

Introduction to R

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Plan for today

01_ R Intro

- Introduction to R
- Data management
- Loops
- Graphics

Outline

01_ R Intro

- 1 Introduction to R
- 2 Importing Data to R
- 3 Description of Data
- 4 Modifying Data
- 5 Loops and Flow Controls in R
- 6 Saving Your Work
- 7 Graphics
 - Histogram
 - Box plot
 - Scatter Plot
 - Line plot

Introduction to R

01_ R Intro

- **R** is a programming *language* and a programming *environment*.
- It is Free! Developed by users under a GNU license.
- Runs on a variety of platforms including Windows, Unix and MacOS. You can even get it for Android.
- Allows for fast implementation of new methods by user demand through packages.
- **R** has state-of-the-art graphics capabilities.

Advantages of R

01_ R Intro

Frank Harrel (my highlighting):

- "One point that hasn't been made very explicitly is one of the greatest advantages of **R**:

Getting your work done better and in less time.

Hundreds of companies hire a multitude of SAS programmers to write code in an archaic language, the SAS macro language. I believe there is a real cost savings from R because of its value as a **data analysis**, **data manipulation**, and **graphics** environment. Instead of programming using an indirect syntax manipulation environment (SAS macros), in R you can program in a dynamic data-sensitive framework".

That was more than 10 years ago. Things have progressed since...

Base R

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- Base **R** and most **R** packages are available for download at the Comprehensive R Archive Network (CRAN).
- <http://www.cran.r-project.org>
- Base **R** includes basic data management, analysis and graphics tools.
- For non-specialized tasks, Base **R** is all you need.
- Specialized tasks may be handled by *packages*.
- We will download, install and use many packages during the course.
- Packages are not all very well-documented (depends on the contributor).
- Want to be sure about what your program does?
 - Use well-established packages only;
 - or write your own code.

- You can work directly in **R**.
- Many prefer another front end (GUI, **G**raphical **U**ser **I**nterface).
- We will use **RStudio**.
- Download from <http://www.posit.co/>

- The GUI **RStudio** has 4 windows.
- One for writing the commands (the "script").
 - Use script for reproducibility.
- One for results and interactive use.
- One for plots, help and packages.
- One showing which objects are resident in the **R** memory.

The screenshot displays the RStudio environment with the following components:

- Source Editor:** Contains R code for a simulation. The code includes comments in Danish and uses the `set.seed()` function. It defines a binomial distribution with $n=10$ and $p=0.5$, and calculates the log-likelihood function $\ell(\theta)$ for a given θ .
- Environment Pane:** Lists the objects in the global environment, including data frames like `coasts`, `country`, `europe`, `frame`, `graticule`, `my.center`, `nuts0.df`, `nuts0.spdf`, `nuts1.df`, `nuts1.spdf`, `nuts2.df`, `nuts2.spdf`, `nuts3.df`, and `nuts3.spdf`.
- Console:** Shows the execution of the code, with the prompt `>` indicating the start of a new line.
- Bottom Status Bar:** Indicates the current session is 'R Session 1'.

R as a calculator

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```
2+2
```

```
[1] 4
```

```
(2*5)+(12/3)-(2^3)
```

```
[1] 6
```

```
exp(log(1))
```

```
[1] 1
```

```
sqrt(25)
```

```
[1] 5
```

```
log(2*2)
```

```
[1] 1.3863
```

```
log(2)+log(2)
```

```
[1] 1.3863
```

Writing commands in R

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- Commands are separated by either a new line or ;
- **R** is case sensitive: id is a different name than ID.
- The character `#` at the beginning of a line shows that the text in this line is a comment. I.e. the text is not executed.
- Help can be found on the internet or in **R** by writing `?` followed by the function you want to help about:

```
?plot
```

- or, in [RStudio](#), highlight the expression and press F1.

Objects in R

01_ R Intro

- Both data and output from analyses are stored as **objects** (if stored);
- Some times, output is just displayed on the screen, and you need to *assign* the object to an identifier to keep it (see below).
- In fact, everything in the **R** memory is stored in **objects**.
- An object could be a vector, a matrix or a data frame.
- Values are assigned to objects using the assignment operator `<-`
- The operator `=` also works, but it is **not recommended** as it may confuse assignments with default values and logical expressions.
- We can see the objects of the current **R** session memory in **RStudio**, or by using the function `ls()`

```
a <- 2+5
```

```
A <- 10
```

```
ls()
```

```
[1] "a" "A"
```

Generating a sequence

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- Specify the first and last values separated by a colon.
- Otherwise use `seq()`

```
0:10
```

```
[1] 0 1 2 3 4 5 6 7 8 9 10
```

```
15:5
```

```
[1] 15 14 13 12 11 10 9 8 7 6 5
```

```
seq(from = 0, to = 1.2, by = 0.1)
```

```
[1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1 1.2
```

```
x <- seq(from = 0, to = 1.5, length = 11); x
```

```
[1] 0.00 0.15 0.30 0.45 0.60 0.75 0.90 1.05 1.20 1.35 1.50
```

Generating repeats using rep()

```
rep(8, 5)
```

```
[1] 8 8 8 8 8
```

```
rep(1:4, each = 2)
```

```
[1] 1 1 2 2 3 3 4 4
```

```
rep(1:4, each = 2, times = 3)
```

```
[1] 1 1 2 2 3 3 4 4 1 1 2 2 3 3 4 4 1 1 2 2 3 3 4 4
```

Functions in R

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We assign a simple function to the identifier f:

```
>f<-function(x){x^2}; f(2)  
[1] 4
```

A function of two variables:

```
>f<-function(x,pow){x^pow}; f(2,2)  
[1] 4
```

A function with a default value:

```
>f<-function(x,pow=2){x^pow}; f(2,2); f(2);f(2,3)  
[1] 4  
[1] 4  
[1] 8
```

Functions in R

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We have already used many functions with and without default values:

- `"+"(2,2)`
- `sqrt(25)`
- `log(2)`
- `ls()`
- `":"(0,10)`
- `seq(from=0.1,to=1.2,by=0.1)`
- `rep(1:4,each=2,time=3)`

Many applications in **R** are built up as functions. You can see default arguments in the help files. Example: `log`.

Data structures in R: Singles

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- Logical, e.g:

```
> TRUE
```

```
[1] TRUE
```

```
> 1==2
```

```
[1] FALSE
```

- Single numbers, e.g:

```
> 1
```

```
[1] 1
```

```
> 1.2
```

```
[1] 1.2
```

- Character, e.g:

```
> "5"
```

```
[1] "5"
```

```
> "abc"
```

```
[1] "abc"
```

Data structures in R: Vectors

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Constructed via the concatenate function `c()`.

- Vector of numbers, e.g:

```
> c(1,1.2,pi,exp(1))  
[1] 1.000000 1.200000 3.141593 2.718282
```

- We can have vectors of other things too, e.g:

```
> c(TRUE,1==2)  
[1] TRUE FALSE  
> c("a","ab","abc")  
[1] "a" "ab" "abc"
```

- But not combinations, e.g:

```
> c("a",5,1==2)  
[1] "a" "5" "FALSE"
```

Note that R just turned everything into characters!

Data structures in R: Matrices

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- Columns of same type and same length:

```
> matrix(c(1,2,3,4,5,6)+pi,nrow=2)
```

```
[,1] [,2] [,3]
```

```
[1,] 4.141593 6.141593 8.141593
```

```
[2,] 5.141593 7.141593 9.141593
```

```
> matrix(c(1,2,3,4,5,6)+pi,nrow=2)<6
```

```
[,1] [,2] [,3]
```

```
[1,] TRUE FALSE FALSE
```

```
[2,] TRUE FALSE FALSE
```

Data structures in R: Data frames

01_R Intro

- Same length of columns but different types; spread-sheet data.
- Created from reading in data from external files;
- or by using the function `data.frame()` on a set of vectors.

```
> data.frame(treatment=c("active","active","placebo"),
+ bp=c(80,85,90))
```

```
  treatment  bp
1   active  80
2   active  85
3 placebo  90
```

- Compare to a matrix created with the `cbind()` command:

```
> cbind(treatment=c("active","active","placebo"),bp=c(80,85,90))
      treatment bp
[1,] "active"  "80"
[2,] "active"  "85"
[3,] "placebo" "90"
```

Data structures in R: Lists

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- Different length of columns and different types.
- Most general object type.

```
> list(a=1,b="abc",c=c(1,2,3),d=list(e=matrix(1:4,2), f=function(x){x^2}))
$a
[1] 1
$b
[1] "abc"
$c
[1] 1 2 3
$d
$d$e
      [,1] [,2]
[1,]    1    3
[2,]    2    4
$d$f
function (x)
{
    x^2
}
```

- The objects returned from many of the built-in functions in R are fairly complicated lists.

Importing Data to R

01_ R Intro

- The easiest is to use data saved as text files.
- Usually values in text files are separated, or delimited, by tabs or commas.
- First tell **R** where you want to find your data using the command `setwd()`.
- Check that all went according to plan with `getwd()`.

```
setwd("C:/Users/ANST/Teaching/02935 January 2025")  
getwd()  
  
[1] "C:/Users/ANST/Teaching/02935 January 2025"
```

Importing Data to R

01_ R Intro

- The function `read.table()` can be used to read data saved as text.
- Wrappers: `read.csv()`, `read.csv2()` and `read.delim()`.
- Notice the option `sep = .`
- We are assigning the loaded data to objects.
- If you have an Excel sheet, then save as text.

```
Births.tab <- read.table("Data/Births.txt", header = TRUE, sep = "\t")
```

```
# SHORT FORM TO READ TAB SEPARATED
```

```
Births.delim <- read.delim("Data/Births.txt")
```

```
# SHORT FORM TO READ ; SEPARATED
```

```
Births.csv2 <- read.csv2("Data/Births.csv")
```

```
# SHORT FORM TO READ , SEPARATED
```

```
Births.csv1 <- read.csv("Data/Births.csv1")
```

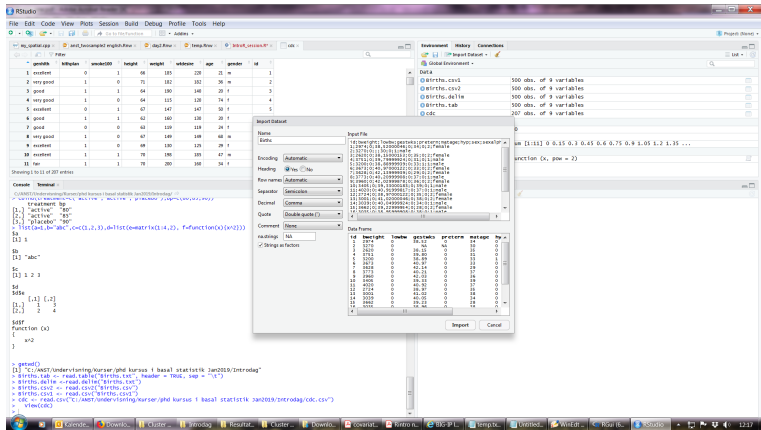
-
- The screenshot displays the RStudio interface with the following components:
- File Editor (Top):** Contains the R script with the following code:


```
## Create a data frame with 1000 rows and 10 columns
set.seed(12345)
df <- data.frame(
  gender = sample(c("M", "F"), 1000, replace = TRUE),
  height = runif(1000, min = 150, max = 200),
  weight = runif(1000, min = 50, max = 150),
  age = runif(1000, min = 18, max = 65),
  blood_pressure = runif(1000, min = 90, max = 140),
  cholesterol = runif(1000, min = 100, max = 300),
  glucose = runif(1000, min = 70, max = 130),
  hba1c = runif(1000, min = 4.0, max = 10.0),
  bmi = runif(1000, min = 18.0, max = 35.0),
  diabetes = sample(c("No", "Yes"), 1000, replace = TRUE)
)
```
 - Environment (Top Right):** Shows the data frame 'df' with 1000 observations and 10 variables. The variables are: gender (factor), height (numeric), weight (numeric), age (numeric), blood_pressure (numeric), cholesterol (numeric), glucose (numeric), hba1c (numeric), bmi (numeric), and diabetes (factor).
 - Console (Bottom):** Shows the execution of the script, including the creation of the data frame and the calculation of the BMI for each observation.
 - Source (Bottom Left):** Shows the R script code, including the creation of the data frame and the calculation of the BMI for each observation.

Importing Data using RStudio

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- In the Objects Window, click "Import Dataset"



Importing Data from other stats programs

- We can read data from a series of other statistical software packages using the package `foreign`. A similar package is `Hmisc`, but we will stick to `foreign`.

```
# INSTALL AN EXTRA PACKAGE  
install.packages("foreign")
```

```
# ACTIVATE THE PACKAGE  
library("foreign")
```

```
SPSS_Data <- read.spss("Data/SPSS_Data.sav", to.data.frame = TRUE)
```

```
Stata_Data <- read.dta("Data/string.dta")
```

- For SAS data not in XPORT format, use the `sas7bdat` package.

Look at Your Data

01_ R Intro

There are several ways to look at the data (or parts of the data).

```
# FIRST FEW OBSERVATIONS
```

```
head(Births.tab)
```

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph
1	1	2974	0	38.52	0	34	0	2	female
2	2	3270	0	NA	NA	30	0	1	male
3	3	2620	0	38.15	0	35	0	2	female
4	4	3751	0	39.80	0	31	0	1	male
5	5	3200	0	38.89	0	33	1	1	male
6	6	3673	0	40.97	0	33	0	2	female

Look at Your Data

01_ R Intro

LAST FEW OBSERVATIONS`tail(Births.tab)`

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph
495	495	2968	0	41.01	0	34	0	1	male
496	496	2852	0	38.45	0	28	0	2	female
497	497	3187	0	38.03	0	38	1	1	male
498	498	3054	0	38.50	0	26	0	2	female
499	499	3178	0	39.92	0	31	0	2	female
500	500	2918	0	37.97	0	31	0	1	male

VARIABLE NAMES`names(Births.tab)`

```
[1] "id"          "bweight" "lowbw"    "gestwks" "preterm" "matage"  "hyp"
[8] "sex"         "sexalph"
```

VIEW THE DATA IN A NEW WINDOW; OFTEN THE HEAD WILL DO THOUGH`View(Births.tab)`

Missing values

01_ R Intro

- In real life examples it is very common to have missing values.
- In **R** missing values are coded as **NA** (not available).
- In your Excel file leave missing values blank, do not set them to 99 or 999.

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph
1	1	2974	0	38.52	0	34	0	2	female
2	2	3270	0	NA	NA	30	0	1	male

Accessing Observations

01_ R Intro

- Data are (usually) stored in a data frame object.
- Observations are the rows.
- Variables, either numerical or categorical, are the columns.
- We can access individual rows, columns and cells in the data frame.
- For this, we use the bracket operator: `object[row, column]`.

Accessing Observations

01_ R Intro

```
# A SINGLE CELL
```

```
Births.tab[345, 4]
```

```
[1] 38.55
```

```
# LEAVING OUT A COLUMN NUMBER INDICATES THAT ALL COLUMNS  
# ARE CHOSEN. HERE ALL COLUMNS IN ROW 224
```

```
Births.tab[224 , ]
```

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph
224	224	3216	0	39.94	0	38	1	1	male

Accessing Observations

01_ R Intro

```
# LEAVING OUT A ROW NUMBER INDICATES THAT ALL ROWS ARE CHOSEN
# HERE ALL ROWS IN COLUMN 5
Births.tab[,5]
```

[illegible]

Accessing Observations

01_R Intro

```
# USE RANGES, ROWS 15 TO 18 COLUMNS 1 TO 4  
Births.tab[15:18, 1:4]
```

	id	bweight	lowbw	gestwks
15	15	3662	0	39.23
16	16	3035	0	38.96
17	17	3351	0	39.35
18	18	3804	0	38.99

Accessing Observations

01_ R Intro

Variables can be accessed directly using their name, either with the `$` operator (`object$variable`), the name (`object[, "variable"]`), or the column number (`object[, k]`).

```
# GET THE BIRTH WEIGHT FOR CHILD 26 TO 36
```

```
Births.tab$bweight[26:36]
```

```
[1] 3585 3798 3164 3739 1780 4022 3942 2887 2391 3911 3509
```

```
Births.tab[26:36, "bweight"]
```

```
[1] 3585 3798 3164 3739 1780 4022 3942 2887 2391 3911 3509
```

```
Births.tab[26:36, 2]
```

```
[1] 3585 3798 3164 3739 1780 4022 3942 2887 2391 3911 3509
```

Subsetting using the `c()` function

01_R Intro

- The concatenate function `c()` concatenates the arguments into a vector. It can be used for many things; one is to access non-sequential rows and columns from a data frame.

```
# GET COLUMNS 2, 5, 7, 8, 9 FOR ROW 33
```

```
Births.tab[33, c(2, 5, 7:9)]
```

```
      bweight preterm hyp sex sexalph
33      2887         0  0  1      male
```

```
# GET bweight, preterm and sexalph FOR ROW 71
```

```
Births.tab[71, c("bweight", "preterm", "sexalph")]
```

```
      bweight preterm sexalph
71      3189         0      male
```

Variable Names

01_ R Intro

If we want to change the variable names we can use `names()`.

```
# NEW VARIABLE NAMES
names(Births.tab) <- c("ID", "Bweight", "LowBW", "GestWks",
                      "Preterm", "Matage", "Hyp", "Sex", "Sexalph")

# JUST THE FIRST VARIABLE NAME
names(Births.tab)[1] <- c("ID_new")

# CHECK HOW IT WENT
names(Births.tab)

[1] "ID_new"  "Bweight" "LowBW"   "GestWks" "Preterm" "Matage"  "Hyp"
[8] "Sex"     "Sexalph"

# RESETTING
names(Births.tab)[1] <- c("ID")
```

Saving/Exporting data

01_ R Intro

- We can save the data to a textfile using either `write.table()` for a tab separated file, or `write.csv()/write.csv2()` for a comma/semicolon separated file (with "." and "," as decimal point, respectively).

```
write.table(Births.tab, file = "Birth_new.txt",  
            sep = "\t", na = ".", row.names= FALSE)  
  
write.csv2(Births.tab, file = "Birth_new.csv")
```

Exercise: Protein Consumption

01_R Intro

- Open [RStudio](#) and set the working directory to where you want to keep the data for the course today.
- Import the data Protein.xlsx to **R**.
- Look at the data.
- What is the protein consumption in Denmark?
- Look at the protein consumption from red meat alone.
- Look at the protein consumption in Denmark, Norway, Sweden from red meat, white meat and eggs.
- Rename the variables “RedMeat” and “WhiteMeat” to “Red” and “White”.
- Save the new version of the protein data as a tab delimited text file “Protein2.txt”.

Description of Data

01_ R Intro

We are still looking at the data set with birth weights for 500 children. Using the function `str()` we can see a description of what our data frame contains (the structure).

```
str(Births.tab)

'data.frame': 500 obs. of  9 variables:
 $ id      : int  1 2 3 4 5 6 7 8 9 10 ...
 $ bweight: int  2974 3270 2620 3751 3200 3673 3628 3773 3960 3405 ...
 $ lowbw   : int   0 0 0 0 0 0 0 0 0 0 ...
 $ gestwks: num   38.5 NA 38.2 39.8 38.9 ...
 $ preterm: int   0 NA 0 0 0 0 0 0 0 0 ...
 $ matage  : int   34 30 35 31 33 33 29 37 36 39 ...
 $ hyp     : int   0 0 0 0 1 0 0 0 0 0 ...
 $ sex     : int   2 1 2 1 1 2 2 1 2 1 ...
 $ sexalph: chr  "female" "male" "female" "male" ...
```

Description of Data: Birth weights

01_ R intro

- `str()` supplies all information about an object. **Much is redundant**, do not use `str()` for report writing but for your own overview only.
- We see that we have a data frame with 500 observations and 9 variables.
- Some are integers but “gestwks” is numeric.
- The variable “sexalph” is a character variable.
- Note that “sexalph” and “sex” describes the same thing. But R does not interpret the character values as group labels.
- Factor: Grouping with informative labels. We can convert “sexalph” to a factor using `as.factor()`.

Description of Data: Birth weights

01_ R intro

```
# TELL R THAT sexalph IS A FACTOR
```

```
Births.tab$sexalph <- as.factor(Births.tab$sexalph)
```

```
levels(Births.tab$sexalph)
```

```
[1] "female" "male"
```

```
str(Births.tab)
```

```
'data.frame': 500 obs. of 9 variables:
```

```
$ id      : int  1 2 3 4 5 6 7 8 9 10 ...
```

```
$ bweight: int  2974 3270 2620 3751 3200 3673 3628 3773 3960 3405 ...
```

```
$ lowbw   : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
$ gestwks: num  38.5 NA 38.2 39.8 38.9 ...
```

```
$ preterm: int  0 NA 0 0 0 0 0 0 0 0 ...
```

```
$ matage  : int  34 30 35 31 33 33 29 37 36 39 ...
```

```
$ hyp     : int  0 0 0 0 1 0 0 0 0 0 ...
```

```
$ sex     : int  2 1 2 1 1 2 2 1 2 1 ...
```

```
$ sexalph: Factor w/ 2 levels "female","male": 1 2 1 2 2 1 1 2 1 2 ...
```

Description of Data: Birth weights

01_ R intro

```
# TELL R THAT sex IS A FACTOR WITH SPECIFIC LEVELS
```

```
Births.tab$sex <- factor(Births.tab$sex, labels = c("Male", "Female"))
levels(Births.tab$sex)
```

```
[1] "Male" "Female"
```

```
str(Births.tab)
```

```
'data.frame': 500 obs. of 9 variables:
```

```
$ id      : int  1 2 3 4 5 6 7 8 9 10 ...
```

```
$ bweight: int  2974 3270 2620 3751 3200 3673 3628 3773 3960 3405 ...
```

```
$ lowbw   : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
$ gestwks: num  38.5 NA 38.2 39.8 38.9 ...
```

```
$ preterm: int  0 NA 0 0 0 0 0 0 0 0 ...
```

```
$ matage  : int  34 30 35 31 33 33 29 37 36 39 ...
```

```
$ hyp     : int  0 0 0 0 1 0 0 0 0 0 ...
```

```
$ sex     : Factor w/ 2 levels "Male","Female": 2 1 2 1 1 2 2 1 2 1 ...
```

```
$ sexalph: Factor w/ 2 levels "female","male": 1 2 1 2 2 1 1 2 1 2 ...
```

Descriptive Statistics

01_ R Intro

- There are some simple functions for summary statistics in **R**.
- Very common extractor functions are `mean()`, `sd()`, `median()`, `max()` and `min()`.

```
mean(Births.tab$bweight)
```

```
[1] 3136.9
```

```
sd(Births.tab$bweight)
```

```
[1] 637.45
```

```
median(Births.tab$bweight)
```

```
[1] 3188.5
```

```
max(Births.tab$bweight)
```

```
[1] 4553
```

```
min(Births.tab[, 2])
```

```
[1] 628
```

The Summary Function

01_ R Intro

- The function `summary()` can be used with many objects in **R**.
- When used on a data frame we get all the main summary statistics.

```
# SUMMARY OF THE DATA FRAME
```

```
summary(Births.tab)
```

id		bweight	lowbw	gestwks	
Min.	: 1	Min. : 628	Min. :0.00	Min.	:24.7
1st Qu.:	126	1st Qu.:2862	1st Qu.:0.00	1st Qu.:	37.9
Median :	250	Median :3188	Median :0.00	Median :	39.1
Mean :	250	Mean :3137	Mean :0.12	Mean :	38.7
3rd Qu.:	375	3rd Qu.:3551	3rd Qu.:0.00	3rd Qu.:	40.1
Max.	:500	Max. :4553	Max. :1.00	Max.	:43.2
				NA's	:10

preterm		matage	hyp	sex	sexalph
Min.	:0.000	Min. :23	Min. :0.000	1:264	female:236
1st Qu.:	0.000	1st Qu.:31	1st Qu.:0.000	2:236	male :264
Median :	0.000	Median :34	Median :0.000		
Mean :	0.129	Mean :34	Mean :0.144		
3rd Qu.:	0.000	3rd Qu.:37	3rd Qu.:0.000		
Max.	:1.000	Max. :43	Max. :1.000		
NA's	:10				

Summaries

01_ R Intro

- We may only want summaries for some of the data, e.g. babies with birth weight < 2900 g.
- We subset the data and then summarize as before:

```
summary(Births.tab[Births.tab$bweight<2900,])
```

id	bweight	lowbw	gestwks
Min. : 3	Min. : 628	Min. : 0.000	Min. : 24.7
1st Qu.: 146	1st Qu.: 2120	1st Qu.: 0.000	1st Qu.: 35.5
Median : 254	Median : 2580	Median : 0.000	Median : 37.4
Mean : 250	Mean : 2355	Mean : 0.441	Mean : 36.6
3rd Qu.: 359	3rd Qu.: 2741	3rd Qu.: 1.000	3rd Qu.: 38.5
Max. : 496	Max. : 2894	Max. : 1.000	Max. : 41.4
			NA's : 2
preterm	matage	hyp	sex sexalph
Min. : 0.000	Min. : 24	Min. : 0.000	1:63 female:73
1st Qu.: 0.000	1st Qu.: 31	1st Qu.: 0.000	2:73 male :63
Median : 0.000	Median : 34	Median : 0.000	
Mean : 0.403	Mean : 34	Mean : 0.243	
3rd Qu.: 1.000	3rd Qu.: 37	3rd Qu.: 0.000	
Max. : 1.000	Max. : 43	Max. : 1.000	
NA's : 2			

Group Summaries

01_ R Intro

- Data may be separated by groups.
- Suppose that we want to calculate the mean birth weight for boys and girls (many ways to do this).
- We will use the `tapply()` function to apply the `mean` function to the two levels of “sexalph”.
- `tapply(<variable to summarize>, <variable to group by>, <function to use>)`.

```
# MEAN BIRTH WEIGHT FOR BOYS AND GIRLS
```

```
tapply(Births.tab$bweight, Births.tab$sexalph, mean)
```

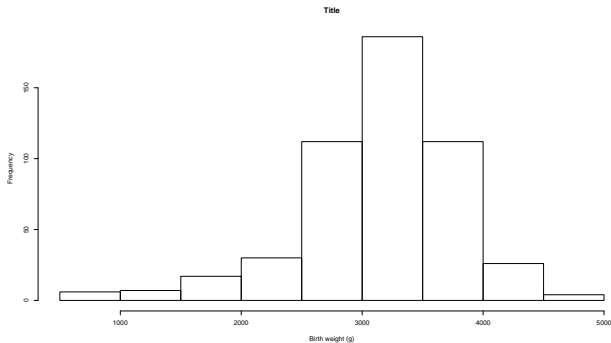
```
female      male  
3032.831 3229.902
```

Histogram

01_R Intro

Often it is easier to get an impression of a distribution using plots. Histograms are typically used for continuous variables.

```
hist(Births.tab$bweight, main = "Title", xlab = "Birth weight (g)" )
```

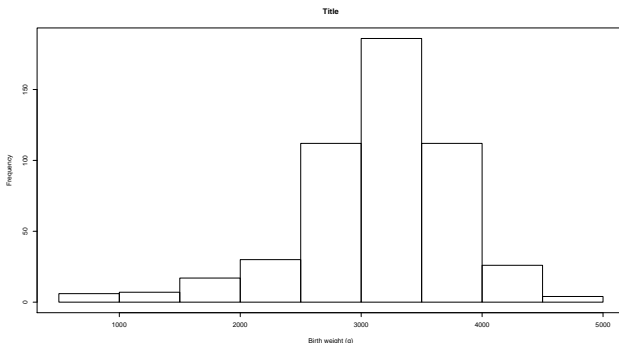


Histogram

01_ R Intro

Often it is easier to get an impression of a distribution using plots. Histograms are typically used for continuous variables. Here with a box on.

```
hist(Births.tab$bweight, main = "Title",  
      xlab = "Birth weight (g)")  
box()
```

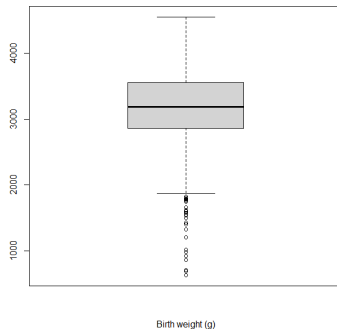


Boxplot

01_ R Intro

Boxplots show the median, upper, lower quartiles and potentially extreme values.

```
boxplot(Births.tab$bweight, xlab = "Birth weight (g)")
```



Exercise: Descriptive Statistics 1

01_R Intro

- Import the dataset `cdc.csv` into **R**.
- Look at the data.
- Describe the structure of the data.
- Change the variable “`smoke100`” to a factor.
- Summarize the variables in the dataset.
- Calculate the mean age by general health.
- Draw a histogram of age.
- Draw a boxplot of age.

Modifying Data

01_ R Intro

We will concentrate on how to modify and rearrange our data.

- Data can be sorted with the `order` function.
- `order` can sort the `Birth.tab` data by “sex“, and then by “bweight“.
- The `order` function returns a vector of sorted indices, which we apply to the rows of the unsorted data frame to get a sorted version.

```
Birth_sort <- Births.tab[order(Births.tab$sex, Births.tab$bweight), ]
```

```
head(Birth_sort)
```

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph
253	253	693	1	30.71	1	34	1	1	male
226	226	981	1	27.99	1	29	1	1	male
181	181	1019	1	28.04	1	31	1	1	male
22	22	1203	1	32.80	1	39	0	1	male
312	312	1500	1	35.27	1	34	0	1	male
313	313	1595	1	30.52	1	33	1	1	male

Creating new variables and deleting old

New variables can be added to a data frame.

```
# ADD A VARIABLE TO DATA FRAME  
Births.tab$log_bweight <- log(Births.tab$bweight)
```

Columns can be dropped from a data frame (log birth weight is column 10):

```
Births.tab <- Births.tab[ , -10]
```

```
# CREATE A VARIABLE AS A SEPARATE OBJECT  
log_bweight <- log(Births.tab$bweight)
```

Objects can be removed from the R memory (cleaning up):

```
rm(log_bweight)
```

Grouping the values of a variable using cut

01_R Intro

You might want to group a continuous variable e.g. mother's age (matage) into the groups:]20-30],]30-35],]35-40],]40-45]:

```
Births.tab$agegrp <- cut(Births.tab$matage,
                        breaks = c(20, 30, 35, 40, 45))
summary(Births.tab[, c("matage", "agegrp")])
```

	matage	agegrp
Min.	:23	(20,30]: 99
1st Qu.:	:31	(30,35]: 215
Median	:34	(35,40]: 174
Mean	:34	(40,45]: 12
3rd Qu.:	:37	
Max.	:43	

Creating new variables: RowSums

01_R Intro

- Often we want to form new variables from other variables.
- For example, we might want to calculate a total score from sub scores.
- We can sum variables using `rowSums`. Related functions are: `rowMeans`, `colSums`, `colMeans`.
- Notice the option `na.rm`.
- If we take a row sum where one of the values is missing then the row sum is set to missing `na.rm= FALSE`.
- If we want to ignore missing values and calculate a sum of the non missing then `na.rm= TRUE`.
- `rowSums`, `rowMeans`, `colSums` and `colMeans` are wrappers of `sapply`, ie. t.ex. `colMeans(x)` is the same as `sapply(x,mean)`. `sapply` can be used with many other functions.

Creating new variables: RowSums

01_R Intro

```
# NEW VARIABLE SCORE SUMMING PRETERM, LOWBW AND HYP
Births.tab$score <- rowSums(Births.tab[,c(3,5,7)], na.rm = FALSE)

#REMOVE MISSING
Births.tab$scoreRM <- rowSums(Births.tab[,c(3,5,7)], na.rm = TRUE)

head(Births.tab)
```

	id	bweight	lowbw	gestwks	preterm	matage	hyp	sex	sexalph	score	scoreRM
1	1	2974	0	38.52	0	34	0	2	female	0	0
2	2	3270	0	NA	NA	30	0	1	male	NA	0
3	3	2620	0	38.15	0	35	0	2	female	0	0
4	4	3751	0	39.80	0	31	0	1	male	0	0
5	5	3200	0	38.89	0	33	1	1	male	1	1
6	6	3673	0	40.97	0	33	0	2	female	0	0

Exercise

01_ R Intro

- Import the data `cdc`.
- Height is in inches, weight and `wt desire` are in pounds. Generate new variables in cm and kg (use Google to find conversion factors).
- Make a factor with 4 *approximately* equally sized groups from the weight variable.
- Sort the data by gender and age.
- Calculate the average of the weight and desired weight for each subject.
- Calculate the mean weight and `wt desire` (in kg) for each level of "genhlth" with the `by` function.

Split Data: Subset

01_ R Intro

- Sometimes we may need to split our data.
- In the Births data we may need to split the data into boys and girls.
- We can use the `subset()` function and assign the new data sets to separate **R** objects.
- Notice `==` (logical expression). We are not assigning a value to “sex“, but asking whether “sex is equal to 1“.

```
Births.Male <- subset(Births.tab, sex == 1)
Births.Female <- subset(Births.tab, sex == 2)
```

- Alternatively the bracket operator:

```
Births.Male <- Births.tab[Births.tab$sex == 1,]
Births.Female <- Births.tab[Births.tab$sex == 2,]
```

Subset

01_ R Intro

- Often data sets come with a lot of variables and we only want to use a few.
- Similarly to the bracket operator `[` the function `subset()` can be used to select the variables we want.
- Notice the `select` option. This is needed to say that we want a subset of columns (on the previous slide it was rows).
- Notice that we do not need quotes in `select`.

```
# SELECT 3 VARIABLES
```

```
Births.new <- subset(Births.tab, select = c(id, bweight, sex))
```

Aggregating data

01_ R Intro

- Sometimes we want to make a new dataframe as a summary of the original dataframe on the basis of factor levels.
- Below we want to make a new dataframe with the mean birthweight for combinations of preterm and sex.

```
PreSex <- aggregate(Births.tab$bweight,
                    by = list(Preterm = Births.tab$preterm,
                              Sex = Births.tab$sexalph), mean)
```

PreSex

	Preterm	Sex	x
1	0	female	3191.6
2	1	female	2020.8
3	0	male	3361.2
4	1	male	2321.6

Add rows: `rbind()`

01_ R Intro

- Data are collected for subgroups of subjects and saved in separate objects.
- The separate objects are appended (stacked) to create a single object.
- This will give an error message if the number of columns differs.

```
# APPEND
```

```
Births.Both <- rbind(Births.Male, Births.Female)  
dim(Births.Both)
```

```
[1] 500  11
```

```
dim(Births.Male)
```

```
[1] 264  11
```

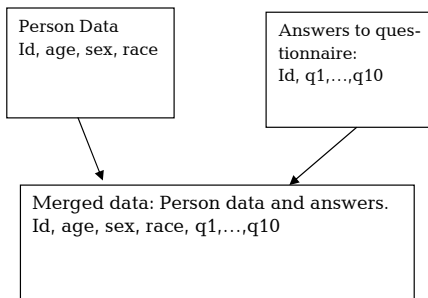
```
dim(Births.Female)
```

```
[1] 236  11
```

Add variables: merge()

01_R Intro

Often you have data in several data sets and want to combine the data sets by merging using one or more variables as *key variables*. Adding variables to a master data set.



Merge

01_ R Intro

We have two data sets with a key variable "id". One with background information and one set with blood pressure measurements.

```
agesex <- read.delim("agesex.txt")
```

```
agesex
```

	id	age	sex
1	99	43	m
2	100	47	f
3	101	NA	f
4	102	67	m

```
bp <- read.delim("bp.txt")
```

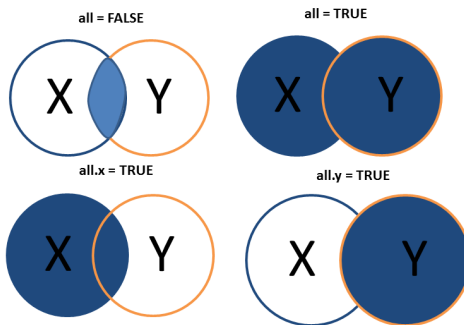
```
bp
```

	id	visit	bp
1	100	1	180
2	100	2	160
3	100	3	155
4	101	1	160
5	102	1	120
6	102	2	140
7	103	1	135

4 Different Merges

01_ R Intro

- In the `merge` function we will look at 4 of the options.
- We have `merge(x, y, by = "key variable", all = TRUE, < all = FALSE, all.x = TRUE, all.y = FALSE >)`.
- Here `x` and `y` are data frames



Merging all=FALSE

01_ R Intro

```
merge_small <- merge(agesex, bp, by = "id", all = FALSE)
merge_small
```

	id	age	sex	visit	bp
1	100	47	f	1	180
2	100	47	f	2	160
3	100	47	f	3	155
4	101	NA	f	1	160
5	102	67	m	1	120
6	102	67	m	2	140

Merging all=TRUE

01_R Intro

```
merge_large <- merge(agesex, bp, by = "id", all = TRUE)
merge_large
```

	id	age	sex	visit	bp
1	99	43	m	NA	NA
2	100	47	f	1	180
3	100	47	f	2	160
4	100	47	f	3	155
5	101	NA	f	1	160
6	102	67	m	1	120
7	102	67	m	2	140
8	103	NA	<NA>	1	135

Merging all.x=TRUE

01_R Intro

```
merge_x <- merge(agesex, bp, by = "id", all.x = TRUE)  
merge_x
```

	id	age	sex	visit	bp
1	99	43	m	NA	NA
2	100	47	f	1	180
3	100	47	f	2	160
4	100	47	f	3	155
5	101	NA	f	1	160
6	102	67	m	1	120
7	102	67	m	2	140

Merging all.y=TRUE

01_R Intro

```
merge_y <- merge(agesex, bp, by = "id", all.y = TRUE)
merge_y
```

	id	age	sex	visit	bp
1	100	47	f	1	180
2	100	47	f	2	160
3	100	47	f	3	155
4	101	NA	f	1	160
5	102	67	m	1	120
6	102	67	m	2	140
7	103	NA	<NA>	1	135

Counting the Missing Observations: The `is.na()` and `sum()` functions

- Suppose that we want to count the number of missing observations.
- The function `is.na` returns a logical vector that is **TRUE** when a value is missing and **FALSE** otherwise.

```
is.na(merge_y$sex)

[1] FALSE FALSE FALSE FALSE FALSE FALSE TRUE
```

```
#COUNT MISSING FOR ONE VARIABLE
```

```
sum(is.na(merge_y$sex))
```

```
[1] 1
```

```
#COUNT FOR DATA FRAME
```

```
colSums(is.na(merge_y))
```

```
id    age    sex visit    bp
0      2      1     0     0
```

Loops in R

01_ R Intro

- In **R**, the **for loop** is used to perform a repetitive task for each element in a set.
- Example:
 - Given a set of integers 1:3:
 - Let a variable i run through the set and print $i + i$:

```
for(i in 1:3) {  
  cat(i, "+", i, "=", i+i, "\n")  
}
```

- Output:

1 + 1 = 2

2 + 2 = 4

3 + 3 = 6

Flow Control: if and if else Statements

01_R Intro

- if statement:

```
for(i in 1:3){
  if (i==2) cat("This index is even:", "\n")
  cat(i, "\n")
}
```

1

This index is even:

2

3

- if else statement:

```
for(i in 1:3){
  if (i==2) cat("The index is 2", "\n") else
    cat("The index is not 2", "\n")
}
```

The index is not 2

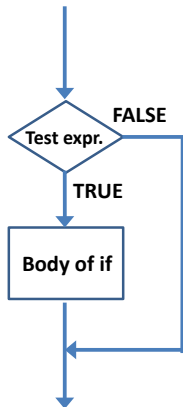
The index is 2

The index is not 2

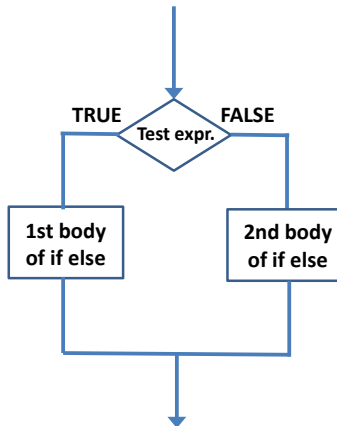
Flow Charts for if and if else Statements

01_R Intro

Enter if statement



Enter if else statement



while and repeat Loops

01_R Intro

The **while** loop:

- `while(condition) expression`

The **repeat** loop:

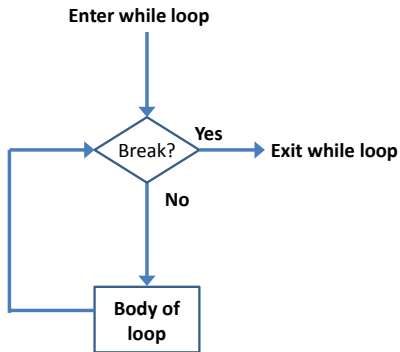
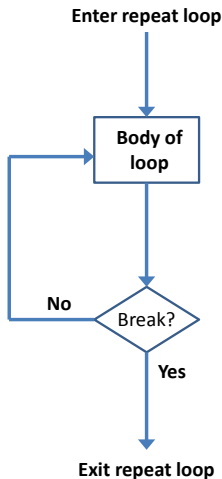
- `repeat expr`

The repeat loop has to be exited manually. Flow controls:

- **next:** Halts the the current iteration and advances to the next immediately;
- **break:** Exits the loop.

Flow Charts for the while and repeat loops

01_R Intro



while Loop Example

01_ R Intro

Storing of machine parts

```
k<-0 # number of big parts (>2)
y<-abs(rnorm(1000)) # simulated part size
i<-0 # index of parts
# loop:
while(k<3 & i<1000){
  i<-i+1
  temp<-y[i]
  k<-k+(temp>2)
}
i
```

```
[1] 42
```

repeat Loop Example

01_ R Intro

Selecting persons without blue or yellow eyes

```

eye.colors<-c("brown","blue","green","yellow","grey")
eyecolor<-data.frame(personId=1:100,color=
                      sample(eye.colors,100,rep=T))

i<-0
list.of.ids<-numeric(0) # patient ID list
#loop:
repeat {
  i<-i+1
  if(eyecolor$color[i]=="yellow" |
     eyecolor$color[i]=="blue") next
  list.of.ids<-c(list.of.ids,eyecolor$personId[i])
  if(i==100 | length(list.of.ids)==20) break
}
list.of.ids

```

```
[1] 5 6 7 9 10 11 12 14 15 18 19 20 21 22 23 24 25 28 29 30
```

Saving your work

01_ R Intro

- Saving your script
- Saving your workspace

Always save your script - do it often if you work in [Rstudio](#).

- Reasons for saving your workspace:
 - Extensive data creations will be there next time you open your workspace.
 - Objects created 'on the fly' (not in your script) will be there.
- Reasons for not saving your workspace:
 - With a well-written script, you can recreate your analysis in seconds, unless you work with huge amounts of data.
 - Edited and saved data where editions have been forgotten may cause havoc on your results.
 - Left-over objects created for various purposes may enter your calculations unintentionally due to the structure of **R**'s search path.

Saving your work

01_ R Intro

How to save your work:

- Script: Click on the script and press 'save' in [Rstudio](#) and the plain R GUI.
- Workspace: Click on the command prompt and press 'save'.
Alternatively, use the [save.image\(\)](#) function
- Both: Accept when asked after terminating [Rstudio](#) or the plain R GUI.

Exercise

01_ R Intro

- Data on exercise habits for the subjects in the cdc data set are found in the data `cdc_exer.csv`. Load and describe these data.
- Merge the cdc data set with the `cdc_exer` data set using `id` as the key variable. How many subjects in the study did not have exercise information?
- List the identifiers for the subjects without exercise information.
- Make a new dataframe with average age for combinations of gender and general health.

Visualizing Data is Important

01_R Intro

- Whenever we want to analyze data the first thing we should do is to **have a look** at it.
- How are the observations spread out?
- What are the most common values?
- Are there any unusual observations?
- Are there any relationships between variables?

This session will not tell you all about graphics in **R** but get you going.

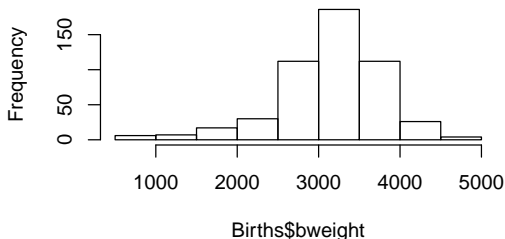
A Basic Histogram

01_ R Intro

- Common way to examine the distribution of a continuous variable.
- The range of the variable is by default divided into equal-width intervals (bins). Plots the number of observations in each bin (unless you specify otherwise).

```
hist(Births$bweight)
```

Histogram of Births\$bweight

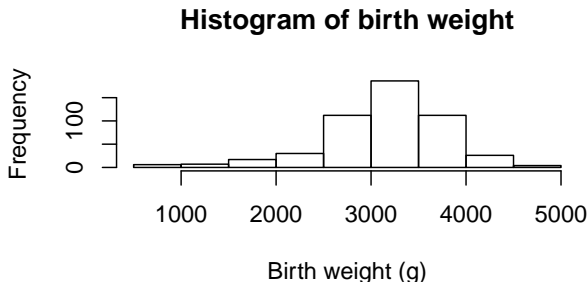


Histogram with a few options

01_R Intro

- Note that **R** automatically has created axis labels and a heading.
- To modify axis labels we set the options `xlab` and `ylab`.
- The heading is set in the option `main`.

```
hist(Births$bweight, xlab = "Birth weight (g)",  
     main = "Histogram of birth weight")
```

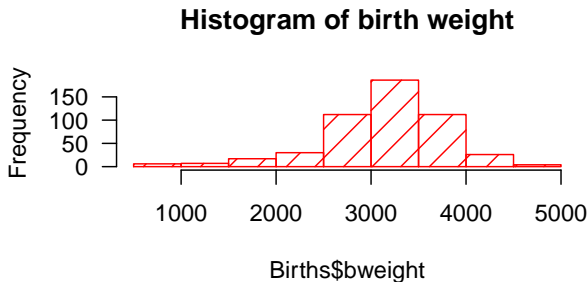


Histogram with more options

01_ R Intro

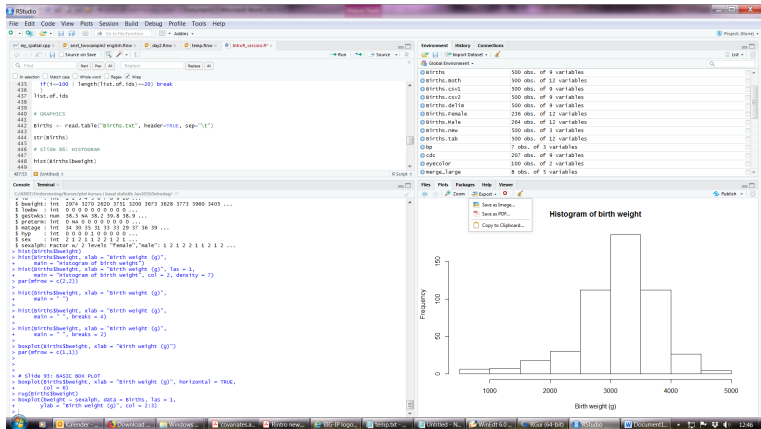
- We could type `?hist` to find more options to customize the histogram.
- The available colours are coded as numbers or one can write `col = "red"`
- If we want shading we can try the `density` function.
- The angle of the numbers on the axes is set by the option `las`.

```
hist(Births$bweight, las = 1, main = "Histogram of birth weight",  
     col = 2, density = 7)
```



How to get your plot from RStudio

01_ R Intro



Writing to a graphics device

01_R Intro

```
pdf("my.histogram.pdf")
hist(Births$bweight, las = 1, main = "Histogram of birth weight",
      col = 2, density = 7)
dev.off()
```

```
svg("my.histogram.svg")
hist(Births$bweight, las = 1, main = "Histogram of birth weight",
      col = 2, density = 7)
dev.off()
```

```
png("my.histogram.png")
hist(Births$bweight, las = 1, main = "Histogram of birth weight",
      col = 2, density = 7)
dev.off()
```

- Options can be specified; see the help files.

Exercise

01_ R Intro

- Load the cdc data set.
- Make a histogram of the weight in kg.
- Add your own title and x-axis label.
- Try different colours and shadings.
- Copy your favorite histogram into a document in e.g. Word.

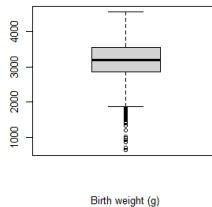
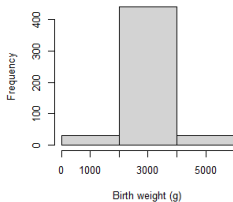
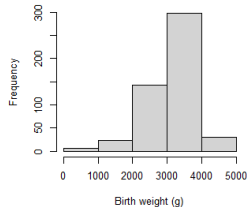
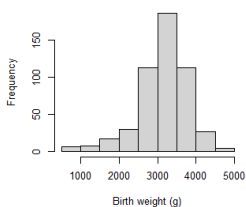
A Basic Box Plot

01_ R Intro

- Box plots show some distributional properties very clearly.
- Box plots show a measure of the location (the median line).
- The spread of the distribution (the length of the box and whiskers).
- Skewness as asymmetry in the upper and lower parts of the box and whisker length.
- We use the function `boxplot(variable)`. Adding labels to the axes and colours is done as for `hist`.

Histograms and a Box Plot

01_R Intro

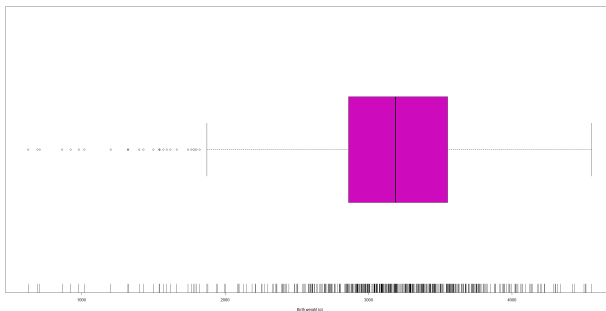


A Basic Box Plot

01_ R Intro

- When describing data we can even add the observations to the plot.
- Notice the function `rug` shows the observations.

```
boxplot(Births$bweight, xlab = "Birth weight (g)", horizontal = TRUE,  
        col = 6)  
rug(Births$bweight)
```



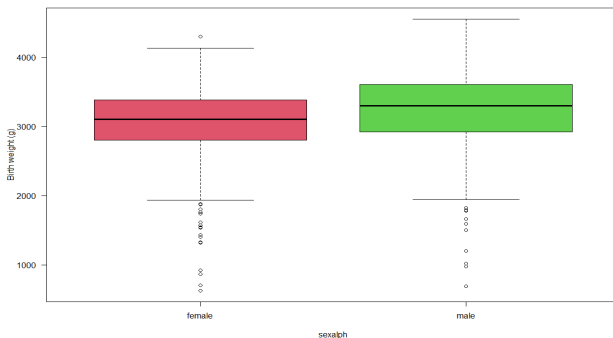
Box Plot for Groups

01_ R Intro

A useful feature is that we can make box plots for different groups next to each other for comparison. Notice the option `data = Births`.

```
# BOX PLOT FOR BOYS AND GIRLS
```

```
boxplot(bweight ~ sexalph, data = Births, las = 1,  
        ylab = "Birth weight (g)", col = 2:3)
```



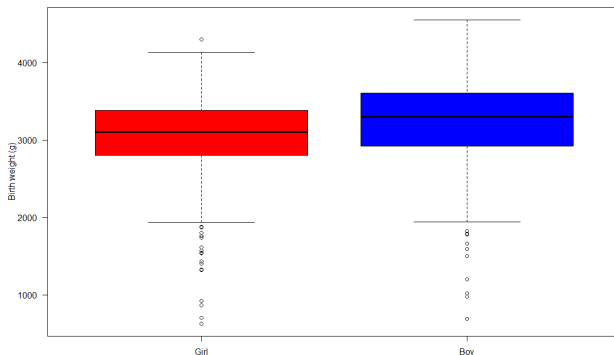
Box Plot for Groups

01_R Intro

Set our own axis. Notice `xast = "n"`.

```
# BOX PLOT WHERE WE WANT TO MAKE OUR OWN AXIS
```

```
boxplot(bweight ~ sexalph, data = Births, las = 1,  
        ylab = "Birth weight (g)", col = c("red", "blue"), xast = "n")  
axis(1, at = c(1,2), labels = c('Girl', 'Boy'))
```



Exercise

01_ R Intro

- Load the cdc data set.
- Make a box plot of the weight in kg showing individual observations. Add your own titles and colours.
- Make a box plot for each level of "genhlth", where each box is a different colour. How were the plots sorted?
- Make a new variable genhlth.num with 5 levels where 1 is "poor", 2 is "fair", 3 is "good", 4 is "very good" and 5 is "excellent".
- Make a new box plot for each level of genhlth.num with labels on the x-axis.
- Does this box plot show any pattern?

The Basic Scatter Plot

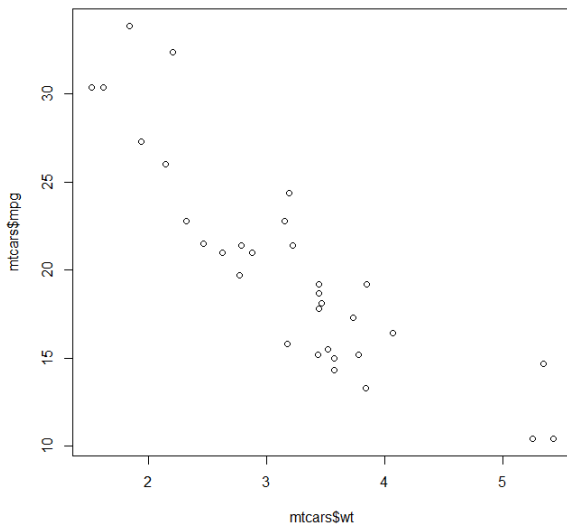
01_ R Intro

- The scatter plot is the standard graph for examining the relationship between two continuous variables.
- The `plot(x,y)` function is used to create scatter plots. Where (x,y) are the points we want to plot.
- We will look at the relationship between car weight (lbs/1000) and miles per gallon for 32 cars.

```
plot(mtcars$wt, mtcars$mpg)
```

The Basic Scatter Plot

01_R Intro

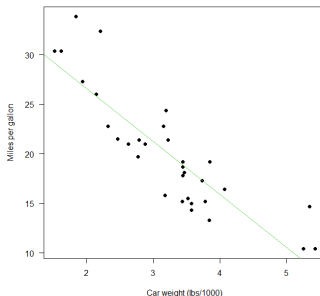


The Scatter Plot

01_ R Intro

- We can customize the scatter plot similar to before.
- The function `abline` adds a straight line to the plot.
- When we write `abline(lm(mpg ~ wt))` we get the best fitting line.

```
plot(mtcars$wt, mtcars$mpg, xlab = "Car weight (lbs/1000)",  
     ylab = "Miles per gallon", las = 1, pch = 19)  
abline(lm(mtcars$mpg ~ mtcars$wt), lty = 1, col = 3)
```

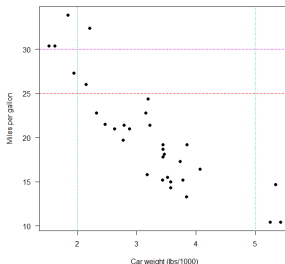


abline

01_ R Intro

- The function `abline` can also add reference lines to a plot.
- A horizontal line, e.g. at 25 and 30 `abline(h = c(25, 30))`
- A vertical line, e.g. at 2 and 5 `abline(v = c(2, 5))`

```
plot(mtcars$wt, mtcars$mpg, xlab = "Car weight (lbs/1000)",  
     ylab = "Miles per gallon", las = 1, pch = 19)  
abline(h = c(25, 30), col = c("red", "magenta"), lty = 2)  
abline(v = c(2, 5), col = 4:5, lty = 3:4)
```



Add a smoothed line

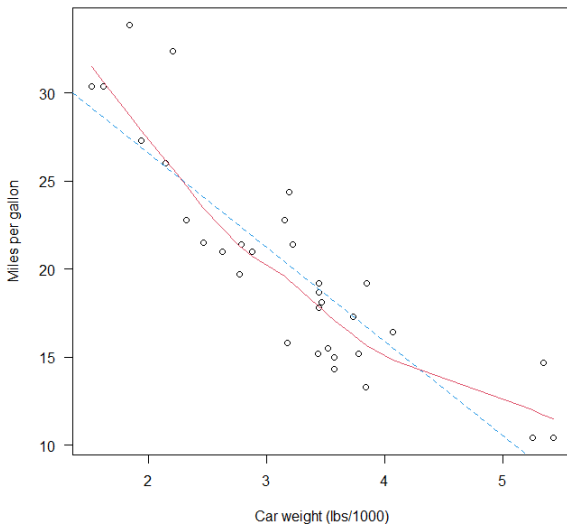
01_ R Intro

Perhaps we do not think the association is linear and try a nonparametric smoothed line.

```
plot(mtcars$wt, mtcars$mpg, xlab = "Car weight (lbs/1000)",  
     ylab = "Miles per gallon", las = 1)  
abline(lm(mtcars$mpg ~ mtcars$wt), lty = 2, col = 4)  
lines(lowess(mtcars$wt, mtcars$mpg), lty = 1, col = 2)
```


Add a smoothed line

01_R Intro



Enhanced graph procedures: Scatter plot example from the "car" package

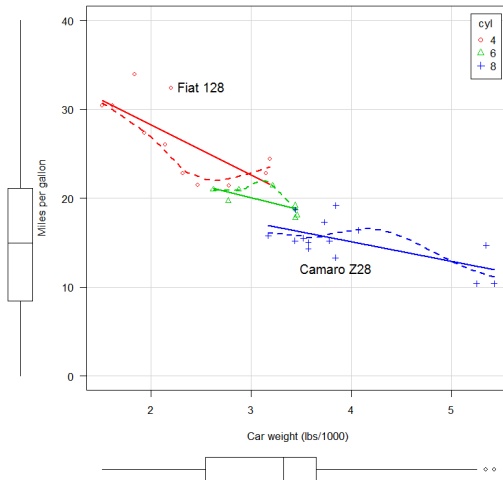
01_R intro

```
scatterplot(mpg ~ wt | cyl, data = mtcars, ylim = c(0,40),  
            xlab = "Car weight (lbs/1000)",  
            ylab = "Miles per gallon", las = 1,  
            legend = list(coords="topright"),  
            id = list(method="identify"),  
            boxplots = "xy", col=2:4)
```

- Here we want to plot miles per gallon versus weight for cars that have 4, 6 or 8 cylinders. We write this as `mpg ~ wt | cyl`.
- By default we get different colours for groups and both a linear and a smoothed line.
- A legend is included in the top right corner of the plot.
- The option `id = list(method="identify")` means that points can be identified by mouse clicks.
- Box plots of miles per gallon and weight included ("xy" option for both axes).
- More possibilities: `?scatterplot`.

The resulting scatter plot

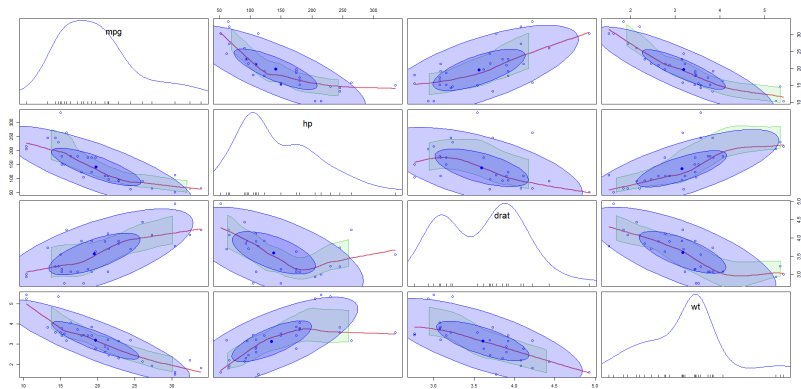
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A scatter plot matrix from the "car" package

01_R Intro

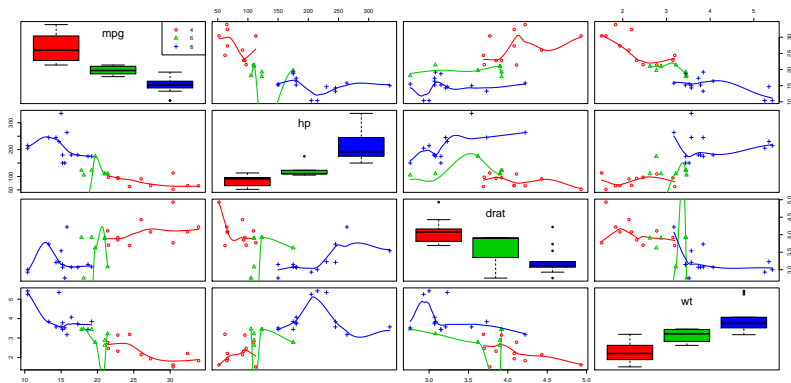
```
scatterplotMatrix(~ mpg + hp + drat + wt, data = mtcars,
  smooth = list(col.smooth=2,col.spread=3,
    lty.smooth=1),
  regLine = FALSE,ellipse = TRUE)
```



A scatter plot matrix with boxplots

01_RIntro

```
scatterplotMatrix( ~ mpg + hp + drat + wt | cyl,
  diagonal = list(method="boxplot"),
  smooth = list(lty.smooth=1),
  regLine = FALSE, col = 2:6, data = mtcars )
```



Exercise

01_ R Intro

- Load the cdc data set.
- Make a basic scatter plot of weight and desired weight with “nice” axes and labels.
- Add a smoothed lined to the plot.
- Make a scatter plot of weight and desired weight for each level of “genhlth” in separate plots, with straight and smoothed lines.
- Install the package “car”.
- Make a scatter plot of weight and desired weight for each level of “genhlth” in one plot.

Exercise

01_ R Intro

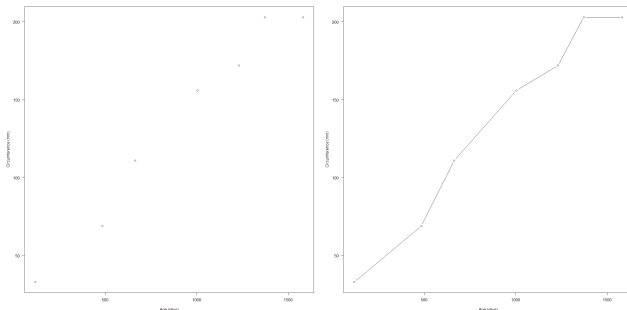
- Load the Protein data set.
- Make a scatter plot matrix of “RedMeat”, “WhiteMeat”, “Eggs”, “Milk” and “Fish”. Can you see any patterns in the protein intake?
- Also make a scatter plot matrix with box plots in the diagonal.

A Line Plot

01_ R Intro

Connecting points in a scatter plot from left to right. Here the growth of a tree. Notice the option `type = "b"` meaning points joined by lines.

```
par(mfrow=c(1,2)),  
plot(TreeA$age, TreeA$circumference, xlab = "Age (days)",  
      ylab = "Circumference (mm)", las = 1)  
plot(TreeA$age, TreeA$circumference, type = "b", xlab = "Age (days)",  
      ylab = "Circumference (mm)", las = 1)
```



Difference between `plot()` and `lines()` functions

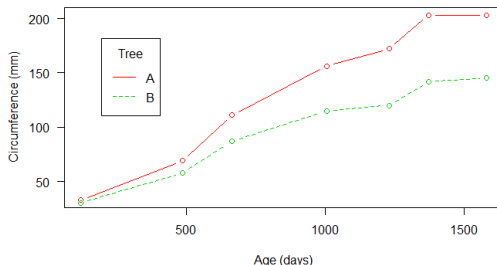
01_R Intro

- We have seen both the `plot` and the `lines` functions.
- The `plot` function creates a new graph. It is a **high-level** plotting function.
- The `lines` function adds information to an existing graph but it cannot produce it's own graph. It is a **low-level** plotting function.
- A **high-level** plotting function can (often) be converted to a **low-level** plotting function with the option `ADD=TRUE`.
- Usually `lines` will be used after a **high-level** plotting function (such as `plot`) has produced a graph.

A line plot and a legend

01_R Intro

```
plot(TreeA$age, TreeA$circumference, type = "b", lty = 1,  
      xlab = "Age (days)", ylab = "Circumference (mm)", las = 1, col = 2)  
lines(TreeB$age, TreeB$circumference, type = "b", col = 3, lty = 2)  
legend(locator(1), # we will place it with a mouse click  
       legend = c("A", "B"), title = "Tree",  
       lty = 1:2, col = 2:3)
```



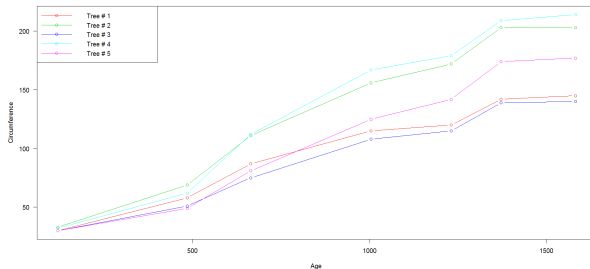
Plot of growth of 5 trees

01_R Intro

```

treedata<-Orange
plot(treedata$age,treedata$circumference,pch=" ",xlab = 'Age',
     ylab='Circumference',las=1)
for(i in 1:5){lines(treedata$age[treedata$Tree==i],
                    treedata$circumference[treedata$Tree==i],type="b",col=i+1)}
legend(x="topleft",paste("Tree #",1:5),pch=1,ltty=1,col=2:6)

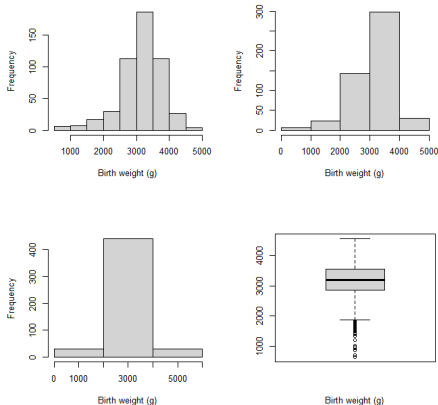
```



Layout of several plots on one graph

01_R intro

Several plots on one graph:



Use the option `par(mfrow = c(2, 2))`, and back to one plot `par(mfrow = c(1, 1))`.

Layout of several plots on one graph

01_R intro

The `layout()` function:

- indicate in matrix form which part of the plot area that you wish to belong to which graph

```
> layout.matrix<-matrix(c(1:3,rep(4,3)),nrow=2,ncol=3,byrow=T)
> layout.matrix
      [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    4    4
```

Layout of several plots on one graph

01_R intro

```
>layout(layout.matrix)
```

