R: language and basic data management

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(initial slides by P. Dalgaard)

Language

- R is a programming language – also on the command line
- (This means that there are *syntax rules*)

On the command line (or a line in a script) one could:

- Print an object by typing its name
- Evaluate an expression
- Call a function, giving the arguments in parentheses – possibly empty
- Notice `objects` vs. `objects()`

R expressions

```
x <- rnorm(10, mean=20, sd=5)
m <- mean(x)
sum((x - m)^2)
```

- Object names
- Explicit constants
- Arithmetic operators
- Function calls
- Assignment of results to names

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Objects

- The simplest object type is *vector*
- Modes: numeric, character, factor, ...
- Operations are vectorized: you can add entire vectors with `a + b`
- Recycling of objects: If the lengths don't match, the shorter vector is reused

Example (numeric vectors)

```
> a <- c(2, 8, 3, 1, 0, 7)
> b <- c(3, 4, 1, 4, 5, 2)
> a+b
[1]  5 12  4  5  5  9
> mean(a)
[1] 3.5
> m <- mean(a)
> m
[1] 3.5
> a - m # notice recycling
[1] -1.5  4.5 -0.5 -2.5 -3.5  3.5

> z <- c(1, 2, 3)
> a - z   #recycling!
[1]  1  6  0  0 -2  4
```

Factors

- Factors are used to describe groupings – these are just integer codes plus a set of names, as labels for the *levels*
- In model specifications, a factor variable is treated as a classification rather than as a quantitative variable

Example:

```
> x<-c(1,3,3,2,1,3,1)
> fx<-factor(x,labels=c("bad","average","good"))

> fx
[1] bad     good    good    average bad     good

 > levels(fx)
[1] "bad"     "average" "good"
```

Lists

- Lists are vectors where the elements can have different types – thus collections of any elements, gathered into one object
- Functions often return lists
- `lst <- list(A=rnorm(5), B="hello")`
- Special indexing:
- `lst$A`
- `lst[[1]]` first element (NB: double brackets)
- Data frames are special type of lists

Matrices

- A matrix is a rectangular collection of data. All columns of a matrix should be of the same type.

```
> A<-matrix(c(1,4,2,6,7,8),nrow=3,ncol=2,
                                        byrow=T)
> A
     [,1] [,2]
[1,]    1    4
[2,]    2    6
[3,]    7    8
```

- One can also construct a matrix from its columns using `cbind`, whereas joining two matrices with equal no of columns (with the same column names) can be done using `rbind`.

Data frames

- Usually a dataset in R is stored in a form of a data frame.
- While reading in data from text files (using `read.table()`, `read.csv()`), a data frame is created.
- A data frame is similar to a matrix, but can have columns (variables) of different types.
- A variable can be extracted using `dataframe$variable` (as data frames are lists)

```
> D<- data.frame(a=c(8,3,5),b=c("X","Z","Y"))
> D
  a b
1 8 X
2 3 Z
3 5 Y
> D$a
[1] 8 3 5
```

Matrices or data frames?

- A (numeric or character) matrix can be converted to a data frame and vice versa (with `as.data.frame(A)` and `as.matrix(B)`).
- Most R functions for statistical analysis work with data frames, but in some cases it is useful to have a matrix (incl the occasions where you want to use some matrix algebra).
- If you need more dimensions than two, there is also `array`.

How to access variables in the data frame?

Different ways to tell R to use variable X from data frame D:

- As mentioned, you can use the `dataframe$variable` notation

```
summary(D$X)
```

- Use the `with` function

```
with(D, summary(X))
```

- Use the `data` argument (does not works for all functions)

```
lm(Y~X, data=D)
```

- Attach the dataframe – DISCOURAGED!
  (seems a convenient solution, but can actually make things more complicated, as it creates a temporary copy of the dataset)

```
attach(D)
summary(X)
detach()
```

Data manipulation

To create a new variable `bmi` in the existing data frame `students`, use either of the two:

```
students$bmi <-
       with(students, weight/(height/100)^2)
students <-
     transform(students, bmi=weight/(height/100)^2)
```

(notice: you need an assignment, to save the transformed object)

Indexing – extracting elements from objects

Square brackets `[ ]` are used for indexing!

Examples:

- Elements of vectors: `a[5]` (5th element); `a[5:7]` (5th to 7th elements); `a[-6]` (all elements except the 6th)
- Logical index: `a[a<3]`, `a[b>2]` , `a[is.na(b)]` (elements of `a` corresponding to missing values of `b`)
- In a data frame or matrix – two dimensions, two indexes: `students[5, 7]`, `students[1:10, c(2,5)]`, `students[1, ]`, `students[ ,3]` (entire row/column)

Examples of indexing

```
>  x<- c(2,7,3,1,5,9,0)
> x[c(1,5,7)]
[1] 2 5 0
> x[x<3]
[1] 2 1 0

> NMRimp[1:2,1:4]    #quick look at a large data
  sample.id XXL.VLDL.P XXL.VLDL.L XXL.VLDL.PL
1    V18566   1.46e-04     0.0313     0.00331
2    V36115   9.00e-05     0.0195     0.00178

> fgsa[is.na(fgsa$height),"age"]
  [1] 18 69 52 41 52 44 73 28 66 20 73 63 26
# ages of those with missing height

# equivalent: fgsa$age[is.na(fgsa$height)]
```

Naming

- Elements of vectors, rows and columns of matrices and data frames can have names

```
> x <- c(boys=1.2, girls=1.1)
> x
 boys girls
  1.2   1.1
> x["boys"]
boys
 1.2
> D[,"a"]  # works for matrices and data frames
[1] 8 3 5
```

- You can extract and set names with `names(x)`; for matrices and data frames also `colnames(x)` and `rownames(x)`;

Classes, generic functions

- R objects have *classes*
- Functions can behave differently depending on the class of an object
- E.g. `summary(x)` or `print(x)` does different things if `x` is numeric, a factor, or a linear model fit

```
> summary(x)  # a numeric vector
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      1       1       2       2       3       3
> summary(fx) # a factor
    bad average    good
      3       1       3
```

Function calls

Round brackets ( ) are used for function calls!

Lots of things you do with R involve calling functions (you have seen that already!).
For instance

```
mean(x, na.rm=TRUE)
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The important parts of this are

- The name of the function
- Arguments: input to the function
- Sometimes, we have named arguments

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Function arguments

Examples:

```
rnorm(10, mean=m, sd=s)
hist(x, main="My histogram")
mean(log(x + 1))
```

Items which may appear as arguments:

- Names of R objects
- Explicit constants
- Return values from another function call or expression
- Some arguments have their *default values*.
- Use `help(`*`function`*`)` or `args(`*`function`*`)` to see the arguments (and their order and default values) that can be given to any function.
- Quite often – first argument is not named, but the others are named

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Example

From R-help (`help(t.test)`):

```
t.test(x, y = NULL,
    alternative = c("two.sided","less","greater"),
    mu = 0, paired = FALSE, var.equal = FALSE,
    conf.level = 0.95, ...)
```

- The first argument (x) does not have a default – you have to provide some data!
- The other arguments can be modified, if you need to.

Example (cont.)

The following lines of code are equivalent:

```
t.test(a, b,  alternative="less", paired=TRUE)
t.test(a, b, paired=TRUE, alt="less")

t.test(a, b, p=T, a="l")    #not a good style!
```

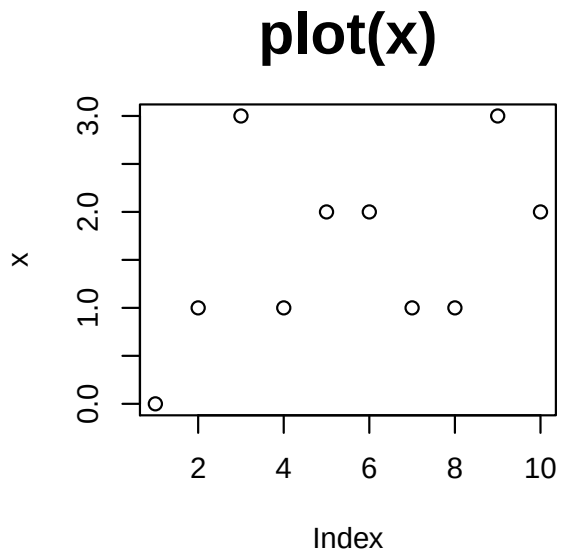
Order does not matter for named arguments!
Partial keyword matching is possible (“alternative" or “alt” or “a")
(partial matching is possible)
For a readable code, the use of explicit argument names is highly recommended!

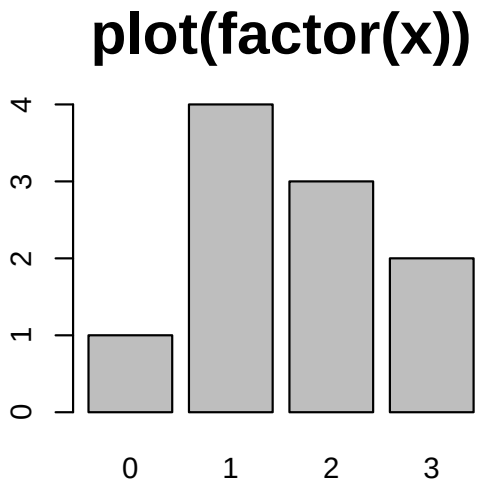
Basic graphics

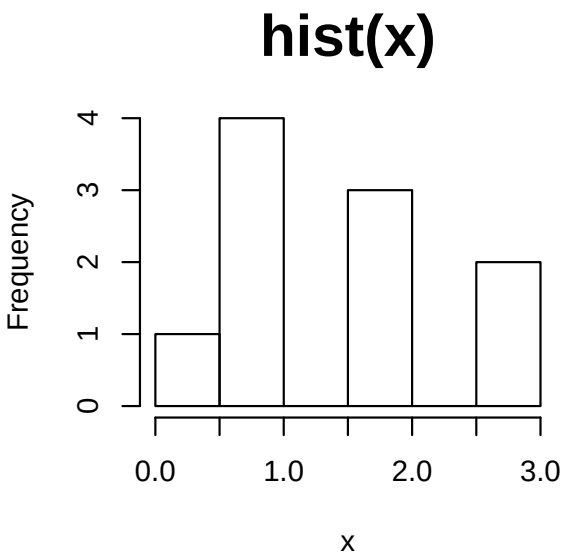
The `plot()` function is a generic function, producing different plots for different types of arguments. For instance, `plot(x)` produces:

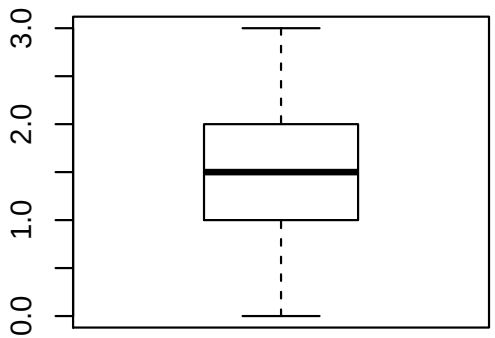
- a plot of observation index against the observations, when `x` is a numeric variable
- a bar plot of category frequencies, when `x` is a factor variable
- a time series plot (interconnected observations) when `x` is a time series
- a set of diagnostic plots, when `x` is a fitted regression model
- Similarly, the `plot(x,y)` produces a scatter plot, when `x` is a numeric variable and a bar plot of category frequencies, when `x` is a factor variable

Some simple plots:









The workspace

- The *global environment* contains R objects created on the command line.
- There is an additional *search path* of loaded packages and attached data frames.
- When you request an object by name, R looks first in the global environment, and if it doesn't find it there, it continues along the search path.
- The search path is maintained by `library()`, `attach()`, and `detach()`
- Notice that objects in the global environment may mask objects in packages and attached data frames

More on factors: the `cut` Function

- The `cut` function converts a numerical variable into groups (a factor variable) according to a set of break points
- The intervals are left-open, right-closed by default (`right=FALSE` changes that)
- . . . and that the lowest endpoint is *not* included by default (set `include.lowest=TRUE` if it bothers you)

Example

```
> age <- c(35,20,21,50,46,23,30)
> agegr<-cut(age, c(20,30,40,50))
> table(agegr)
agegr       # the 20-year old is not included!
(20,30] (30,40] (40,50]
      3       1       2
> agegr<-cut(age, c(20,30,40,50),right=FALSE)
> table(agegr)
agegr     # the 50-year old is not included!
[20,30) [30,40) [40,50)
      3       2       1
> agegr<-cut(age, c(20,30,40,50),
+                              include.lowest=TRUE)
> table(agegr)
agegr
[20,30] (30,40] (40,50]
4       1       2
```

Working with Dates

- Dates are usually read as character or factor variables
- Use the `as.Date` function to convert them to objects of class `"Date"`
- If data are not in the default format (YYYY-MM-DD) you need to supply a format specification

```
> as.Date("11/3-1959",format="%d/%m-%Y")
[1] "1959-03-11"
```

- You can calculate differences between `Date` objects. The result is an object of class `"difftime"`. To get the number of days between two dates, use

```
> as.numeric(as.Date("2017-6-1")-
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Creating your own functions

A very simple example:

```
logit <- function(p)  log(p/(1-p))
```

The function `logit` requires one argument *p* and produces the logit of *p*. Try `logit(0.5)`, or `logit(0.25)`,...

More complex (but still simple):

```
simpsum <- function(x, dec=5) {
m <- mean(x, na.rm=TRUE)
s  <- sd(x, na.rm=TRUE)
 round(c(mean=m,sd=s), dec) }
```

The function `simpsum` requires one argument *x*, but the second argument `dec` (no of decimal points in the output) has a default value 5. Try `simpsum(a)`, or `simpsum(a,dec=2)`.