], pch = 19, color = rep(c("green", "red", "blue"), each = 50),
              grid = TRUE, box = FALSE, mar = c(3, 3, 0.5, 3))
```



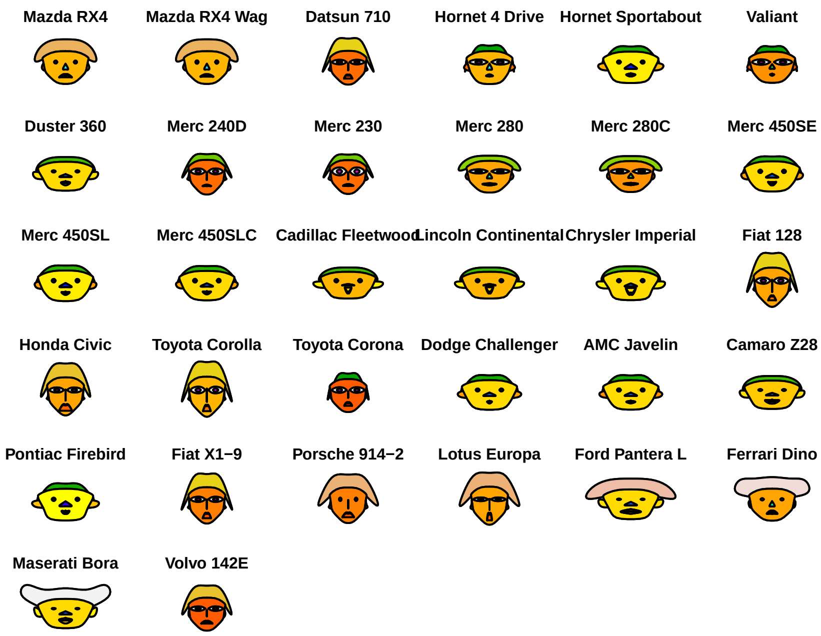
Parallel Coordinate Plot

```
dat <- iris[, 1:4]
par(mar = c(3, 3.5, 0.5, 1), mgp = c(2, 1, 0), las = 1,
    family = "serif", font = 3)
parcoord(log(dat)[ , c(3, 4, 1, 2)], # Order the axes
col = rep(c("green", "red", "blue"), each = 50))
```



Chernoff Faces

```
library(aplpack)
par(mar = rep(0, 4))
faces(mtcars, cex = 0.8)
```



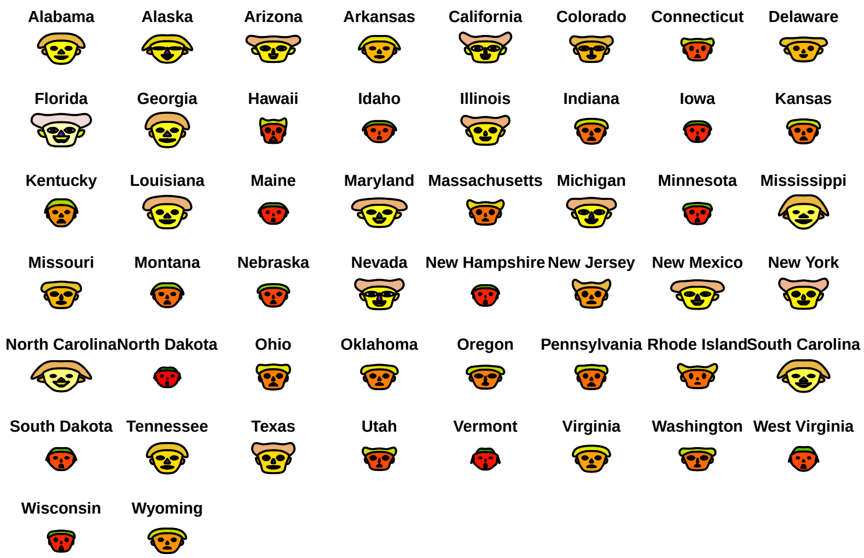

```
## effect of variables:
##  modified item       Var
##  "height of face   " "mpg"
##  "width of face    " "cyl"
##  "structure of face" "disp"
##  "height of mouth  " "hp"
##  "width of mouth   " "drat"
##  "smiling          " "wt"
##  "height of eyes   " "qsec"
##  "width of eyes    " "vs"
##  "height of hair   " "am"
##  "width of hair   "  "gear"
##  "style of hair   "  "carb"
##  "height of nose  "  "mpg"
##  "width of nose   "  "cyl"
##  "width of ear    "  "disp"
##  "height of ear   "  "hp"
```

```
USArrests
```

```
##                  Murder Assault UrbanPop Rape
## Alabama            13.2     236       58 21.2
## Alaska             10.0     263       48 44.5
## Arizona             8.1     294       80 31.0
## Arkansas            8.8     190       50 19.5
## California          9.0     276       91 40.6
## Colorado            7.9     204       78 38.7
## Connecticut         3.3     110       77 11.1
## Delaware            5.9     238       72 15.8
## Florida            15.4     335       80 31.9
## Georgia            17.4     211       60 25.8
## Hawaii              5.3      46       83 20.2
## Idaho               2.6     120       54 14.2
```

```
## Illinois          10.4     249        83 24.0
## Indiana            7.2     113        65 21.0
## Iowa               2.2      56        57 11.3
## Kansas             6.0     115        66 18.0
## Kentucky           9.7     109        52 16.3
## Louisiana         15.4     249        66 22.2
## Maine              2.1      83        51  7.8
## Maryland          11.3     300        67 27.8
## Massachusetts      4.4     149        85 16.3
## Michigan          12.1     255        74 35.1
## Minnesota          2.7      72        66 14.9
## Mississippi       16.1     259        44 17.1
## Missouri           9.0     178        70 28.2
## Montana            6.0     109        53 16.4
## Nebraska           4.3     102        62 16.5
## Nevada            12.2     252        81 46.0
## New Hampshire      2.1      57        56  9.5
## New Jersey         7.4     159        89 18.8
## New Mexico        11.4     285        70 32.1
## New York          11.1     254        86 26.1
## North Carolina    13.0     337        45 16.1
## North Dakota       0.8      45        44  7.3
## Ohio               7.3     120        75 21.4
## Oklahoma           6.6     151        68 20.0
## Oregon             4.9     159        67 29.3
## Pennsylvania       6.3     106        72 14.9
## Rhode Island       3.4     174        87  8.3
## South Carolina    14.4     279        48 22.5
## South Dakota       3.8      86        45 12.8
## Tennessee         13.2     188        59 26.9
## Texas             12.7     201        80 25.5
## Utah               3.2     120        80 22.9
## Vermont            2.2      48        32 11.2
## Virginia           8.5     156        63 20.7
## Washington         4.0     145        73 26.2
## West Virginia      5.7      81        39  9.3
## Wisconsin          2.6      53        66 10.8
## Wyoming            6.8     161        60 15.6
```

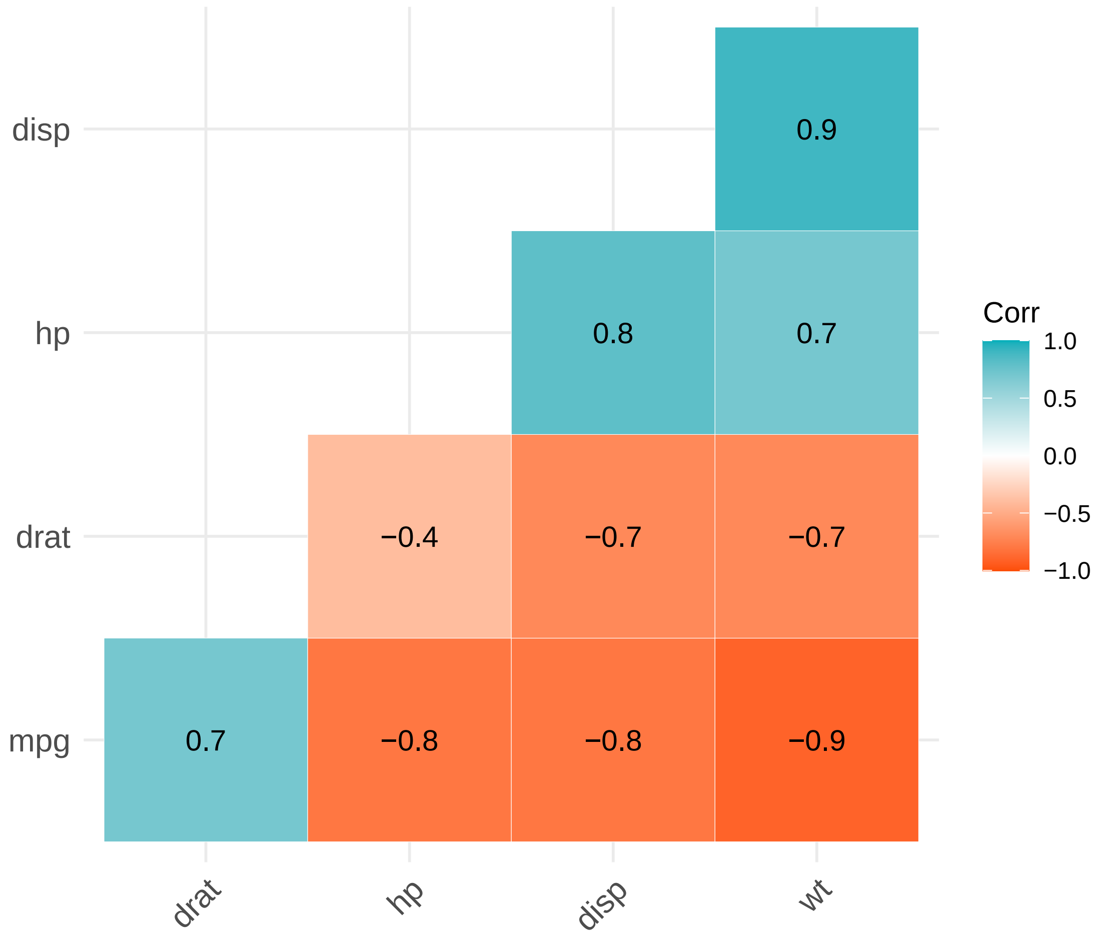
```r
faces(USArrests, cex = 0.8)
```




```
## effect of variables:
##  modified item       Var
##  "height of face   " "Murder"
##  "width of face    " "Assault"
##  "structure of face" "UrbanPop"
##  "height of mouth  " "Rape"
##  "width of mouth   " "Murder"
##  "smiling          " "Assault"
##  "height of eyes   " "UrbanPop"
##  "width of eyes    " "Rape"
##  "height of hair   " "Murder"
##  "width of hair   "  "Assault"
##  "style of hair   "  "UrbanPop"
##  "height of nose  "  "Rape"
##  "width of nose   "  "Murder"
##  "width of ear    "  "Assault"
##  "height of ear   "  "UrbanPop"
```

Visualizing Summary Statistics

```r
library(ggcorrplot)
# Compute a correlation matrix
corr <- round(cor(car), 1)
# Visualize
ggcorrplot(corr, p.mat = cor_pmat(car),
           hc.order = TRUE, type = "lower",
           color = c("#FC4E07", "white", "#00AFBB"),
           outline.col = "white", lab = TRUE)
```


Corr
1.0
0.5
0.0
−0.5
−1.0
disp
hp
drat
mpg
drat
hp
disp
wt
0.9
0.8
0.7
−0.4
−0.7
−0.7
0.7
−0.8
−0.8
−0.9