Lecture 7: Descriptive statistics with R: Part I - Quantitative variables

This lecture covers descriptive statistics and corresponding graphical representations for quantitative variables.

Descriptive statistics

- for the whole dataset
- for a single quantitative variable
- for quantitative variables by groups
- for two quantitative variables.

7.1 For the whole dataset

In [1]:

```
# ?ToothGrowth
tg <- ToothGrowth
rbind(head(tg, 3), tail(tg, 3))
```

A data.frame: 6 × 3

	len	supp	dose
	<dbl>	<fct>	<dbl>
1	4.2	VC	0.5
2	11.5	VC	0.5
3	7.3	VC	0.5
58	27.3	OJ	2.0
59	29.4	OJ	2.0
60	23.0	OJ	2.0

In [2]:

```
# Check the dimension
dim(tg)
```

60 3

In [3]:

```
# Summary
summary(tg)
# Note the difference for categorical and numeric variables.
```

```
      len        supp         dose      
 Min.   : 4.20   OJ:30   Min.   :0.500  
 1st Qu.:13.07   VC:30   1st Qu.:0.500  
 Median :19.25           Median :1.000  
 Mean   :18.81           Mean   :1.167  
 3rd Qu.:25.27           3rd Qu.:2.000  
 Max.   :33.90           Max.   :2.000  
```

7.2 For a single quantitative variable

7.2.1 Numerical representation

A lot of statistics, such as,

mean, variance, standard deviation, median, minimum, maximum, range, quantiles, etc...

In [4]:

```
var(tg$len)
```

58.5120225988701

$Var(x)$ in R calculates the variance of the sample x - sample variance thus denominator is $n-1$.

$Var(\boldsymbol{x}) = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$

In [5]:

```
n.sample = dim(tg)[1]
sum((tg$len - mean(tg$len))^2)/(n.sample - 1)
```

58.5120225988701

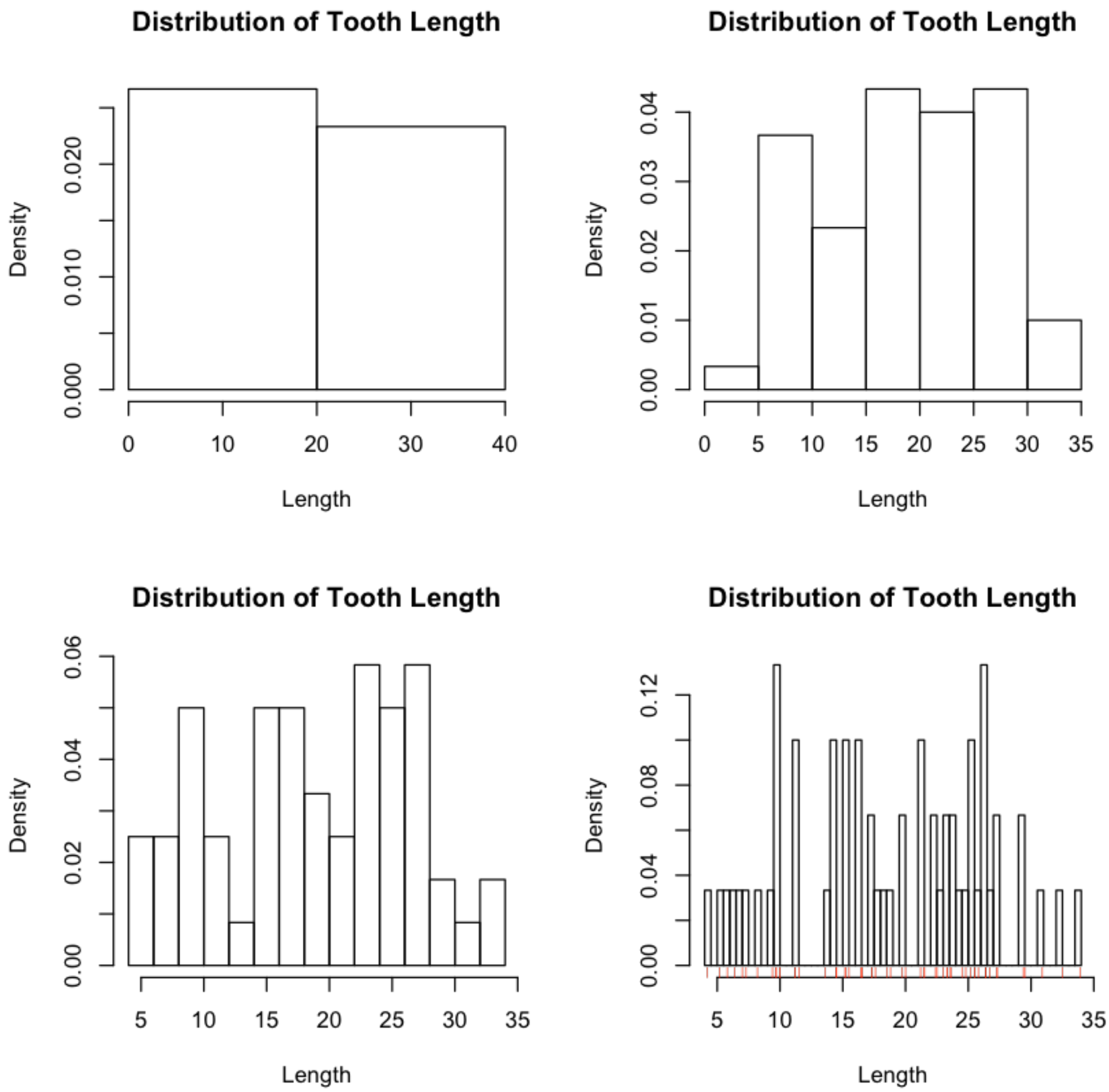
7.2.2 Graphical representation

Check the overall distribution. Check normality in many cases.

i. Histogram

In [6]:

```
par(mfrow=c(2 ,2))
hist(tg$len,
     main = "Distribution of Tooth Length",
     xlab = "Length",
     freq = F,    # F gives probability, T gives count
     breaks = 2) # Number of bars
hist(tg$len,
     main = "Distribution of Tooth Length",
     xlab = "Length",
     freq = F,
     breaks = 5)
hist(tg$len,
     main = "Distribution of Tooth Length",
     xlab = "Length",
     freq = F,
     breaks = 20)
hist(tg$len,
     main = "Distribution of Tooth Length",
     xlab = "Length",
     freq = F,
     breaks = 100)
rug(tg$len, col = "red")# Add ticks at the data points on the x
axis.

# Is the distribution normal?
# See how different number of bins can affect our arbitrary judg
ement of the distribution.
```

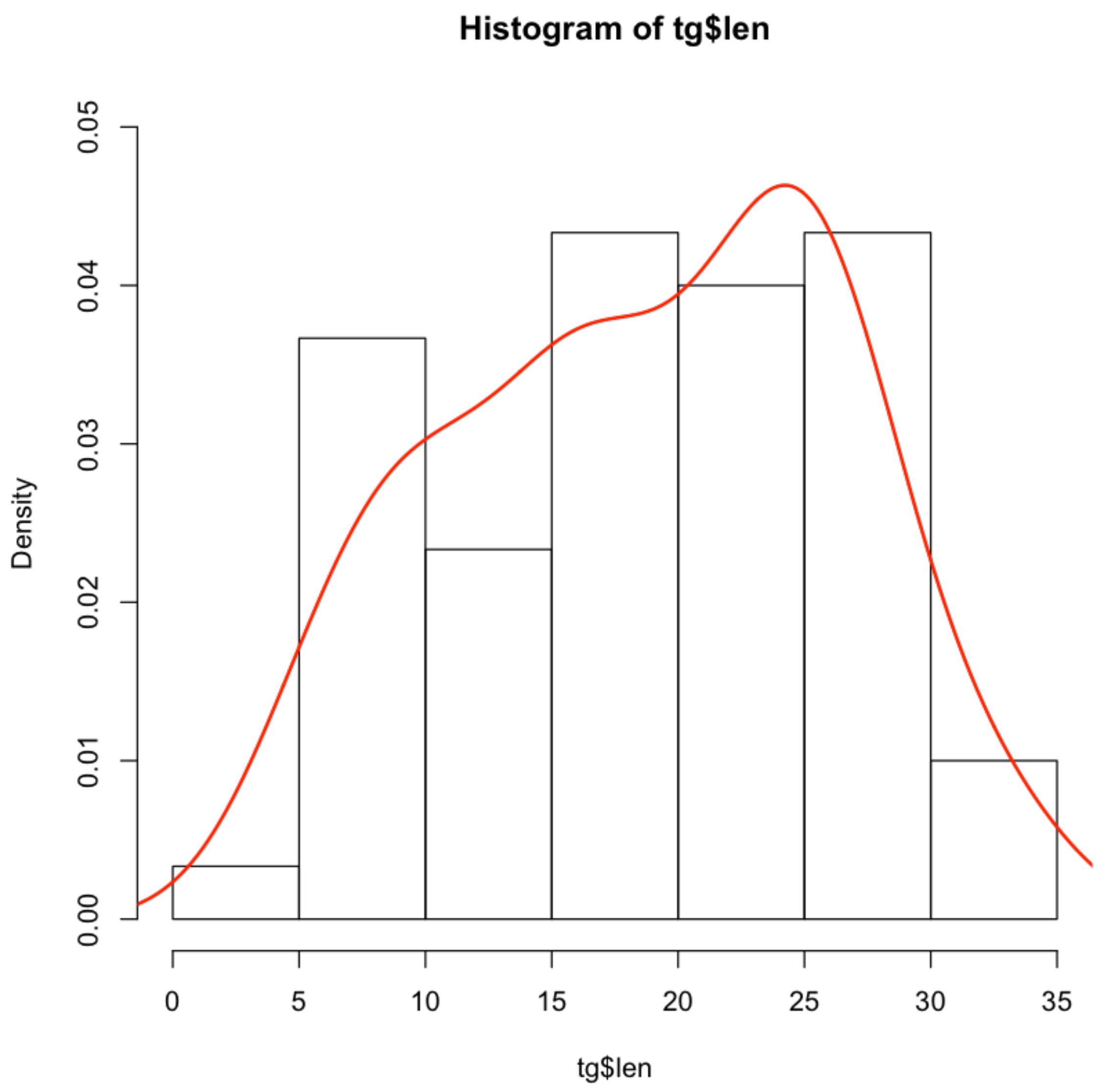


ii. Kernel density*

Non-parametric statistics

In [7]:

```
hist(tg$len, freq = F, ylim = c(0, 0.05))
lines(density(tg$len), col = "red", lwd = 2)
```

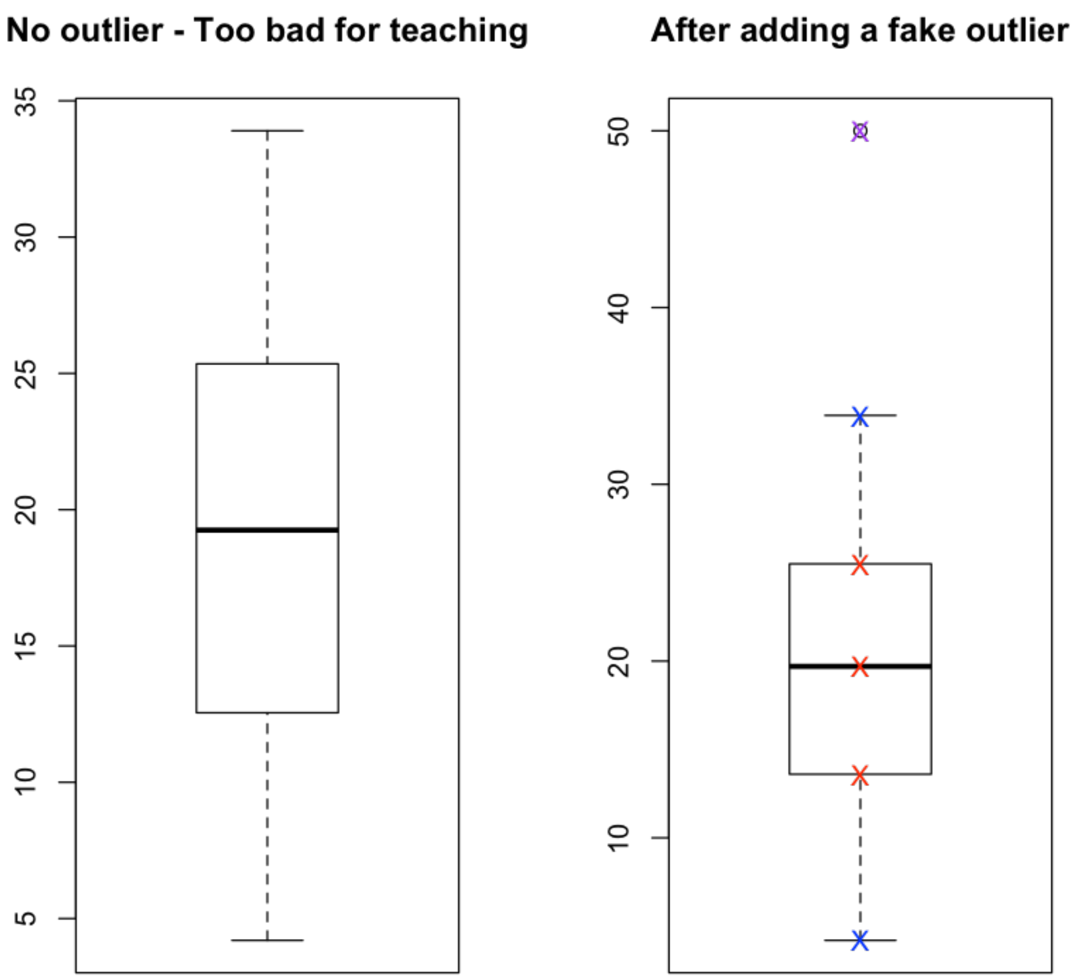


iii. Boxplot

Detect outliers

In [8]:

```
par(mfrow = c(1, 2))
boxplot(tg$len, main = "No outlier - Too bad for teaching")
fake.len <- c(tg$len, 50)
boxplot(fake.len, main = "After adding a fake outlier")
points(x = rep(1,3), quantile(fake.len, seq(0.25, 0.75, 0.25)),
pch = "X", col = "red")
points(x=rep(1,2), c(min(tg$len), max(tg$len)), pch = "X", col =
"blue")
points(x=1, max(fake.len), pch = "X", col = "purple")
# Box: IQR - 25th and 75th quantile
# Whiskers: the lowest datum still within 1.5 IQR of the lower q
uartile,
# and the highest datum still within 1.5 IQR of the upper quarti
le
```



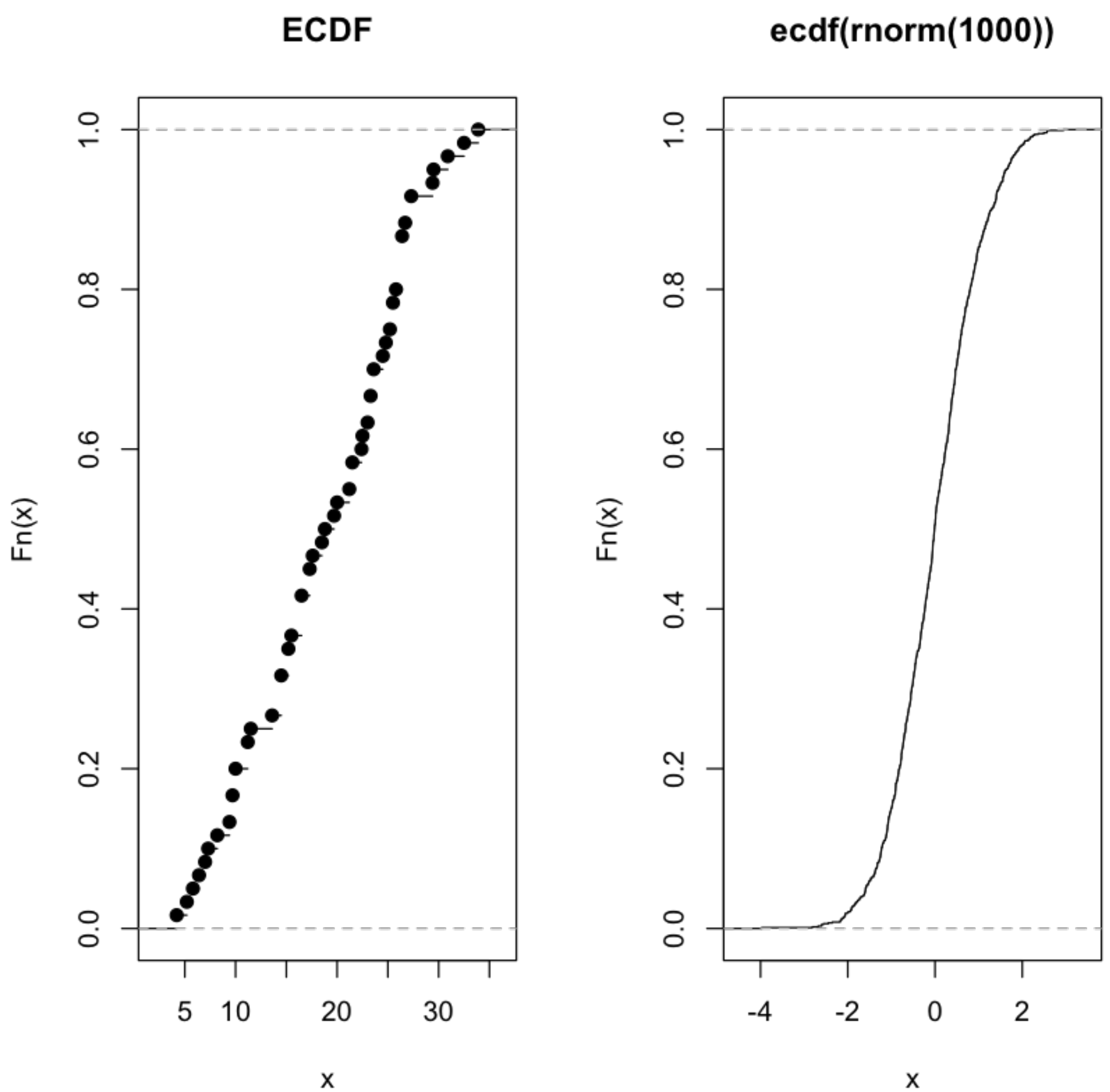
iv. Empirical CDF*

The empirical cumulative distribution function. Again non-parametric statistics.

$$\hat{F}_n(t) = \frac{1}{n}\sum_{i-1}^{n} \mathbf{1}_{(x_i \le t)}$$

In [9]:

```
set.seed(613)
par(mfrow = c(1,2))
plot(ecdf(tg$len), main = "ECDF")
plot(ecdf(rnorm(1000)))
```



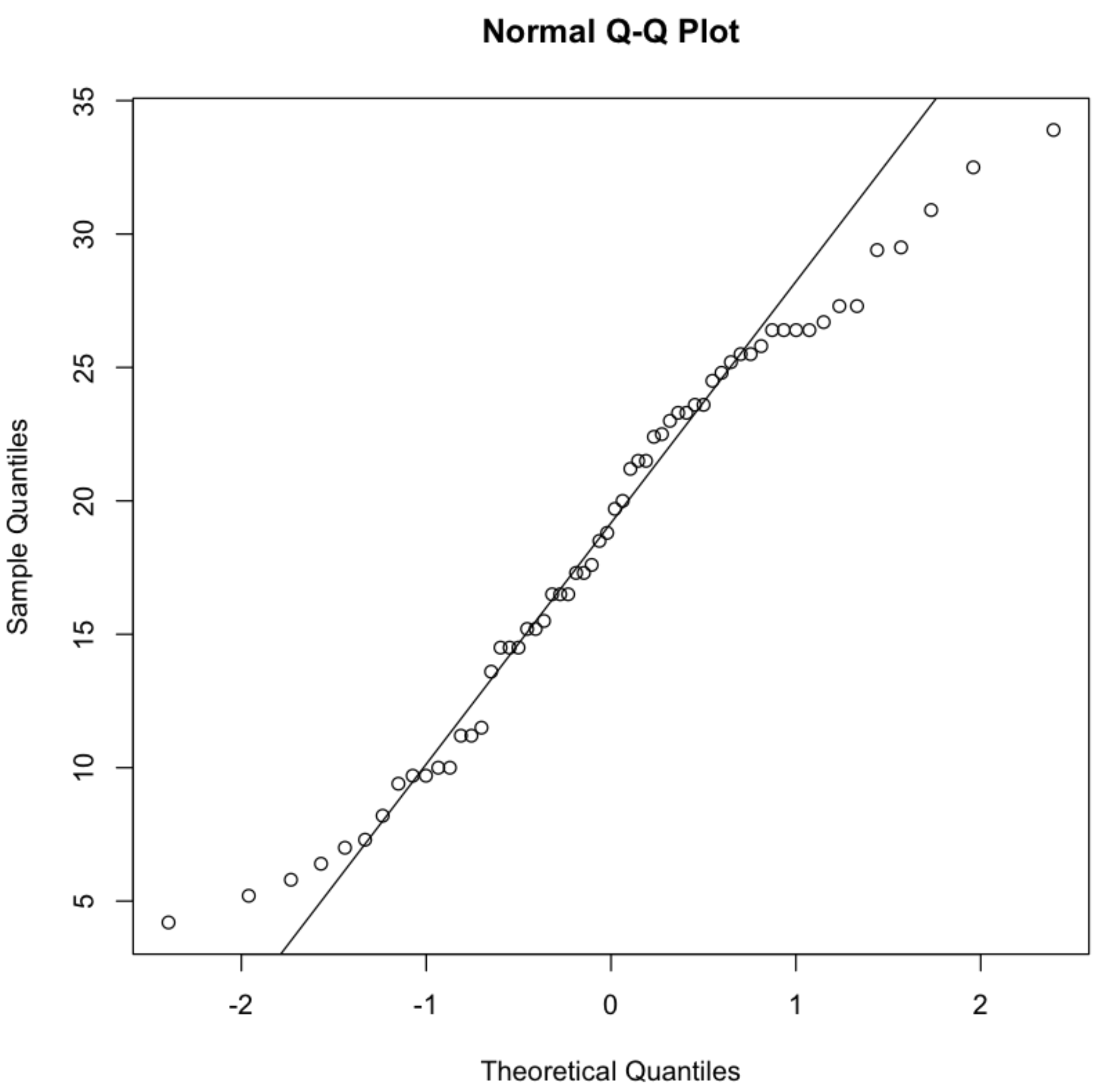
v. Q-Q Plot

quantile-quantile plot

Normal Q-Q plot checks normality.

In [10]:

```
qqnorm(tg$len)
qqline(tg$len)
```



7.3 For quantitative variables by groups

7.3.1 Numerical representation

The following three functions are closely related.

```
- aggregate()
- tapply()
- by()
```

In ToothGrowth dataset, there are 2 different supp, 3 different dose, mean length in all 6 categories.

When the result of your function (FUN) is 1D.

In [11]:

```
# recall aggregate( )
aggregate(len~., data = tg, FUN = mean)
```

A data.frame: 6 × 3

supp	dose	len
<fct>	<dbl>	<dbl>
OJ	0.5	13.23
VC	0.5	7.98
OJ	1.0	22.70
VC	1.0	16.77
OJ	2.0	26.06
VC	2.0	26.14

In [12]:

```
tapply(tg$len,
       INDEX = list(tg$supp, tg$dose),
       FUN = mean)
```

A matrix: 2 × 3 of type dbl

	0.5	1	2
OJ	13.23	22.70	26.06
VC	7.98	16.77	26.14

In [13]:

```
by(tg$len,
   INDICES = list(supp = tg$supp, dose = tg$dose),
   FUN = mean)
```

```
supp: OJ
dose: 0.5
[1] 13.23
----------------------------------------------------
--------
supp: VC
dose: 0.5
[1] 7.98
----------------------------------------------------
--------
supp: OJ
dose: 1
[1] 22.7
----------------------------------------------------
--------
supp: VC
dose: 1
[1] 16.77
----------------------------------------------------
--------
supp: OJ
dose: 2
[1] 26.06
----------------------------------------------------
--------
supp: VC
dose: 2
[1] 26.14
```

When the result of your FUN is multi-dimensional

In [14]:

```
# aggregate(len~., data = tg, FUN = range)
# Gives an error - has to be 1D.
```

In [15]:

```
# A list of length 6
print(tapply(tg$len,
             INDEX = list(tg$supp, tg$dose),
             FUN = range))
# One of the 6 items in the list.
tapply(tg$len,
       INDEX = list(tg$supp, tg$dose),
       FUN = range)[[1]]
```

```
   0.5       1         2
OJ Numeric,2 Numeric,2 Numeric,2
VC Numeric,2 Numeric,2 Numeric,2
```

8.2 21.5

In [16]:

```
by(tg$len,
   INDICES = list(supp = tg$supp, dose = tg$dose),
   FUN = range)
```

```
supp: OJ
dose: 0.5
[1]  8.2 21.5
----------------------------------------------------
--------
supp: VC
dose: 0.5
[1]  4.2 11.5
----------------------------------------------------
--------
supp: OJ
dose: 1
[1] 14.5 27.3
----------------------------------------------------
--------
supp: VC
dose: 1
[1] 13.6 22.5
----------------------------------------------------
--------
supp: OJ
dose: 2
[1] 22.4 30.9
----------------------------------------------------
--------
supp: VC
dose: 2
[1] 18.5 33.9
```

7.3.2 Graphical representation

Compare plots of the subsets. We can use aggregate( ), tapply( ) or by( ).

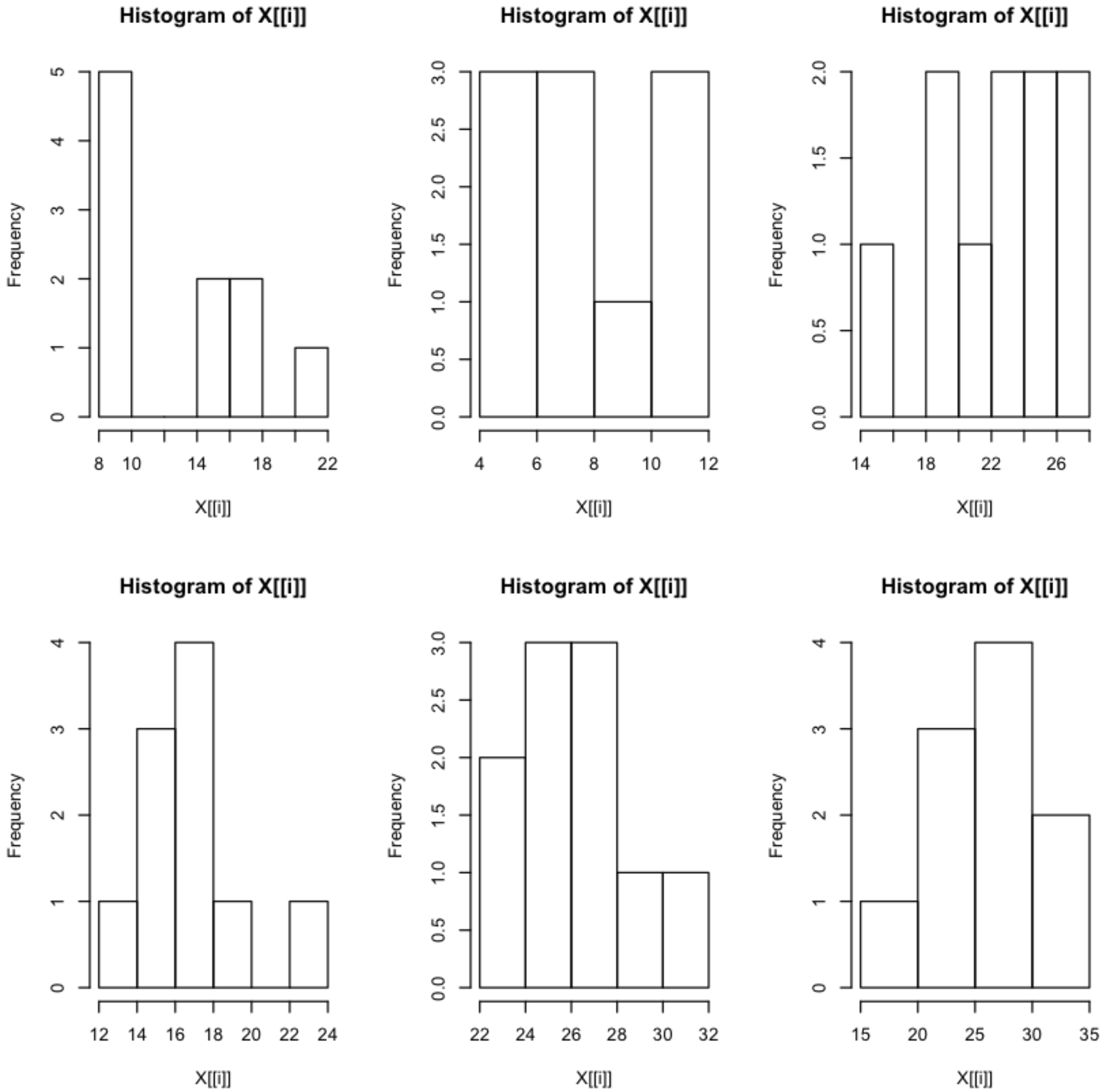
The FUN can be more complicated , e.g. plot( )

In [17]:

```
par(mfrow = c(2,3))
aggregate(len~., data = tg, FUN = hist)
```

A data.frame: 6 × 3

supp	dose	len
<fct>	<dbl>	<list[,6]>
OJ	0.5	8, 10, 12, 14, 16, 18, 20, 22, 5, 0, 0, 2, 2, 0, 1, 0.25, 0.00, 0.00, 0.10, 0.10, 0.00, 0.05, 9, 11, 13, 15, 17, 19, 21, X[[i]], TRUE
VC	0.5	4, 6, 8, 10, 12, 3, 3, 1, 3, 0.15, 0.15, 0.05, 0.15, 5, 7, 9, 11, X[[i]], TRUE
OJ	1.0	14, 16, 18, 20, 22, 24, 26, 28, 1, 0, 2, 1, 2, 2, 2, 0.05, 0.00, 0.10, 0.05, 0.10, 0.10, 0.10, 15, 17, 19, 21, 23, 25, 27, X[[i]], TRUE
VC	1.0	12, 14, 16, 18, 20, 22, 24, 1, 3, 4, 1, 0, 1, 0.05, 0.15, 0.20, 0.05, 0.00, 0.05, 13, 15, 17, 19, 21, 23, X[[i]], TRUE
OJ	2.0	22, 24, 26, 28, 30, 32, 2, 3, 3, 1, 1, 0.10, 0.15, 0.15, 0.05, 0.05, 23, 25, 27, 29, 31, X[[i]], TRUE
VC	2.0	15, 20, 25, 30, 35, 1, 3, 4, 2, 0.02, 0.06, 0.08, 0.04, 17.5, 22.5, 27.5, 32.5, X[[i]], TRUE

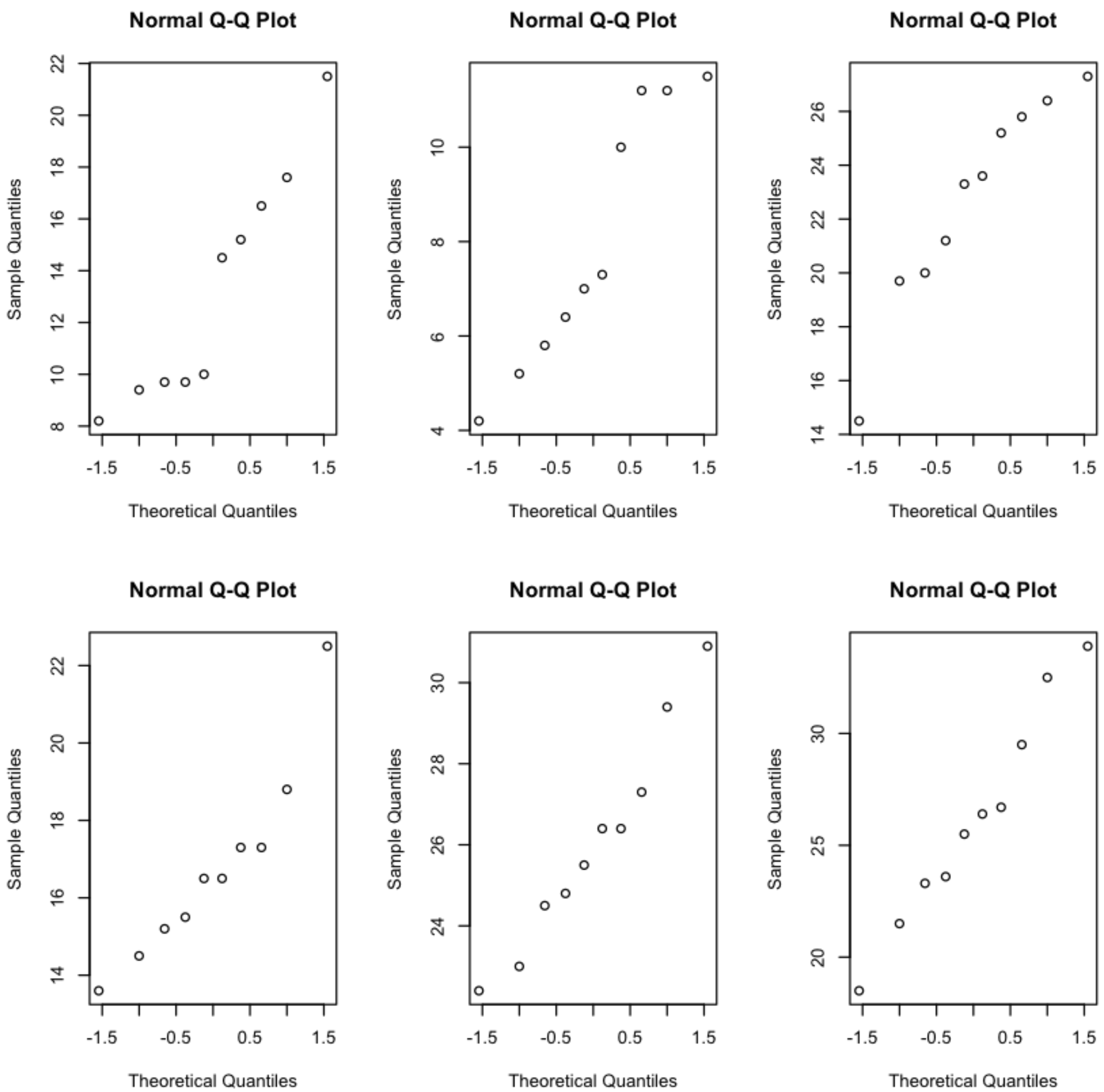


In [18]:

```
par(mfrow = c(2,3))
tapply(tg$len,
       INDEX = list(tg$supp, tg$dose),
       FUN = qqnorm)
```

A matrix: 2 × 3

	0.5	1	2			
	<named list>	<named list>	<named list>	<named list>	<named list>	<named list>
OJ	0.3754618, 1.5466353, 1.0004905, -0.6554235, 0.1225808, -0.1225808, -1.5466353, -1.0004905, 0.6554235, -0.3754618, 15.2000000, 21.5000000, 17.6000000, 9.7000000, 14.5000000, 10.0000000, 8.2000000, 9.4000000, 16.5000000, 9.7000000	-1.0004905, -0.1225808, 0.1225808, 1.0004905, -0.6554235, 0.3754618, 0.6554235, -0.3754618, -1.5466353, 1.5466353, 19.7000000, 23.3000000, 23.6000000, 26.4000000, 20.0000000, 25.2000000, 25.8000000, 21.2000000, 14.5000000, 27.3000000	-0.1225808, 0.1225808, -1.5466353, -0.6554235, -0.3754618, 1.5466353, 0.3754618, 0.6554235, 1.0004905, -1.0004905, 25.5000000, 26.4000000, 22.4000000, 24.5000000, 24.8000000, 30.9000000, 26.4000000, 27.3000000, 29.4000000, 23.0000000			
VC	-1.5466353, 1.5466353, 0.1225808, -0.6554235, -0.3754618, 0.3754618, 0.6554235, 1.0004905, -1.0004905, -0.1225808, 4.2000000, 11.5000000, 7.3000000, 5.8000000, 6.4000000, 10.0000000, 11.2000000, 11.2000000, 5.2000000, 7.0000000	-0.1225808, 0.1225808, -0.6554235, 0.3754618, 1.5466353, 0.6554235, -1.5466353, -1.0004905, 1.0004905, -0.3754618, 16.5000000, 16.5000000, 15.2000000, 17.3000000, 22.5000000, 17.3000000, 13.6000000, 14.5000000, 18.8000000, 15.5000000	-0.3754618, -1.5466353, 1.5466353, -0.1225808, 0.1225808, 1.0004905, 0.3754618, -1.0004905, -0.6554235, 0.6554235, 23.6000000, 18.5000000, 33.9000000, 25.5000000, 26.4000000, 32.5000000, 26.7000000, 21.5000000, 23.3000000, 29.5000000			



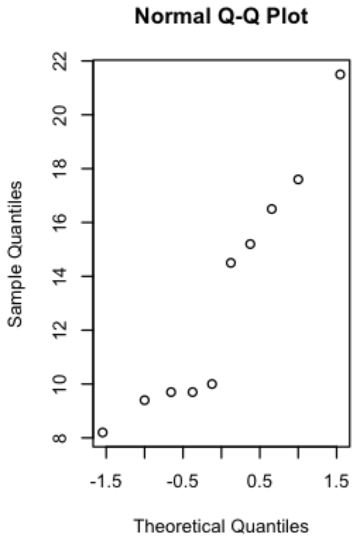
In [19]:

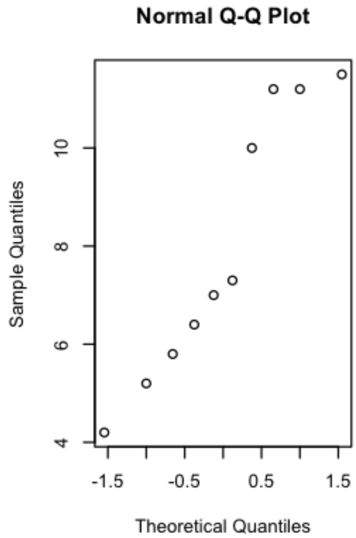
```
par(mfrow = c(2,3))
by(tg$len,
   INDICES = list(supp = tg$supp, dose = tg$dose),
   FUN = qqnorm)
```

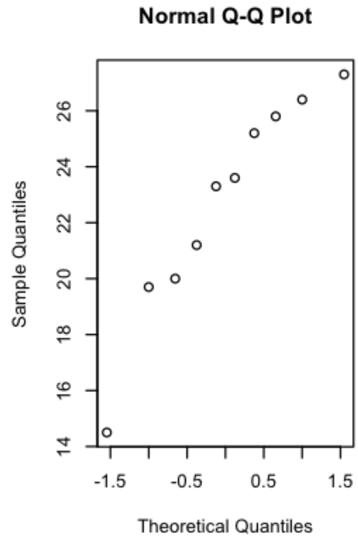
```
supp: OJ
dose: 0.5
$x
 [1]  0.3754618  1.5466353  1.0004905 -0.6554235  0.
1225808 -0.1225808
 [7] -1.5466353 -1.0004905  0.6554235 -0.3754618

$y
 [1] 15.2 21.5 17.6  9.7 14.5 10.0  8.2  9.4 16.5  9
.7
```

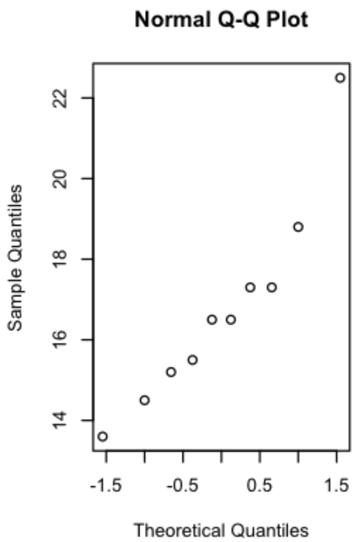
```
------------------------------------------------------------
--------
supp: VC
dose: 0.5
$x
 [1] -1.5466353  1.5466353  0.1225808 -0.6554235 -0.
3754618  0.3754618
 [7]  0.6554235  1.0004905 -1.0004905 -0.1225808

$y
 [1]  4.2 11.5  7.3  5.8  6.4 10.0 11.2 11.2  5.2  7
.0

------------------------------------------------------------
--------
supp: OJ
dose: 1
$x
 [1] -1.0004905 -0.1225808  0.1225808  1.0004905 -0.
6554235  0.3754618
 [7]  0.6554235 -0.3754618 -1.5466353  1.5466353

$y
 [1] 19.7 23.3 23.6 26.4 20.0 25.2 25.8 21.2 14.5 27
.3

------------------------------------------------------------
--------
supp: VC
dose: 1
$x
 [1] -0.1225808  0.1225808 -0.6554235  0.3754618  1.
5466353  0.6554235
 [7] -1.5466353 -1.0004905  1.0004905 -0.3754618

$y
 [1] 16.5 16.5 15.2 17.3 22.5 17.3 13.6 14.5 18.8 15
.5

------------------------------------------------------------
--------
supp: OJ
dose: 2
$x
```

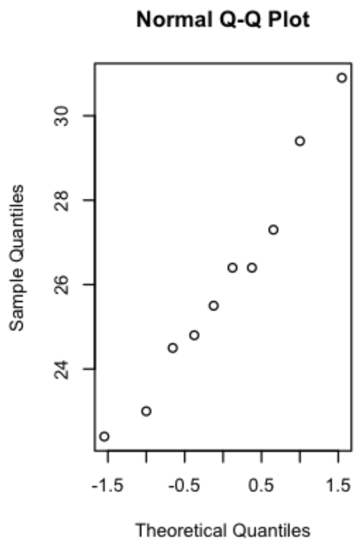
```
 [1] -0.1225808  0.1225808 -1.5466353 -0.6554235 -0.
3754618  1.5466353
 [7]  0.3754618  0.6554235  1.0004905 -1.0004905

$y
 [1] 25.5 26.4 22.4 24.5 24.8 30.9 26.4 27.3 29.4 23
.0

----------------------------------------------------
--------
supp: VC
dose: 2
$x
 [1] -0.3754618 -1.5466353  1.5466353 -0.1225808  0.
1225808  1.0004905
 [7]  0.3754618 -1.0004905 -0.6554235  0.6554235

$y
 [1] 23.6 18.5 33.9 25.5 26.4 32.5 26.7 21.5 23.3 29
.5
```

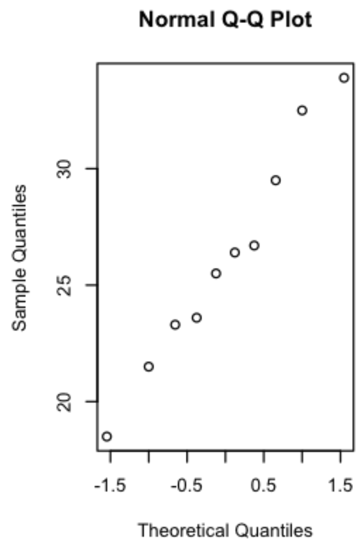

Normal Q-Q Plot
Sample Quantiles
8 10 12 14 16 18 20 22
Theoretical Quantiles
-1.5 -0.5 0.5 1.5


Normal Q-Q Plot
Sample Quantiles
4 6 8 10
Theoretical Quantiles
-1.5 -0.5 0.5 1.5


Normal Q-Q Plot
Sample Quantiles
14 16 18 20 22 24 26
Theoretical Quantiles
-1.5 -0.5 0.5 1.5


Normal Q-Q Plot
Sample Quantiles
14 16 18 20 22
Theoretical Quantiles
-1.5 -0.5 0.5 1.5


Normal Q-Q Plot
Sample Quantiles
24 26 28 30
Theoretical Quantiles
-1.5 -0.5 0.5 1.5


Normal Q-Q Plot
Sample Quantiles
20 25 30
Theoretical Quantiles
-1.5 -0.5 0.5 1.5

7.4 For two quantitative variables

7.4.1 Numerical representation

```
- Covariance
- Correlation
```

Examine whether the following variables are correlated

- **mpg** --- miles per gallon, fuel economy
- **cyl** --- no. of cylinders, e.g. L4, V6, engine structure
- **dis** --- displacement, e.g. 2.0T, 2.5L, engine size
- **hp** --- horsepower, engine power

In [20]:

```
head(mtcars)
```

A data.frame: 6 × 11

	mpg	cyl	disp	hp	drat	wt	qsec	vs	
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<d
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	

In [21]:

```
cov(mtcars[, c("mpg", "cyl", "disp", "hp")])
```

A matrix: 4 × 4 of type dbl

	mpg	cyl	disp	hp
mpg	36.324103	-9.172379	-633.0972	-320.7321
cyl	-9.172379	3.189516	199.6603	101.9315
disp	-633.097208	199.660282	15360.7998	6721.1587
hp	-320.732056	101.931452	6721.1587	4700.8669

In [22]:

```
cor(mtcars[, c("mpg", "cyl", "disp", "hp")])
```

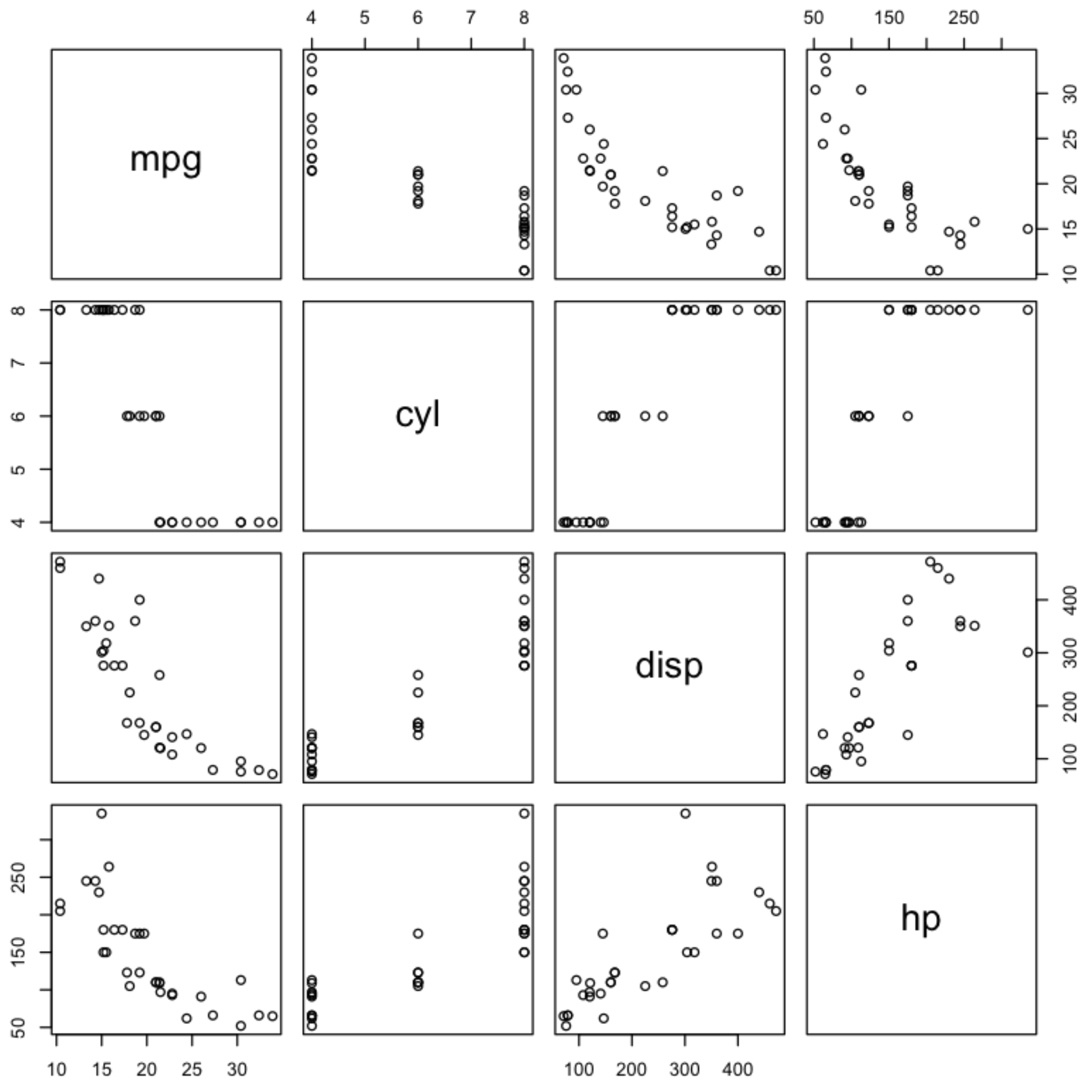
A matrix: 4 × 4 of type dbl

	mpg	cyl	disp	hp
mpg	1.0000000	-0.8521620	-0.8475514	-0.7761684
cyl	-0.8521620	1.0000000	0.9020329	0.8324475
disp	-0.8475514	0.9020329	1.0000000	0.7909486
hp	-0.7761684	0.8324475	0.7909486	1.0000000

7.4.2 Graphical representation

In [23]:

```
plot(mtcars[, c("mpg", "cyl", "disp", "hp")])
# See how powerful the plot function is.
```



Exercise!

As epidemiologists and public health specialists, we should not use statistical softwares packages and functions as black boxes.

We need to understand the theories behind!!!

1. Perform the calculation of sample covariance $cov(mpg, disp)$ from scratch

$$Cov(x,y) = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})$$

In [24]:

```
cov(mtcars$mpg, mtcars$disp)
```

-633.09720766129

2. Reproduce the qqnorm( ) plot using plot( )

If you understand the Q-Q plot, the main problem is - what are the quantiles of the 60 sample points?

1. $1/60^{th}, 2/60^{th}, \dots, 60/60^{th}$?
   - Does the 100% quantile of standard normal distribution exist?
2. $0/60^{th}, 2/60^{th}, \dots, 59/60^{th}$?
   - Does the 0% quantile of standard normal distribution exist?
3. Something else?

In [25]:

```
str(qqnorm(tg$len))
```

```
List of 2
 $ x: num [1:60] -2.394 -0.701 -1.331 -1.732 -1.569
...
 $ y: num [1:60] 4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5
.2 7 ...
```