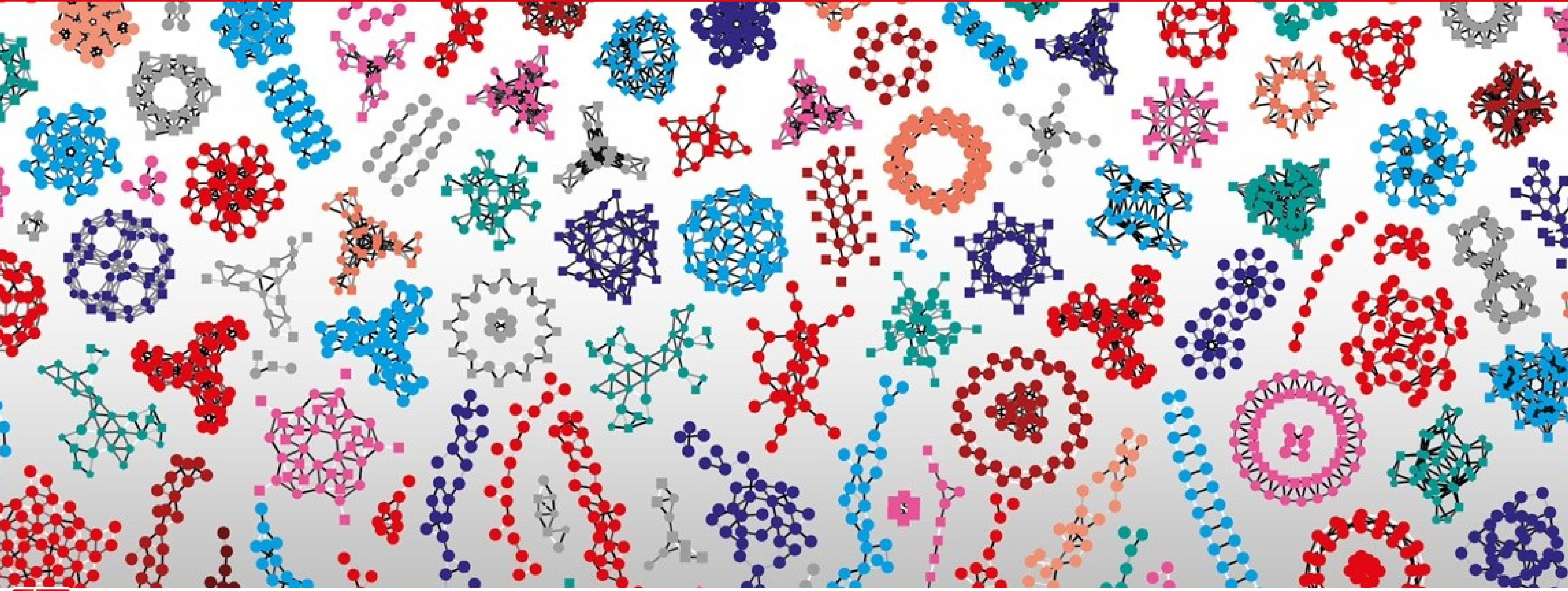


First steps with R in Life Sciences: Graphics

February, 2022 - Streamed

Wandrille Duchemin

-- with slides from Diana Marek, Wandrille Duchemin, Leonore Wigger

www.sib.swiss

Exam – for 0.5 ECTS credit points

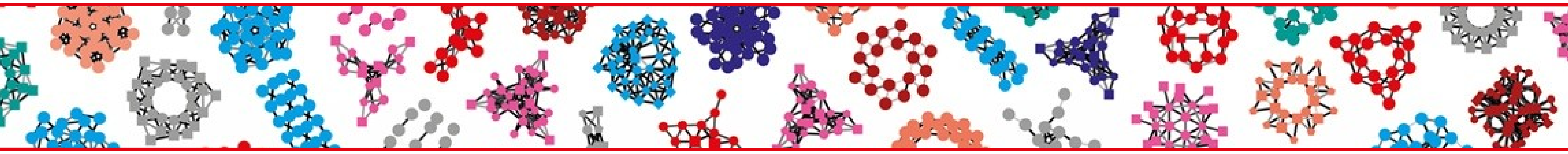
Take-home exam: data analysis tasks, available on course page.

Exam is graded as "pass" or "fail".

- Submit analysis by **February 23, 2022, 23:59:59**
- **(e-mail in the chat + google doc)**.
- You will receive a certificate of achievement from the SIB Training Team, which you can submit to your educational institution.

- If you don't take the exam, you will receive a certificate of attendance.

Outline

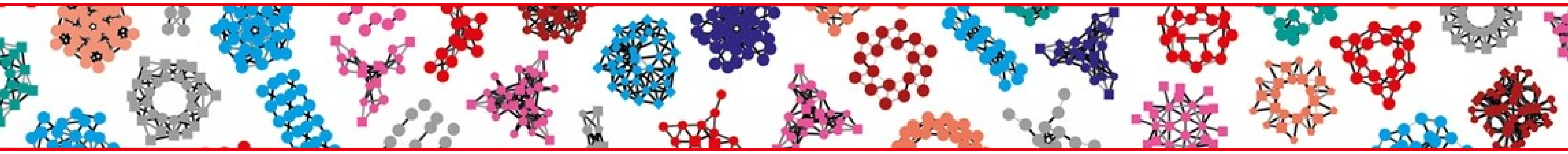


Day 2

06 **Building graphics in R (basic plotting)**

07 **Starting with statistics in R (hypothesis testing, simple linear regression)**

Examples and exercises are integrated in the chapters



06 Building graphics in R

R graphics

R is powerful for plotting graphs and figures. It provides several plotting systems:

- base (widely used, comes with basic R installation)
- ggplot2 (widely used)
- lattice (mainly used for specialized needs, e.g. 3D plots)

They have very different syntax, cannot be mixed, and need to be learned separately. This course gives an introduction to the R base plotting system

R base plotting system

Plots are built up step-by-step with multiple function calls.

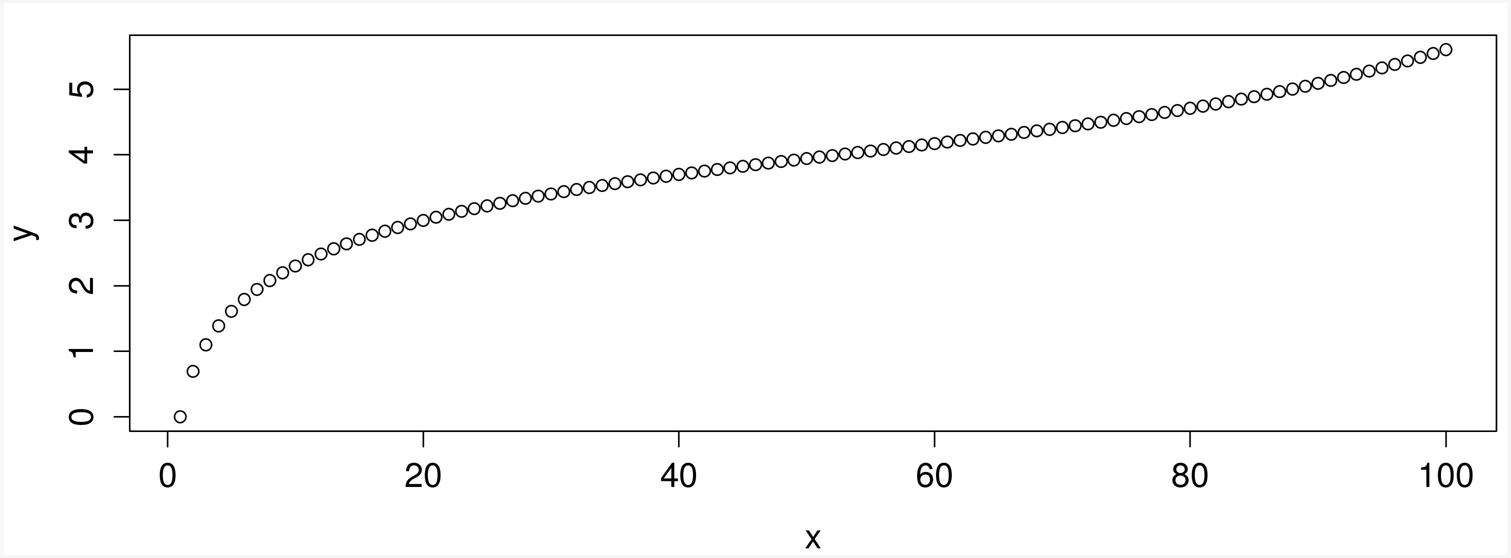
- High level graphics functions:
  - Draw a new plot. Tailor its appearance with optional arguments.

- Low level graphics functions:
  - Add graphical elements to an existing plot, piece by piece.

Plotting - the basics

- The generic function to use is **plot()**, which plots a variable y against a variable x.
- Takes the argument **type** to indicate the type of plot ("**l**" for lines, "**p**" for points and "**b**" for both). The default is **points**.

```
> x <- 1:100
> y <- log(x) + (x/100)^5
> plot(x,y) # equivalent to plot(x, y, type
```

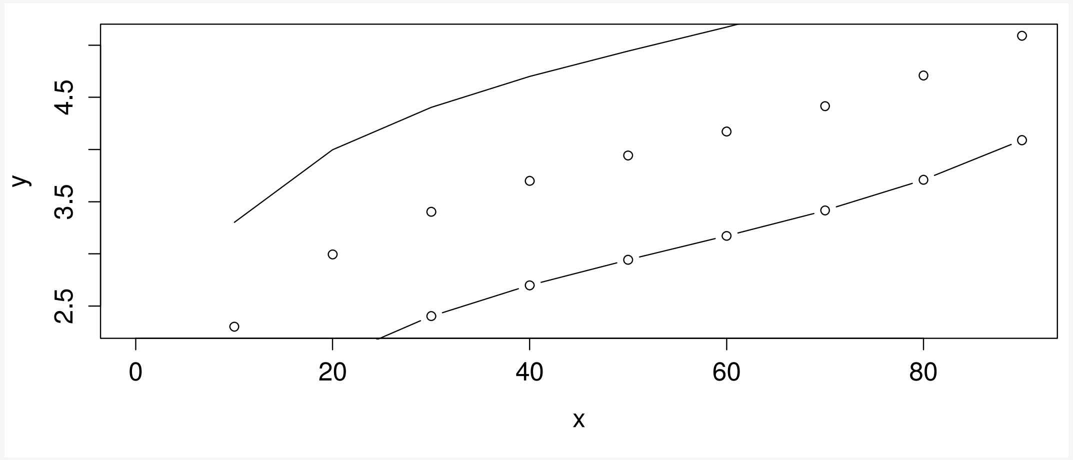


Adding elements to a plot

- Every time the plot function is called, a new plot is created.
- In order to add more graphical elements to an already existing plot, low-level plotting commands can be used, such as:
  - **points()** to add points to an existing plot
  - **lines()** to add a line to an existing plot

  The **type** argument can also be provided to those functions ("**l**" for lines, "**p**" for points and "**b**" for both). Default for points(): **"p"**, default for lines(): **"l"**.

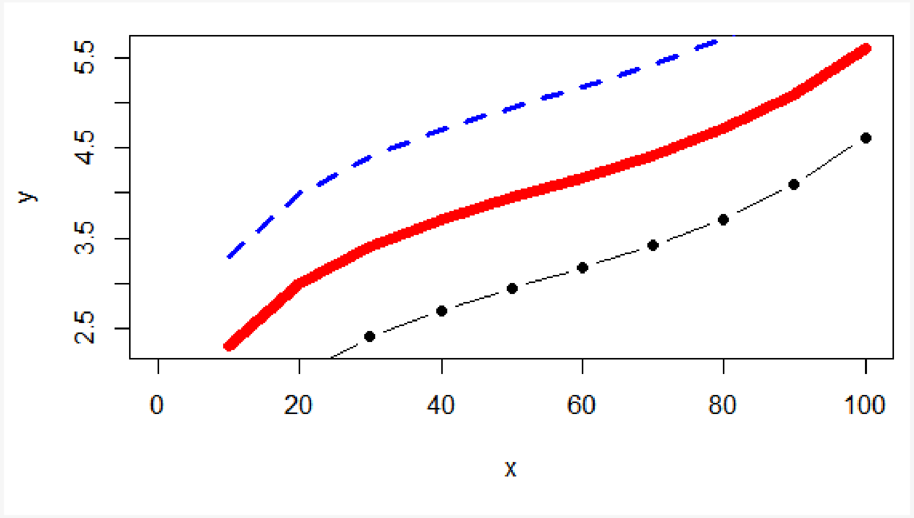
```
>x <- seq(0,100, by=10)
>y <- log(x) + (x/100)^5

>plot(x,y)
>lines(x,y+1)
>points(x,y-1, type
```



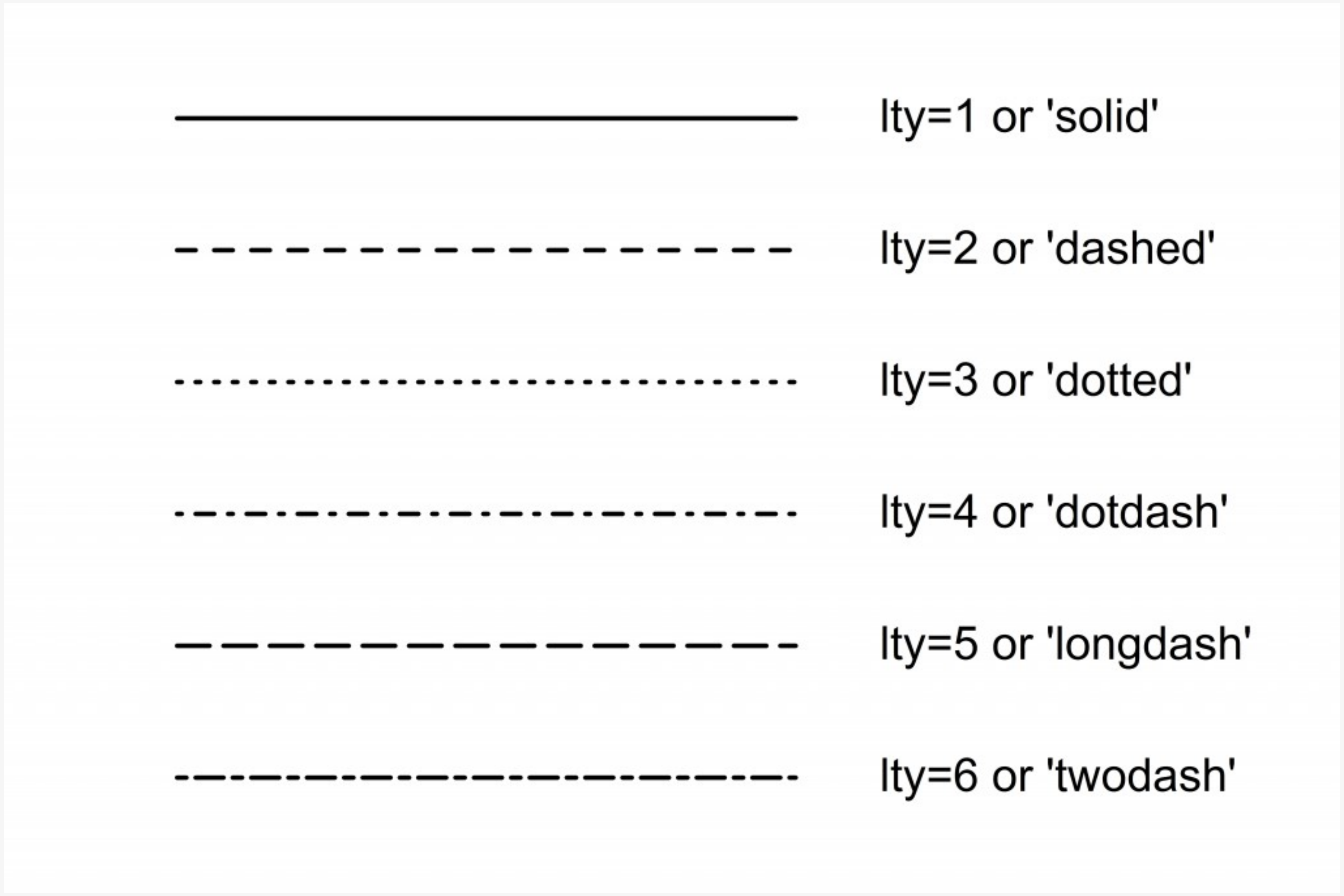
Customizing plots – Part 1

- **plot()**, **points()** and **lines()** all take customizing arguments, including:
  - **col** indicating the colour
  - **lwd** indicating the line width
  - **lty** indicating the line type
  - **pch** indicating the plotting character (symbol)

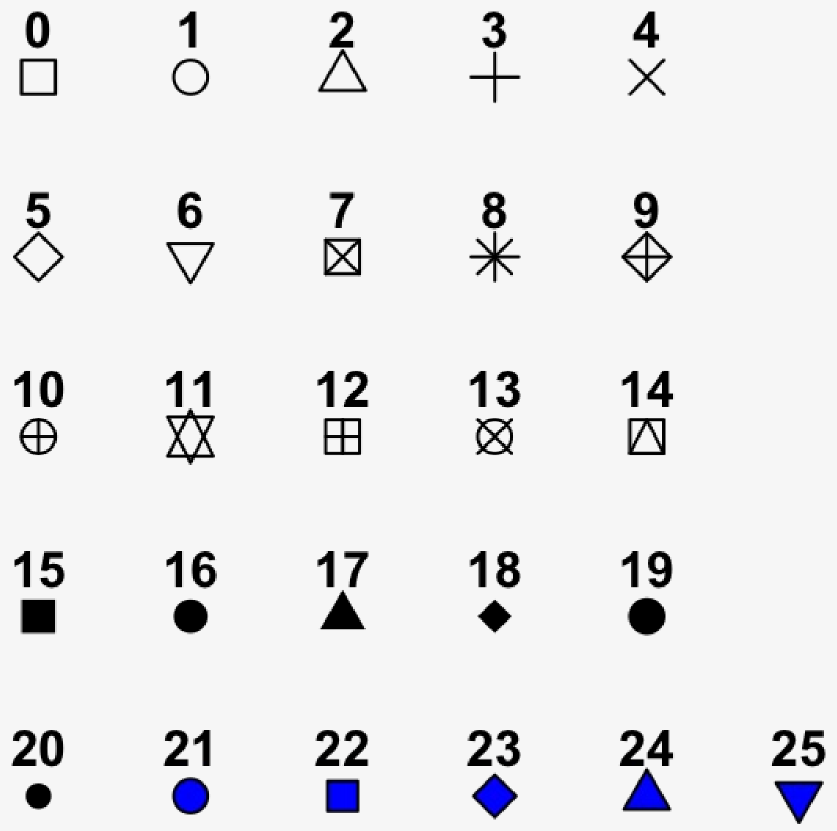
```
>plot(x, y, type="l", col="red", lwd=7)
>lines(x, y+1,
         col="blue",
         lty="dashed")
>points(x, y-1, type="b",
            pch=19)
```



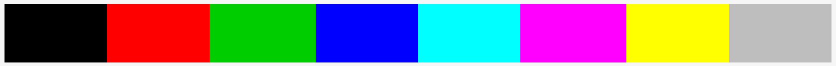
R line types, to use with lty

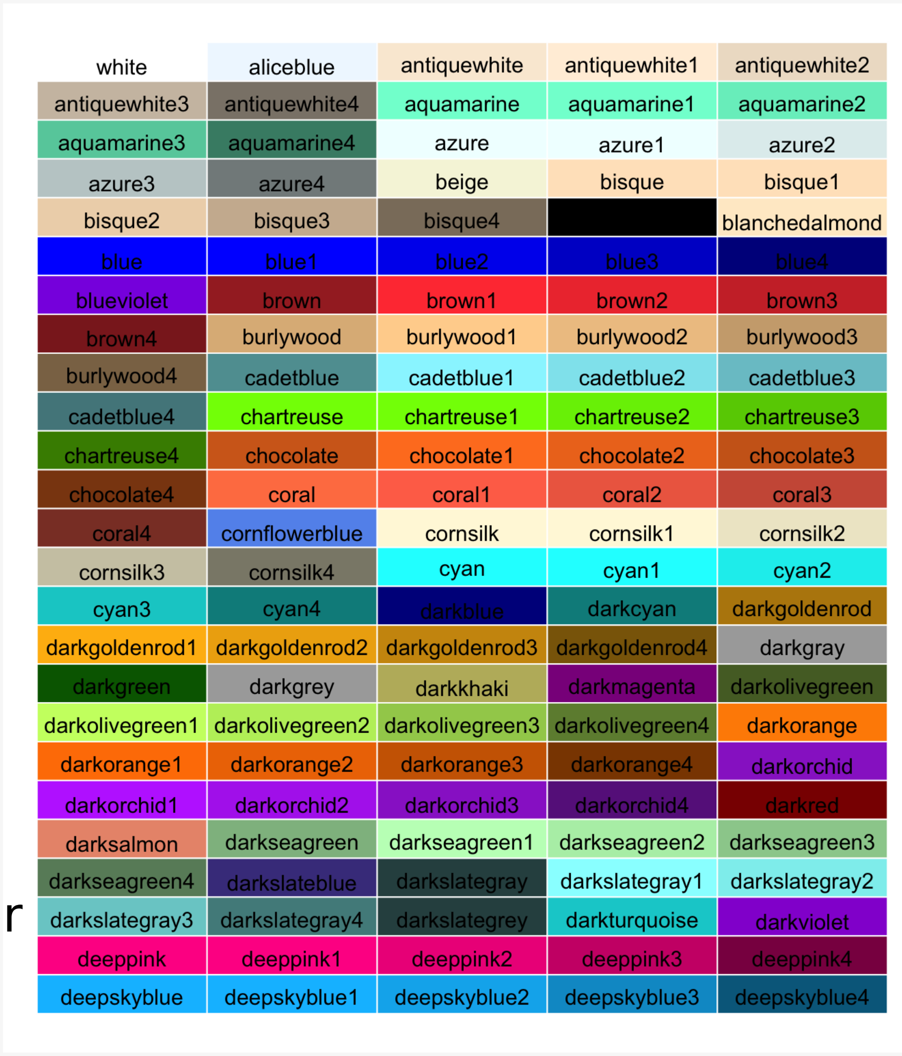


R plotting characters, to use with pch



R color

- default palette : 1 to 8 
- Hexadecimal :
  - "#1492AD"
  - "#BC520088" ← transparency
- 657 built-in color names,
  - here is a subset:
- **colors()** will output a list of all color names



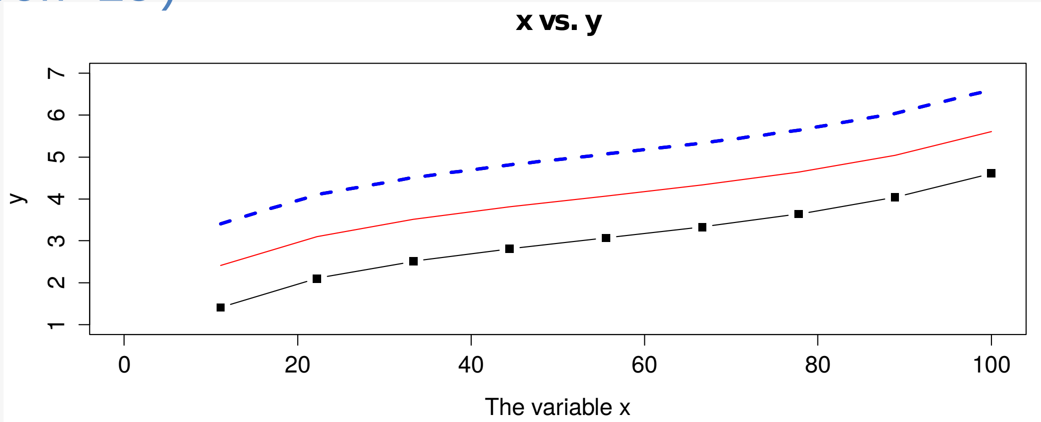
white	aliceblue	antiquewhite	antiquewhite1	antiquewhite2
antiquewhite3	antiquewhite4	aquamarine	aquamarine1	aquamarine2
aquamarine3	aquamarine4	azure	azure1	azure2
azure3	azure4	beige	bisque	bisque1
bisque2	bisque3	bisque4		blanchedalmond
blue	blue1	blue2	blue3	blue4
blueviolet	brown	brown1	brown2	brown3
brown4	burlywood	burlywood1	burlywood2	burlywood3
burlywood4	cadetblue	cadetblue1	cadetblue2	cadetblue3
cadetblue4	chartreuse	chartreuse1	chartreuse2	chartreuse3
chartreuse4	chocolate	chocolate1	chocolate2	chocolate3
chocolate4	coral	coral1	coral2	coral3
coral4	cornflowerblue	cornsilk	cornsilk1	cornsilk2
cornsilk3	cornsilk4	cyan	cyan1	cyan2
cyan3	cyan4	darkblue	darkcyan	darkgoldenrod
darkgoldenrod1	darkgoldenrod2	darkgoldenrod3	darkgoldenrod4	darkgray
darkgreen	darkgrey	darkkhaki	darkmagenta	darkolivegreen
darkolivegreen1	darkolivegreen2	darkolivegreen3	darkolivegreen4	darkorange
darkorange1	darkorange2	darkorange3	darkorange4	darkorchid
darkorchid1	darkorchid2	darkorchid3	darkorchid4	darkred
darksalmon	darkseagreen	darkseagreen1	darkseagreen2	darkseagreen3
darkseagreen4	darkslateblue	darkslategray	darkslategray1	darkslategray2
darkslategray3	darkslategray4	darkslategrey	darkturquoise	darkviolet
deeppink	deeppink1	deeppink2	deeppink3	deeppink4
deepskyblue	deepskyblue1	deepskyblue2	deepskyblue3	deepskyblue4

See R color cheat sheet for the full color chart and other ways to define colors

Customizing plots – Part 2

- The **plot()** command takes further arguments to customize the plotting area:
  - **xlim** and **ylim** to set the limits on the x- and y-axis, respectively
  - **xlab** and **ylab** to set the labels for the x- and y-axis, respectively
  - **main** to set a title

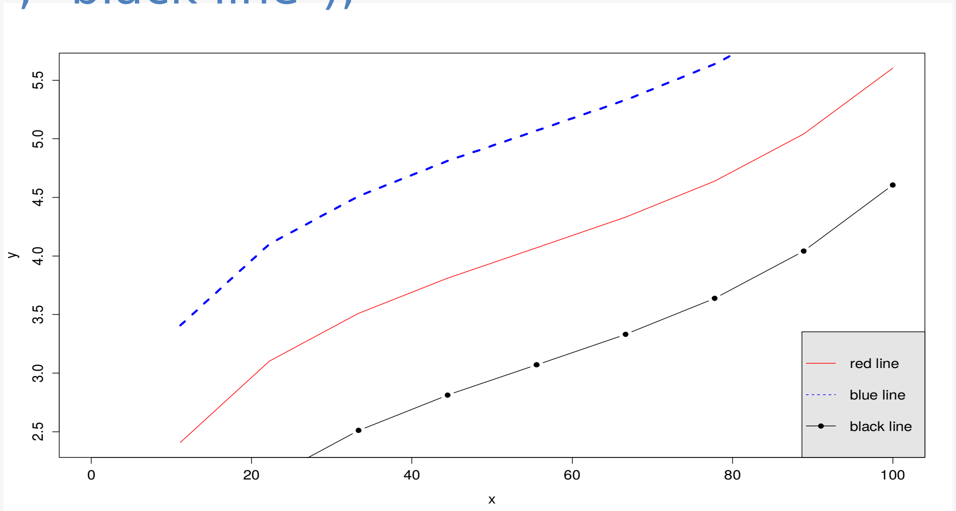
```
> x <- seq(0, 100, length.out=10)
> y <- log(x) + (x/100)^5
> plot(x,y, type="l", col="red", ylim=c(1,7),
       xlab="The variable x", main ="x vs. y" )
> lines(x, y+1, lwd=3,lty="dashed", col="blue")
> points(x, y-1, type="b", pch=15)
```



Customizing plots – Part 3

- The **legend()** command can be used to add legends to plots:
  - **x** , **y** to set the numeric coordinates for positioning the legend.
    - x can be used by itself with a keyword for legend position: "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", "center"
  - **legend** to set the text to appear in the legend
  - **col , lty , lwd , pch** : set graphical elements in the legend
  - **bty** for box type around the legend ("o" for box, "n" for no box)
  - **bg** for background color

```
> legend(x="bottomright",
        legend=c("red line","blue line", "black line"),
        lty=c(1,2,1),
        pch=c(NA,NA,19),
        col=c("red", "blue", "black"),
        bg="gray90")
```



How to get data for practicing and playing

R can easily simulate data drawn from a given distribution.
The function rnorm() generates normally distributed data.

Example:

```
>rnorm(10)  #numeric vector with 10 values
            #drawn from normal distribution,
            #mean=0, standard deviation=1 (function defaults)
```

```
[1]  1.1053564  0.7937635  0.2743762  0.3574477 -0.7677099  [2]  0.5838973
0.6616164  0.1203090 -0.4060265  0.2778585
```

How to get data for practicing and playing

R can easily simulate data drawn from a given distribution.
The function rnorm() generates normally distributed data.

Example:

```
>rnorm(10)  #numeric vector with 10 values
            #drawn from normal distribution,
            #mean=0, standard deviation=1 (function defaults)
[1]  1.1053564  0.7937635  0.2743762  0.3574477 -0.7677099  [2]  0.5838973
0.6616164  0.1203090 -0.4060265  0.2778585
```

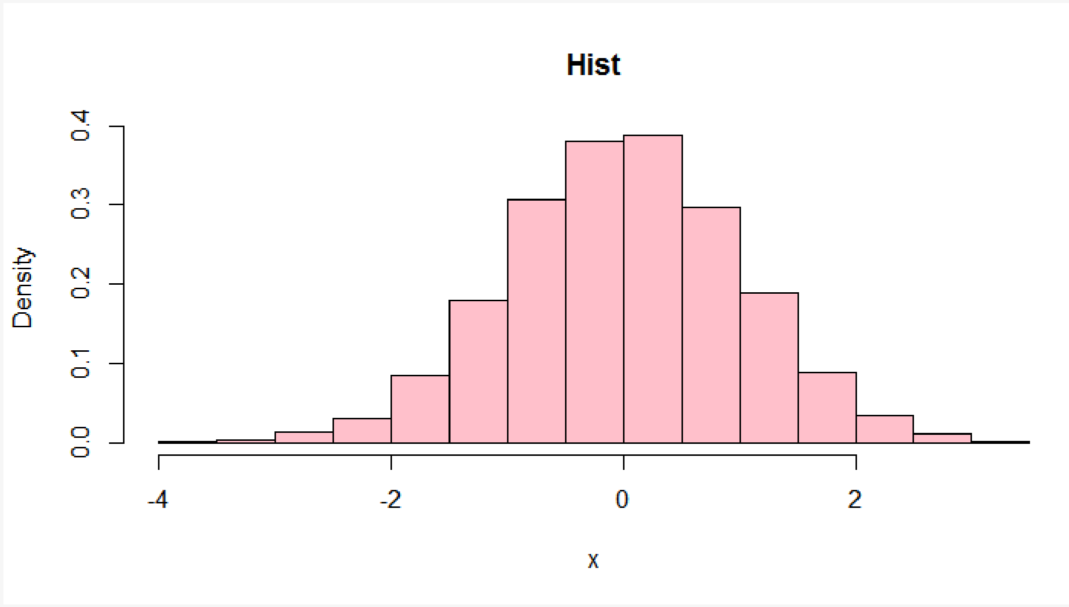
```
>rnorm(10, mean=10, sd=2) #customized mean and sd
[1]  6.253392  9.527140  9.398857 11.932284 11.472909
[2] 10.714245  7.656026 11.302829  9.332930 10.264157
```

If you want data from other distributions than normal:
rpois() for poisson, rbinom() for binomial (see R help)

The hist() function

- The function **hist()** produces a histogram, which counts the number of observations that fall into different ranges (bins)
- Rough visual representation of the distribution of the data.
  - **x** vector of data values for which the histogram will be constructed
  - **breaks** either a vector indicating breakpoints between histogram bins, or a single number for the number of bins (used as suggestion)
  - **freq** logical. If TRUE, cell height represents counts per bin. If FALSE, cell height is the fraction of values that fall into each bin (probability density).

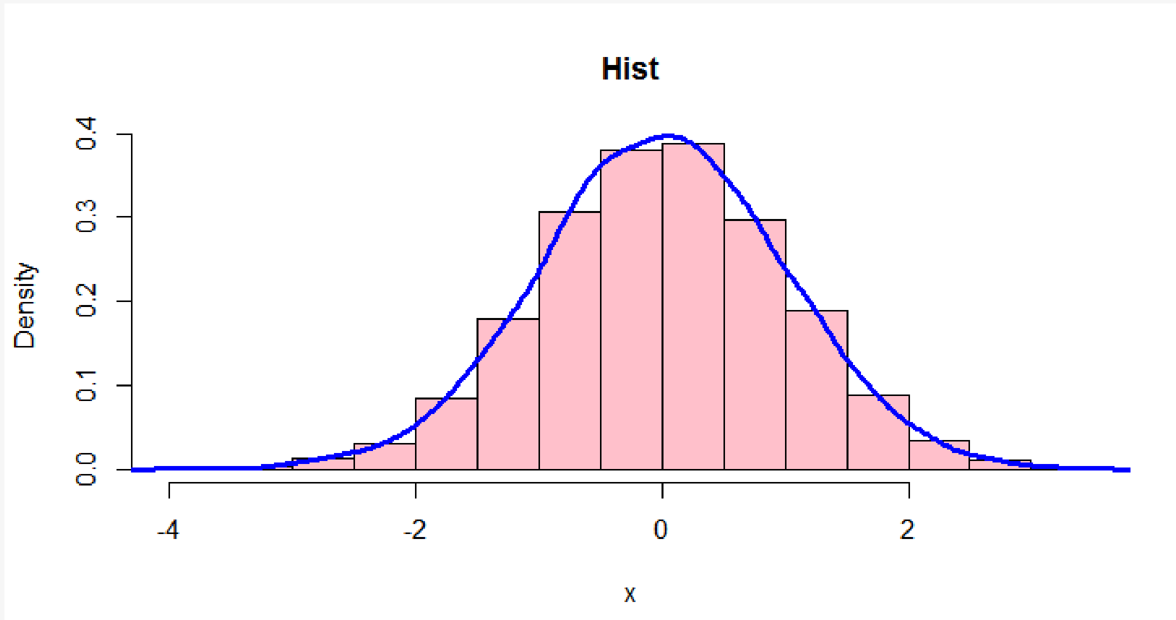
```
> x <- rnorm(10000)
> hist(x, breaks=20, freq=FALSE,
  main="Hist", col="pink")
```



The hist() and density() functions

- To add a smooth line to a histogram, use density(), which computes estimates of the probability density (kernel density estimates).
- This works as a complementary representation of the histogram only when freq = FALSE
- The line produced by density() often reflects the distribution better than a histogram.
- Use lines() to plot the result as a line on top of the histogram.

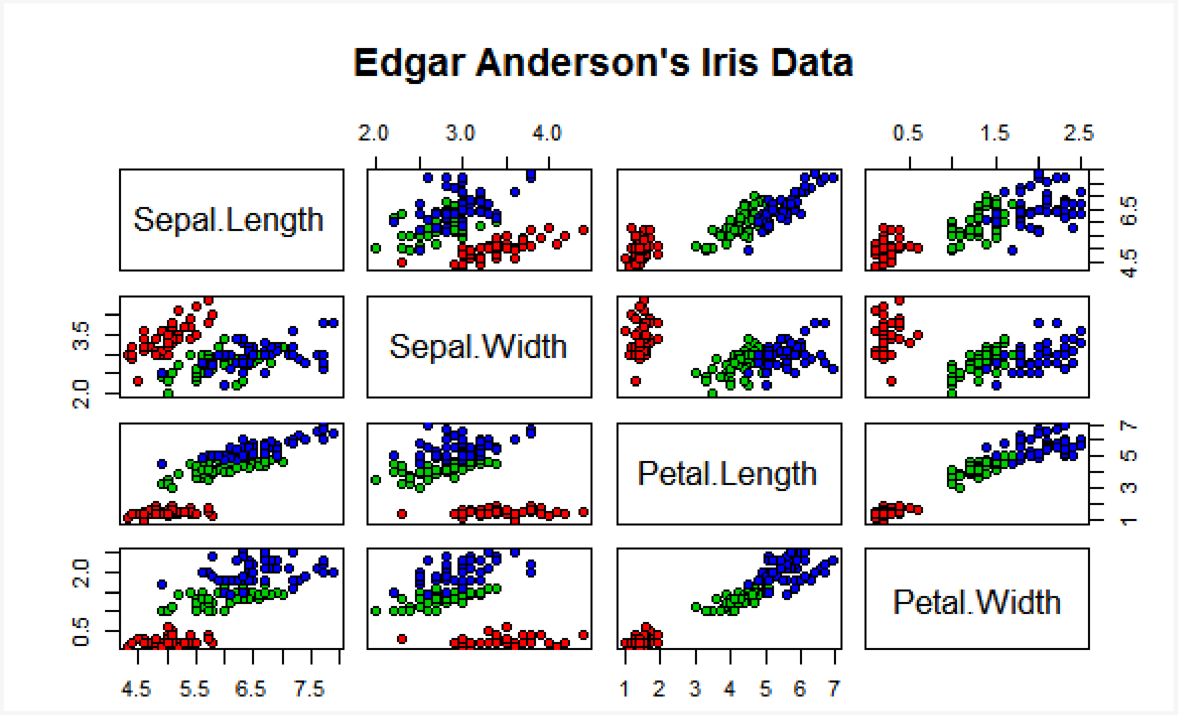
```
> x <- rnorm(10000)
> hist(x, freq=FALSE,
     main="Hist", col ="pink")
> lines(density(x),
     col="blue", lwd=3)
```



Draftsman's or Pairs Scatter Plots - **P5S**

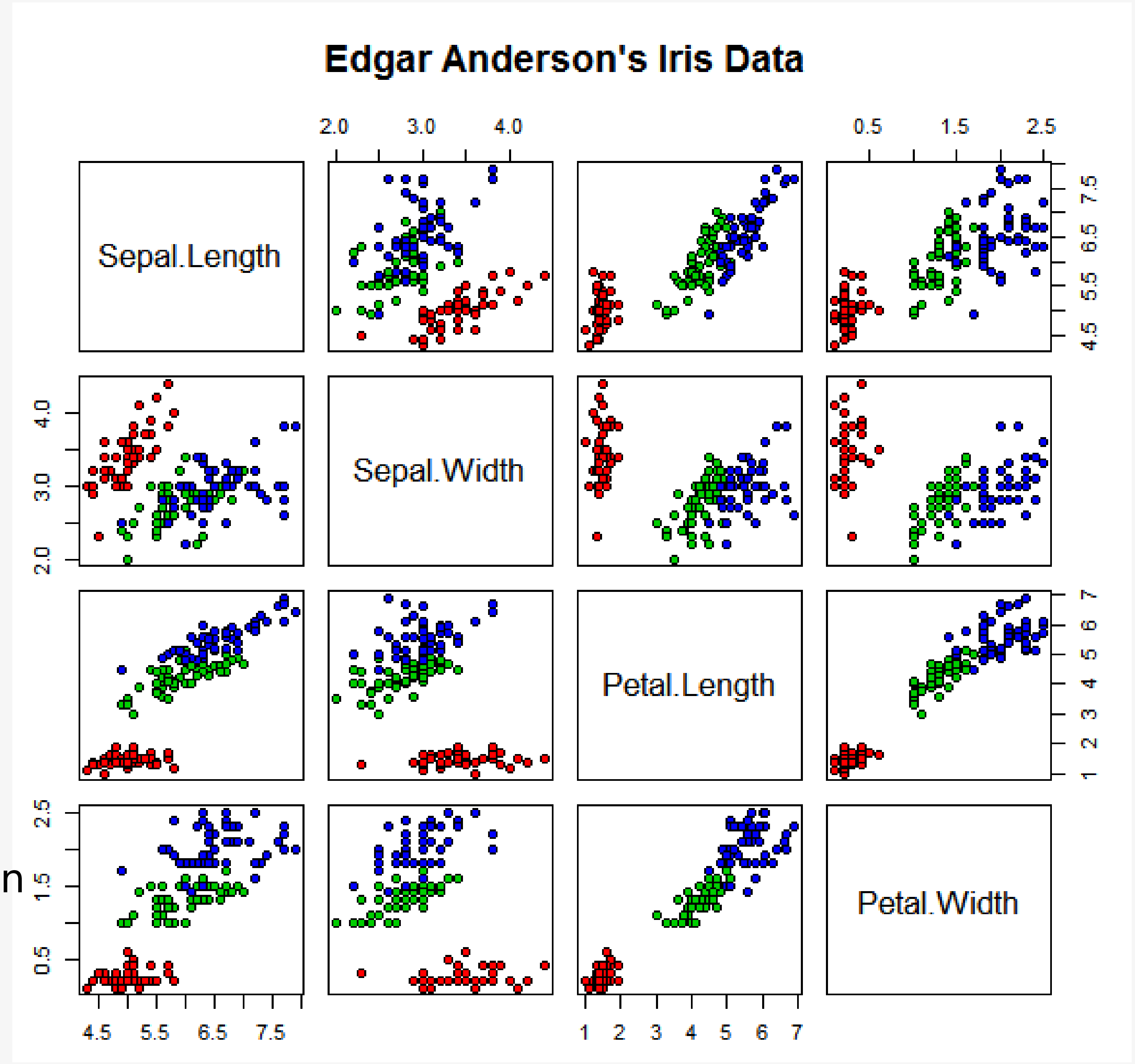
- If x is a matrix or a data frame, **pairs()** draws all possible bivariate plots between the columns of x.

```
> data(iris) #contains 4 measurements for 150 flowers from 3   species of iris
(Iris setosa, versicolor and virginica)

> pairs(iris[,1:4], main="Edgar Anderson's Iris Data",
  pch=21, bg=c("red", "green3", "blue")[iris$Species])
```



bg:
color fill of circles ●

Colors:
setosa in red
versicolor in green
virginica in blue



Colors:
setosa in red
versicolor in green
virginica in blue

Excursus: Coloring data points in the iris data(I)

```
bg=c("red", "green3", "blue")[iris$Species])  #color fill
```

How does this work?

```
iris$Species  #factor with 3 levels
```

```
 [1] setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa
 [14] setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa
 [27] setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa
 [40] setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     setosa     versicolor versicolor
 [53] versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor
 [66] versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor
 [79] versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor
 [92] versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor versicolor virginica  virginica  virginica  virginica
[105] virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica
[118] virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica
[131] virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica  virginica
[144] virginica  virginica  virginica  virginica  virginica  virginica  virginica
Levels: setosa versicolor virginica
```

```
as.numeric(iris$Species) #factor coerced to numeric
```

```
[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [44] 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [87] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
[130] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
```

Excursus: Coloring data points in the iris data (II)

The coloring strategy in the iris draftman's plot involves **subsetting** and **coercion:**

```
bg=c("red", "green3", "blue")[iris$Species]
```

is equivalent to

bg=c("red", "green3", "blue")[**as.numeric(**iris$Species**)**]

is equivalent to

```
bg=c("red","green3",blue")
[c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2
,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3,3,3,3,3,
3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3
)]
```

Inside the square brackets [] , the factor is automatically coerced to a numeric

Excursus: Coloring data points in the iris data (III)

This results in a vector of color terms with 150 entries in the correct order.

```
> bg=c("red", "green3", "blue")[iris$Species]  #color fill

> bg
```

```
 [1] "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"
 [14] "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"
 [27] "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"
 [40] "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "red"    "green3"
"green3"
 [53] "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3"
"green3" "green3" "green3"
 [66] "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3"
"green3" "green3" "green3"
 [79] "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3"
"green3" "green3" "green3"
 [92] "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "green3" "blue"   "blue"
"blue"   "blue"
[105] "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"
"blue"
[118] "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"
"blue"
[131] "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"
"blue"
[144] "blue"   "blue"   "blue"   "blue"   "blue"   "blue"   "blue"
```

Let’s practice - 7

Let's come back to the mice dataset stored in the "mice_data" data frame (Let’s practice – 3). If mice_data is not currently in your workspace, either get it back by loading the .Rdata file or import the data again from the original .csv file.

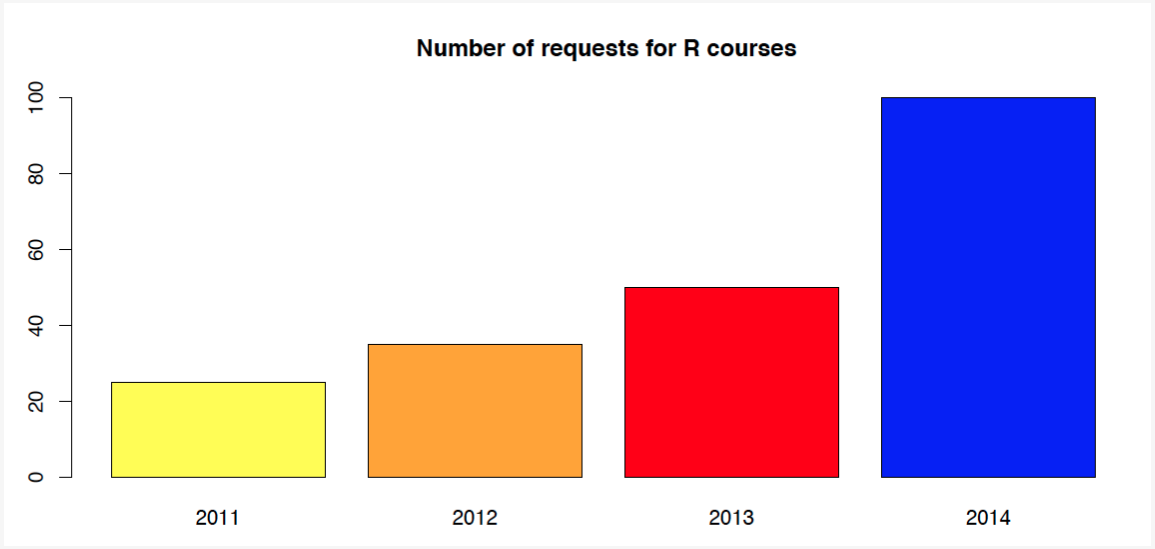
1) Check your data frame: did it load correctly? Make sure genotype and diet are factor variables.

2) Plot an histogram of mouse weight and customize it with colours, labels, title and represent the density line on top.

3) Make a scatter plot of mouse weights using the function plot(), with no additional arguments. (You do not need to define values for a second axis.) Inspect the plot - what appears on the two axes? Then re-do the plot by adding function arguments: Use solid circles as plotting symbol, add a title, customise the y-axis label, and colour the points **by genotype.** Add a legend.

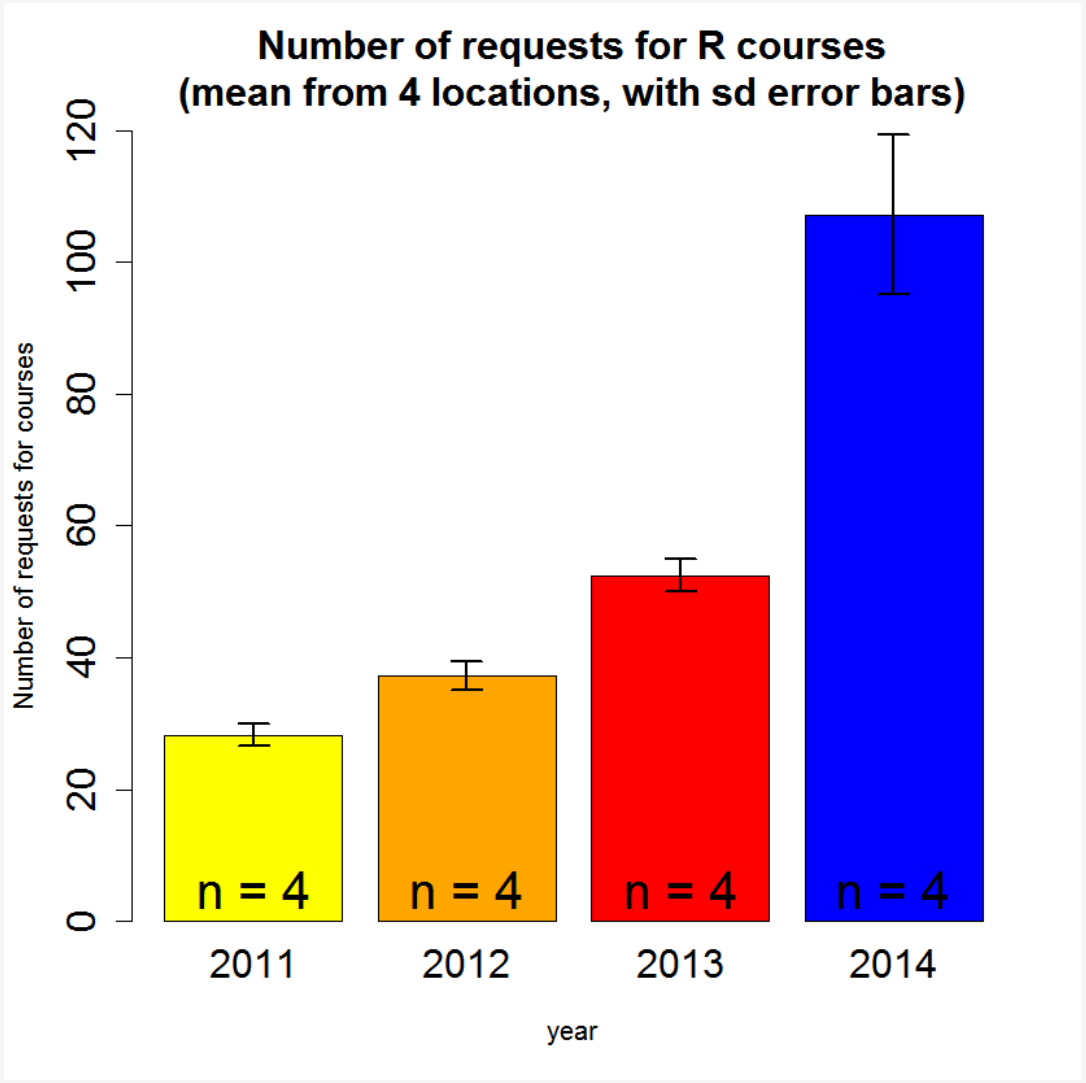
The barplot() function

- Barplots allow simple visualization of counts or numeric data.
- Optional arguments can be used to customize the plot.



```
>course_data <- c(yr2011=25, yr2012=35, yr2013=50, yr2014=100)
>barplot(course_data, main="Number of requests for R courses",
      names.arg=c("2011", "2012","2013", "2014"),
      col=c("yellow", "orange","red", "blue"))
```

Customized barplot with sd error bars



Each year, R course requests were counted in 4 cities.

Bar heights: mean across all cities per year

Custom plotting using low level functions:
- add error bars (std dev.)
- add text to each bar (n=4)

Customized barplot with sd error bars (I)

```
# Create a data frame
df <- data.frame(
        year = c("2011","2012","2013","2014",
                "2011","2012","2013","2014",
                "2011","2012","2013","2014",
                "2011","2012","2013","2014"),
       city =  c("A","A","A","A", "B","B","B","B",
                "C","C","C","C", "D","D","D","D"),
       nb_requests_courses = c(30,36,50,98, 26,35,54,101,
                            28,38,51,105, 29,40,55,125))
# Check what is inside
> head(df)
 year        city    nb_requests_courses
1 2011        A                   30
2 2012        A                   36
3 2013        A                   50
4 2014        A                   98
5 2011        B                   26
```

Customized barplots with sd error bars (II)

Compute summary statistics

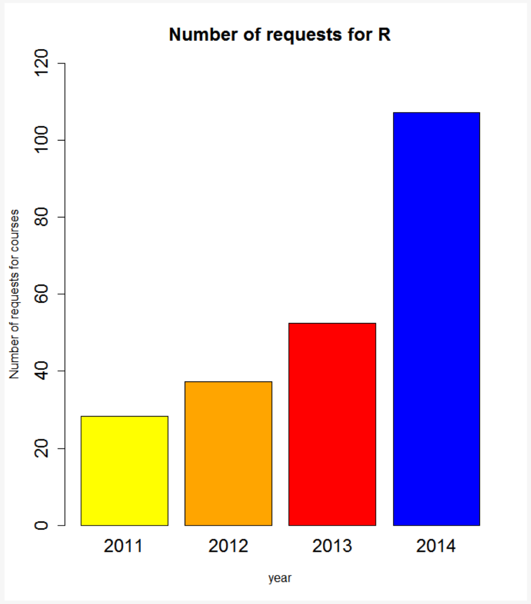
```
# Compute mean, sd, number of observations per year
mean_nb  <- tapply(df$nb_requests_courses, df$year, mean)
sd_nb    <- tapply(df$nb_requests_courses, df$year, sd)
n_values <- tapply(df$nb_requests_courses, df$year, length)
```

```
> mean_nb
 2011   2012   2013   2014
 28.25  37.25  52.50  107.25

> sd_nb
 2011      2012      2013      2014
 1.707825  2.217356  2.380476  12.175796

> n_values
 2011 2012 2013 2014
 4    4    4    4
```

Customized barplots with sd error bars (III)

High-level: Generate plot

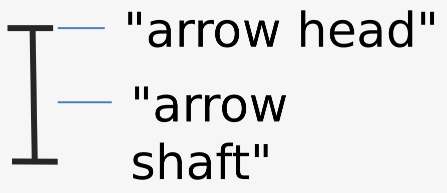
```
# Make a barplot using the means returned by tapply
mids <- barplot(mean_nb,
        xlab="year",ylab="Number of requests for courses",
        ylim=c(0,120),
         col=c("yellow", "orange","red", "blue"),
         cex=1.5, cex.axis=1.5, cex.main=1.5, cex.names=1.5,
        main= "Number of requests for R")

# mids contains the location of the middle
of the bars on the x-axis

> mids
     [,1]
[1,]  0.7
[2,]  1.9
[3,]  3.1
[4,]  4.3
```



Customized barplots with sd error bars (IV)

Low-level: Add elements (error bars and text)

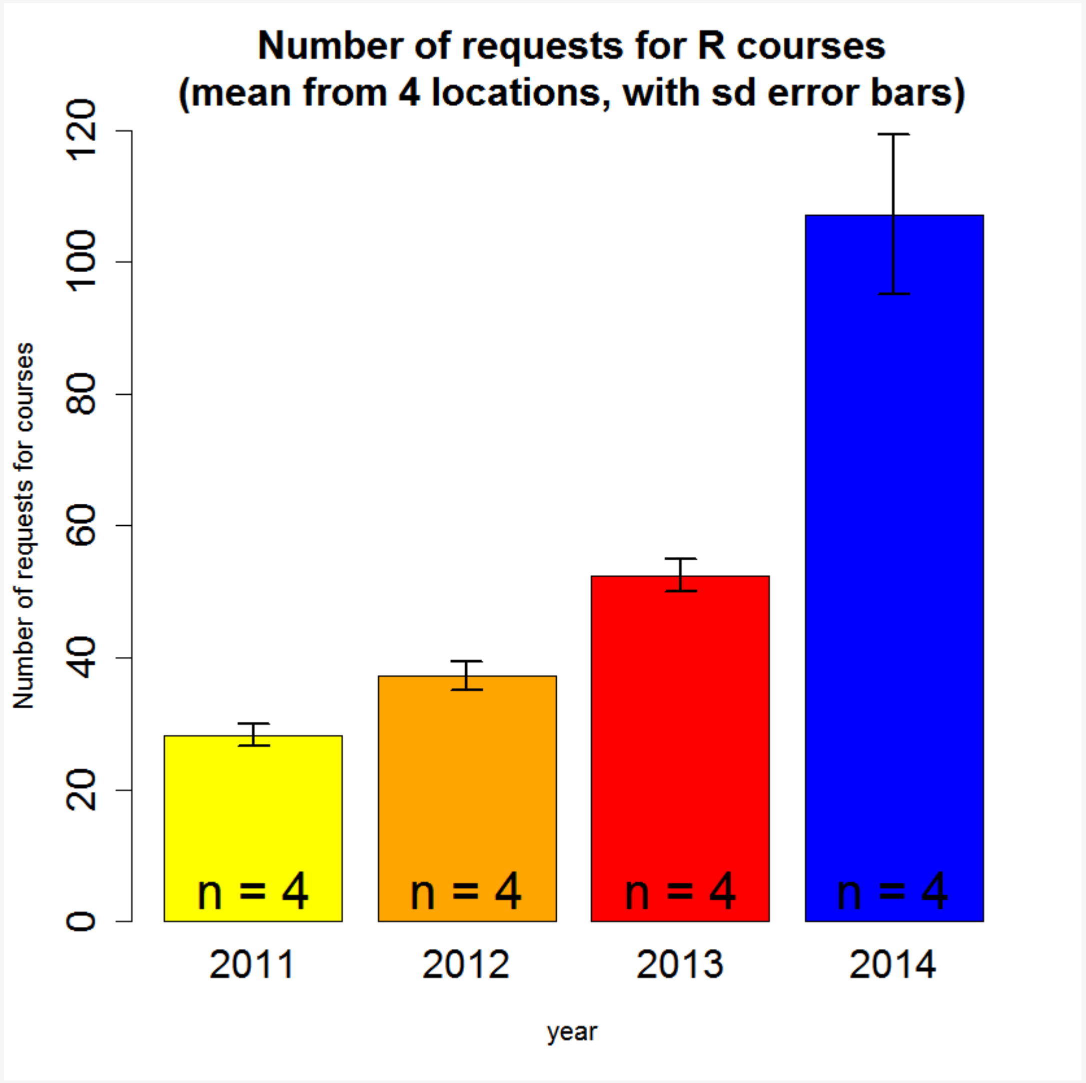
# Use arrows() to put **sd error bars** on the plot



```
arrows(mids, mean_nb-sd_nb, # coordinates of lower point
      mids, mean_nb+sd_nb, # coordinates of upper point
       code=3,       # type of arrow: "head at both ends"    angle=90,    # angle between shaft and head of arrow
      length=0.1,  # length of edges of arrow head
       lwd=2)       # line width
```

```
# Add text at the midpoints and at height 5 on the y-axis: number of observations
text(x=mids, y=5, paste("n =",n_values), cex=2
```

Customized barplot with sd error bars



Barplot digression...

- Bar plots with error bars are widely used in biology
- Be aware: different ways of calculating error bars (sd or sem*)
  (standard deviation or standard error of the mean)
- Often not the most informative way to look at the data, combine them with other plots (box plot, violin plots, scatter plot)

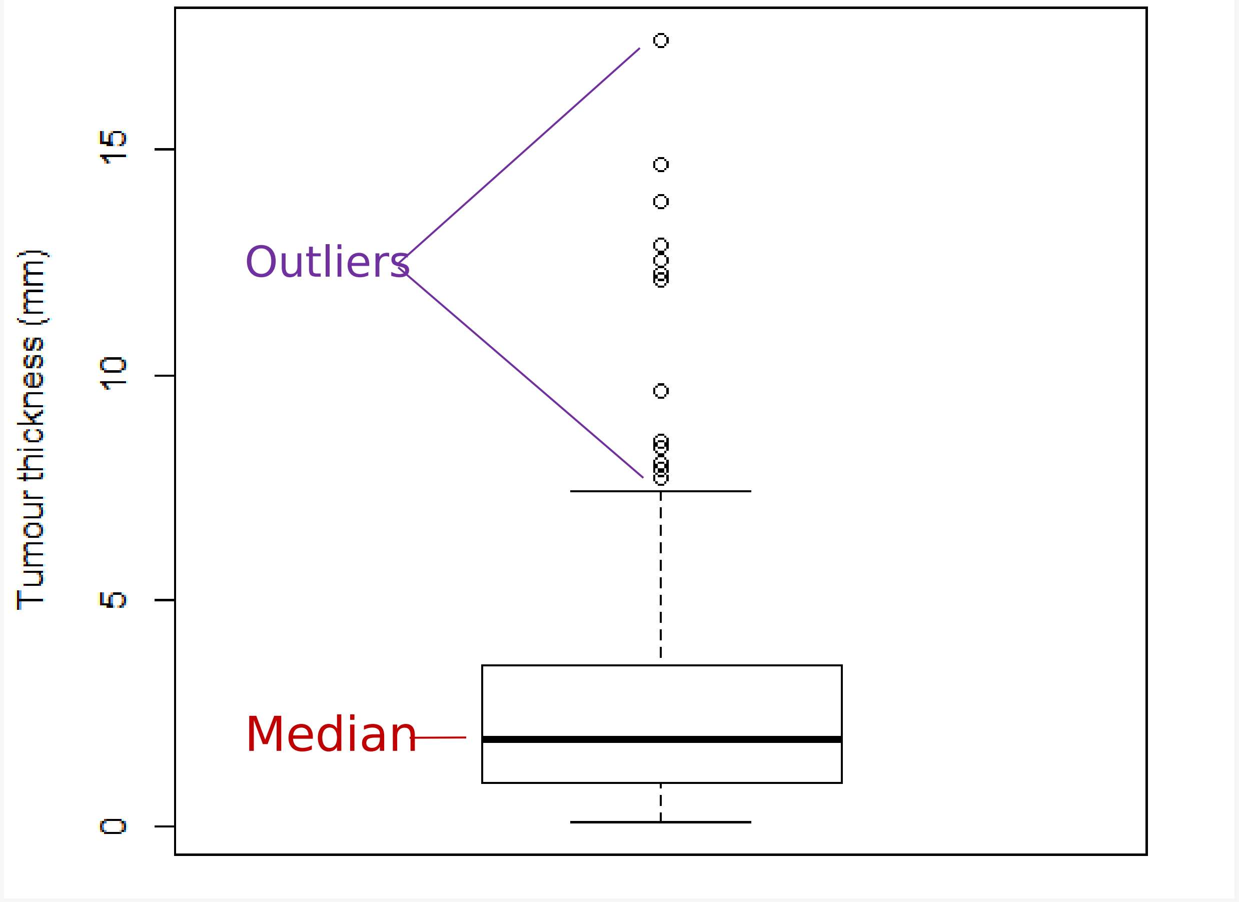
- https://stekhoven.shinyapps.io/barplotNonsense/

*sd: standard deviation
sem: standard error of the mean

The boxplot() function

Convenient way of depicting the spread of numerical data

- **Box**: Interquartile range (IQR), contains 50% of points
- **Whiskers**: Extend from box, indicate variability outside upper and lower quartiles
- **Outliers**: May be plotted as individual points

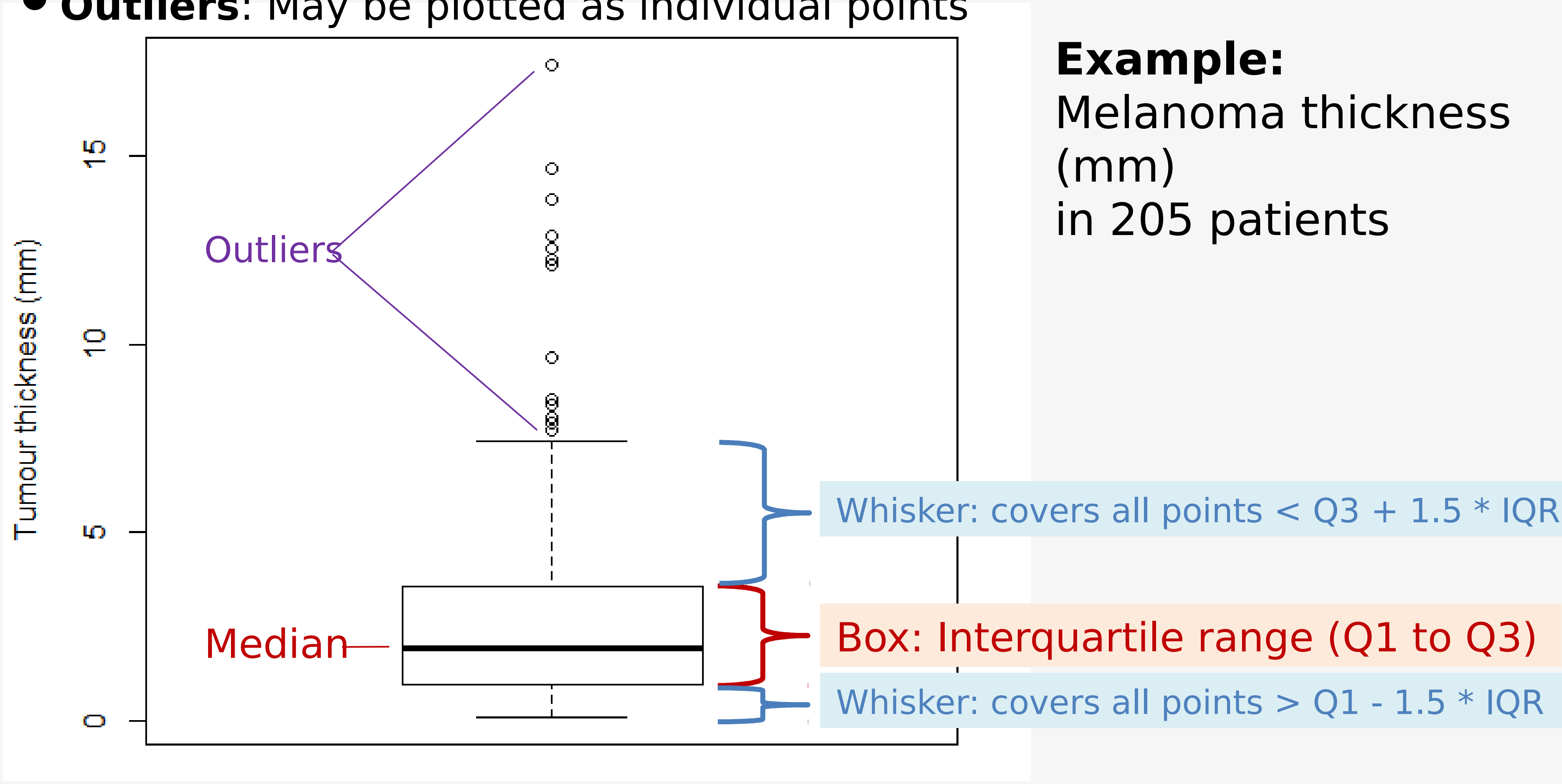


Example:
Melanoma thickness (mm) in 205 patients

The boxplot() function

Convenient way of depicting the spread of numerical data

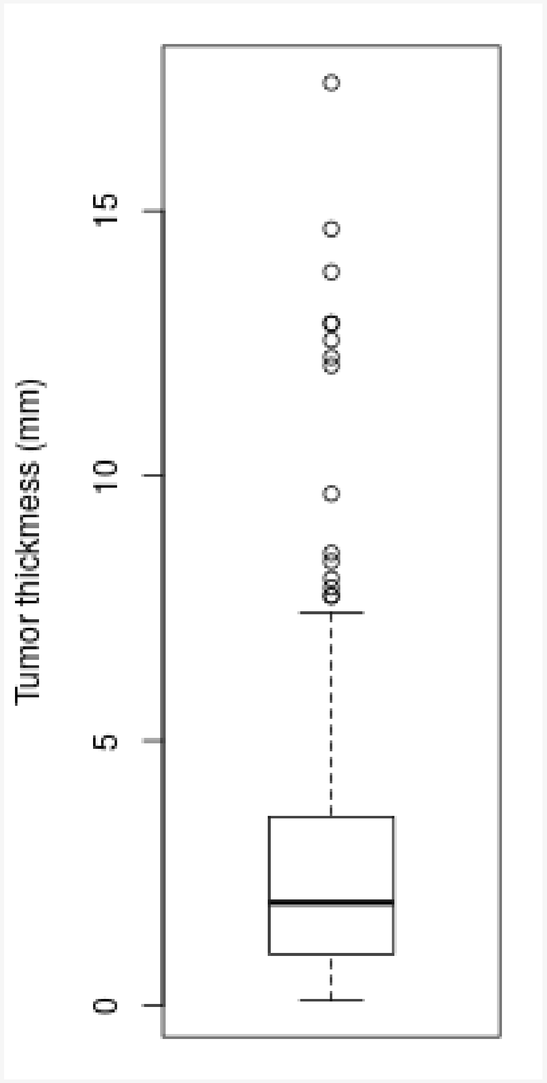
- **Box**: Interquartile range (IQR), contains 50% of points
- **Whiskers**: Extend from box, indicate variability outside upper and lower quartiles
- **Outliers**: May be plotted as individual points



Example:
Melanoma thickness (mm)
in 205 patients

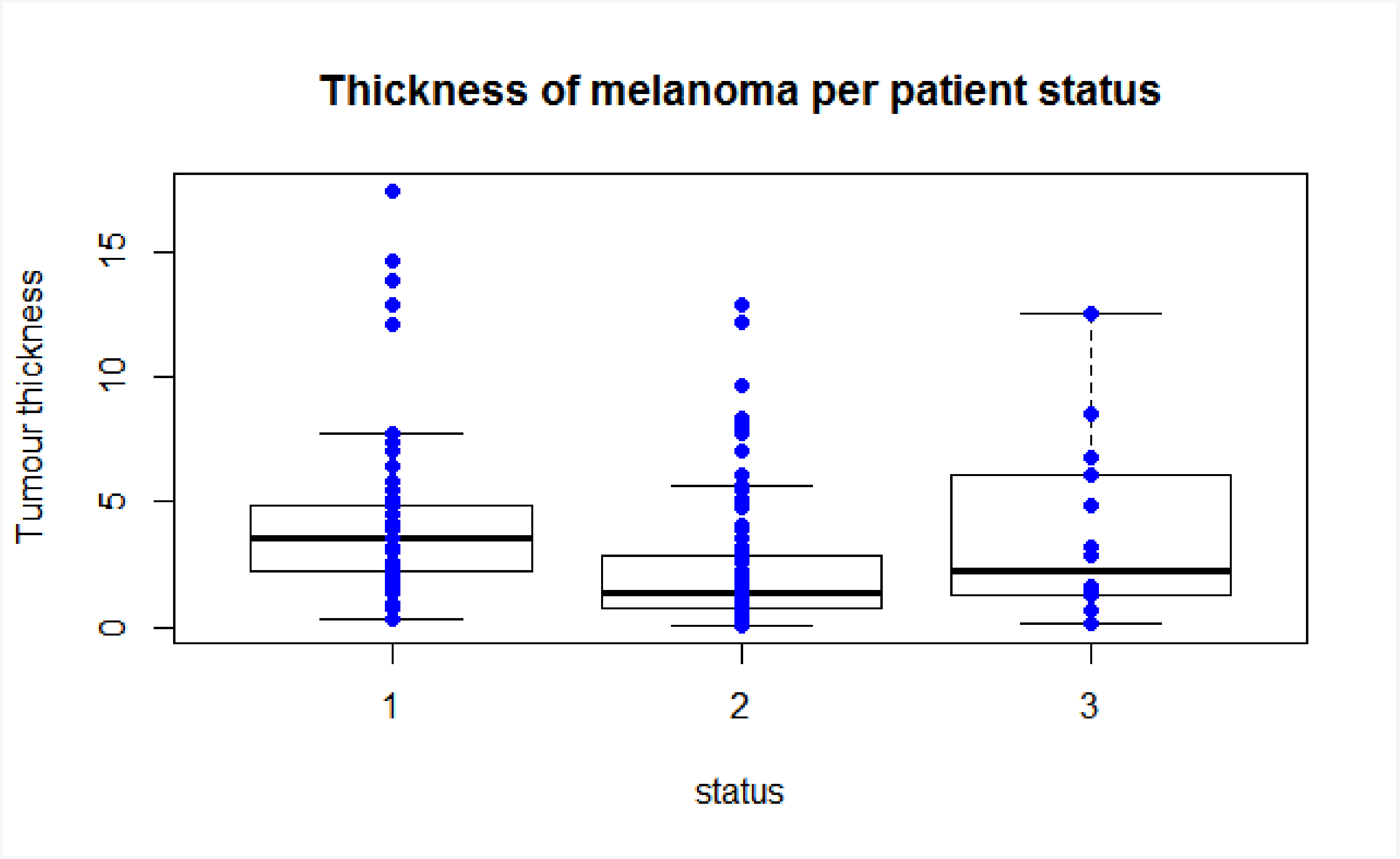
Boxplot: data and plotting code

```
>library(MASS)
>data(Melanoma) #Data from MASS package. 205 patients in Denmark
with malignant melanoma

>head(Melanoma) #look inside the data set
 time status sex age year thickness ulcer
1   10      3   1  76 1972      6.76      1
2   30      3   1  56 1968      0.65      0
3   35      2   1  41 1977      1.34      0
4   99      3   0  71 1968      2.90      0
5  185      1   1  52 1965     12.08      1
6  204      1   1  28 1971      4.84      1


>boxplot(Melanoma$thickness,
        ylab="Tumour thickness (mm)")
```



More boxplots

- Make separate boxplots for subgroups of data
- Plot individual data points as an overlay of the boxplots.



status: 1 died from melanoma, 2 alive, 3 dead from other causes

More boxplots: data preparation

```
#check if the grouping variable is a factor (it is not!)
>str(Melanoma)
'data.frame':     205 obs. of  10 variables:
 $ time     : int  10 30 35 99 185 204 210 232 232 279 ...
 $ status   : int  3 3 2 3 1 1 1 3 1 1 ...
 $ sex      : int  1 1 1 0 1 1 1 0 1 0 ...
 $ age      : int  76 56 41 71 52 28 77 60 49 68 ...
 $ year     : int  1972 1968 1977 1968 1965 1971 1972 1974
 $ thickness: num  6.76 0.65 1.34 2.9 12.08 ...
 $ ulcer    : int  1 0 0 0 1 1 1 1 1 1


#coerce the grouping variable to factor
>Melanoma$status <- factor(Melanoma$status)
```

More boxplots: plotting code

Method 1: Data subsets

```
>boxplot(Melanoma$thickness[Melanoma$status=="1"],
         Melanoma$thickness[Melanoma$status=="2"],
         Melanoma$thickness[Melanoma$status=="3"],
        main="Thickness of melanoma per patient status",
        xlab="status", ylab="Tumour thickness",
        names=c("1","2","3"))

>points(Melanoma$status, Melanoma$thickness,
       col="blue",pch=19) #adds the actual data points to the plot
```

Method 2: Formulas

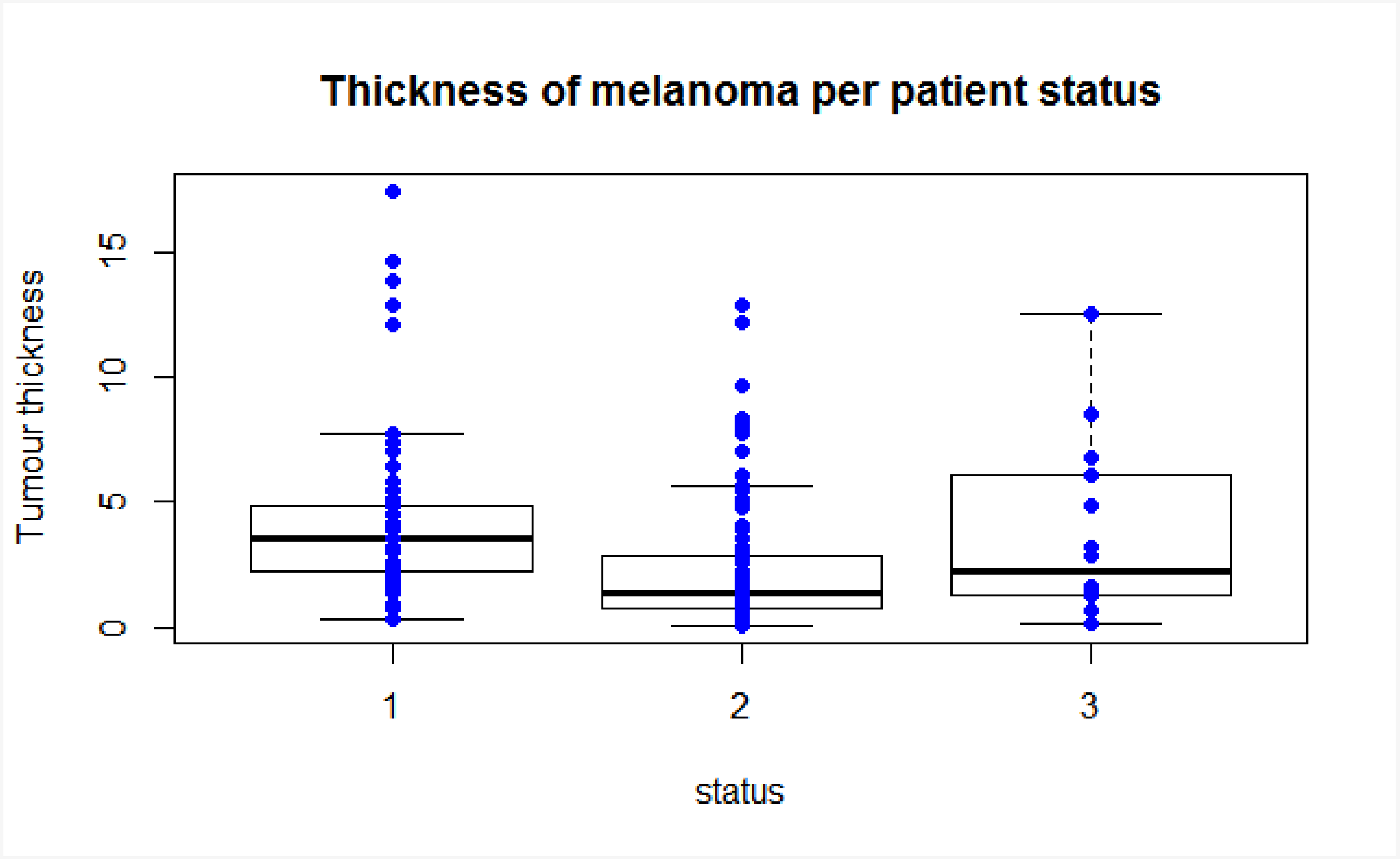
```
>boxplot(thickness ~ status, data=Melanoma,
        main="Thickness of melanoma per patient status",
        xlab="status", ylab="Tumour thickness")

>points(thickness ~ status, data=Melanoma,
        col="blue", pch=19) #adds the actual data points to the plot
```

More boxplots: plotting code - P5S

Method 1: Data subsets – boxplot(df$y[df$x==’a’] ,
df$y[df$x==’b’])

Method 2: Formulas - boxplot(y ~ x , data=df)

→ give the same plot



The abline() function

abline() adds one or more straight lines through the current plot – vertical, horizontal or sloped.

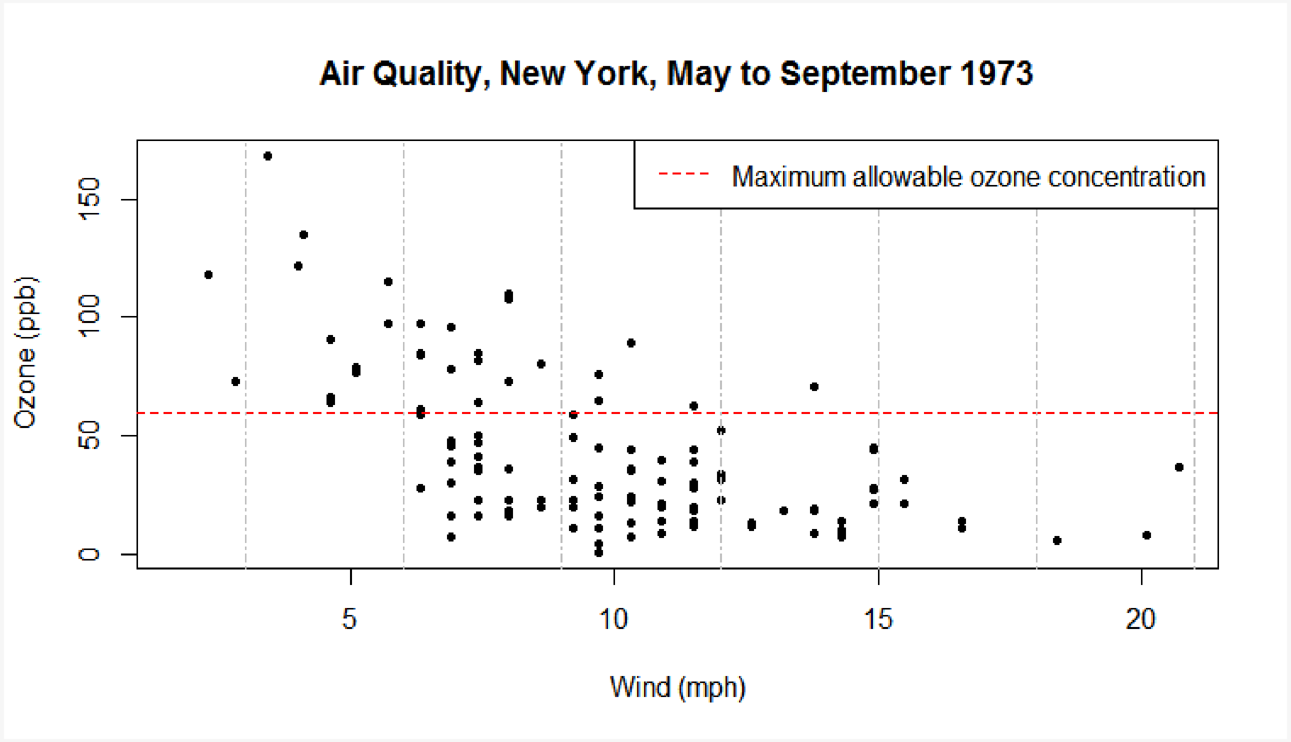
Useful for

- showing boundaries and cutoffs
- fitting straight trend lines through the data (cf. ?lm)

Arguments:

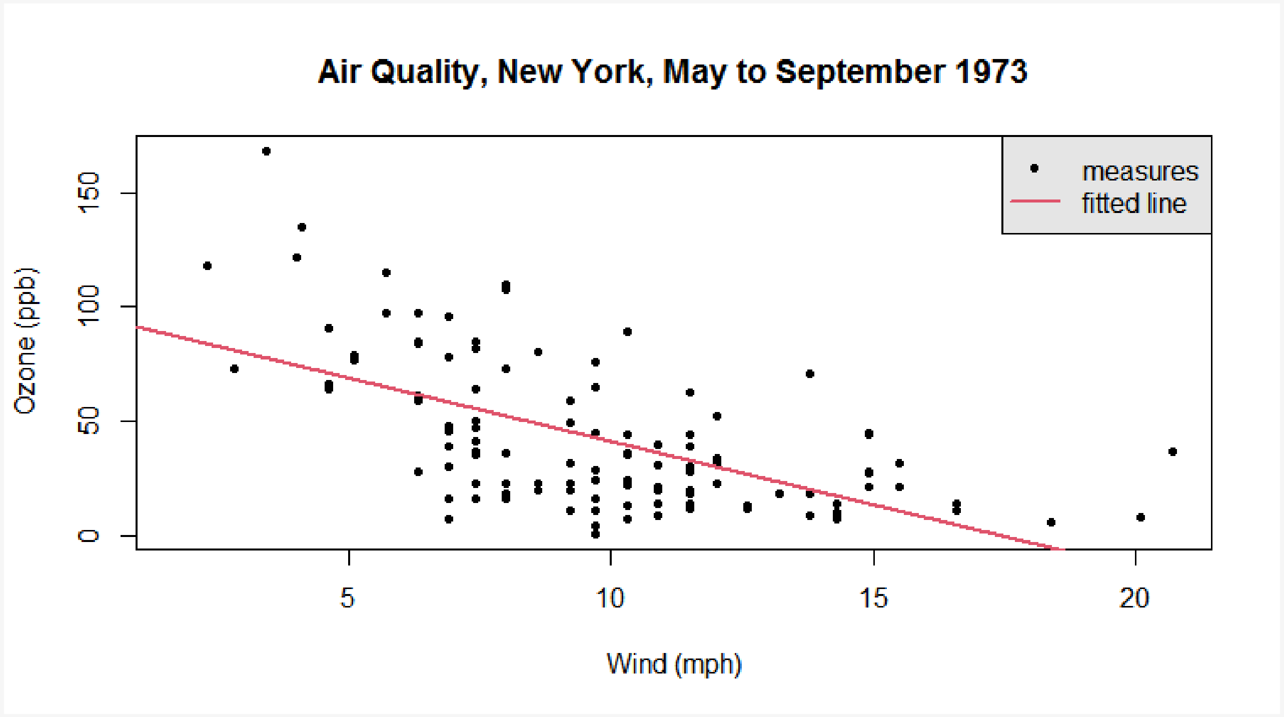
- abline(**v**=c(...)): add vertical line(s) at the given x value(s)
- abline(**h**=c(...)): add horizontal line(s) at the given y value(s)
- abline(**a**= ,**b**=): add an affine line with intercept a and slope b
- abline(**reg**=**lm**(...)): add a trend line from a linear regression equivalent to abline(lm(...))

Example 1: Horizontal and vertical lines



```
> data(airquality) # Daily measurements, New York, May-Sept. 1973
> plot(airquality$Wind, airquality$Ozone, pch=20,
    xlab= "Wind (mph)", ylab="Ozone (ppb)")

> abline(h=60, col="red", lty="dashed")
> abline(v=seq(3,21,3), col="grey", lty="dotdash")

> legend("topright", "Maximum allowable ozone concentration",
     col="red", lty="dashed")
```

Example 2: Fitting a trend line



```
> plot(airquality$Wind, airquality$Ozone, pch=20,
    xlab= "Wind (mph)", ylab="Ozone (ppb)")
```

`> abline(lm(airquality$Ozone ~ airquality$Wind), col=2, lwd=2)`

```
> legend("topright", legend= c("measures","fitted line"),
  pch= c(20, NA), lty = c(0, 1), lwd=c(NA, 2),
  col = c(1, 2), bg = "gray90")
```

Let’s practice - 8

Let's come back to the mice dataset stored in the "mice_data" data frame (Let’s practice – 3). If mice_data is not currently in your workspace, either get it back by loading the .Rdata file or import the data again from the original .csv file.

1) Make boxplots of weights from WT and KO mice. Customise with title, labels, colours.
2) Make a barplot of the mean weights of WT and KO mice, using the means returned by tapply(). Customise the barplot with title, labels, colours.
   - *Optional: Add number of observations to each bar.*
   - *Optional: add errors bars.*

Permanent Graphic Changes (I)

- The function **par()** allows to change the default values of many plotting parameters. All future calls to graphics functions will be affected.

- Example 1: set plotting colors and symbols

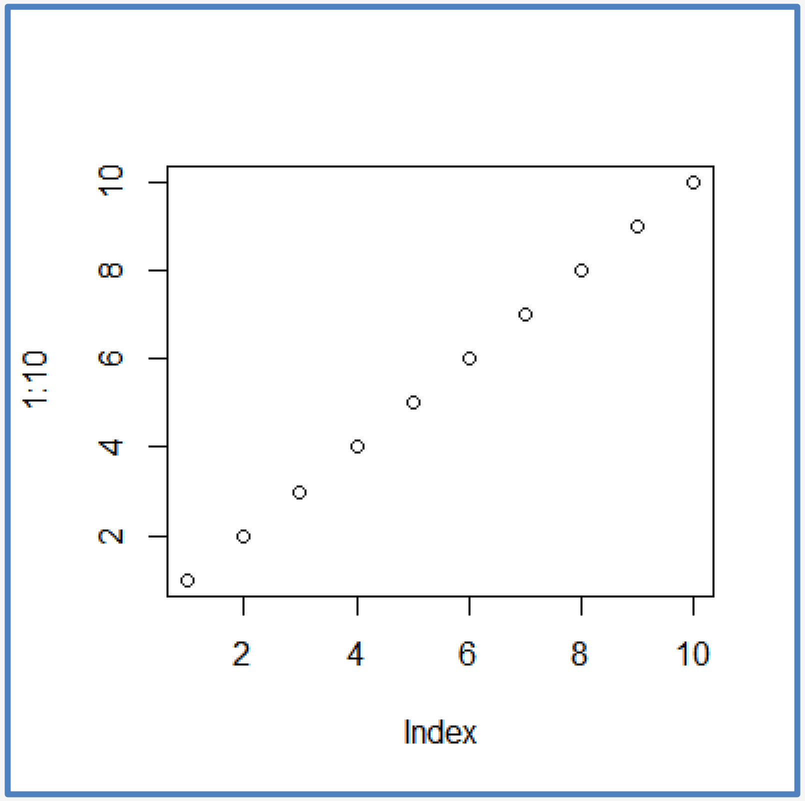
```
>par(col="red", pch=15)
```

- Example 2: set margin widths for subsequent plots
  - **mar** sets plot margins in number of lines
  - **mai** sets plot margins in inches
  - use vectors of 4 values (c(0,1,1,2)) for the bottom, left, top, and right margins

```
>par(mar=c(5.1,4.1,4.1,2.1))     #set margins in lines
>par(mai=c(1.02,0.82,0.82,0.42)) #set margins in inches
```

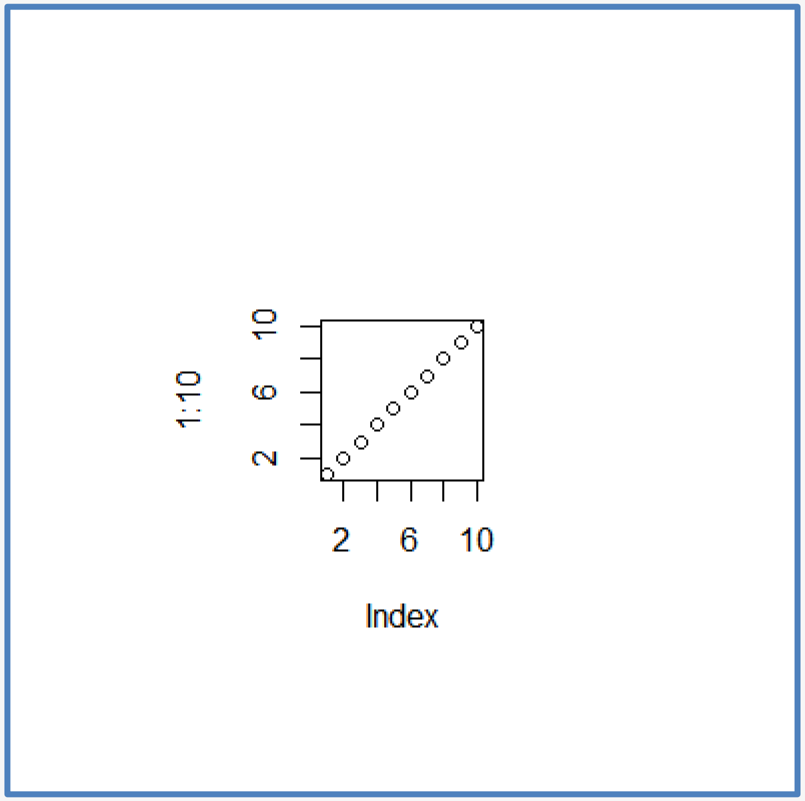
Normal Margins (bottom, left, top right):

```
>par(mar=c(5.1,4.1,4.1,2.1))
>plot(1:10)
```



Wide Margins (bottom, left, top, right):

```
>par(mar=c(8.1,8.1,8.1,8.1))
>plot(1:10)
```

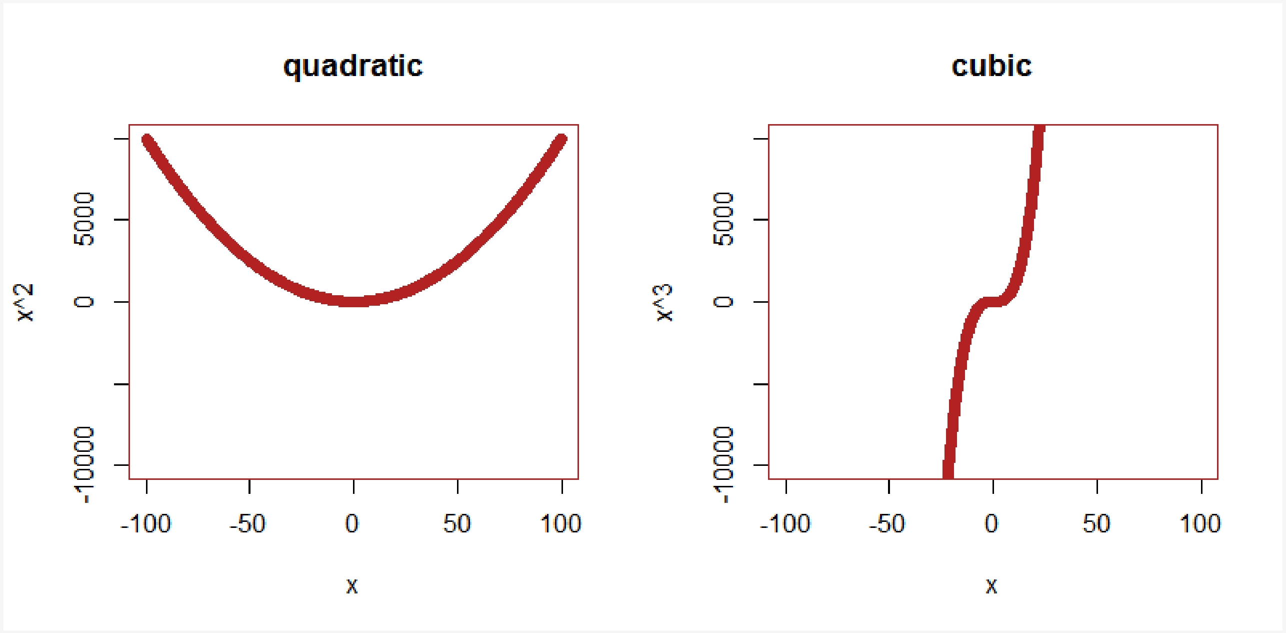


Permanent Graphic Changes (II)

- **Example 3:** Generate multi-panel figures using **par()**

mfrow (or mfcol): A vector of the form c(nr, nc). Subsequent figures will be drawn in an nr-by-nc array by rows (or columns, respectively).

```
> par(mfrow=c(1,2),col="firebrick", pch=19)  #1x2 plot array
> x <- seq(-100, 100, 0.1)
> plot(x, y=x^2, ylim = c(-10000,10000), "quadratic")
> plot(x, y=x^3, ylim = c(-10000,10000), "cubic")
```



Current settings of par() - P5S

- Calling par() without parameters displays current settings
- If you changed nothing, all parameters are at default values

Resetting par()

- par() is automatically reset to defaults when you:
  - **Restart R** or close/switch **Rstudio projects**
  - Run **dev.off(),** which closes the most recent plot/plotting device
  - Run **graphics.off(),** which closes plots/plotting devices
  - **In RStudio, clear** all plots using the broom icon

Saving figures to files

- By default, R plots all graphics to the screen.
- R offers functions to export graphics to many formats (pdf, postscript, bmp, jpeg, png, tiff). The basic concept is to redirect the graphics output to a different "device".
- Use **pdf()** to start redirection to a .pdf file, **png()** for a .png file, etc.
- Use **dev.off()** to close the redirection.

```
> pdf(file="quadratic_cubic.pdf", width=10, height=5,
    paper="a4")
> par(mfrow=c(1,2),col="firebrick", pch=19)
> x <- seq(-100, 100, 0.1)
> plot(x, y=x^2, ylim=c(-10000,10000), "quadratic")
> plot(x, y=x^3, ylim=c(-10000,10000), "cubic")
> dev.off()
```

- Alternatively you can use the RStudio interface:
  - Plots > *Export > Save as Image* (PNG,JPEG,TIFF,BMP,...)
  - Plots > *Save as PDF*.

Arguments to graphics export functions

- Use correct file extension:
  - postscript(file="a_name.ps", ...)
  - pdf(file="...pdf", ...)
  - jpeg(file=" ...jpg", ...)
  - png(file=" ....png", ...)

- Each graphics device has a specific set of arguments that dictate characteristics of the outputted file : height=, width=, horizontal=, res=, paper=, pointsize=
- For png, jpeg, tiff (raster formats), the width and height of the graphics are given in pixels.
- For pdf and postscript (vector formats), the width and height of the graphics region are given in inches. Default values are 7. (Tip: A4 = 8.3" x 11.7“; set the width and height a little smaller for printing to A4 size).
- Only pdf() and postscript have an argument "paper". This can be set to common paper formats (paper="a4" for A4 in portrait orientation, paper="

Multi-page vs single page output

- Files in png, jpeg, tiff (raster formats) can only have one page.
- Files in pdf and postscript formats (vector format) receive multiple pages by default. You can deactivate this behaviour using the onefile argument.

One Multi-page file

```
> pdf(file="my_file.pdf")
... #make a few plots, each will go on a separate page     #in the same file
> dev.off()
```

Several one-page files

```
> pdf(file="my_file_%d.pdf", onefile= FALSE )
... #make a few plots, each will go into its own file
> dev.off()
```

The format specifier %d causes the resulting files to be numbered:

Choosing an image file format

Raster graphics (png, tiff, jpeg):
file sizes depend on the image size (number of pixels)
once created, stretching the image leads to poor quality

Vector graphics (pdf, ps, eps, svg):
file sizes depend on the number of drawing actions
(e.g. number of points, lines,...)
all elements can be scaled as desired

Embedding image files in MS Office documents (Word, PowerPoint):
In Windows, png and tiff work best, pdf can get blurry.
In macOS, pdf works well.

Publication-quality figures:
Vector graphics (pdf, eps) tend to be easier to adapt as they can be resized

File size tip: pdfs can become large in file size and slow to display when a large number of points is plotted. When this is an issue, consider png.

Let’s practice – 9

1) Make a multi-panel figure with the **four graphics on one page**, exporting the figure to a **png** file. Set width and height arguments in the call to png() to make it look nice.

2) **Optional:** Perform the steps of the 2 previous practice sessions, but for diet in place of genotype. (Step 2 will not change). This time, make a **pdf** with two pages and **two graphics on each page**. Again, set width and height arguments in the call to pdf() to make it look nice.

3) **Optional:** Look at the multi-panel figures. Are your impressions about mouse weight from yesterday's exploration of data summaries confirmed by today's visualizations?

In a nutshell

- Introduction to high-level and low-level plotting functions in R
  - plot(), lines(), points(), hist(), barplot(), boxplot() …
- Customization of plotting functions
  - Colours, line types, line widths, plotting characters…
  - Titles, labels, legend…
- Permanent graphic changes
- Exporting graphics