chapter 3

Introduction to R plot

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Contents

- creat/save a plot
- symbol, line and color
- title and range
- text and mtext
- add lines
- legend
- combine multiple plots

Why plot?

When we analyze data, the first thing is to look at the data, and check its patterns, for example,

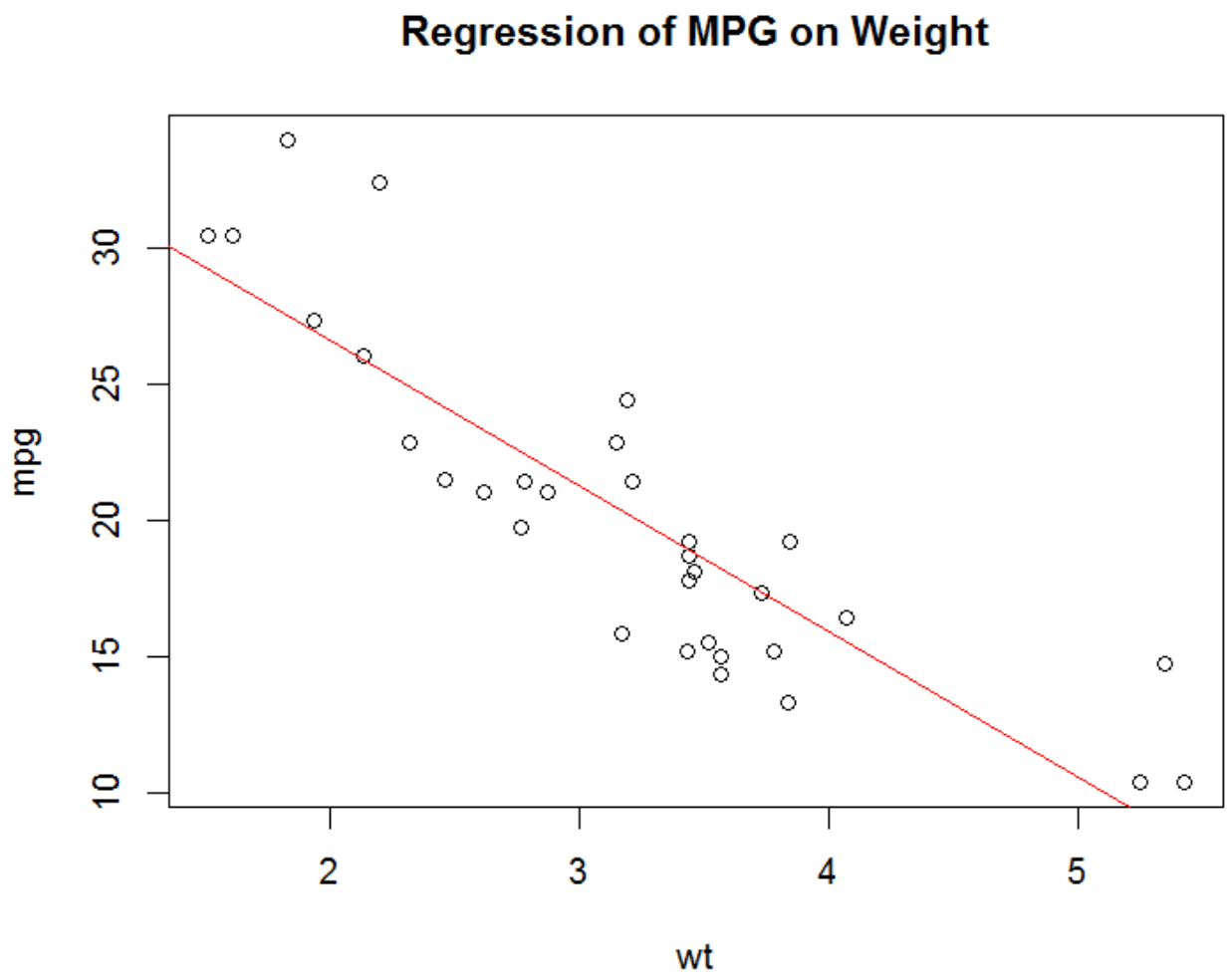
- the range of the data
- symmetric or left, right skew?
- the most common values
- any outlier?

data example

	mpg	cyl	am
Mazda RX4	21.0	6	1
Mazda RX4 Wag	21.0	6	1
Toyota Corolla	33.9	4	1
Merc 280C	17.8	6	0
Ford Pantera L	15.8	8	1
Ferrari Dino	19.7	6	1
...	...	...	...

Example 1

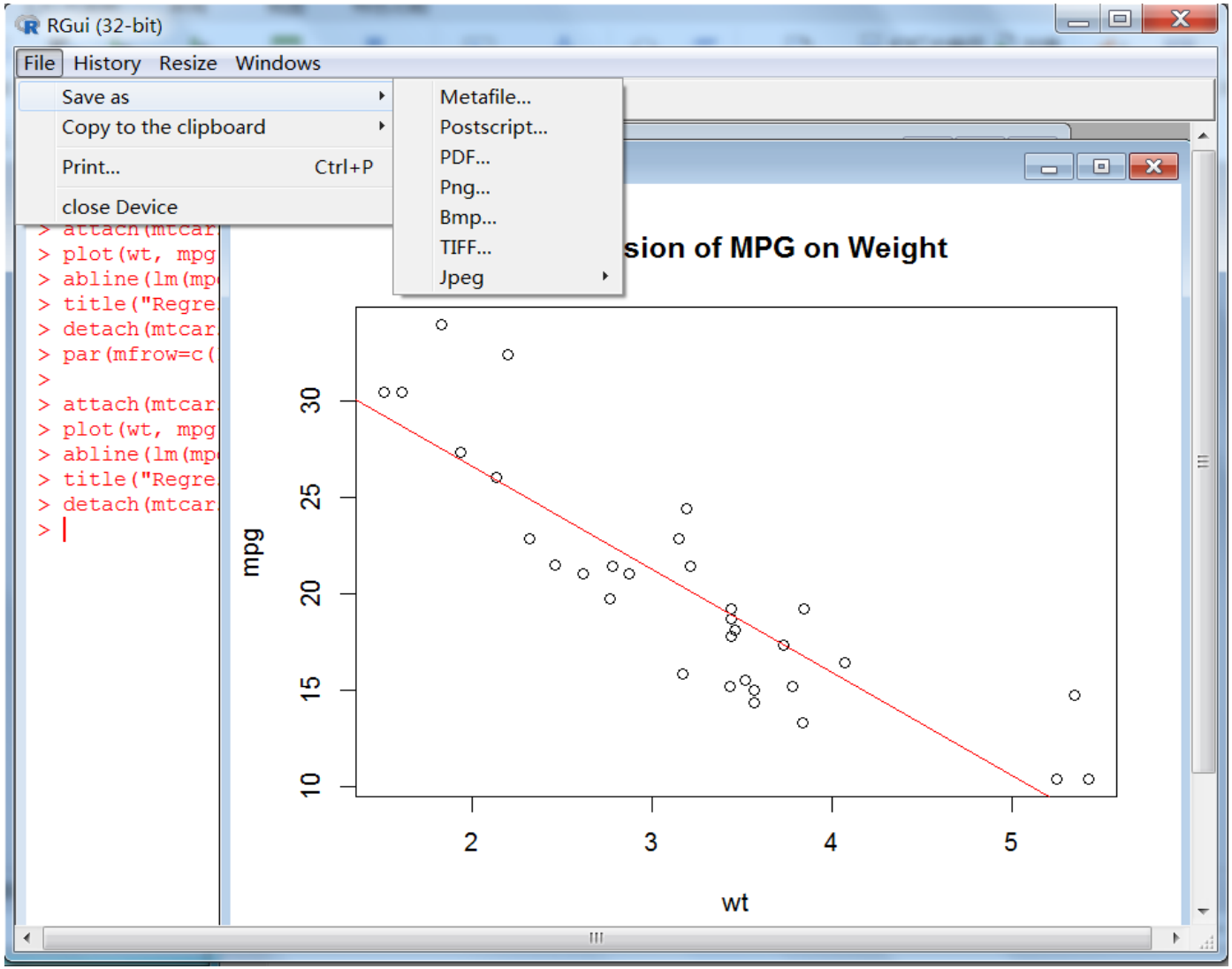
```
attach(mtcars)
plot(wt, mpg, col=1)
abline(lm(mpg~wt), col=2)
title("Regression of MPG on Weight")
detach(mtcars)
```


Regression of MPG on Weight
mpg
10
15
20
25
30
2
3
4
5
wt

Creat a plot

To creat a plot, there are two methods:

- directly plot, then save it under the graphics window, by clicking file -> save as -> choose the graph type
- start a device, then plot, after that close the device


RGui (32-bit)
File History Resize Windows
Save as
Copy to the clipboard
Print... Ctrl+P
close Device
Metafile...
Postscript...
PDF...
Png...
Bmp...
TIFF...
Jpeg
> plot(wt, mpg
> abline(lm(mp
> title("Regre
> detach(mtcar
> par(mfrow=c(
> attach(mtcar
> plot(wt, mpg
> abline(lm(mp
> title("Regre
> detach(mtcar
sion of MPG on Weight
mpg
10
15
20
25
30
2
3
4
5
wt

Example 2

```
jpeg("mygraph.jpeg")
attach(mtcars)
plot(wt, mpg, col=1)
abline(lm(mpg~wt), col=2)
title("Regression of MPG on Weight")
detach(mtcars)
dev.off()
```

Open multiple graph windows

In R, it will open one graph window by default. To open multiple graph windows, use

```
#make a new plot
dev.new()
#make another new plot
dev.new()
```

A simple plot

Example 3

```
dose <- c(20, 30, 40, 45, 60)
drugA <- c(16, 20, 27, 40, 60)
drugB <- c(15, 18, 25, 31, 40)

plot(dose, drugA, type="b")
```

Graph parameters

In R, we could set the parameters of par() to make a plot, for instance, the type and the color of a line, the size of the graph.

To save the original graph parameters, use opar <- par(no.readonly=TRUE). After finishing the plot, reset the paramters to their original values by using par(opar).

Example 4

```
opar <- par(no.readonly=TRUE)
par(lty=2, pch=17)
plot(dose, drugA, type="b")
par(opar)
```

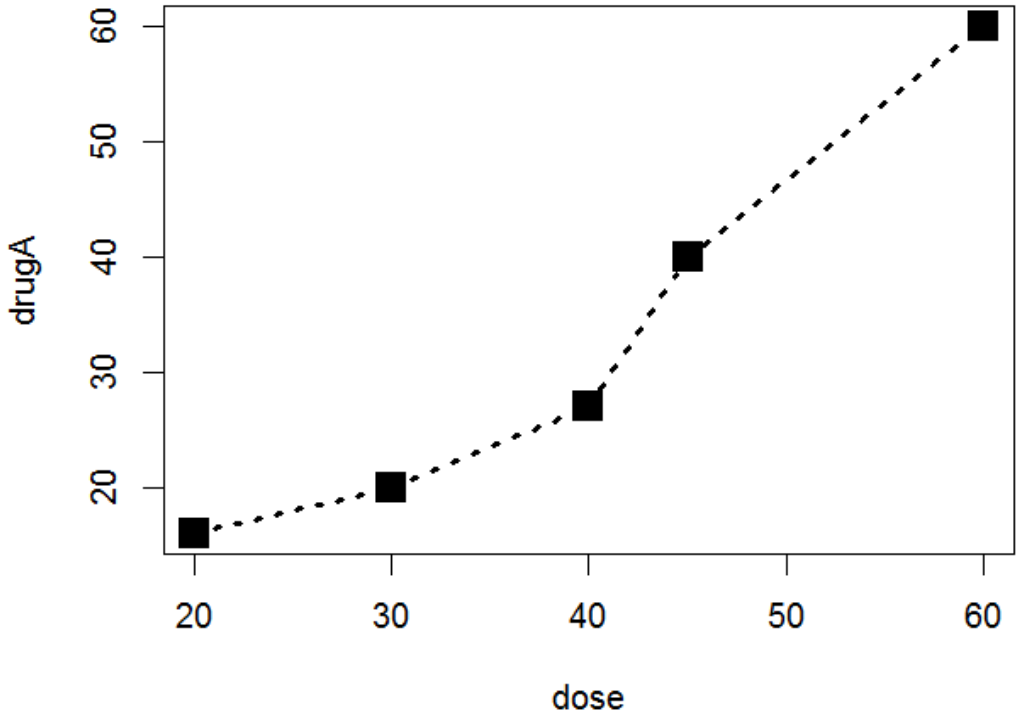
Symbol and line

The parameters for setting the type and magnitude of symbol and lines are

- pch=? the type of a symbol
- cex=? the magnitude of a symbol
- lty=? the type of a line
- lwd=? the width of a line

Example 5

```
plot(dose, drugA, type="b", lty=3, lwd=3, pch=15,
cex=2)
```


drugA
20
30
40
50
60
20
30
40
50
60
dose

col

To specify the color for plotting, set col=?

We use set col=”red”, col=”black”, col=”blue” or col=1, col=2,....

Other color parameters:

col.axis, col.lab, col.main, col.sub

Size of a graph

- pin=c(a, b): size of a graph in inch with width=a, height=b
- mai=c(a, b, d, f): the marginal size of a graph in inch, with bottom=a, left=b, up=d, right=f

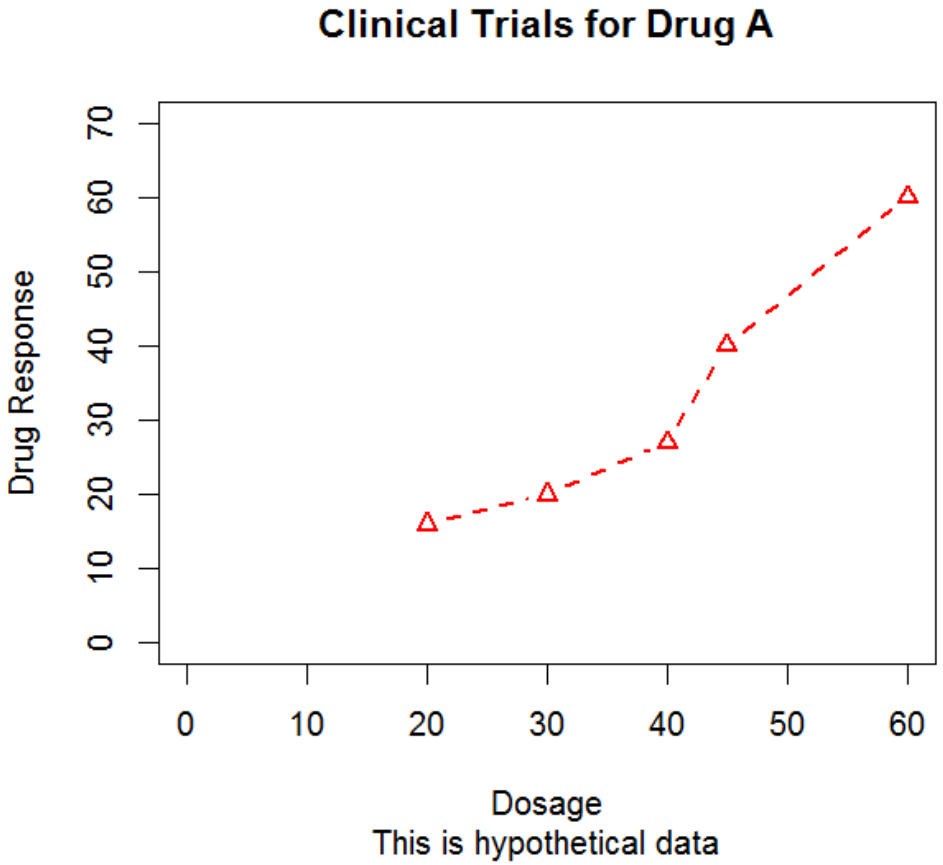
Example 6

```
opar <- par(no.readonly=TRUE)
par(pin=c(2,3))
par(lwd=2, cex=1.5)
par(cex.axis=0.75, font.axis=3)
plot(dose, drugA, type="b", pch=19, lty=2, col="red")
dev.new()
plot(dose, drugB, type="b", pch=23, lty=6, col="blue",
bg="green")
par(opar)
```

title and range of plotting

Example 7

```
plot(dose, drugA, type="b", col="red", lty=2, pch=2,
lwd=2, main="Clinical Trials for Drug A", sub="This
is hypothetical data", xlab="Dosage", ylab="Drug
Response", xlim=c(0, 60), ylim=c(0, 70))
```


Clinical Trials for Drug A
Drug Response
0
10
20
30
40
50
60
70
0
10
20
30
40
50
60
Dosage
This is hypothetical data

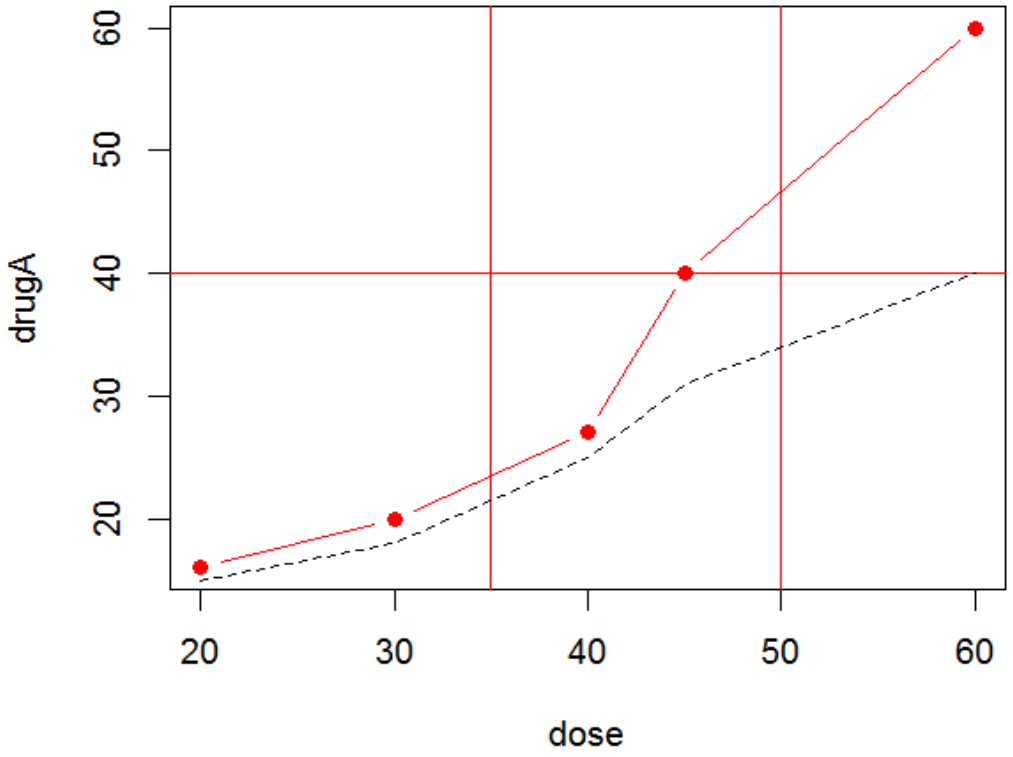
Add lines

To add lines to the graph, there are several methods:

- abline(h=yvalues, v=xvalues, col=?, lty=?)
- lines(x,y, col=?, lty=?)

Example 8

```
plot(dose, drugA, type="b", pch=19, lty=1,
col="red")
abline(h=40,v=c(35, 50), col=2)
lines(dose, drugB, lty=2)
```


drugA
20
30
40
50
60
dose
20
30
40
50
60

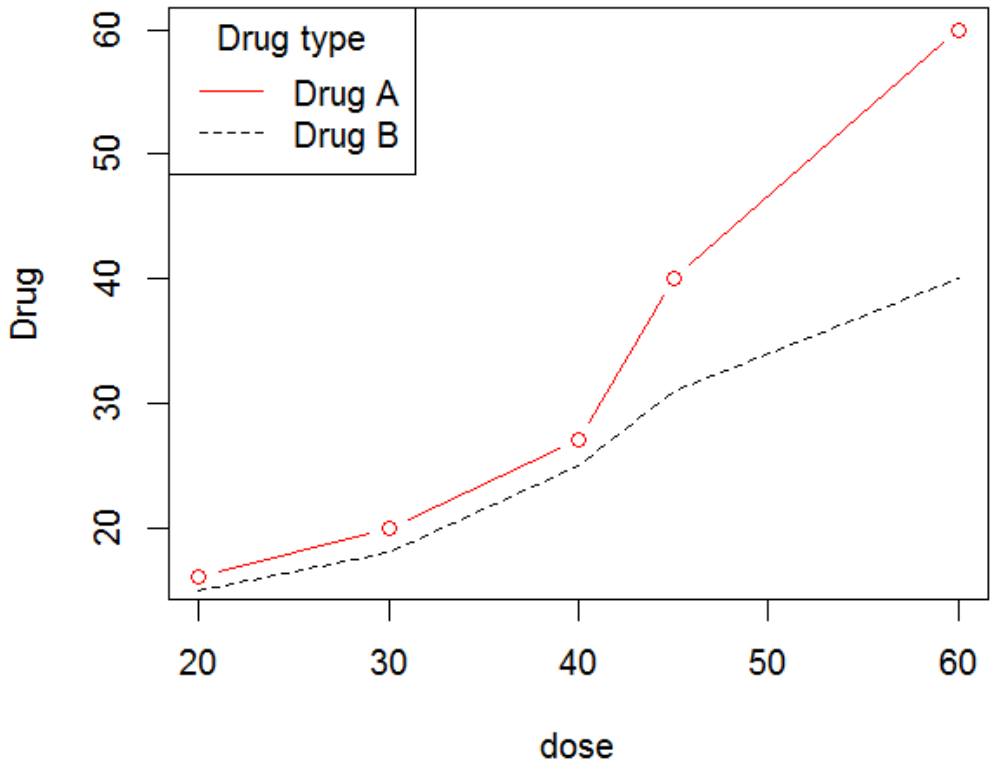
legend

When we have multiple lines in a graph, we need to use legend to tell their specific information to distinguish them.

legend(location, title, legend, lty, col,...)

Example 9

```
plot(dose, drugA, type="b", lty=1, col="red", ylab="Drug")
lines(dose, drugB, lty=2)
legend("topleft", title="Drug type", legend=c("Drug A", "Drug B"), lty=c(1,2), col=c("red",1))
```


Drug type
Drug A
Drug B
Drug
20
30
40
50
60
dose

text()

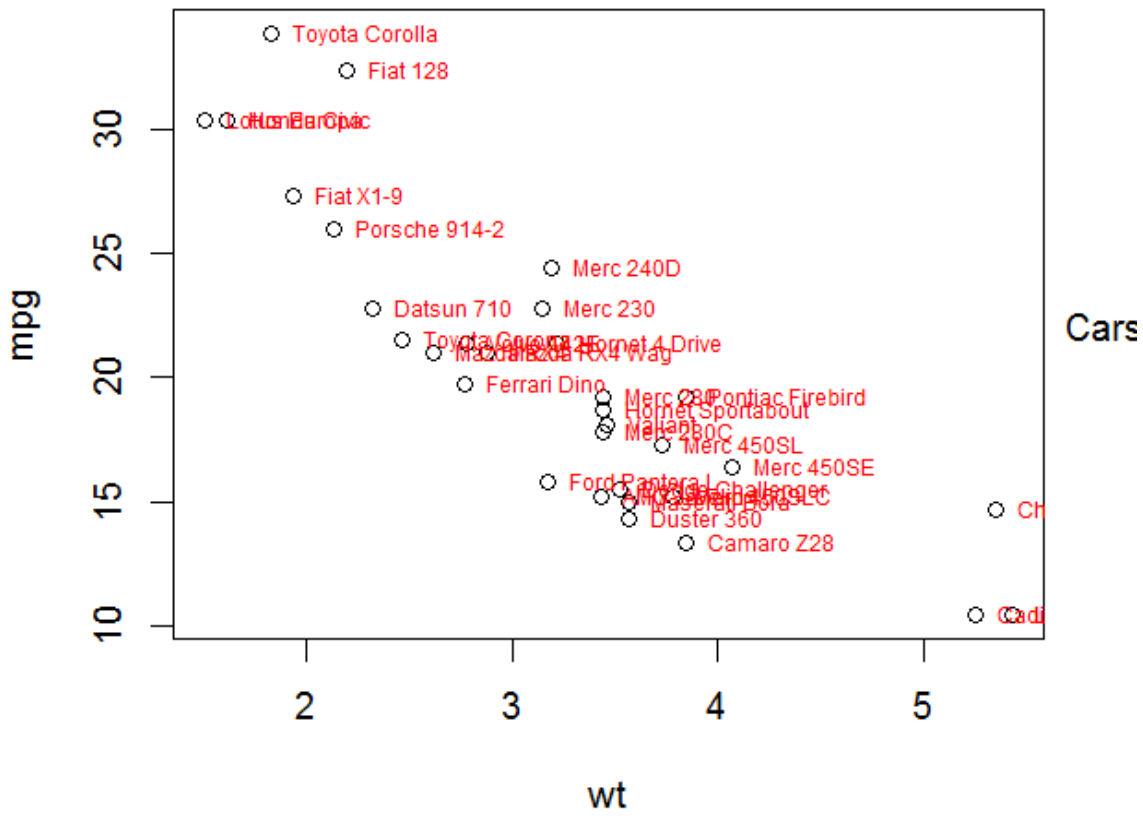
To add text in specific location, use

text(location, “text to write”, pos,...)

mtext(“text to write”, side, line,...)

Example 10

```
attach(mtcars)
plot(wt,mpg)
text(wt,mpg, row.names(mtcars), cex=0.6, pos=4, col="red")
mtext("Cars", side=4, las=2, line=0.5)
detach(mtcars)
```


Toyota Corolla
Fiat 128
Fiat X1-9
Porsche 914-2
Merc 240D
Datsun 710
Merc 230
Ferrari Dino
Pontiac Firebird
Hornet Sportabout
Merc 450SL
Merc 450SE
Duster 360
Camaro Z28
mpg
wt
Cars
10
15
20
25
30
2
3
4
5

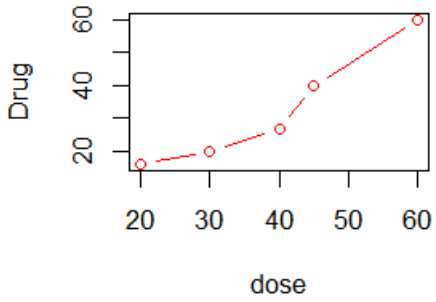
Combine multiple plots

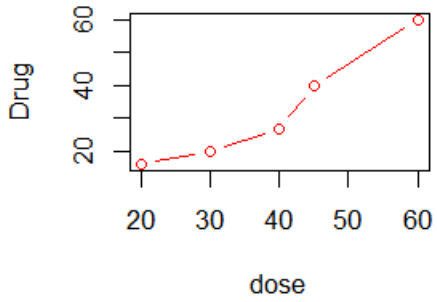
If we would like to show multiple plots together, we need to specify the number of plots and how to place them.

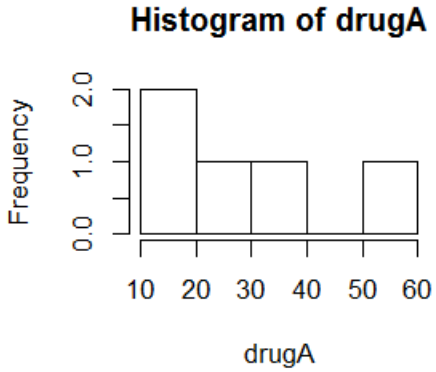
```
# We will draw m*n plots, row by row
par(mfrow=c(m,n))

# We will draw m*n plots, column by column
par(mfcol=c(m,n))
```

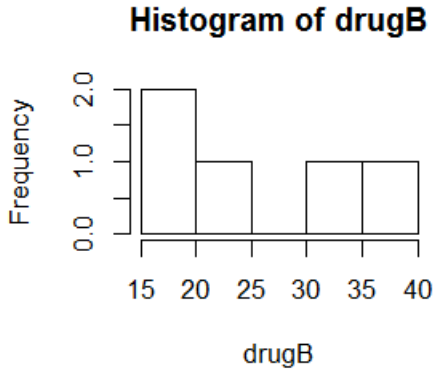
Example 10

```
par(mfrow=c(2,2))
plot(dose, drugA, type="b", lty=1, col="red", ylab="Drug")    #plot 1
plot(dose, drugA, type="b", lty=1, col="red", ylab="Drug")   #plot 2
hist(drugA)   #plot 3
hist(drugB)   #plot 4
```


Drug
20
40
60
20
30
40
50
60
dose


Drug
20
40
60
20
30
40
50
60
dose

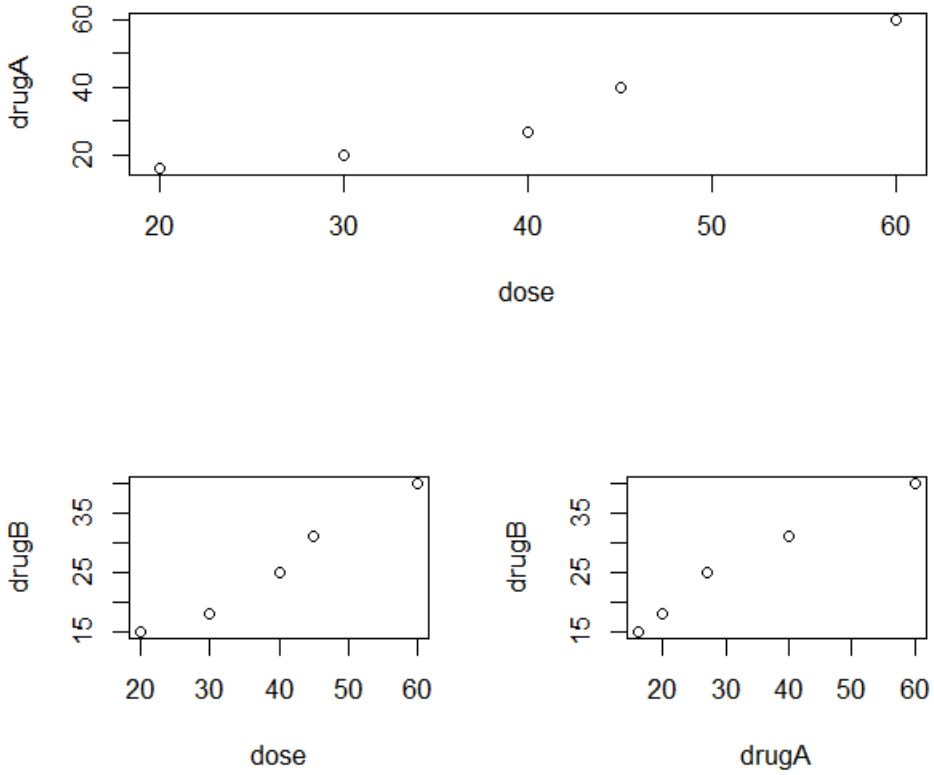

Histogram of drugA
Frequency
0.0
1.0
2.0
10
20
30
40
50
60
drugA


Histogram of drugB
Frequency
0.0
1.0
2.0
15
20
25
30
35
40
drugB

layout()

Example 11

```
layout(matrix(c(1,1,2,3), 2,2, byrow=T),
widths=c(2,2), heights=c(3,3))
plot(dose, drugA)
plot(dose, drugB)
plot(drugA, drugB)
```


drugA
20
40
60
20
30
40
50
60
dose
drugB
15
25
35
20
30
40
50
60
dose
drugB
15
25
35
20
30
40
50
60
drugA

Try the examples and enjoy plotting!