Introductionary + advanced R course

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Hints and corrections are very welcome!

Download the current slides, source code and datasets at

github.com/brry/course

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Outline

R course info
Course plan
1. One-Session-Intro
2. Getting started: Background, GUI and first steps
3. Objects
4. "Real" data
5. Plotting
6. Character Operations
7. Conditions & loops
8. Functions & packages
9. Distributions
10. Statistics
11. Time series handling and analysis
12. Spatial data and GIS functionality
13. Final tasks

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- Session 4/4: if-else statements, for loops
- Session 5/4: Additional material
- Feedback

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- perform and visualize linear regression

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- `hist(vals)`; `plot(x,y, las=1, pch=16, type="b")`

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- BONUS: Read about Simpson's paradox and solve the first corresponding exercise, see slide 332 et sequentes.

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  - apply a function to each element in a list (or vector)

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- `rbind` and `cbind` to join data.frames, `merge` to (surprise) merge them.

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Please email me the approximate time you spend on each task separately, so I can manage your future homework load. Please note how much you needed the solutions.
You can send me your homework if you want comments.

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- create a plot with multiple panels
- reproducibly save plots with useful settings

Session 3: Task small research project

Please write down the answers to the following questions / instructions as pseudocode

- What do you do to start a (small) research project?
- Read a file into R where columns are tab-separated and the decimal marker is German.
- In a data set with monthly weather records (Potsdam.txt): Get the average temperature of months with more than 90 mm rainfall.
- Visually compare wind speed and rainfall.
- Describe and visualize the distribution of relative humidity.

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- Export graphics with `png` or `pdf` with good size and resolution settings.

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Enter the competition to win a 32GB 3.0 USB-Drive with R goodies: Send in your graphic per email (PNG preferred) along with the R script and approximate time needed. The class will pick a winner from the submissions based on graph appearance, artistic creativity, programming level and scientific relevance.

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Unicode

Collaborative editing can quickly become a textual rap battle fought with increasingly convoluted invocations of U+202a to U+202e (xkcd.com/1137)

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- instead: vectorize, use lapply, write C++ code

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Please email me how much time you spent on each task and how solvable it was (did you need to look into my solutions?)

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- Session 1/4: Why R, read file, select and plot data
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- Session 3/4: small research project, export of publication-ready graphics
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recap if else I

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```
x <- -5:8
y <- ifelse(x<0, -x, x)
y

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

recap if else II

```
(  requireNamespace("some_package", quietly=TRUE)  )

## [1] FALSE
```

invisibly returns TRUE if it succeeds loading a package. The outer brackets are for printing in the slides.

1. Use it to conditionally install the package quantmod (i.e. if it is not already available).

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1. Use it to conditionally install the package quantmod (i.e. if it is not already available).

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if(!requireNamespace("quantmod")) install.packages("quantmod")

## Loading required namespace:  quantmod
```

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Please fill out the feedback form at

goo.gl/jVgqge

(it only takes 2 minutes)

Thanks!

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print("Hello world!")

- Berry Boessenkool → berry-b@gmx.de

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- Geoecology @ Potsdam University

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- The standard for data analysis in many universities and industries

In the future, programming will save you time!

I find that when someone's taking time to do something right in the present, they're a perfectionist with no ability to prioritize, whereas when someone took time to do something right in the past, they're a master artisan of great foresight. (xkcd.com/974)

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Exercise 2: Vector indexing

1. Create a vector with body sizes of people around you. You can also use the values 1.75, 1.76, 1.83, 1.84, 1.77, 1.76, 1.77, 1.66, 1.86, 1.76. Assign it to an object with a useful name (`YourObject` is not one!).
2. What does `3:6` create? What does `YourObject[3:6]` do?
3. What does `YourObject[-4]` do?
4. BONUS (for fast people): Analyze the descriptive statistics: `mean(YourObject), median, min, max, range, quantile`
5. BONUS 2: Help your peers - there's no reason to be bored ;-)

Vector task solutions

```
size <- c(1.75, 1.76, 1.83, 1.84, 1.77, 1.76,
          1.77, 1.66, 1.86, 1.76)
3:6 # A vector with consecutive integers
size[3:6] # Select the corresponding elements of a vector
size[-4] # Select all but the fourth value
```

```
c(mean(size), median(size), min(size), max(size)); range(size); quantile(size)
```

```
## [1] 1.776 1.765 1.660 1.860
## [1] 1.66 1.86
##    0%   25%   50%   75%  100%
## 1.660 1.760 1.765 1.815 1.860
```

`mean` and `median` are similar, hinting at a symmetric data distribution
`range` returns a composite of `min`imum and `max`imum
`quantile` returns quantiles (now that is surprising...)

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Reading files

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You need to set the argument `header`.

Solution to exercise 3: Reading files

```
treesize <- read.table(file="treesize.txt", header=TRUE)
```

Objects: data.frames

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Exercise 4: Data.frame indexing

From the dataset `treesize` from the previous exercise, obtain:

1. The first 5 values in column 2
2. The maximum "Height" (the maximum of the values in that column)
3. For each entry: is the measurement equal to (==) A?
4. BONUS 1: The height entries for trees older than 23.5 years
5. BONUS 2: All rows, excluding rows 3, 7,8,9,...,20

Solution to exercise 4: subsetting data.frames I

```
treesize[1:5, 2]

## [1] 32.7 26.0 27.9 35.4 26.4

max(treesize$height)  ;   max(treesize[ ,"age"])

## [1] 40.1
## [1] 24.8

treesize$measurement=="A"

##   [1]  TRUE  TRUE  TRUE  TRUE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE
##  [13]  TRUE  TRUE  TRUE FALSE  TRUE FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE
##  [25]  TRUE FALSE  TRUE FALSE FALSE FALSE FALSE  TRUE  TRUE FALSE FALSE FALSE
##  [37] FALSE  TRUE FALSE  TRUE FALSE FALSE  TRUE  TRUE  TRUE FALSE FALSE FALSE
##  [49]  TRUE FALSE  TRUE  TRUE  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE
##  [61]  TRUE  TRUE FALSE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE FALSE FALSE
##  [73] FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE FALSE FALSE  TRUE  TRUE  TRUE
##  [85] FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE FALSE  TRUE  TRUE FALSE
##  [97]  TRUE FALSE  TRUE  TRUE
```

Solution to exercise 4: subsetting data.frames II

```
##  [1] 32.7 38.4 40.1 34.0 32.3 32.6 34.4 23.2 34.6
## [10] 35.9
```

```
treesize[ -c(3,7:20) , ]

##     age height measurement
## 1  24.4   32.7           A
## 2  13.6   26.0           A
## 4  21.2   35.4           A
## 5  19.8   26.4           B
## 6   7.7    7.2           B
## 21  5.1    7.2           A
## 22 15.6   17.7           B
## 23 19.4   29.2           A
## 24  7.8   10.2           A
## 25  5.7   11.1           A
## 26 19.6   17.5           B
## 27 12.8   20.1           A
## ...
```

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Plotting I

General code for scatterplots: `plot(x, y, ...)`

Plotting I

General code for scatterplots: `plot(x, y, ...)`

```
plot(x=Indometh$time, y=Indometh$conc,
     col="orange", pch=16, main="Awesome Graph!")
```

Plotting I

General code for scatterplots: `plot(x, y, ...)`

```
points(4, 1.5, pch=22, bg="yellow", cex=4, col="red")
# PointCHaracter, BackGround, Character EXpansion
```

Plotting I

General code for scatterplots: `plot(x, y, ...)`

```
lines(x=c(2,5,6,7), y=c(1,2.3,-3,1),
      col=4, type="b", lwd=5)
```

Plotting II: Our treesize dataset

```
treesize <- read.table(file="data/treesize.txt", header=TRUE)
```

Plotting II: Our treesize dataset

```
treesize <- read.table(file="data/treesize.txt", header=TRUE)
```

```
plot(x=xvalues, y=y_values, xlab="nice axis label",
     main="graph title", las=1)
```

Plotting II: Our treesize dataset

```
treesize <- read.table(file="data/treesize.txt", header=TRUE)
```

```
plot(x=xvalues, y=y_values, xlab="nice axis label",
     main="graph title", las=1)
```

Exercise 5: Scatterplots, sample distribution graphs

1. Plot tree height over age.
2. Add labels to the plot.
3. Change the point character (`pch`) and color (`col`).
4. BONUS 1: Use a vector for colors, e.g. treesize$measurement
5. BONUS 2: Compare the histogram (`hist`) of the heights with the `boxplot` and `quantile(x, probs=c(0.1, 0.8))`.

Solution for exercise 5: Scatterplots

```
treesize <- read.table(file="data/treesize.txt", header=TRUE)

plot(treesize$age, treesize$height)
plot(treesize$age, treesize$height, las=1, ylab="Tree height [m]",
     xlab="Tree age [years]", col=treesize$measurement,
     main="Older trees are larger", pch=3)
quantile(treesize$height, probs=c(0.1, 0.8))

##   10%   80%
##  8.93 32.36
```

Solution for exercise 5: Scatterplot

Solution for exercise 5: Histogram

```
hist(treesize$height, col=6, breaks=20, las=1)
```

Solution for exercise 5: Boxplot

```
boxplot(treesize$height, col=5, horizontal=TRUE, notch=TRUE)
```

commonly needed plot arguments

```
plot(x, y, # point coordinates
col="lightblue", # point color
pch=0, # point character (symbol)
xlab="My label  [km]", ylab="", # axis labels
main="Graph title", # title
cex=1.8, # character expansion (symbol size)
type="l", # draw lines instead of points
lwd=3, # line width (thickness of lines)
las=1, # label axis type (axis numbers upright)
xaxt="n" # axis type (none to suppress axis)
)
```

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- `library("ggplot2")` to load it
  (needed in every new R session) Put this in the script for reproducibility
- Better to use the `package::function` syntax
- Regularly run `update.packages()` or use the Rstudio button
- Rarely needed: `remove.packages("packagename")`

Packages and linear regression

Exercise 6: Packages, linear regression

1. Install and load the package `berryFunctions`
2. How can we pass the treesize data to `?linReg` with a formula?
3. Describe the resulting graph (height vs age).
4. Look into the source code of `linReg`. What is actually the backbone for the calculation of the function?
5. Feed the data into `lm`, assign the output to an object (useful name!).
6. Briefly explain the `summary` of the linear model.

Solution for exercise 6: Linear regression

```
library("berryFunctions")
linReg(height~age, data=treesize)
linReg
browseURL("https://github.com/brry/berryFunctions")
# go to R/linReg.R  -  working horse: lm
linear_model <- lm(height~age, data=treesize)
summary(linear_model)
```

blog.yhathq.com/posts/r-lm-summary.html

stats.stackexchange.com/questions/5135/interpretation-of-rs-lm-output

Time to put all of this into practice

Exercise 7: Reading files, subsetting, comparison

1. Start a new session of R. Read in the tree size data.
2. Check that everything is read correctly with `str`.
3. `which` rows of the data.frame have measurement equal to (`==`) B?
4. Plot the linear regression for measurement method B, then add the points and regression line for A in a different color and shape.
5. BONUS 1: use `boxplot` with a formula (`height~measurement`) for an automatic boxplot comparison with median difference notches.
6. BONUS 2: Visually compare the effect of Girth and Height on Volume in the dataset `trees`. Here's one idea (of many possible): Plot with two panels below each other (`par(mfrow=c(2,1))`), with the linear regression plots (`berryFunctions::linReg`) for each variable. Make it look nice with the graphical `par`ameters `mar` and `mgp`, as well as by specifying some of the linReg arguments.

Solution for exercise 7: Reading files, subsetting

```r
setwd("D:/my/path")
treesize <- read.table(file="data/treesize.txt", header=TRUE)
str(treesize)
```

```r
which(treesize$measurement=="B")

##  [1]  5  6 12 16 18 19 20 22 26 28 29 30 31 34 35
## [16] 36 37 39 41 42 46 47 48 50 55 56 59 60 63 64
## [31] 66 68 70 71 72 73 74 75 76 78 80 81 85 86 87
## [46] 88 90 93 96 98

treeA <- treesize[treesize$measurement=="A", ]
treeB <- treesize[treesize$measurement=="B", ]
library("berryFunctions")
linReg(height~age, data=treeA, pos1="topleft")
linReg(height~age, data=treeB, add=T, col=4,
       pos1="bottomright", inset=0.05)
points(height~age, data=treeB, pch=3, col=4)
```

Solution for exercise 7: Plotting, linear Regression

Solution for exercise 7.BONUS 1

```
boxplot(height~measurement, data=treesize,
        col=c("blue","orange"), notch=TRUE)
```

Solution for exercise 7.BONUS 2

```
par(mfrow=c(2,1), mar=c(3,3,1.5,0.5), mgp=c(1.9,0.7,0), las=1)
linReg(Volume~Height, data=trees, col="blue", pos1="topleft")
linReg(Volume~Girth, data=trees, col="forestgreen", pos1="topleft")
```

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R - What and Why?

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- R is a standard environment for statistical computing
- and an object-oriented programming language.
- It is developed and maintained by the R development core team
- and has thousands of add-on packages written by the community.
- There are mailing lists where users (& developers) help users
- and blogs to communicate analysis and coding to the public.
- R allows complex data analysis of big data sets with current methods
- and the creation of advanced professional (even interactive) graphics.
- Coding and programming forces you to keep track of your work
- and allows you to efficiently customize and automatize your analysis.
- R is very versatile: you can write your own functions and packages,
- implement new methods and make them available to everyone.
- Being capable of programming helps finding a job
- and the best part: R is open source and free!

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fantasyfootballanalytics.net/2014/01/why-r-is-better-than-excel.html
thegrantlab.org/bio3d/tutorials/79-static-content/85-why-use-r

interpreter language - no compilation

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xkcd.com/303

Where to get R

- base R itself: r-project.org.
  Official and helpful hints for Linux Ubuntu users.
- Use an Editor to work with script files:
- R-Studio (widely spread, easy to use)
- Tinn-R (only for Windows OS, flexible window arrangement).
  Needs some initial tweaking, see Berry's TinnR Page

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RStudio

RUN CODE
SCRIPTS
OBJECTS IN WORKSPACE
DOCUMENTATION
PLOTS
CODE EXECUTION

RStudio configuration

keyboard shortcuts (ALT+SHIFT+K)

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Recommended settings for reproducible research under
Tools - Global Options - General
ON: Restore previously open source documents at startup
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Tools - Global Options - Code - Display
ON: Show margin (Margin column:80) *People **hate** horizontal scrolling!*

Tools - Global Options - Code - Saving
Line ending conversion: **Windows (CR/LF)**

Tinn R

Figure: screenshot Tinn-R

```
# enable sending of blocks up to the next blank line:
.trPaths <- paste(Sys.getenv('LOCALAPPDATA'),
'\\Temp\\Tinn-R', c('', 'search.txt', 'objects.txt',
'file.r', 'selection.r', 'block.r','lines.r'),sep='\\')
# write this in  C:/Program Files/R/R-3.2.2/etc/Rprofile.site
```

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Getting help: Inside R

R-Help

```
help("apply") # get help for the function
?apply # The same. saves typing effort.
# Press F1 while the cursor is at a command.

apropos("apply")
help.search("apply")
??apply

help.start() # html help Manuals, Material, search engine
```

Getting help: Outside R

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  - ONLY post on mailing lists when all other options are exploited and you are sure there's no answer out there. FIRST read the posting guide.

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get started, comments

Please start R via the editor you like.

Comments start with a hash key #

```
17-42 # This is a comment, thus not executed

## [1] -25
```

Please calculate the following tasks

Exercise 8: Basic operators

1. 4 * 9
2. 2 + 4,8 (International decimal sign: ".")
3. 3^2
4. $\frac{\pi}{2}$
5. sinus of 15 °. Must be 0.26. Remember: $radians = degrees * \frac{\pi}{180\,^\circ}$
6. $\sqrt{81}$ (square root)
7. $|-12|$ (absolute value)
8. log(100) (–> should return 2, as $10^2 = 100$)
9. 5! (factorial)
10. e^3 (exponential function)
11. Bonus: How is 3.91 * 10^{-3} written in scientific notation?

Solution for exercise 8.1-8: Basic operators

```
4*9 # this is our first calculation with a comment
2 + 4.8
3^2
pi/2
sin(15*pi/180)
?sqrt # get the offline help about the function sqrt
sqrt(81) # square root
abs(-12) # absolute value
log(100)
help(log) # natural logarithm
log10(100) # log base 10
log(100, base=10) # another way
```

Solution for exercise 8.9-11: Basic operators

```r
factorial(5)
e^3 # does not work
??exponential
exp(3) # exponential function
exp(1) # the value of e
3.91 * 10^-3
3.91e-3 # no spaces possible in scientific notation
help.start() # offline search, manuals, etc
```

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   Graphical user interfaces
   Getting help
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   Source code of R commands
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8. Functions & packages
9. Distributions
10. Statistics
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12. Spatial data and GIS functionality
13. Final tasks

Source code: github.com/wch/r-source/src/library/base (or stats, utils, ...)
CRAN packages source code: github.com/cran
HTML Documentation: www.rdocumentation.org

excellent post
ncol - .Primitive("dim") - NROW head.matrix
https://github.com/wch/r-source/blob/trunk/src/library/utils/R/head.R
https://github.com/wch/r-source/blob/trunk/src/library/base/R/matrix.R

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Assignment: Create an object with data in the workspace I

```
a <- 15.4
```

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```
a <- 15.4
```

```
a

## [1] 15.4
```

Assignment: Create an object with data in the workspace I

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a <- 15.4
```

```
a

## [1] 15.4
```

```
a > 2 # is a bigger than 2?  --> logical value (boolean)

## [1] TRUE
```

Assignment: Create an object with data in the workspace I

```
a <- 15.4
```

```
a

## [1] 15.4
```

```
a > 2 # is a bigger than 2?  --> logical value (boolean)

## [1] TRUE
```

```
A # not an existing object (R is case sensitive)

## Error in eval(expr, envir, enclos):  object 'A' not found
```

Assignment: Create an object with data in the workspace II

Don't assign to existing objects or functions like `mean, c, T, data, sin`; Later on, you will hardly be able to distinguish what object (original or custom) you are referring to.

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As R is Case SeNsitivE, `Data` would be OK, but it's not useful. Use object names that are short, but still meaningful.

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```
# Rstudio: press 'ALT' + '-'  for   " <- "
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```
# Rstudio: press 'ALT' + '-'  for   " <- "
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Don't use = for assignments. R users usually prefer " <- ", (style guide) and "=" is only allowed on the top level.

Assignment: Create an object with data in the workspace II

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```
# Rstudio: press 'ALT' + '-'  for   " <- "
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Don't use `=` for assignments. R users usually prefer " <- ", (style guide) and "=" is only allowed on the top level.
`median(x <- 1:10)` also creates the object in `globalenv()`, while `median(x=1:10)` does not. Used in `NCOL`, for example.

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Don't assign to existing objects or functions like `mean, c, T, data, sin`; Later on, you will hardly be able to distinguish what object (original or custom) you are referring to.
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http://blog.revolutionanalytics.com/2008/12/use-equals-or-arrow-for-assignment.html
https://csgillespie.wordpress.com/2010/11/16/assignment-operators-in-r-vs/

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Vectors I

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b <- c(3, 7, -2.5, 11, 3.8, 9)
```

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spaces make code easier to read:

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```

spaces make code easier to read:

```
b<-c(3,7,-2.5,11,3.8,9)
b <- c(3, 7, -2.5, 11, 3.8, 9)
```

```
print(b) # or just write   b

## [1]  3.0  7.0 -2.5 11.0  3.8  9.0
```

Vectors II: Other ways to generate vectors

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```
1:5  # integer numbers  from : to

## [1] 1 2 3 4 5
```

Vectors II: Other ways to generate vectors

```
1:5  # integer numbers  from : to

## [1] 1 2 3 4 5
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```
rep(1:4, times=3) # repeat entries several times

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

Vectors II: Other ways to generate vectors

```
1:5  # integer numbers  from : to

## [1] 1 2 3 4 5
```

```
rep(1:4, times=3) # repeat entries several times

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

```
v <- rep(1:3, each=3, times=2)
v

##  [1] 1 1 1 2 2 2 3 3 3 1 1 1 2 2 2 3 3 3
```

Vectors III: Yet other ways to generate vectors

Vectors III: Yet other ways to generate vectors

```
seq(from=5, to=-1, by=-0.5) # Sequence
# by must be negative for descending sequences

##  [1]  5.0  4.5  4.0  3.5  3.0  2.5  2.0  1.5  1.0
## [10]  0.5  0.0 -0.5 -1.0
```

Vectors III: Yet other ways to generate vectors

```r
seq(from=5, to=-1, by=-0.5) # Sequence
# by must be negative for descending sequences

##  [1]  5.0  4.5  4.0  3.5  3.0  2.5  2.0  1.5  1.0
## [10]  0.5  0.0 -0.5 -1.0
```

```r
seq(1.32, 6.1, length.out=15) # 15 elements

##  [1] 1.320000 1.661429 2.002857 2.344286 2.685714
##  [6] 3.027143 3.368571 3.710000 4.051429 4.392857
## [11] 4.734286 5.075714 5.417143 5.758571 6.100000
```

Vectors III: Yet other ways to generate vectors

```
seq(from=5, to=-1, by=-0.5) # Sequence
# by must be negative for descending sequences

##  [1]  5.0  4.5  4.0  3.5  3.0  2.5  2.0  1.5  1.0
## [10]  0.5  0.0 -0.5 -1.0
```

```
seq(1.32, 6.1, length.out=15) # 15 elements

##  [1] 1.320000 1.661429 2.002857 2.344286 2.685714
##  [6] 3.027143 3.368571 3.710000 4.051429 4.392857
## [11] 4.734286 5.075714 5.417143 5.758571 6.100000
```

```
seq(1.32, 6.1, len=15) # abbreviate argument names
?seq # read more about it...
```

Indexing on vectors (subsets) I: square brackets

```
b # remember b?

## [1]  3.0  7.0 -2.5 11.0  3.8  9.0

b[1] # first element

## [1] 3
```

Indexing on vectors (subsets) I: square brackets

```
b # remember b?

## [1]  3.0  7.0 -2.5 11.0  3.8  9.0

b[1] # first element

## [1] 3
```

```
b[2:4] # several elements

## [1]  7.0 -2.5 11.0

b[ c(2,5,1,6,1) ] # flexible

## [1] 7.0 3.8 3.0 9.0 3.0
```

Indexing on vectors (subsets) II

```
b

## [1]  3.0  7.0 -2.5 11.0  3.8  9.0

b[-2] # all but the second element

## [1]  3.0 -2.5 11.0  3.8  9.0
```

Indexing on vectors (subsets) II

```
b

## [1]  3.0  7.0 -2.5 11.0  3.8  9.0

b[-2] # all but the second element

## [1]  3.0 -2.5 11.0  3.8  9.0
```

```
a <- seq(from=1, to=100, by=0.1)

head(a) # only first 6 elements (or rows)

## [1] 1.0 1.1 1.2 1.3 1.4 1.5
```

Indexing on vectors (subsets) III

```
head(a)

## [1] 1.0 1.1 1.2 1.3 1.4 1.5

a[2] <- 87 # manipulate single elements of object
head(a)

## [1]  1.0 87.0  1.2  1.3  1.4  1.5
```

```
ls() # list objects in workspace

## [1] "a" "b" "v"

rm(b) # remove an object
```

Data types

R can handle data of a variety of types: Numbers like `42.6`, characters like `"R rocks"`, complex numbers like `8+4i`, categories with `as.factor(c("blue", "green"))`, logical or boolean values `c(TRUE, FALSE)` and a few others. They should usually not be mixed. For example, you can't perform algebraic computation on characters:

Data types

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```
(p9 <- "1.3")     # show assignment result
2*p9              # error, as p9 is a character
2*as.numeric(p9)  # make it a number first
p9                # p9 itself has not changed
is.numeric(p9)    # FALSE
mode(p9)          # character
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3            # TRUE
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3          # TRUE
```

```
0.5 - 0.2  ==  0.3    # TRUE
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3          # TRUE
```

```
0.5 - 0.2  ==  0.3    # TRUE
```

```
0.4 - 0.1  ==  0.3    # FALSE
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3            # TRUE
```

```
0.5 - 0.2  ==  0.3      # TRUE
```

```
0.4 - 0.1  ==  0.3      # FALSE
```

```
print(0.4-0.1 , digits=22)

## [1] 0.30000000000000004
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3            # TRUE
```

```
0.5 - 0.2  ==  0.3      # TRUE
```

```
0.4 - 0.1  ==  0.3      # FALSE
```

```
print(0.4-0.1 , digits=22)

## [1] 0.30000000000000004
```

```
round(0.4-0.1, digits=6)  ==  round(0.3, 6)

## [1] TRUE
```

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3            # TRUE
```

```
0.5 - 0.2  ==  0.3      # TRUE
```

```
0.4 - 0.1  ==  0.3      # FALSE
```

```
print(0.4-0.1 , digits=22)

## [1] 0.30000000000000004
```

```
round(0.4-0.1, digits=6)  ==  round(0.3, 6)

## [1] TRUE
```

Test for equality only with integers / with rounding (see also `signif`), or use `all.equal`.

Integer vs decimal numbers: arithmetic precision

```
6  ==  3 + 3            # TRUE
```

```
0.5 - 0.2  ==  0.3      # TRUE
```

```
0.4 - 0.1  ==  0.3      # FALSE
```

```
print(0.4-0.1 , digits=22)

## [1] 0.30000000000000004
```

```
round(0.4-0.1, digits=6)  ==  round(0.3, 6)

## [1] TRUE
```

Test for equality only with integers / with rounding (see also `signif`), or use `all.equal`. More pitfalls like this in the R inferno.

Exercise 9: Vectors and statistics

1. Repeat your favorite number 6 times using `rep`.
2. With `sequence`, generate one vector from -1 to 4 in steps of 0.5 and one with a length of 21 elements. Then add a number to the vector.
3. Assign a vector with the body heights of a few people around you to an object with a useful name.
4. Print only the 4th and 2nd element (one single vector). BONUS: All but the 2nd to 4th elements.
5. `sort` the numbers decreasingly.
6. Calculate the average size (`mean`), the variance (`var`) and the standard deviation (`sd`) of this dataset, as well as the `min`, `max`, `median` and 80% `quantile` (20% of the entries are larger than this value).
7. BONUS 1: Explain what `length` does.
8. BONUS 2: Generate the numbers from 1 to 10 in three different ways.
9. BONUS 3: Explain and relate to each other: mean, var, sd, median, quantile.

Solution for exercise 9.1-2: Vectors

```
# repeat and sequence:
rep(5, times=6)
seq(from=-1, to=4, by=0.5)
vec2 <- seq(-1, 4, length.out=21)
seq(-1, 4, len=21)
```

You can leave argument names away, if you specify their content in the right order. If it is unambiguous, you can use partial argument names.

```
# add a number to a vector:
c(vec2, 8) # does not change vec2
vec3 <- c(vec2, 8) # creates a new object
vec2 <- c(vec2, 8) # changes the object vec2
# Another way:
vec2 <- seq(-1, 4, length.out=21)
vec2[21] <- 5 # changing one element
vec2
vec2[22] # returns NA - there is no value here
vec2[26] <- 8
vec2 # is now changed
```

Solution for exercise 9.3-6: Vectors

```
# vector with body heights:
heights <- c(192, 171, 178, 175, 185, 145, 164) # cm
# print selected elements:
heights[ c(4,2) ]
# sort:
sort(heights, decreasing=T)
# statistics:
mean(heights)
var(heights) # cm^2
sd(heights) # cm
min(heights)
max(heights)
median(heights)
quantile(heights, probs=0.80)
```

Solution for exercise 9.BONUS: Vectors

```
length(heights) # number of elements in vector
# Numbers from 1 to 10:
1:10  ;  seq(1,10)  ;  c(1,2,3,4,5,6,7,8,9,10)
# mean vs median:
mean(   replace(heights, 1, 292) ) # subject to outliers
median( replace(heights, 1, 292) ) # indifferent to extrema
```

70% of values in a normal distribution lie between mean-sd and mean+sd:

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data.frames

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Columns as well as rows can have names (`colnames, rownames`). If these start with a number, an "X" will be prefixed. This happens frequently when reading data, which is usually stored as a `data.frame` in R.

```
?data.frame
```

Creating data.frames

```
df <- data.frame(col_a=11:14, ColName2=letters[1:4],
                 LogicalCol=(1:4)>2)
df

##   col_a ColName2 LogicalCol
## 1    11        a      FALSE
## 2    12        b      FALSE
## 3    13        c       TRUE
## 4    14        d       TRUE

str(df)

## 'data.frame': 4 obs. of  3 variables:
##  $ col_a     : int  11 12 13 14
##  $ ColName2  : Factor w/ 4 levels "a","b","c","d": 1 2 3 4
##  $ LogicalCol: logi  FALSE FALSE TRUE TRUE
```

Subsetting data.frames by index numbers

```
nrow(df)

## [1] 4

ncol(df) # see also dim(df)

## [1] 3
```

Subsetting data.frames by index numbers

```
nrow(df)

## [1] 4

ncol(df) # see also dim(df)

## [1] 3
```

```
df[ 3 , 1] # 3rd row, 1st column

## [1] 13

df[   , 2] # all rows, 2nd column (as vector)

## [1] a b c d
## Levels: a b c d
```

Subsetting data.frames by names

```
df[ "LogicalCol" ] # no comma -> data.frame

##   LogicalCol
## 1      FALSE
## 2      FALSE
## 3       TRUE
## 4       TRUE
```

Bad practice, unclear whether rows or columns are indexed!

```
df[ , "LogicalCol", drop=FALSE ]  # better
```

Subsetting data.frames by names

```
df[ "LogicalCol" ] # no comma -> data.frame

##   LogicalCol
## 1      FALSE
## 2      FALSE
## 3       TRUE
## 4       TRUE
```

Bad practice, unclear whether rows or columns are indexed!

```
df[ , "LogicalCol", drop=FALSE ]  # better
```

```
df$col_a

## [1] 11 12 13 14
```

Subsetting data.frames by names

```
df[ "LogicalCol" ] # no comma -> data.frame

##   LogicalCol
## 1      FALSE
## 2      FALSE
## 3       TRUE
## 4       TRUE
```

Bad practice, unclear whether rows or columns are indexed!

```
df[ , "LogicalCol", drop=FALSE ]  # better
```

```
df$col_a

## [1] 11 12 13 14
```

```
df[2, ] # full row

##   col_a ColName2 LogicalCol
## 2    12        b      FALSE
```

Some hints about data.frames

- If `nrow(df)` returns `NULL`, `df` might in fact be a vector.

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- Also, remember you can check the object with `class` and `mode`, as well as `is.vector`.

Some hints about data.frames

- If `nrow(df)` returns `NULL`, `df` might in fact be a vector.
- `NROW(df)` will show `length(df)` if `df` is a vector.
- Also, remember you can check the object with `class` and `mode`, as well as `is.vector`.
- `colnames(df)` will show the column names. (see also `rownames`)

Exercise 10: data.frames

Working with the dataset `state.x77`

1. Change the object type to a data.frame
2. What are the 3 ways to select the population column? Which one doesn't work for Life expectancy? Why not?
3. How can you subset a single column, without the result being simplified to a vector? (you want to keep it as a data.frame, but with one single column only. Hint: `?"["`)
4. How could the `$` subsetting method be dangerous when misspelling columns?
5. By which two ways can you select the Income and Illiteracy columns?
6. How can you select all the states (=rows) with an income above 5000?
7. BONUS: Why does `state.x77$Income` not work on the original dataset? (use `rm(state.x77$Income)` to remove your changed object from the workspace, if you didn't assign it to a different name.)

Solution to exercise 10: subsetting data.frames

```
state <- as.data.frame(state.x77)
state[,1] # not safe, columns could be in different position
state[ , "Population"] # safe and readable
state$Population # quicker to type, has autocomplete
# $  doesn't work (at least not without quotation marks)
   # with a space, it's an invalid column name
state[ , "Population", drop=FALSE]
state$Illeeteeraacyy # does not give an error!!!
state[ , c("Income","Illiteracy")]
state[ , 2:3]
state[state$Income>=5000, ]
# Because it is a matrix, not a data.frame
```

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Creating matrices

```r
matrix(data=1:6 , nrow=2, ncol=3)

##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

Creating matrices

```
matrix(data=1:6 , nrow=2, ncol=3)

##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

```
m <- matrix(1:6 , nrow=2, ncol=3, byrow=T)
print(m)

##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
```

Manipulating matrices, row and column names

```
colnames(m) <- c("A", "B", "C")
m[1,1] <- c(989)
print(m)

##        A B C
## [1,] 989 2 3
## [2,]   4 5 6
```

Manipulating matrices, row and column names

```
colnames(m) <- c("A", "B", "C")
m[1,1] <- c(989)
print(m)

##        A B C
## [1,] 989 2 3
## [2,]   4 5 6
```

```
rownames(m) <- c("row1", "row2")
m

##      [,1] [,2] [,3]
## row1  989    2    3
## row2    4    5    6
```

Matrices only have one single data type

```
m[1,1] <- "a"
m

##      [,1] [,2] [,3]
## row1 "a"  "2"  "3"
## row2 "4"  "5"  "6"
```

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Lists

Lists store every R data type (vectors, data.frames, . . .) in one variable

```
list("df"=df[c(1:2), ], matrix=m, character="TEXT")

## $df
##   col_a ColName2 LogicalCol
## 1    11        a      FALSE
## 2    12        b      FALSE
##
## $matrix
##      [,1] [,2] [,3]
## row1 "a"  "2"  "3"
## row2 "4"  "5"  "6"
##
## $character
## [1] "TEXT"
```

List basics I

```
# create a list: an object with several 'objects' inside it
L1 <- list(first="result of function 'list'",
           second=345:287, third=rnorm(10),
           fourth=data.frame(a=6:3, b=rexp(4)),
           fifth=LETTERS, sixth=letters,
           seventh=sample(300), eigth="goodbye")
```

List basics I

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# create a list: an object with several 'objects' inside it
L1 <- list(first="result of function 'list'",
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```
# print the whole thing:
L1
```

List basics I

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           fifth=LETTERS, sixth=letters,
           seventh=sample(300), eigth="goodbye")
```

```
# print the whole thing:
L1
```

```
# print only the first 4 elements of the list
head(L1,4)
tail(L1) # or the last n elements (by default 6)
```

List basics II

```r
# Structure of the list
str(L1, max.level=1, vec.len=3)

## List of 8
##  $ first  : chr "result of function 'list'"
##  $ second : int [1:59] 345 344 343 342 341 340 339 338 ...
##  $ third  : num [1:10] 1.083 0.953 0.269 1.076 ...
##  $ fourth :'data.frame': 4 obs. of  2 variables:
##  $ fifth  : chr [1:26] "A" "B" "C" ...
##  $ sixth  : chr [1:26] "a" "b" "c" ...
##  $ seventh: int [1:300] 19 216 192 48 161 46 73 117 ...
##  $ eigth  : chr "goodbye"
```

List basics II

```r
# str down to each level of the list
str(L1, vec.len=3) # see the df for the difference

## List of 8
##  $ first  : chr "result of function 'list'"
##  $ second : int [1:59] 345 344 343 342 341 340 339 338 ...
##  $ third  : num [1:10] 1.083 0.953 0.269 1.076 ...
##  $ fourth :'data.frame': 4 obs. of  2 variables:
##   ..$ a: int [1:4] 6 5 4 3
##   ..$ b: num [1:4] 0.275 0.441 1.693 0.96
##  $ fifth  : chr [1:26] "A" "B" "C" ...
##  $ sixth  : chr [1:26] "a" "b" "c" ...
##  $ seventh: int [1:300] 19 216 192 48 161 46 73 117 ...
##  $ eigth  : chr "goodbye"
```

List indexing I

```
# Assessing list elements (indexing) with double square brackets:
L1[[3]]

##  [1]  1.08270524  0.95297954  0.26906649
##  [4]  1.07597085 -0.86401751  0.06248087
##  [7]  0.13752332  0.01085314  0.75895050
## [10] -1.11800498
```

List indexing I

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# Assessing list elements (indexing) with double square brackets:
L1[[3]]

##  [1]  1.08270524  0.95297954  0.26906649
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##  [7]  0.13752332  0.01085314  0.75895050
## [10] -1.11800498
```

```
# What's different if you use only single brackets?
L1[3]

## $third
##  [1]  1.08270524  0.95297954  0.26906649
##  [4]  1.07597085 -0.86401751  0.06248087
##  [7]  0.13752332  0.01085314  0.75895050
## [10] -1.11800498

# HINT: look at the class of the results
```

List indexing II

```
# Assesing elements by name
L1$eight # NULL if not existent, so watch out with spelling!

## NULL

L1$eigth

## [1] "goodbye"
```

List indexing II

```
# Assesing elements by name
L1$eight # NULL if not existent, so watch out with spelling!

## NULL

L1$eigth

## [1] "goodbye"
```

```
names(L1) # as with names(VECTOR) or rownames(DATAFRAME)

## [1] "first"   "second"  "third"   "fourth"
## [5] "fifth"   "sixth"   "seventh" "eigth"

names(L1)[2] <- "second elem."
```

List indexing III

```
# Several elements of the list (the result is still a list):
L1[4:5]

## $fourth
##   a         b
## 1 6 0.2754568
## 2 5 0.4412032
## 3 4 1.6930600
## 4 3 0.9602851
##
## $fifth
##  [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K"
## [12] "L" "M" "N" "O" "P" "Q" "R" "S" "T" "U" "V"
## [23] "W" "X" "Y" "Z"
```

List indexing IV

```
# changing elements:
L1[c(3,6)]  <- c(77777777, 3333333)
head(L1)
```

L-apply

```
typeof(L1[[1]])

## [1] "character"
```

L-apply

```r
typeof(L1[[1]])

## [1] "character"
```

```r
# Apply a function to each element of the list:
lapply(X=L1, FUN=typeof)
```

L-apply

```r
typeof(L1[[1]])

## [1] "character"
```

```r
# Apply a function to each element of the list:
lapply(X=L1, FUN=typeof)
```

```
## $first
## [1] "character"
##
## $`second elem.`
## [1] "integer"
##
## $third
## [1] "double"
##
## $fourth
## [1] "list"
```

```
## $fifth
## [1] "character"
##
## $sixth
## [1] "character"
##
## $seventh
## [1] "integer"
##
## $eigth
## [1] "character"
```

S-apply I

```r
# simplify that output (if possible):
    sapply(X=L1, FUN=typeof)

##        first second elem.        third       fourth
##  "character"    "integer"     "double"       "list"
##        fifth        sixth      seventh        eigth
##  "character"  "character"    "integer"  "character"
```

S-apply I

```
# simplify that output (if possible):
    sapply(X=L1, FUN=typeof)

##        first second elem.        third       fourth
##  "character"    "integer"     "double"       "list"
##        fifth        sixth      seventh        eigth
##  "character"  "character"    "integer"  "character"
```

```
# simplifying not possible if FUN(L1[[1]]) and FUN(L1[[2]])
# return different results:
sapply(X=L1, FUN=head)
```

S-apply II

```
# List with vectors:
L2 <- list(3:7, 8:4, 5:9)
L2

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

S-apply II

```r
# List with vectors:
L2 <- list(3:7, 8:4, 5:9)
L2

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

```r
sapply(L2, I)

##      [,1] [,2] [,3]
## [1,]    3    8    5
## [2,]    4    7    6
## [3,]    5    6    7
## [4,]    6    5    8
## [5,]    7    4    9
```

`I` basically returns the input as is. This is useful for `tapply` results!

S-apply III

```
# That doesn't work for vectors of different lengths:
L3 <- list(AB=c(6,9,2,6), BC=1:8, CD=c(-3,2) )
sapply(L3, I)

## $AB
## [1] 6 9 2 6
##
## $BC
## [1] 1 2 3 4 5 6 7 8
##
## $CD
## [1] -3  2
```

S-apply IV

```r
# the solution: berryFunctions::l2df
# list to data.frame conversion
if(!require(berryFunctions)) install.packages("berryFunctions")
library(berryFunctions)

l2df(L3)

##    V1 V2 V3 V4 V5 V6 V7 V8
## AB  6  9  2  6 NA NA NA NA
## BC  1  2  3  4  5  6  7  8
## CD -3  2 NA NA NA NA NA NA

# vectors are padded with NAs, names are kept
```

S-apply V

```
L3

## $AB
## [1] 6 9 2 6
##
## $BC
## [1] 1 2 3 4 5 6 7 8
##
## $CD
## [1] -3  2

# nested subsetting: get the third element of each vector:
sapply(L3, "[", 3)

## AB BC CD
##  2  3 NA
```

apply functions to vectors & further arguments

```
sample(x=1:100, size=5)

## [1] 49 39 35 98 74
```

apply functions to vectors & further arguments

```
sample(x=1:100, size=5)

## [1] 49 39 35 98 74
```

```
lapply(c(6,2,13), sample, x=1:100)

## [[1]]
## [1] 10 35 87 80 88 39
##
## [[2]]
## [1] 76 98
##
## [[3]]
##  [1] 16 80 73  9 90  8 64 74 99 45 53 71 77
```

Practice matrices and lists

Exercise 11: matrix, list

1. Create a matrix with some numbers you like, with a useful amount of rows and columns.
2. Create a list (with meaningful element names!) that contains the previous matrix, your name, the current `Sys.time()`, the number of this exercise, and the haircolors of at least two of your neighbours.
3. BONUS 1: Using `sapply`, get the `length` for each element. What is surprising about he result?
4. BONUS 2: Make the haircolors element a `factor`. Inspect the result with `str`.

matrix + list: solutions

```
mat <- matrix(c(42,007,123,7777,-17,88), ncol=2)
mylist <- list(matrix=mat, creator="Berry",
     created=Sys.time(), exerciseNumber=11,
     haircolor=c("brunette", "red", "blonde", "blonde")  )
sapply(mylist, length) # matrix length is 6 (=ncol*nrow)
mylist$haircolor <- as.factor(mylist$haircolor)
str(mylist)
```

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Determine the class of an object

Everything is an object that belongs to an existing class!!

```
class(v)

## [1] "integer"

class(df)

## [1] "data.frame"

class(m)

## [1] "matrix"
```

Usage of class in functions

```
x <- 10
class(x) <- c("a", "b")
# error:
if( class(x) == "b"   ) message("class of x contains b")

## Warning in if (class(x) == "b") message("class of x
contains b"):  the condition has length > 1 and only the
first element will be used

# use this instead
if( inherits(x, "b")  ) message("good coding!")

## good coding!
```

Examining objects

Every object class has attributes and methods:

```
str(v)

##  int [1:18] 1 1 1 2 2 2 3 3 3 1 ...

str(df)

## 'data.frame': 4 obs. of  3 variables:
##  $ col_a     : int  11 12 13 14
##  $ ColName2  : Factor w/ 4 levels "a","b","c","d": 1 2 3 4
##  $ LogicalCol: logi  FALSE FALSE TRUE TRUE

str(m)

##  chr [1:2, 1:3] "a" "4" "2" "5" "3" ...
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:2] "row1" "row2"
##   ..$ : NULL
```

Overview of some useful functions

```
length(v)

## [1] 18

names(df)

## [1] "col_a"       "ColName2"   "LogicalCol"

dim(m)

## [1] 2 3

which(v > 4)

## integer(0)
```

Please note ...

Parentheses and square brackets of functions and objects

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objects are variables and contain your data. The indexing (accessing of items) is done by brackets `[ ]`

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With `newtable <- edit(oldtable)`, you can change cells in a table by hand. As this is not reproducible, this is bad practice!. `fix` is even worse, as it changes the object itself.
With `View`, you can look at a table in an external viewer. This is useful for large tables, as the console is not cluttered with data.

Overview: data types

In order of coercion (if mixed, TRUE is converted to 1, 3.14 to "3.14" etc)

Description	example	`typeof`	`class`
empty set	NULL	NULL	NULL
not available	NA	logical	logical
logical	c(T, F, FALSE, TRUE)	logical	logical
category	factor("left")	integer	**factor**
integer number	4:6	integer	integer
decimal	8.7	double	**numeric**
complex	5+3i	complex	complex
character string	"homer rocks"	character	character
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adv-r.had.co.nz/Data-structures.

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Overview: Object types

Object	example	`typeof`	`class`
vector	*see data types*	...	...
matrix	matrix(9:15, ncol=2)	...	matrix
array	array(letters[1:24], dim=c(2,6,4))	...	array
data.frame	data.frame(C1=4:5, C2=c("a","b"))	list	data.frame
list	list(el1=7:15, el2="big")	list	list
function	function(x) 12+0.5*x	closure	function
...	lm(b ∼ a)	list	lm

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A `matrix` consists of only one data type. If you accidentally change one element to a character, all are converted and calculations are not possible any more (See coercion order in previous slide).

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`list`s can combine anything, even other lists.

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Object	example	`typeof`	`class`
vector	*see data types*	...	...
matrix	matrix(9:15, ncol=2)	...	matrix
array	array(letters[1:24], dim=c(2,6,4))	...	array
data.frame	data.frame(C1=4:5, C2=c("a","b"))	list	data.frame
list	list(el1=7:15, el2="big")	list	list
function	function(x) 12+0.5*x	closure	function
...	lm(b ∼ a)	list	lm

A `matrix` consists of only one data type. If you accidentally change one element to a character, all are converted and calculations are not possible any more (See coercion order in previous slide).

`data.frame`s can have multiple data types, but a column in itself also has only one type.

`list`s can combine anything, even other lists.

`is.atomic(Object)` returns TRUE (vector, matrix, array) or FALSE

Overview: Object types

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`data.frame`s can have multiple data types, but a column in itself also has only one type.

`list`s can combine anything, even other lists.

`is.atomic(Object)` returns TRUE (vector, matrix, array) or FALSE

`as.matrix(Object)` converts the class of an object by force.

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Data I/O functions (Input / Output)

R **reads and writes** data formats like ASCII files, GEOTIFF, GRIB, NETCDF, HDF ...

Data I/O functions (Input / Output)

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```
read.csv("relative/path/to/input/file.csv")
# Combined with a variable assignment:
mydata <- read.table("C:/path/to/input/file.txt")
write.table(x=mynewdata, file="output.txt")
```

Windows users: change all \ to \\ or /

Data I/O functions (Input / Output)

R **reads and writes** data formats like ASCII files, GEOTIFF, GRIB, NETCDF, HDF ...

```
read.csv("relative/path/to/input/file.csv")
# Combined with a variable assignment:
mydata <- read.table("C:/path/to/input/file.txt")
write.table(x=mynewdata, file="output.txt")
```

Windows users: change all \ to \\ or /

Relative file names (minimal changing of working directory):

```
setwd("C:/Users/berry/Desktop") # set working directory
dir() # show files in current folder
mydata <- read.table("filename.txt", header=TRUE, sep="\t")
# use a better object name!
```

Folder management

```r
setwd("..") # sets working directory path up one level
getwd() # shows the current wd path
dir(recursive=TRUE) # also list items in subfolders
dir("../other_subfolder") # list files in different folder
file.create() # some file operations
file.rename()
file.remove() # see also unlink()
file.copy()
dir.create() # some folder (directory) operations
file.exists()
dir.exists()
```

Some of the arguments for read.table

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Alternatives to read.table:

scan	At the core of read.table - for complicated things
read.csv	comma separated values (different defaults than read.table)
read.fwf	fixed width formatted data
read_excel	Excel files (install package, see github.com/hadley/readxl)

Practice reading tables and subsetting data.frames

Exercise 12: data.frames - working with tables

1. Read the file "animals.txt" with the correct settings for each needed argument and assign it to an object.
2. Check whether everything is read correctly with `str`.
3. Print only the first column (BONUS: in 3 different ways of subsetting).
4. `which` element of this vector is equal to (==) "Sparrow"?
5. Can the elephant fly? Find out with a logical query.
6. Find out how many legs the mammals have on average. Interpret the result.
7. BONUS 1: Use `tapply` to find the average cuteness score for each animal class.
8. BONUS 2: Read the file "days.txt" in a way that days, months, and years each have their own column. What other function besides `read.table` might be useful for that?

Solution for exercise 12.1-2: data.frames

```
# set working directory to path with files:
setwd("C:/Dokumente und Einstellungen/hydro/Desktop")
# which files are there:
dir()
# step by step, specify the arguments of read.table...
animals <- read.table("animals.txt", sep="\t",
                      header=TRUE, dec=",")
animals
str(animals) # ... until all numbers are num.
```

Solution for exercise 12.3-5: data.frames

```
# first column, and which is Sparrow:
animals$Name
animals[ ,"Name"] # too much typing
animals[ ,1] # hard to read later on
animals$Name == "Sparrow"
which( animals$Name == "Sparrow" )

# Can the elephant fly? Automatic query:
animals[4,3]
animals[ animals$Name == "Elephant" , 3 ]
animals[ animals$Name == "Elephant" , "can_fly" ]
animals[ animals$Name == "Sparrow"  , "can_fly" ]
```

Solution for exercise 12.6-7: data.frames

```r
# How many legs do the mammals have on average?
animals[ animals$Class == "Mammal" , "n_legs" ]
mean( animals[ animals$Class == "Mammal" , "n_legs" ] )
# How cute are they, on average?
mean( animals[ animals$Class == "Mammal" , "cuteness" ] )

# How cute is each category of animals?
tapply(X=animals$cuteness, INDEX=animals$Class, FUN=mean)
# separates cuteness into groups, categorized by Class,
# then calculates mean for each group
```

Solution for exercise 12.8: data.frames

```r
# Read "days.txt" with columns for days, months and years
dir()
days <- read.table("days.txt", sep=".")
head(days)
str(days)

# custom names of columns
colnames(days) <- c("day", "month", "year")
head(days)

# other way:
read.fwf("data/days.txt", widths=c(2,1,2,1,4))

# usage example: return months for e.g. vegetation index:
days$month
```

Frequent mistakes with `read.table`

Error in scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, : line _ did not have _ elements	usually `header`, `sep` or `fill` is given incorrectly.

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`str(DataframeIreadIn)` yields "factor" in some numeric columns	Check data file! `dec` may need to be corrected

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```
as.numeric( as.character(df$col) )
as.numeric( gsub(pattern=",", replacement=".", x=df$col) )
# If you try to read data in the format "3,590.18", run
df$col <- as.numeric(gsub(",", "", df$col))
```

Frequent mistakes with `read.table`

Error in scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, : line _ did not have _ elements	usually `header`, `sep` or `fill` is given incorrectly.
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```

Note: errors stop function execution, warnings can influence function performance and should only be ignored if you know what they really mean.

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Factors = categorical variables

```
iris$Species[63] # how factors are printed

## [1] versicolor
## Levels: setosa versicolor virginica

class(iris$Species)

## [1] "factor"

levels(iris$Species)

## [1] "setosa"     "versicolor" "virginica"

# R saves factors as numbers internally
as.numeric(iris$Species)[c(1,63,105)]

## [1] 1 2 3
```

factors, explained with animals.txt: the danger

factors, explained with animals.txt: the danger

```
ac <- read.table(file="data/animals.txt", sep="\t", header=T)$cuteness
ac # R calls  print.factor ,  see methods(print)

## [1] 1,3 6,5 9,8 6,3 5,8 4,5
## Levels: 1,3 4,5 5,8 6,3 6,5 9,8
```

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```

```
class(ac); typeof(ac)

## [1] "factor"
## [1] "integer"
```

factors, explained with animals.txt: the danger

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ac <- read.table(file="data/animals.txt", sep="\t", header=T)$cuteness
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## Levels: 1,3 4,5 5,8 6,3 6,5 9,8
```

```
class(ac); typeof(ac)

## [1] "factor"
## [1] "integer"
```

```
as.numeric(ac) # don't ever do this!!

## [1] 1 5 6 4 3 2
```

factors, explained with animals.txt: the danger

```
ac <- read.table(file="data/animals.txt", sep="\t", header=T)$cuteness
ac # R calls  print.factor ,  see methods(print)

## [1] 1,3 6,5 9,8 6,3 5,8 4,5
## Levels: 1,3 4,5 5,8 6,3 6,5 9,8
```

```
class(ac); typeof(ac)

## [1] "factor"
## [1] "integer"
```

```
as.numeric(ac) # don't ever do this!!

## [1] 1 5 6 4 3 2
```

```
char <- as.character(ac)
as.numeric(sub(",",".", char))

## [1] 1.3 6.5 9.8 6.3 5.8 4.5
```

factors, explained with animals.txt: the solution

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```
df <- read.table(file="data/animals.txt", sep="\t", header=T, as.is=TRUE)
str(df)

## 'data.frame': 6 obs. of  6 variables:
##  $ Name    : chr  "Frog" "Merl" "Doe" "Elephant" ...
##  $ Class   : chr  "Amphibian" "Bird" "Mammal" "Mammal" ...
##  $ can.fly : logi  FALSE TRUE FALSE FALSE TRUE FALSE
##  $ color   : chr  "green" "black" "brown" "gray" ...
##  $ n.legs  : int  4 2 4 4 4 2
##  $ cuteness: chr  "1,3" "6,5" "9,8" "6,3" ...
```

Now Name and cuteness are character strings instead of factors. `as.is=TRUE` is a special case of `stringsAsFactors=FALSE`: with the first you can specify the latter per column (I use it because I can type it more quickly).

factors are very useful to apply a function per group

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```
str(PlantGrowth)

## 'data.frame': 30 obs. of  2 variables:
##  $ weight: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53 5.33 5.14 ...
##  $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1 1 1 1 1 ...
```

factors are very useful to apply a function per group

```
str(PlantGrowth)
```

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##  $ weight: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53 5.33 5.14 ...
##  $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
tapply(X=PlantGrowth$weight, INDEX=PlantGrowth$group, FUN=mean)
```

```
##  ctrl  trt1  trt2
## 5.032 4.661 5.526
```

factors are very useful to apply a function per group

```
str(PlantGrowth)

## 'data.frame': 30 obs. of  2 variables:
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##  $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
tapply(X=PlantGrowth$weight, INDEX=PlantGrowth$group, FUN=mean)

##  ctrl  trt1  trt2
## 5.032 4.661 5.526
```

This part of Hadley's book is a good intro to factors.

factors are also useful for plotting specifics

col can be a factor vector, integers correspond to `palette()`

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col can be a factor vector, integers correspond to `palette()`

```
plot(rate~conc, data=Puromycin, col=state, pch=16, las=1)
legend("bottomright", levels(Puromycin$state), col=1:2, pch=16)
```

practice working with categories

Exercise 13: Factors, tapply

1. Plot the Puromycin dataset, but use the 3rd and 4th color of the default `palette()`
2. BONUS 1: Use custom colors.
   Hint: create a vector with the colors, then index from it.
3. BONUS 2: In the `iris` dataset, add a row for the *Iris sintenisii*.
   Hint: add a level to the factor first.
4. Using `tapply`, find out what you should feed chickens according to the measurements in `chickwts`.

Solution for exercise 13: factors, tapply

```
plot(rate~conc, data=Puromycin, col=as.integer(state)+2, pch=16)

mycol <- c("orange", "mediumpurple2")
plot(rate~conc, data=Puromycin, col=mycol[state], pch=16)

levels(iris$Species) <- c(levels(iris$Species), "sintensii" )
iris[151, ] <- c(6,3,5,2,"sintensii")
```

Solution for exercise 13: factors, tapply

```
plot(rate~conc, data=Puromycin, col=as.integer(state)+2, pch=16)

mycol <- c("orange", "mediumpurple2")
plot(rate~conc, data=Puromycin, col=mycol[state], pch=16)

levels(iris$Species) <- c(levels(iris$Species), "sintensii" )
iris[151, ] <- c(6,3,5,2,"sintensii")
```

```
sort(tapply(chickwts$weight, chickwts$feed, median))

## horsebean   linseed   soybean  meatmeal sunflower    casein
##     151.5     221.0     248.0     263.0     328.0     342.0

sort(tapply(chickwts$weight, chickwts$feed, min))

## horsebean   linseed  meatmeal   soybean    casein sunflower
##       108       141       153       158       216       226
```

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Merge (join) tables

Exercise 14: Merge

1. Read the files mergeApples1.txt and mergeApples2.txt into separate data.frames.
2. Use `rbind` to combine both tables line-wise and assign the output to e.g. `apples`.
3. Read mergeAge.txt into e.g. `age`.
4. Describe what `merge(age, apples, by.x="Name", by.y="Person")` does.
5. What happens if you set `all` or `all.x` = TRUE?
6. BONUS 1: What is the difference between `cbind` and `rbind`?
7. BONUS 2: Why does `cbind` not work with age and apples?

Solution for exercise 14: Merge

```
ma1 <- read.table("data/mergeApples1.txt", header=T)
ma2 <- read.table("data/mergeApples2.txt", header=T)
apples <- rbind(ma1, ma2)
apples
age <- read.table("data/mergeAge.txt", header=T)

merge(age, apples, by.x="Name", by.y="Person")
# combine the information from both datasets
# for names that occur in both tables

merge(age, apples, by.x="Name", by.y="Person", all=T)
# Keep all entries, pad with NAs

# rbind: combine rows below each other
# cbind: bind columns beside each other
# dimensions and names must be correct
```

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NA-values (NA=not available)

Creating a table with **NA** values

```
# create some test data. "c" around ":" is not necessary
df <- data.frame(x= c(1:10), y=11:20 )
df[3,2] <- NA
head(df)

##   x  y
## 1 1 11
## 2 2 12
## 3 3 NA
## 4 4 14
## 5 5 15
## 6 6 16
```

NA-values

Handling of **NA** values

```
plot(df$x, df$y, pch=19, col="red")
```

NA-values

Checking for **NA** values

```
is.na(df)

##            x     y
##  [1,] FALSE FALSE
##  [2,] FALSE FALSE
##  [3,] FALSE  TRUE
##  [4,] FALSE FALSE
##  [5,] FALSE FALSE
##  [6,] FALSE FALSE
##  [7,] FALSE FALSE
##  [8,] FALSE FALSE
##  [9,] FALSE FALSE
## [10,] FALSE FALSE
```

NA-values

Checking for **NA** values

```
is.na(df)

##             x     y
##  [1,] FALSE FALSE
##  [2,] FALSE FALSE
##  [3,] FALSE  TRUE
##  [4,] FALSE FALSE
##  [5,] FALSE FALSE
##  [6,] FALSE FALSE
##  [7,] FALSE FALSE
##  [8,] FALSE FALSE
##  [9,] FALSE FALSE
## [10,] FALSE FALSE
```

```
na.omit(df)

##     x  y
## 1   1 11
## 2   2 12
## 4   4 14
## 5   5 15
## 6   6 16
## 7   7 17
## 8   8 18
## 9   9 19
## 10 10 20
```

NA-values

```
##     x  y
## 1   1 11
## 2   2 12
## 3   3 NA
## 4   4 14
## 5   5 15
## 6   6 16
## 7   7 17
## 8   8 18
## 9   9 19
## 10 10 20
```

NA-values

```
##     x  y
## 1   1 11
## 2   2 12
## 3   3 NA
## 4   4 14
## 5   5 15
## 6   6 16
## 7   7 17
## 8   8 18
## 9   9 19
## 10 10 20
```

```r
mean(df$x) ; mean(df$y)
```

```
## [1] 5.5
## [1] NA
```

NA-values

```
##     x  y
## 1   1 11
## 2   2 12
## 3   3 NA
## 4   4 14
## 5   5 15
## 6   6 16
## 7   7 17
## 8   8 18
## 9   9 19
## 10 10 20
```

```r
mean(df$x) ; mean(df$y)
```

```
## [1] 5.5
## [1] NA
```

```r
mean(df$y, na.rm=TRUE) # dangerous with sums
```

```
## [1] 15.77778
```

apply: execute a function on each row (col) of a `matrix`

apply: execute a function on each row (col) of a matrix

```
# Compute the column- and row sums of a data.frame (df)
apply(X=df, MARGIN=2, FUN=sum) # column wise

##  x  y
## 55 NA
```

apply: execute a function on each row (col) of a matrix

```r
# Compute the column- and row sums of a data.frame (df)
apply(X=df, MARGIN=2, FUN=sum) # column wise

##  x  y
## 55 NA
```

```r
apply(df, 1, sum) # line by line

##  [1] 12 14 NA 18 20 22 24 26 28 30
```

apply: execute a function on each row (col) of a matrix

```r
# Compute the column- and row sums of a data.frame (df)
apply(X=df, MARGIN=2, FUN=sum) # column wise

##  x  y
## 55 NA
```

```r
apply(df, 1, sum) # line by line

##  [1] 12 14 NA 18 20 22 24 26 28 30
```

```r
apply(df, 2, sum, na.rm=TRUE) # with further arguments

##   x   y
##  55 142
```

apply: execute a function on each row (col) of a matrix

```
# Compute the column- and row sums of a data.frame (df)
apply(X=df, MARGIN=2, FUN=sum) # column wise

##  x  y
## 55 NA
```

```
apply(df, 1, sum) # line by line

##  [1] 12 14 NA 18 20 22 24 26 28 30
```

```
apply(df, 2, sum, na.rm=TRUE) # with further arguments

##   x   y
##  55 142
```

Exercise 15: apply

Compute the median of each column in the dataset `iris`.
Hint: leave out the non-numeric column.

apply practice solution

```
apply(iris[ ,-5], MARGIN=2, median)

## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##         5.80         3.00         4.35         1.30
```

apply practice solution

```
apply(iris[ ,-5], MARGIN=2, median)

## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##         5.80         3.00         4.35         1.30
```

```
apply(iris[ ,-5], MARGIN=2, mean)

## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##     5.843333     3.057333     3.758000     1.199333
```

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Working with Scripts

For any real data analysis, you should work with scripts that save your code.

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They may also develop into packages...
Before sending, close R, open a clean (!) session, and check whether everything is running.
Scripts should have lots of comments! `# seriously.`

Creating documents, Organizing your files

Rstudio - file - new -
- R HTML (no LaTeXrequired on system)
- R markdown (easy to learn, creates .pdf or .docx)
- R sweave (very powerful through LaTeX. This is what I use for these slides.)

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I use knitr, as it is more advanced than the default sweave. For that, set:
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There are tips online on how to organize data, scripts, plots etc.
stackoverflow: How to organize large R programs
stackexchange: How to efficiently manage a statistical analysis project?
Here are some tips by Hadley: http://r-pkgs.had.co.nz/style.html

Real Datasets online

- NOAA (USA) weather data: www1.ncdc.noaa.gov/pub/data/normals
- DWD Climate Data Center: CDC/observations_germany/climate

```
library(rdwd) # github.com/brry/rdwd
clim <- dataDWD(selectDWD(id=02080, res="daily", var="kl",
                          time="hist"), dir=tempdir())
```

- data.unicef.org (potentially add .xls etc as file extension)
- https://github.com/okulbilisim/awesome-datascience#data-sets
- https://github.com/caesar0301/awesome-public-datasets
- http://ropensci.org/packages/index.html
- http://dataviz.tools/category/data-sources/

Exercise 16: Real Data

Download a dataset that interests you, read it into R and do some analyzing / plotting.

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Plot I: the dataset

```
head(beaver2, 4)

##   day time  temp activ
## 1 307  930 36.58     0
## 2 307  940 36.73     0
## 3 307  950 36.93     0
## 4 307 1000 37.15     0

str(beaver2)

## 'data.frame': 100 obs. of  4 variables:
##  $ day  : num  307 307 307 307 307 307 307 307 307 307 ...
##  $ time : num  930 940 950 1000 1010 1020 1030 1040 1050 1100 ...
##  $ temp : num  36.6 36.7 36.9 37.1 37.2 ...
##  $ activ: num  0 0 0 0 0 0 0 0 0 0 ...
```

Plot II

```r
# The basic syntax is plot(x, y, adjustments)
plot(beaver2$time, beaver2$temp)
#
```

Plot III

```
plot(beaver2$time, beaver2$temp, ylab="Body temperature  [ \U00B0 C]",
     main="Beavers get warm late in the evening",
     xlab="Observation time [0330 for 3:30AM]", col="red")
```

Plot IV

```
plot(beaver2$time, beaver2$temp, pch=2, cex=2.8, las=1)
# pch: PointCHaracter, cex: CharacterEXpansion
# las: LabelAxisStyle (numbers upright)
```

Overview of Point CHaracters (more in Rclick Anhang)

plot (x, y, pch = _)

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Plot with lines I

```
k <- c(3,0,-10,8,6,3)   ; l <- c(-4,2,-6,-12,7,-3)
plot(k)  # standard (default) type: "p" for points
```

Plot with lines II

```r
plot(k, type="l")
# type="l" for lines
```

Plot with lines III

```
plot(k, type="b", lwd=4)
# type="b" for both points and lines. # lwd: line width
```

Plot with lines IV

```
plot(k, type="o", lty=2)
# type="o" for both overplotted. # lty: line type
```

Overview of types (more in Rclick Anhang)

plot (x, y, type = _)

Overview of line types (more in Rclick Anhang)

plot (x, y, lty = _)

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One data.frame instead of two vectors

Default method if x is a data.frame:

```
plot( beaver2[ ,2:3] )
```

Plot limits I

xlim with a two-value vector with lower and upper limit.

```
plot(beaver2[ ,2:3], xlim=c(-1000,3000),  ylim=c(36,40))
```

Plot limits II

xaxis decreasing (can be very misleading!):

```
plot(beaver2[ ,2:3], xlim=c(3000,-1000), ylim=c(36,40))
```

Adding datapoints

```
plot(beaver2[ ,2:3])
points(100, 37.5, pch=21, bg=5, cex=4, col=2, lwd=3)
lines(x=c(5,120,514,918), y=c(37,39,38,37.5), col=3, type="b")
```

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Saving plots to a file

In the menu of the graphics window, you can save the current plot by hand. For reproducible sizes and if you're creating many plots, use

Saving plots to a file

In the menu of the graphics window, you can save the current plot by hand. For reproducible sizes and if you're creating many plots, use

```
png("FileName.png", width=12, height=9, units="in",
           res=300, bg="transparent", pointsize=14)
  plot(1:20)
  title(main="Plot title")
  points(5,9)
dev.off() # to close the external device
```

Saving plots to a file

In the menu of the graphics window, you can save the current plot by hand. For reproducible sizes and if you're creating many plots, use

```
png("FileName.png", width=12, height=9, units="in",
           res=300, bg="transparent", pointsize=14)
  plot(1:20)
  title(main="Plot title")
  points(5,9)
dev.off() # to close the external device
```

The functions `pdf`, `jpeg`, etc. are also available.

multiple figure layout I

```
# 3 rows, 2 columns:
par(mfrow=c(3,2), mar=c(3,3,1,1), mgp=c(1.9, 0.7, 0), las=1)
plot(stackloss[ ,1:2]) # 6 plot commands
```

multiple figure layout II

```
lay <- layout(matrix(c(1,1,2,2,
                       5,5,2,2,
                       3,3,4,4,
                       3,3,4,4), ncol=4, byrow=TRUE),
              widths=c(6,6,4,4))
layout.show(lay)
```

multiple figure layout III

From the example in `?layout`:

Box

Y−Axis
0.8
0.6
0.4
0.2
0.0
1
2
3
4
5
6
box(_)
1.4
1.0
0.6
'plot'
'figure', after par(mfrow) or layout()
'inner'
'outer', if outer margins were set by par(oma)

Now it's your turn...

Exercise 17: Plotting

1. Plot a dataset of your choice (eg from `library(help = "datasets")`).
2. Add some red dotted lines between big quadratic points, filled with blue color.
3. Label the axis and give your graph a big italic header with `cex.main`, `font.main`, see `?par`.
4. Plot with a logarithmic scale on one axis.
5. Set the axis to a certain limit. With `yaxs`, suppress the default 4% range extension.
6. Using `xaxt`, plot without an x-axis. Look in the help of `par` how this can be done. Then add a custom `axis`.
7. Add a `legend` to the plot and thick-lined `box` around the final plot.

Solution for exercise 17: Plotting I

```
# generate "random" data:
set.seed(42) ; numbers <- cumsum(rnorm(40)) + 20
x <- c(10, 15, 31, 33); y <- c(19, 22, 17, 23)
# Basic plot:
plot(numbers, type="l", xlab="Time",
     main="Fake Time Series", cex.main=3, font.main=3,
     log="y", xlim=c(0,50), xaxs="i", xaxt="n" )
# Add points and lines
points(x=x, y=y, pch=22, type="p", cex=3, col="orange",
      bg="green")
lines(x=c(10, 15, 31, 33), y=c(-6, -3, -8, -2)+25, col=2,
      lty="dashed")
# Custom axis, legend and box around plot:
axis(side=1, at=c(0, 15, 30, 45)  )
legend("topright", legend=c("ts", "more fake stuff"),
       lty=c(1,2), col=c(1,2) )
box(lwd=5)
```

Solution for exercise 17: Plotting II

Graphing paths: NA lines between entry groups

```
library("berryFunctions") # >= 1.9.2 (2015-10-22) for insertRows, colPoints
tfile <- system.file("extdata/rivers.txt", package="berryFunctions")
rivers <- read.table(tfile, header=TRUE, dec=",")
colPoints(x,y,n, data=rivers, add=FALSE, lines=TRUE, lwd=3,
          legargs=c(y1=0.8,y2=1, density=FALSE) )
```

Base R vs ggplot2

This has all been graphing with the possibilities of base R.
There is also the package `ggplot2` which a lot of people love to use.
I get everything done with base R and don't see a need to learn ggplot grammar.
You can do whatever you want - it's both R, both have their advantages.
A very good place to start comparing things is:
http://flowingdata.com/2016/03/22/comparing-ggplot2-and-r-base-graphics/
Be sure to follow the links in the beginning of the article...

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   Character strings: Intro
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Character strings I

```
paste("NiceThing", 3:5) # Creates vector of Mode character

## [1] "NiceThing 3" "NiceThing 4" "NiceThing 5"

paste(2, "hot", 4, "U", sep="_")

## [1] "2_hot_4_U"

letvec <- c("some different", "let", "ters")
letvec

## [1] "some different" "let"
## [3] "ters"
```

Character strings II

```r
length(letvec)

## [1] 3

nchar(letvec)

## [1] 14  3  4

paste("nice", letvec, sep="_")

## [1] "nice_some different" "nice_let"
## [3] "nice_ters"
```

Character strings III

```
paste(letvec, sep="")

## [1] "some different" "let"
## [3] "ters"

paste(letvec, collapse="")

## [1] "some differentletters"

# remove spaces: substitute " " in letvec with ""
sub(" ", "", letvec)

## [1] "somedifferent" "let"
## [3] "ters"
```

Character strings IV

```
substr("Monster Party", start=2, stop=5)

## [1] "onst"

# If you need several string segments:
substring("Monster Party", first=c(1,3,5), last=c(2,5,9) )

## [1] "Mo"    "nst"   "ter P"

strsplit("Die Aerzte - Monster Party", split=" - ")[[1]]

## [1] "Die Aerzte"    "Monster Party"
```

Backslash "\" : Escape Character

"\n" for return or line break (newline), eg in graphictitles and -texts
"\t" for Tabstop, e.g. for `write.table("path/file.txt", yourdata, sep="\t")`
"\\" for Backslash as symbol in `title, text, legend` etc.
"\"" for " as character
"\U" for Unicode, e.g.:

```
plot(1)
# average symbol without using "expression":
mtext(paste("\U00D8", 5.4, "\U00B0 C"), col=2)
```

Time to practice...

Exercise 18: character string operations

In the German chocolate industry, we love

```
schoko <- c("Ritter Sport", "Lindor", "Frigor", "Milka", "Frey",
"More Lindor")
```

1. which element **is** or **contains** "Lindor"?
   Find out with `match`, `grep`, `%in%` and `grepl`. What are the differences between those?
2. Replace "or" with "nicor" using `sub` and `gsub`.
3. What's the problem with `"Ritter sport" %in% schoko`?
4. What does `"Ritter [s,S]port" %in% schoko` do?

Solution for exercise 18.1: Character strings

```r
schoko <- c("Lindor", "Ritter Sport", "Frigor", "Milka",
            "Frey", "More Lindor")
# Which element in schoko IS Lindor
match("Lindor", schoko)
match(schoko, "Lindor")
match(schoko, c("Lindor", "Frigor") )

# Which element in schoko CONTAINS Lindor
grep("Lindor", schoko)
grep("or", schoko)
grepl("Lindor", schoko) # logical value

# Is one of the elements of schoko == "Lindor" at all?
"Lindor" %in% schoko
any(  grepl("Lindor", schoko)  ) # any TRUE?
all(  grepl("Lindor", schoko)  ) # All TRUE
! grepl("Lindor", schoko)
```

Solution for exercise 18.2-41: Character strings

```r
# Replace Character strings (substitute)
sub(pattern="or", replacement="nicor", schoko)
# Replace all occurences (global substitution)
gsub(pattern="or", replacement="nicor", schoko)

# Avoid capitalization issues with
tolower(schoko)
"Ritter [s,S]port" %in% schoko
# Does not work!!
```

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   For Loops
   lapply, Rcpp
   Repeat + While Loops
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to R or not to R

to R or not to R

Lucius Annaeus Seneca (4BC - 65AD):

to R or not to R

Lucius Annaeus Seneca (4BC - 65AD):

To err is human

to R or not to R

Lucius Annaeus Seneca (4BC - 65AD):

To err is human

to R is better

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

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```

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ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

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```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

```
7-3 > 2
class(7-3 > 2 )
if(7-3 > 2) 18
if(7-3 > 5) 18
if(7-3 > 5) 18 else 17
```

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

```
7-3 > 2                    TRUE
class(7-3 > 2 )
if(7-3 > 2) 18
if(7-3 > 5) 18
if(7-3 > 5) 18 else 17
```

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

`7-3 > 2`	TRUE
`class(7-3 > 2 )`	logical = truth value, boolean
`if(7-3 > 2) 18`	
`if(7-3 > 5) 18`	
`if(7-3 > 5) 18 else 17`	

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

`7-3 > 2`	TRUE
`class(7-3 > 2 )`	logical = truth value, boolean
`if(7-3 > 2) 18`	Condition is TRUE, so 18 is returned
`if(7-3 > 5) 18`	
`if(7-3 > 5) 18 else 17`	

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

`7-3 > 2`	TRUE
`class(7-3 > 2 )`	logical = truth value, boolean
`if(7-3 > 2) 18`	Condition is TRUE, so 18 is returned
`if(7-3 > 5) 18`	Condition is FALSE, so nothing happens
`if(7-3 > 5) 18 else 17`	

Conditional execution I

Syntax for a single logical value:

```
if(this_is_true) {do_something} else {do_other_thing}
```

Syntax for a vector with several T/F values:

```
ifelse(condition, expression1, expression2)
```

If condition == TRUE, then expression1 is evaluated, if condition == FALSE, then expression2 is evaluated.

`7-3 > 2`	TRUE
`class(7-3 > 2 )`	logical = truth value, boolean
`if(7-3 > 2) 18`	Condition is TRUE, so 18 is returned
`if(7-3 > 5) 18`	Condition is FALSE, so nothing happens
`if(7-3 > 5) 18 else 17`	Condition FALSE, so 17 is returned.

Conditional execution II

```
# Several commands must be held together with curly braces:
if(TRUE)
  {
  plot(1:10, main="TRUE in code")
  box("figure", col=4, lwd=3)
  } else
# do something else: plot random numbers
    {
    plot(rnorm(500), main="FALSE in code")
    }
# these last brackets can (but should not) be left away
# indenting code makes it readable for humans

par(mfrow=c(1,2), cex=1, las=1)
```

Conditional execution III

Vectorising: if(c) e1 else e2 vs ifelse(c, e1, e2)

```
v <- c(13, 14, 15, 16, 17)
v>14

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

Vectorising: if(c) e1 else e2 vs ifelse(c, e1, e2)

```
v <- c(13, 14, 15, 16, 17)
v>14

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

```
ifelse(v>14, v+10, NA) # can handle vector of input

## [1] NA NA 25 26 27
```

Vectorising: if(c) e1 else e2 vs ifelse(c, e1, e2)

```
v <- c(13, 14, 15, 16, 17)
v>14

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

```
ifelse(v>14, v+10, NA) # can handle vector of input

## [1] NA NA 25 26 27
```

```
if(v>14) v+10 else NA

## Warning in if (v > 14) v + 10 else NA: the condition has
length > 1 and only the first element will be used

## [1] NA
```

Time to practice

Exercise 19: if else - Conditional code execution

1. `sqrt` returns NaN for the negative values in `v <- -3:5` and warns about it. With a conditional expression, pass 0 instead of negative values to `sqrt`.
2. Construct a statement that checks whether the variable `input <- 4` is a number smaller than 3. Let it write a useful `message` to the console (for both cases). Now test it with `input <- 1.8` and `input <- -17`.
3. Now restrict the correct value of input to *positive* numbers <3, i.e. the number must be <3 AND ≥ 0.
4. BONUS 1: What happens if `input <- "2"` or if `input <- "b"`?
5. BONUS 2: Create a character variable that, depending on the result of `rnorm(1)`, is initiated with probable or unlikely.
6. BONUS 3: `replicate` this experiment 1000 times and examine the result with `table`.
7. BONUS 4: How could you do this with `ifelse`?

Solution for exercise 19.1: if else

```
v <- -3:5
sqrt(v)

## Warning in sqrt(v):  NaNs produced

## [1]    NaN    NaN    NaN 0.0000 1.0000 1.4142 1.7321 2.0000 2.2361
```

```
ifelse( v >= 0, sqrt(v), 0)

## Warning in sqrt(v):  NaNs produced

## [1] 0.0000 0.0000 0.0000 0.0000 1.0000 1.4142 1.7321 2.0000 2.2361
```

```
sqrt(ifelse( v >= 0, v, 0))

## [1] 0.0000 0.0000 0.0000 0.0000 1.0000 1.4142 1.7321 2.0000 2.2361
```

Solution for exercise 19.2: if else

```
input <- 4
if( input >= 3 ) message("Input was wrong.
                         It should be <3") else
                 message("Input OK")

## Input was wrong.
##                         It should be <3

# run it again after
input <- 1.8
input <- -17
```

Solution for exercise 19.3: if else

```
# three different solutions:
if( input >= 3 ) message("Input is > 3") else
if( input < 0 )  message("Input is < 0") else
                 message("Input OK")

if( input >= 3 |  input < 0)
   message("Input outside 0...3") else
   message("Input OK")

if( input > 0  &  input <= 3 )   message("Input OK") else
           message("Input (",input,") outside 0...3")
```

Solution for exercise 19.3: if else BONUS

```
result <- if(rnorm(1)>2) "unlikely" else "probable"

result <- replicate(n=1000, expr=
             if(rnorm(1)>2) "unlikely" else "probable")
table(result)

result <- ifelse(rnorm(1000)>2, "unlikely", "probable")
table(result)
```

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- Logical (boolean) values F and T internally are often converted to integers 0 and 1, thus `sum(c(T,F,F,T,T,T,F,F,T))` is the number of TRUEs in a vector, `mean` yields the proportion of TRUEs.

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- `which(logicalVec)` gives the indices (positions) of TRUE values.
- `Vec[logicalVec]` returns only the values of vec corresponding to TRUE in logicalVec (No need to wrap it into `which`).

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- `which(logicalVec)` gives the indices (positions) of TRUE values.
- `Vec[logicalVec]` returns only the values of vec corresponding to TRUE in logicalVec (No need to wrap it into `which`).
- Logical operators: `!`, `&`, `|`, `xor()` (not, and, or, exclusive or)

Notes on conditional code execution

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```
if(cond)
  {
  ex1a
  ex1b
  }
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- `if(c){ex1}` is valid code, thus R doesn't expect else anymore.
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```
if(cond)
  {
  ex1a
  ex1b
  }
else
  ex2
```

- `if(logicalValue==TRUE) ...` is usually unnecessary, you can write `if(logicalValue) ...`, but sometimes, `if(isTRUE(logicalValue)) ...` helps to deal with NAs.

Actual usage of if else statements

See the `hist` source code:
github.com/wch/r-source -> src / library / graphics / R / hist.R

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```
mad
```

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```
mad
```

Multiple nested conditionals
`if(a) b else if(c) d else e`
can be avoided with `switch`.

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For loops

Execute a block of code several times, with different input values.

Syntax: `for(aRunningVariable in aSequence){ doSomething }`

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```
help("for") # needs quotation marks!
```

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print(1:2)
print(1:5)
print(1:9)
```

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help("for") # needs quotation marks!
```

```
print(1:2)
print(1:5)
print(1:9)
```

This is easier and less prone to human errors with:

```
for(i in c(2,5,9) ) { print(1:i) }

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

For loops: fill a vector

```
v <- vector(mode="numeric", length=20)
v

##  [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

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```
for(i in 3:17)  {  v[i] <- (i-2)^2  }
```

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```

```
for(i in 3:17)  {  v[i] <- (i-2)^2  }
```

```
v # this code was executed once for each i

##  [1]   0   0   1   4   9  16  25  36  49
## [10]  64  81 100 121 144 169 196 225   0
## [19]   0   0
```

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```

See Rclick 10.4 for a realistic for loop example.

For loops: fill a vector

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for(i in 3:17)  {  v[i] <- (i-2)^2  }
```

```
v # this code was executed once for each i

##  [1]   0   0   1   4   9  16  25  36  49
## [10]  64  81 100 121 144 169 196 225   0
## [19]   0   0
```

See Rclick 10.4 for a realistic for loop example.
In R, `for` loops are slow. Always try to vectorize (the best option, not always possible) or use `lapply` (saves you the initiation of the empty vector, easier to parallize).

For loops: execute code multiple times I

$$y = f(x, n) = \frac{12.5 * n}{(n-1)!} * \left(\frac{nx}{8}\right)^{(n-1)} * e^{-\frac{nx}{8}}$$

For loops: execute code multiple times II

```
x <- seq(0,25,0.1)
plot(x,x, type="n", ylab="y = f(x,n)")
lines(x, 12.5*5/factorial(5-1)*(x/8*5)^(5-1)*exp(-x/8*5), col=2)
lines(x, 12.5*6/factorial(6-1)*(x/8*6)^(6-1)*exp(-x/8*6), col=2)
```

For loops: execute code multiple times II

```
x <- seq(0,25,0.1)
plot(x,x, type="n", ylab="y = f(x,n)")
lines(x, 12.5*5/factorial(5-1)*(x/8*5)^(5-1)*exp(-x/8*5), col=2)
lines(x, 12.5*6/factorial(6-1)*(x/8*6)^(6-1)*exp(-x/8*6), col=2)
```

For loops: execute code multiple times III

```
x <- seq(0,25,0.1)
plot(x,x, type="n", ylab="y = f(x,n)")
for (n in 5:25)
lines(x, 12.5*n/factorial(n-1)*(x/8*n)^(n-1)*exp(-x/8*n), col=2)
```

stocks data from finance.yahoo.com

```
# Download current datasets:
if(!requireNamespace(quantmod)) install.packages("quantmod")
if(!requireNamespace(pbapply))  install.packages("pbapply")
dummy <- pbapply::pblapply(c("F","VLKAY", "AMZN","AAPL","GOOG","YHOO"),
   function(x) zoo::write.zoo(x=quantmod::getSymbols(x, auto.assign=FALSE)[,6],
                              file=paste0("data/finance/",x,".txt"), col.names=T))

# read single files to R and merge into one file:
stocks <- lapply(dir("data/finance", full=TRUE),
                 read.table, as.is=TRUE, header=TRUE)
stocks <- Reduce(function(...) merge(..., all=T), stocks)

# Get nicer column names:
names <- sapply(strsplit(colnames(stocks), ".", fix=TRUE),"[", 1)
colnames(stocks) <- c(Index="Date", F="FORD", VLKAY="VOLKSWAGEN",
              AMZN="AMAZON", AAPL="APPLE", GOOG="GOOGLE", YHOO="YAHOO")[names]

# Save to disc:
write.table(stocks, file="data/stocks.txt", row.names=F, quote=F)
```

For loops: multipanel graphics: the task

Exercise 20: for loop

1. Read stocks.txt, so that there are no factors in the data.frame
2. Change the first column type from `char` to `date` with `?as.Date`
3. What do you get with `plot(stocks[ ,1:2])`? Make it a line graph.
4. With `par(mfrow...`, set up a two by three panel plot
5. With a for loop, fill those with each stock time series
6. BONUS 1: Make good annotations, including a main title (par oma, `mtext` with the outer argument)
7. BONUS 2: Make the plot margins smaller (par mar), turn y axis labels upright (las) and move the axis labels closer to the plots (mgp).
8. BONUS 3: Understand and comment each line of the data preparation.

For loops: multipanel graphics: the solution

```
stocks <- read.table("data/stocks.txt", header=T, as.is=T)
stocks$Date <- as.Date(stocks$Date)
par(mfrow=c(2,3), mar=c(2,4,1,1), mgp=c(2.5,0.7,0),oma=c(0,0,2,0),las=1)
for(i in 2:7) plot(stocks[ ,c(1,i)], type="l")
mtext("stocks this decade", line=0, outer=TRUE)
```

For loops: multipanel graphics: beautifuller

```
par(mfrow=c(1,2), mar=c(4,4,2,0.1), mgp=c(2.5,0.7,0), cex=0.7, las=1)
for(i in 2:3)
 {
 plot(stocks[ stocks$Date>as.Date("2015-04-01") , c(1,i) ],
      main=colnames(stocks)[i], xaxt="n", type="l", xlab=" ",
      ylab=if(i==2) "Adjusted daily share price  [USD]" else "")
 berryFunctions::monthAxis(ym=TRUE)
 }
```

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for -> lapply I: basics

```
files <- dir("../rawdata", pattern="*.csv", full=TRUE)

#
```

for -> lapply I: basics

```
files <- dir("../rawdata", pattern="*.csv", full=TRUE)

# bad and slow way:
dfs <- list() # initiate empty list
for(i in 1:length(files))
   dfs[[i]] <- read.csv(files[i], as.is=TRUE)

#
```

for -> lapply I: basics

```
files <- dir("../rawdata", pattern="*.csv", full=TRUE)

# bad and slow way:
dfs <- list() # initiate empty list
for(i in 1:length(files))
   dfs[[i]] <- read.csv(files[i], as.is=TRUE)

# much better way: apply function to each file
dfs <- lapply(X=files, FUN=read.csv, as.is=TRUE)

#
```

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# bad and slow way:
dfs <- list() # initiate empty list
for(i in 1:length(files))
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# much better way: apply function to each file
dfs <- lapply(X=files, FUN=read.csv, as.is=TRUE)

# single data.frame if all files have n columns:
df <- do.call(rbind, dfs)

#
```

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files <- dir("../rawdata", pattern="*.csv", full=TRUE)

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dfs <- list() # initiate empty list
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   dfs[[i]] <- read.csv(files[i], as.is=TRUE)

# much better way: apply function to each file
dfs <- lapply(X=files, FUN=read.csv, as.is=TRUE)

# single data.frame if all files have n columns:
df <- do.call(rbind, dfs)

# PS: much faster in this example could be
library("data.table")
dfs <- lapply(X=files, FUN=fread, sep=",")
df <- rbindlist(dfs)
```

for -> lapply II: progress bar, names, indexing etc

```
dfs <-   lapply(X=files, FUN=read.csv, as.is=TRUE)

#
```

for -> lapply II: progress bar, names, indexing etc

```
dfs <-   lapply(X=files, FUN=read.csv, as.is=TRUE)

# progress bar with remaining time
library("pbapply")
dfs <- pblapply(X=files, FUN=read.csv, as.is=TRUE)

#
```

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dfs <-   lapply(X=files, FUN=read.csv, as.is=TRUE)

# progress bar with remaining time
library("pbapply")
dfs <- pblapply(X=files, FUN=read.csv, as.is=TRUE)

# nice additional stuff:
names(dfs) <- files
str(dfs, max.level=1)
dfs[[2]] # second list element

#
```

for -> lapply II: progress bar, names, indexing etc

```
dfs <-   lapply(X=files, FUN=read.csv, as.is=TRUE)

# progress bar with remaining time
library("pbapply")
dfs <- pblapply(X=files, FUN=read.csv, as.is=TRUE)

# nice additional stuff:
names(dfs) <- files
str(dfs, max.level=1)
dfs[[2]] # second list element

# get third column / fifth row from each df:
sapply(dfs, "[",  , j=3)
sapply(dfs, "[", 5,    )
```

for -> lapply IIIa: parallel on multiple CPU cores

```
library("parallel") # already comes with R
# -> don't try to  install.packages("parallel")
nc <- detectCores()-1

#
```

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nc <- detectCores()-1

# multicore parallel execution
dfs <-        lapply(X=files, FUN=read.csv, as.is=TRUE)
dfs <-      mclapply(X=files, FUN=read.csv, as.is=TRUE,
                     mc.cores=nc) # easy on linux

#
```

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dfs <-      mclapply(X=files, FUN=read.csv, as.is=TRUE,
                     mc.cores=nc) # easy on linux

# more code needed on windows:
cl <- makePSOCKcluster(nc)
dfs <- parLapply(cl, X=files, fun=read.csv, as.is=TRUE)
stopCluster(cl)

#
```

for -> lapply IIIa: parallel on multiple CPU cores

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library("parallel") # already comes with R
# -> don't try to  install.packages("parallel")
nc <- detectCores()-1

# multicore parallel execution
dfs <-        lapply(X=files, FUN=read.csv, as.is=TRUE)
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                     mc.cores=nc) # easy on linux

# more code needed on windows:
cl <- makePSOCKcluster(nc)
dfs <- parLapply(cl, X=files, fun=read.csv, as.is=TRUE)
stopCluster(cl)

# sometimes needed before parLapply call:
clusterExport(cl, c("files","otherObjects"))
clusterEvalQ(cl, library("somePackage"))
```

for -> lapply IIIb: parallel AND progress bar

```
library(parallel)
library(pbapply) # (>2016-10-30)
cl <- makeCluster( detectCores()-1 )
myfun <- function(...) mean(rnorm(1e6))
clusterExport(cl, "myfun")
dfs1 <- pblapply(X=1:500, FUN=myfun) # 36 sec on 1 CPU core
dfs2 <- pblapply(X=1:500, FUN=myfun, cl=cl) # 10 s on 7
stopCluster(cl)

# selects windows or linux method for you!
# Peter Solymos and Zygmunt Zawadzki are awesome!
```

for -> lapply IV: code timing

```
begintime <- Sys.time(); begintime
parLapply(cl, X, fun)
Sys.time() - begintime ; rm(cl, begintime)
```

for -> lapply IV: code timing

```
begintime <- Sys.time(); begintime
parLapply(cl, X, fun)
Sys.time() - begintime ; rm(cl, begintime)
```

```
#install.packages("microbenchmark")
library(microbenchmark)
forbad <- function(n)  # fibonacci
  {
  fibvals <- c(1,1)
  for (i in 3:n) fibvals[i] <- fibvals[i-1]+fibvals[i-2]
  fibvals
  }
forgood <- function(n)
  {
  fibvals <- rep(1,n)
  for (i in 3:n) fibvals[i] <- fibvals[i-1]+fibvals[i-2]
  fibvals
  }
mb <- microbenchmark(forbad(2000), forgood(2000))  ;  mb

## Unit: milliseconds
##            expr      min       lq      mean   median       uq       max neval
##   forbad(2000) 7.379511 8.905075 11.612078 9.033072 9.179138 134.80383   100
##  forgood(2000) 2.677982 2.722405  2.802097 2.756889 2.825856   3.83025   100
```

for -> C++ code: Rcpp

Loops are fast in C++, so outsource that part of your code into C. The package Rcpp will compile it for you and make it available as a normally accessible R function.

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To find the slow parts of your code, you perform a process called "profiling":
https://www.r-bloggers.com/profiling-r-code
https://www.rdocumentation.org/packages/utils/topics/Rprof?
https://adv-r.had.co.nz/Profiling.html

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https://adv-r.had.co.nz/Profiling.html
New and very promising:
https://blog.rstudio.org/2016/05/23/profiling-with-rstudio-and-profvis
https://support.rstudio.com/hc/en-us/articles/218221837-Profiling-with-RStudio

For loop: Fibonacci

The Fibonacci sequence consists of the following integers:
1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144, ...
The first two values are 1, the following values are always the sum of the previous two elements.

Exercise 21: Fibonacci

1. Create the first 100 numbers of the fibonacci sequence with a for loop
2. BONUS 1: "forget" to create an empty vector of the correct length first, and compare the computational time of the two expressions. Hint: Use `install.packages("microbenchmark"); library(microbenchmark); mb <- microbenchmark(...)`
3. BONUS 2: Can you also do this with sapply?
4. BONUS 3: Find a fast fibonacci creator function online and compare the timings of that as well
5. BONUS 4: With the package `Rcpp`, write the for loop in C++ and compare the speed with the other variants

Fibonacci solution

```
len <- 20
fn <- rep(1, len)
for(i in 3:len)  fn[i] <- fn[i-1] + fn[i-2]
fn

##  [1]    1    1    2    3    5    8   13
##  [8]   21   34   55   89  144  233  377
## [15]  610  987 1597 2584 4181 6765
```

Fibonacci solution II

```
#install.packages("microbenchmark")
library(microbenchmark)
#install.packages("numbers")
suppressWarnings(library(numbers))
forbad <- function(n)
  {fibvals <- c(1,1)
  for (i in 3:len) fibvals[i] <- fibvals[i-1]+fibvals[i-2]
  fibvals
  }
forgood <- function(n)
  {fibvals <- rep(1,n)
  for (i in 3:len) fibvals[i] <- fibvals[i-1]+fibvals[i-2]
  fibvals
  }
numfib <- function(n) suppressWarnings(fibonacci(n, seq=T))
applfib <- function(n)
  {fibvals <- rep(1,n)
  sapply(3:n, function(i) {fibvals[i]<<-fibvals[i-1]+fibvals[i-2]})
  }
mb <- microbenchmark(numfib(2000), forbad(2000), forgood(2000), applfib(2000))
mb


## Unit: microseconds
##           expr      min        lq       mean   median       uq      max neval
##   numfib(2000) 2822.199 3094.8970 3424.04161 3258.544 3458.969 5941.757   100
##   forbad(2000)   24.519   29.5075   36.10796   34.497   39.914   63.578   100
##  forgood(2000)   22.808   27.9400   36.00247   30.648   36.207  301.065   100
##  applfib(2000) 3380.140 3713.4205 3986.06967 3827.176 4030.023 5847.675   100
```

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Repeat loops

Syntax: `repeat {expressions}`

```
next  # jump to next iteration
break # leave the loop
```

Repeat loops

Syntax: `repeat {expressions}`

```
next  # jump to next iteration
break # leave the loop
```

```
i <- 0 # Create object i with the value 0
repeat # keep repeating the following block of code
   {                        # Codeblock begins
   i <- i + 1               # overwrite object i with new number
   if (i < 3)  print(i) # conditional output to console
   if (i == 3)   break  # conditional leaving of loop
   }                        # Codeblock ends

## [1] 1
## [1] 2
```

What is now the value of i?

Repeat loops

Syntax: `repeat {expressions}`

```
next  # jump to next iteration
break # leave the loop
```

```
i <- 0 # Create object i with the value 0
repeat # keep repeating the following block of code
   {                        # Codeblock begins
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   if (i < 3)  print(i) # conditional output to console
   if (i == 3)   break  # conditional leaving of loop
   }                        # Codeblock ends

## [1] 1
## [1] 2
```

What is now the value of i? i is now 3, because in the last iteration, 1 was added to 2 and the result saved as i.

While loops

Syntax: `while(condition){expressions}`

The following code is executed as long as (while) i is lesser then 3:

```
i <- 0
while(i < 3) i <- i + 1
i

## [1] 3
```

repeat loops are hardly ever used in R, and while loops fairly seldom as well.

Practice while loops

Exercise 22: while loop

1. Why is the character string `folder <- "path/to/file///"` unsuitable for reading in a file?
2. With a while loop, make it suitable. Hints: `substring`, `nchar`
3. BONUS: enable your solution to deal with \\ at the end as well. Hint: `%in%`.

Solution to exercise 22: while loop

`folder <- "path/to/file///"` would link to empty-named subfolders at the end

```
folder <- "path/to/file///"
while(substring(folder, nchar(folder))=="/")
     folder <- substring(folder, 1, nchar(folder)-1)

while( substring(folder, nchar(folder)) %in% c("/", "\\") )
     folder <- substring(folder, 1, nchar(folder)-1)
```

The grand duel (http://www.janko.at/Raetsel/Mathematik/095.a.htm)

Sir Adam and Sir Bart confront each other in a duel with pistols. By good old English custom, the two shoot at each other alternately, until one of them dies. Being gentlemen, they decide that the worse shooter may fire the first shot. Sir Adam has a hit ratio of 30% and Sir Bert one of 40%. What are the chances of survival for each of the two?

Exercise 23: while loop duel

1. BONUS 1: Derive the probabilities mathematically.
2. Simulate the duel numerically. Hint: repeat the experiment `while` both are alive. In each step, let Sir Bert die with a 30% change; if he survives, let Sir Adam die with a 40% change.
3. BONUS 2: Write a function simulating the duel and returning the outcome.
4. Run the simulation 1000 (10k) times and assess Sir Bert's chance of survival.
5. BONUS 3: How many rounds are fought on average? (How is that quantity distributed?)

The grand duel - resolved

```
plot(cumsum(sapply(0:20, function(i) 0.42^i*0.3)), type="l",
     ylim=c(0.26,0.58), main="cumulative death chance per round")
lines(cumsum(sapply(0:20, function(i) 0.42^i*0.7*0.4)), col=2)
```

The grand duel - resolved

```
duel_simulation <- function()
{
a <- b <- TRUE # TRUE = 1 = alive
n <- 0 # number of rounds
while(a&b)
  {
  if(  runif(1)<0.3) b <- FALSE # = 0 = dead
  if(b&runif(1)<0.4) a <- FALSE
  n <- n+1
  }
# return simulation result
c(a=a,b=b, n=n)
}
```

The grand duel - resolved

```
simu_res <- replicate(10000, duel_simulation())
# head(t(simu_res), 30)
apply(simu_res, 1, table) # / 10000 *100

## $a
##
##    0    1
## 4844 5156
##
## $b
##
##    0    1
## 5156 4844
##
## $n
##
##    1    2    3    4    5    6    7    8    9   10   11
## 5730 2526 1052  414  163   70   27    6    8    2    2
```

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Functions I

http://r4ds.had.co.nz/functions.html

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```
?"function"
```

Functions I

http://r4ds.had.co.nz/functions.html

```
?"function"
```

Syntax:

```
Functionobjectname <- function(argument1, argument2, ...)
{"DoSomething"}
```

Functions I

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`?"function"`

Syntax:

`Functionobjectname <- function(argument1, argument2, ...) {"DoSomething"}`

```
myfunct <- function(grappig)
       {plot(grappig, type="l"); return(grappig*7)  }
```

Functions I

http://r4ds.had.co.nz/functions.html

`?"function"`

Syntax:

`Functionobjectname <- function(argument1, argument2, ...) {"DoSomething"}`

```
myfunct <- function(grappig)
       {plot(grappig, type="l"); return(grappig*7)  }
```

After `return()`ing, the execution of the function is terminated, so it should only be positioned at the end. It can also be left away, the last instruction ("expression") will then be returned.

Functions II

```
myfunct(   c(5,11,3,7)  )

## [1] 35 77 21 49
```

Functions with more arguments

```
myfunct <- function(x, type="o", ...) plot(x, type=type, ...)
# type="o" is now the default, thus used unless specified
# The ellipsis (...) passes arguments to other functions
myfunct(  c(5,11,3,7) , col="red", las=1)
```

Functions: example I

If you needed to find the zeros of quadratic functions very often, you could use

```
pq <- function(p,q) # y = x^2 + px + q
               {
               w <- sqrt( p^2 / 4 - q )
               c(-p/2-w, -p/2+w)
               } # End of function

pq(3, -12)

## [1] -5.274917  2.274917
```

Functions: example II

```
x <- seq(-10, 10, len=100)
plot(x,  x^2 +3*x -12, type="l", col=2)
abline(h=0, v=0)
```

Exercise: add circles with given radius

```
plot(1:10, asp=1) # aspect ratio y/x of graph range
grid(col=1) # the next part sould go into a function:
x <- 8 ;  y <- 6 ;  r <-2
p <- seq(0, 2*pi, len=50)
cx <- x+r*cos(p) ;  cy <- y+r*sin(p)
polygon(cx, cy)
```

Time to practice programming

Exercise 24: Writing functions

Write a function that

1. - draws a circle with a certain radius at user-specified locations of an existing plot (see last slide).
2. - uses ellipsis to allow the user to customize the appearance
3. - checks all the arguments and gives useful warnings if the wrong type of input is provided
4. - has useful explanations for each argument (documentation)
5. - has readable indentation, spacing and comments explaining the code
6. Now let your neighbor use it without explaining how it is to be used (this should be inferred from the code and comments!)
7. Use your neighbor's function with a vector to draw several circles at once. (unintended use?) What happens?

```r
# Small helper function drawing circles into existing graphics
# Berry Boessenkool, berry-b@gmx.de, 2012
circle <- function(
  x, # x-coordinate of points, numeric value of length 1
  y, # ditto for y
  r, # radius of the circle, in the graphic's units
  locnum=100, # number of points on circle (more means smoother but slower)
  ...) # Further Arguments passed to polygon, like col, border, lwd
 {
 # input checking - only one circle can be drawn:
 if(length(x) >1 | length(y) >1 | length(r) >1 | length(locnum) >1)
   {
   warning("Only the first element of the vectors is used.")
   x <- x[1]; y <- y[1]; r <- r[1]; locnum <- locnum[1]
   }
 # input checking - is every value numeric?
 if(!is.numeric(x)) stop("x must be numeric")
 if(!is.numeric(y)) stop("y must be numeric")
 if(!is.numeric(r)) stop("r must be numeric")
 # prepare circle line coordinates:
 cx <- x+r*cos( seq(0,2*pi,len=locnum) )
 cy <- y+r*sin( seq(0,2*pi,len=locnum) )
 polygon(cx, cy, ...) # actually draw it
 }
# Note: if circles look like ellipsis, use plot(... asp=1)
```

Solution for exercise 24 II: functions

```
plot(1:20, type="n", asp=1, cex=2)
circle(5,5, r=3)
circle(15,10, r=4, locnum=12, col=2, border=4, lwd=3)
```

Solution for exercise 24 III: functions

```
# can not be vectorized:
x <- sample(1:20, 15) ;  y <- sample(1:20, 15) ; r <- runif(20)*4
circle(x,y,r, col=rgb(1,0.5,0,alpha=0.4), border=NA)

## Warning in circle(x, y, r, col = rgb(1, 0.5, 0, alpha = 0.4), border = NA):
Only the first element of the vectors is used.

for(i in 1:15) circle(x[i],y[i],r[i], col=rgb(1,0.5,0,alpha=0.4), border=NA)
```

Coding elegance I

Suppose you have two related vectors, perhaps as a result from `approx`:

```
a:  1   2   3   4   5 ...
b:  1 2 3 4 5 6 7 8 9 ...
```

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For any element *i* in `a`, you want to select the corresponding surrounding values of `b`.

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Coding elegance I

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```

For any element *i* in a, you want to select the corresponding surrounding values of b. Example: if i=3, you want to select the elements 4,5 and 6. However, at the border, you cannot select with negative indices.

Coding elegance I

Suppose you have two related vectors, perhaps as a result from `approx`:

```
a:  1   2   3   4   5 ...
b:  1 2 3 4 5 6 7 8 9 ...
```

For any element *i* in a, you want to select the corresponding surrounding values of b. Example: if i=3, you want to select the elements 4,5 and 6. However, at the border, you cannot select with negative indices.

Exercise 25: Elegant Coding: surrounding indices

1. Write a function using conditionals that performs the task described above.
2. BONUS: If it's not a "one-liner", try to find a different approach.

Coding elegance II

Here is how to write this with conditional statements:

Coding elegance II

Here is how to write this with conditional statements:

```
index_1 <- function(i)
{
if(i == 1)                          1 : 2
else if(i == length(a))  ((i-1)*2) : (i*2-1)
else                     ((i-1)*2) : (i*2)
}
```

Coding elegance II

Here is how to write this with conditional statements:

```
index_1 <- function(i)
{
if(i == 1)                          1 : 2
else if(i == length(a))  ((i-1)*2) : (i*2-1)
else                     ((i-1)*2) : (i*2)
}
```

Here's the elegant way:

```
index_2 <- function(i)
  pmax((i-1)*2, 1) : pmin(i*2, length(a)*2-1)
```

Coding elegance III

Both functions yield the same result:

```
a <- 1:5
index_1(1); index_2(1)

## [1] 1 2
## [1] 1 2

index_1(3); index_2(3)

## [1] 4 5 6
## [1] 4 5 6

index_1(5); index_2(5)

## [1] 8 9
## [1] 8 9
```

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Why you should write R packages

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- Collect your own functions in one place

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- Combine functions and documentation in the right way

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Good introductions linked here: github.com/brry/misc

Package development: devtools + github

We'll create a cat package together following the instructions in packdev.R.

Version control with git:

- Once only: Create a github account (free), set up git on your computer, connect it to Rstudio. This is all very unfun and tedious, but at least there is a good guide that also includes a first test of the system: r-bloggers.com/rstudio-and-github. See also kbroman.org/github_tutorial for a good intro.
- github.com, log in, on "+" in top-right select "New repository", initialize with readme!
- On the green field "clone or download": copy link
- Rstudio - file - new project - version control - git: paste url and create
- `devtools::setup()` instead of `create`, choose option number to Overwrite 'yourPackage.Rproj'
- Work. Commit. Push. Repeat.

Package exercise

Exercise 26: create LSC package (solutions on next 2 slides)

1. Create a package for linear storage cascade functions (lsc)
2. BONUS: Use git from the beginning, commit often!
3. Check the package, correct description file and check again
4. Now add the functions in lsc_functions.zip to the R folder
5. Done? Help your peers.
6. Document the nse function (we'll do this one together)
7. Create datasets within the package (following instructions in data.R)
8. Document the rmse function
9. Check and install the package

Solution for exercise 26: create LSC package

```r
library(devtools)
create("lsc") # or devtools::setup() if using git
document() # calls roxygen2::roxygenise()
check() # will also update documentation
install() # install the package locally
load_all(".") # CTRL + SHIFT + L    - faster than install!
```

Solution for exercise 26: Documenting functions

```
#' @title       Nash-Sutcliffe efficiency
#' @description Nash-Sutcliffe efficiency as a measure of goodness of fit.
#'              Removes incomplete observations with a warning.
#' @return      Single numerical value
#' @export
#' @seealso     \code{\link{rmse}}
#' @references  based on eval.NSeff in RHydro Package
#'              \url{https://r-forge.r-project.org/R/?group_id=411}
#' @examples
#' x <- rnorm(20) ; y <- 2*x + rnorm(20)
#' x[2:4] <- NA
#' nse(x,y)
#'
#' @param obs Numerical vector with observed values
#' @param sim Simulated values (Num vector with same length as \code{obs})
#'
nse <- function(obs, sim)
{
if(!(is.vector(obs) & is.vector(sim))) stop("Input is not a vector.")
if(length(obs) != length(sim)) stop("Vectors are not of equal length.")
#[...]
1 - ( sum((obs - sim)^2) / sum((obs - mean(obs))^2) )
}
```

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Debugging

- Your code throws an error. You didn't call the mentioned function. Obviously, your code calls some function calling some function calling some function calling [you get the idea] which in the end creates an error. To trace back this path, you can use `traceback()`.

Debugging

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- Now that you know where the error originates from, you set `options(error=recover)`. You run your code again, but this time R waits at the level creating an error. You examine the environment within the function, play around with the objects and internal function code, until the bug has been fixed. You have just debugged a function.

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- You want to step into the function you are developing at a specific point. You add `browser()` at that point of the code. You want to go line by line in one specific function. You set `debug(thatFunction)`.
- You want to learn about lexical scoping (Where does R find variables?). http://trestletech.com/2013/04/package-wide-variablescache-in-r-package/ http://adv-r.had.co.nz/Environments.html

Debugging: useful functions

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source("projectFuns.R") execute complete file

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source("projectFuns.R")	execute complete file
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Debugging: useful functions

source("projectFuns.R")	execute complete file
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options(warn=2)	warnings to error. default 0
browser()	go into function environment: `n`, `s`, `f`, `c`, `Q`
options(error=recover)	open interactive session where error occurred

Debugging: useful functions

source("projectFuns.R")	execute complete file
traceback()	find error source in sequence of function calls
options(warn=2)	warnings to error. default 0
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debug(funct)	toggle linewise function execution

Debugging: useful functions

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Debugging: useful functions

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```
if(length(input)>1) stop("length must be 1, not ", length(input))
```

Debugging: useful functions

source("projectFuns.R")	execute complete file
traceback()	find error source in sequence of function calls
options(warn=2)	warnings to error. default 0
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```
if(length(input)>1) stop("length must be 1, not ", length(input))
```

`stop`: Interrupts function execution and gives error
`warning`: continues but gives warning
`message`: to inform instead of worry the user

Debugging: useful functions

source("projectFuns.R")	execute complete file
traceback()	find error source in sequence of function calls
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```
if(length(input)>1) stop("length must be 1, not ", length(input))
```

`stop`: Interrupts function execution and gives error
`warning`: continues but gives warning
`message`: to inform instead of worry the user

R. Peng (2002): Interactive Debugging Tools in R
D. Murdoch (2010): Debugging in R
H. Wickham (2015): Advanced R: debugging
Example: Pete Werner Blog Post (2013)

Practice debugging

Exercise 27: Debugging

1. Load your package and the datasets. Correct the functions until `lsc(calib$P, calib$Q, area=1.6)` returns the result below.
2. BONUS: commit each change to git.

Solution for exercise 27: Debugging

- `stupid error you can easily remove` - traceback - find location of error - lsc#75 - just comment it out
- `harder to find but still stupid` - traceback - nse#22 - ditto
- `Error in plot:  need finite 'ylim' value` - debug/browser/options(error=recover) - lsc#107 - NAs in Q - range(Q, na.rm=TRUE) - also in other applicable locations
- `There were 50 or more warnings` - come from rmse being called in optimization - add argument quietNA (or similar) to lsc that is passed to rmse in lsc#81

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Chapter practice: sample size dependency

Exercise 28: Programming part 1 - functions

1. Write a function (#1) that computes the backtransformed arithmetic average of logtransformed values. It should `stop` with a useful error message if there are `any` negative values in the input vector.
2. Write a second function (#2) taking a vector of values that returns the mean, sd, coefficient of variation and the output of function #1.
3. It should return these values with names as in `c(a=5,b=-3)`.
4. If the average is zero, it should inform the user that the CV cannot be computed. Remember to check only rounded values for equality.
5. Test both functions with `c(88,31,73,21,08,52,66,48)`, with `c(4,7,5,6,4,5,3,NA,6,4,5,6,8,5)` and with `c(0,0,0)`.
6. Write a function (#3) taking **`n`**, **`mean`** and **`sd`** that
   - breaks if **`n`** is not a single value
   - draws **`n`** random numbers from the normal distribution with **`mean`** and **`sd`**
   - returns the output of function #2 of that sample.

Programming practice solutions part 1 - functions 1

backtransformed arithmetic average of logtransformed values

```
logmean <- function(x)
  {
  if(any(x<0)) stop("x has ", sum(x<0), " negative values.")
  lx <- log10(x)
  10^mean(lx)
  }

logmean(c(88,31,73,21,08,52,66,48))

## [1] 39.14336

#logmean(c(4,7,5,6,4,5,3,NA,6,4,5,6,8,5))
logmean(c(0,0,0))

## [1] 0
```

Programming practice solutions part 1 - functions 2

Statistical properties of a vector

```
meanvar <- function(vals)
  {
  m <- mean(vals) # average
  s <- sd(vals) # root of variation
  if(round(m)==0) stop("mean is 0, CV cannot be computed")
  c(mean=m, sd=s, CV=s/m, logmean=logmean(vals))
  }

meanvar(c(88,31,73,21,08,52,66,48))

##       mean          sd          CV    logmean
## 48.3750000 27.2078639  0.5624365 39.1433623

#meanvar(c(4,7,5,6,4,5,3,NA,6,4,5,6,8,5))
#meanvar(c(0,0,0))
```

Programming practice solutions part 1 - functions 3

Dependency on sample size

```
dep_n <- function(n, mean, sd)
  {
  if(length(n)!=1) stop("n must be a single value, not ",
                        length(n))
  # draw n numbers randomly from normal distribution:
  v <- rnorm(n, mean=mean, sd)
  meanvar(v)
  }

dep_n(20, 70,5)

##        mean          sd          CV     logmean
## 70.95960010  6.56314211  0.09249125 70.65816749

#
```

Chapter practice: sample size dependency

Exercise 29: Programming part 2 - debugging

1. Test function #3 with `n=20:30, mean=70,sd=5`
2. What happens if you use it with `n=NA, mean=70,sd=5`?
3. After you call it with `n=20, mean=-70,sd=5`, run `traceback()` Explain the result.
4. What is the result of `ls.str()`?
5. Set you upper level function #3 to `debug`ging mode. Now call it again. What happens? What is now the result of `ls.str()`?

- With enter, you can now execute the function line by line and observe how objects (variables) in functions change over execution time, thus making it easier to find the source of an error.
- Don't forget to `undebug` your function again.
- If you only want to step into the function at a certain point, write `browser()` at that position, redefine the function and call it again.

Programming practice solutions part 2 - debugging

```r
dep_n(20, -70,5)

## Error in logmean(vals):  x has 20 negative values.
```

```r
traceback()
```

```
4:  stop("x has ", sum(x < 0), " negative values.") at #3
3:  logmean(vals) at #6
2:  meanvar(v) at #5
1:  dep_n(20, -70, 5)
```

In debugging mode, you step into the function when it is called (visible by `Browse[2]>` in the console). `ls.str()` now returns the structures of the objects defined within the function environment.

Chapter practice: sample size dependency

Exercise 30: Programming part 3 - loops for computation

For this task, use `n <- rep(1:50, each=100)`

1. Create an empty `data.frame` with the column names according to the output of function #3.
2. With a for loop, fill each row with the result of the n-corresponding call to function #3.
3. Obtain the computing time by either wrapping it in `system.time` or calling `Sys.time()` before and afterwards and computing the `difftime`.
4. Time the usage of `sapply` for the same task. How many times is it faster? What does that imply for a 5-hour for loop computation?
5. BONUS: Get uncertainties on the computing time estimation with `microbenchmark` (You might want to reduce the length of n for that).

Programming practice solutions part 3 - loops computation

```
n <- rep(1:50, each=100)
results_for <- data.frame(mean=NA, sd=NA, CV=NA, logmean=NA)
system.time( for(i in 1:length(n))
  {results_for[i, ] <- dep_n(n[i], 70,5)})

##    user  system elapsed
##    2.31    0.01    2.32

tail(results_for, 5)

##          mean       sd         CV  logmean
## 4996 70.07647 4.851932 0.06923768 69.90943
## 4997 70.30274 4.788358 0.06811055 70.14381
## 4998 69.69953 5.420097 0.07776375 69.49969
## 4999 69.35405 4.780247 0.06892527 69.19216
## 5000 68.47572 4.488871 0.06555420 68.32956
```

Programming practice solutions part 3 - loops computation

```
system.time(res_lapply <- sapply(n, dep_n, mean=70,sd=5)  )

##    user  system elapsed
##    0.20    0.01    0.22
```

In this case with (only) 5000 iterations, lapply is ca 7 times faster than the badly initiated for loop. 5 hrs of computation would reduce to 40 minutes. Notice you get similar to lapply speed results for properly initiated data.frames with the correct dimension.
For more speed hints, read win-vector.com efficient accumulation in R.
Remember: your code is much cleaner with lapply:

```
results <- matrix(NA, ncol=4, nrow=length(n2))
for(i in 1:length(n2)) results[i, ] <- dep_n(n2[i], 70,5)

results <- sapply(n2, dep_n, mean=70,sd=5)
```

Programming practice solutions part 3 - loops computation

```
n2 <- rep(1:50, each=10)

dep_n_for <- function()
 {results <- data.frame(mean=NA, sd=NA, CV=NA, logmean=NA)
  for(i in 1:length(n2)) results[i, ] <- dep_n(n2[i], 70,5)}

dep_n_for_good <- function()
 {results <- matrix(NA, ncol=4, nrow=length(n2))
  for(i in 1:length(n2)) results[i, ] <- dep_n(n2[i], 70,5)}

dep_n_sapply <- function()
{results <- sapply(n2, dep_n, mean=70,sd=5)}

mb <- microbenchmark(dep_n_for(), dep_n_for_good(),
                     dep_n_sapply())
save(mb, file="data/mb.Rdata")
```

Programming practice solutions part 3 - loops computation

```
load("data/mb.Rdata"); library(microbenchmark)
boxplot(mb, yaxt="n"); berryFunctions::logAxis(2)
```

Chapter practice: sample size dependency

Exercise 31: Programming part 4 - loops for plotting

1. Plot the mean estimate over sample size, using fully colored but semitransparent dots (see `rgb` or `berryFunctions::addAlpha`).
2. Add a nicely visible horizontal line at the population mean. (we drew random samples from some defined distribution, which is the general population whose parameters are usually unknown in real life).
3. BONUS: add lines limiting the 90% confidence region.
4. Set up a multipanel plot to automatically hold a figure for each of the rows of the previous results (mean, sd, CV, logmean). To automatically dimension the panels, you could use `berryFunctions::panelDim(n)`
5. With a for loop, fill each of the panels and add nice annotations.

Programming practice solutions part 4 - loops plotting

```
transp <- rgb(0,0,0, alpha=0.1)
plot(n, res_lapply["mean", ], pch=16, col=transp, cex=0.6)
abline(h=70, col=4, lwd=2)
```

Programming practice solutions part 4 - loops plotting

```
conf <- tapply(res_lapply["mean", ], n, quantile, probs=c(0.05, 0.95))
conf <- sapply(conf, I)
conf_x <- as.numeric(colnames(conf))
for(i in 1:2) lines(conf_x, conf[i, ], col=2, lwd=2)
```

Programming practice solutions part 4 - loops plotting

```
library(berryFunctions) # for panelDim

par(mfrow=panelDim(nrow(res_lapply)), mar=c(2,4,1,1),
    mgp=c(2.5,0.7,0), las=1 )

truevals <- c(mean=70, sd=5, CV=5/70, logmean=70)
for(nm in rownames(res_lapply))
  {
  plot(n, res_lapply[nm, ], ylab=nm, pch=16, col=transp)
  abline(h=truevals[nm], col=4, lwd=2)
  if(nm=="sd") points(60,2, col=2)
  }
```

Programming practice solutions part 4 - loops plotting

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A quick example I

```
grades <- c(3.0, 2.3, 5, 1.3, 4, 1.7)
grades          # Show the object

## [1] 3.0 2.3 5.0 1.3 4.0 1.7

mode(grades)    # numeric

## [1] "numeric"

sum(grades)     # sum of all values

## [1] 17.3

diff(grades)    # difference from one value to the next

## [1] -0.7  2.7 -3.7  2.7 -2.3
```

```r
mean(grades)   # Average

## [1] 2.883333

median(grades) # median*

## [1] 2.65

var(grades)    # variance

## [1] 1.997667

sd(grades)     # Standard deviation

## [1] 1.413388
```

* If you sort all the numbers ascendingly, the median is in the middle. Thus, it is not as sensitive to outliers as the mean. We'll get back to this later on.

The dataset we'll be looking at

sources: mirlab.org, desirableplants.com, 3.bp.blogspot.com

iris data set

```r
head(iris)

##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

Exercise 32: EDA - Exploratory Data Analysis

1. Look at `iris` with `summary`.
2. Assign `iris$Sepal.Length` to an object with a short name.
3. Calculate `min` and `max`, the `median` and the median absolute deviation (`mad`), the quartiles and octiles (via `quantile`), the fourthspread (`IQR`) and `diff(range)` of the iris values.
4. With `par(mfrow=c(2,1))`, set the graphic device to contain two graphics.
5. Draw a horizontal `boxplot` in the upper window and compare it with the statistics calculated above. Interpret them.
6. What happens when the argument `notch` is set to true?
7. Draw a `hist`ogram with the bars filled with orange color, and experiment with the number of breaks.
8. BONUS: What are the (dis-)advantages of boxplots and histograms?

Mean vs. Median etc.

mathwithbaddrawings.com/2016/07/13/why-not-to-trust-statistics

Mean vs. Median etc.

mathwithbaddrawings.com/2016/07/13/why-not-to-trust-statistics

Similar boxplots...

... different distributions!

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Random numbers

R has a very good random number generator. If you want to set a starting point for it, you can use `set.seed(n)`, with n being some number you like. After R has set the seed, it will always generate the same "random" numbers. This creates reproducible numbers.

Exercise 33: Random numbers

1. With `sample`, put the numbers 5 to 15 in random order. Out of the possible numbers 1:3, draw 25 realizations.
2. Via `?Distributions`, find out how to generate 200 random numbers from the exponential distribution and look at those with a boxplot and a histogram (BONUS: look at `ecdf` and `density`).

Solution for exercise 33: random numbers

```
sample(5:15)  ;  sample(1:3, 25, replace=TRUE)  ;  r <- rexp(200)
par(mfrow=c(2,1), mar=c(2,2,0,0))
hist(r, breaks=20, col=3)
boxplot(r, horizontal=T, notch=T, col=3)
lines(density(r)$x, density(r)$y +par("usr")[3], lwd=3)
lines(0:50/10, dexp(0:50/10) +par("usr")[3], col=2)
```

Distributions: normal distribution I

Distributions: normal distribution II

Distributions: normal distribution II

`pnorm(q=1, mean=0, sd=1)` = 84% of the values of a standard normal distribution (SND) with $\mu = 0$ and $\sigma = 1$ are smaller than 1.

Get familiar with the Gaussian distribution

Exercise 34: normal distribution

In 1981, Fries and Crapo estimated future life expectancy to be 85 years with a standard deviation of 4.5 years.

Fries, J., Crapo, L.: Vitality and Aging: Implications of the Rectangular Curve. Freeman & Co Publishers, San Francisco (1981)

1. Plot the distribution density curve
2. Plot it again using `normPlot` in the package `berryFunctions`.
3. What proportion of people would die before age 75?
   Is that a realistic likelihood?
4. How many Germans (pop ~80 mio) would exceed 90 years?
5. In which symmetric age range would 95% of the people die?
   Give the rough estimate and the exact number.
6. How likely is it to die at age 85.3?
7. What are the biggest problems with this task?

Solution for exercise 34: Normal distribution I

Examples taken from: Wolfgang Tschirk (2014): Statistik: Klassisch oder Bayes - Zwei Wege im Vergleich

```
plot(70:100, dnorm(70:100, 85, 4.5), type="l")
berryFunctions::normPlot(85, 4.5)
pnorm(75, 85, 4.5)*100 #  1.3%
(1-pnorm(90, 85, 4.5))*80e6   # 10.7 mio
85-4.5*2; 85+4.5*2 # 76, 94
qnorm(c(0.025, 0.975), 85, 4.5) # 76.2 - 93.8
```

The probability to die at age 85.3 is 0 percent, as there are infinite possibilities in a continuous distribution. (You could also die at 85.331761 years). That's why we look at probability "density" in intervals.
But: we don't know if life expectancy is normally distributed. We also don't know whether it is parametrized correctly.

Solution for exercise 34: Normal distribution II

```
## [1] 1.313415
## [1] 10660821
## [1] 76.18016 93.81984
```

Test for normality of a distribution

```
data <- rnorm(1000, mean=97, sd=8.9)
shapiro.test(data)
ks.test(data, "pnorm", mean(data), sd(data))
# if p > 0.05: accept Nullhypothesis
# (that data are normally distributed.)
```

More on slide 338 et sequentes.

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Get familiar with the discrete Binomial distribution

Exercise 35: binomial distribution

149'291 of 279'371 students in Austria are female. Statistik Austria: Studierende in OEsterreich im Wintersemester 2009/10. Statistik Austria, Wien (2010). This is a population for which we know the actual proportion, which happens rarely in inferential statistics. 100 students are randomly chosen.

1. Guess how likely it is that the majority (at least half) of those are female.
2. Plot the probability for each reasonable possible outcome using `dbinom`. (This is the actual probability, not probability density, for each discrete number of females in a group of 100 randomly chosen students). Now guess again.
3. Actually calculate the probability.
4. At which proportion of females would you accuse the experimenter of selection bias (or cheating)?

Solution for exercise 35: Binomial distribution

```
plot(30:70, dbinom(x=30:70, size=100, prob=149291/279371))
abline(v=c(49.5, 53.438), h=0.025)
1-pbinom(q=49.5, size=100, prob=149291/279371)

## [1] 0.7852772
```

If the probability of the result happening by chance is under 5%, in this case ≤ 45 or ≥ 61 females (two-sided confidence interval).

Other distributions: density

Other distributions: cumulated

Overview of distributions in R

prefix	meaning	usage
d	**d**ensity	calculate probability (density) for value x
p	cumulated **p**robability	area under density curve up until value x
q	**q**uantile	reciprocal to p: calculate value x for a given cumulated probability
r	**r**andom	draw random numbers from distribution

Overview of distributions in R

prefix	meaning	usage
d	**d**ensity	calculate probability (density) for value x
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q	**q**uantile	reciprocal to p: calculate value x for a given cumulated probability
r	**r**andom	draw random numbers from distribution

distribution	parameters	type
binom	size, prob	discrete
pois	lambda	
norm	mean, sd	continuous
exp	rate	
beta	shape1, shape2	

Exercise 36: classical statistical analysis

1. Calculate `mean`, `var`, `sd` and standard error of the mean (SEM $= \frac{\sigma}{\sqrt{n}}$) of the `iris` sepal length data and interpret these values.
2. Visualize the theoretical distribution of the dataset. Use a sequence of values and calculate `pnorm` and `dnorm` on it with mean and sd according to the previous task.
3. Compare this with the actual distribution of the sample. First draw a histogram with `freq=FALSE`, then add the theoretical distribution with `lines`.
4. If this distribution were from the general and complete "population" of iris sepal lengths, we could say: 20% of the sepal lengths are smaller than a certain value. Use `qnorm` to find out this value. What is the limit of this approach?
5. BONUS: What are the (dis-)advantages of mean and median?

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Beta distribution: motivating example

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Imagine you are the scientific advisor to the government of India.

Beta distribution: motivating example

Imagine you are the scientific advisor to the government of India.
It has recently been found that some of the millions (yes, millions) of wells contain dangerous levels of arsenic.

Beta distribution: motivating example

Imagine you are the scientific advisor to the government of India.
It has recently been found that some of the millions (yes, millions) of wells contain dangerous levels of arsenic.
If more than 25% of the wells are affected, the government will pass a law constraining well construction.

Beta distribution: motivating example

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It has recently been found that some of the millions (yes, millions) of wells contain dangerous levels of arsenic.
If more than 25% of the wells are affected, the government will pass a law constraining well construction.
You sample 10 wells and find that 2 surpass the safety limit of arsenic concentration.

Beta distribution: motivating example

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To graph the uncertainty, you want to use the beta distribution.

Beta distribution: motivating example

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You remember (from this class) that for a binomial trial, the two parameters can be defined as:

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$\alpha - 1 =$ number of successes

Beta distribution: motivating example

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It has recently been found that some of the millions (yes, millions) of wells contain dangerous levels of arsenic.
If more than 25% of the wells are affected, the government will pass a law constraining well construction.
You sample 10 wells and find that 2 surpass the safety limit of arsenic concentration. What will you do?
To graph the uncertainty, you want to use the beta distribution.
You remember (from this class) that for a binomial trial, the two parameters can be defined as:
$\alpha - 1 =$ number of successes
$\beta - 1 =$ number of failures

Beta distribution: motivating example

Imagine you are the scientific advisor to the government of India.
It has recently been found that some of the millions (yes, millions) of wells contain dangerous levels of arsenic.
If more than 25% of the wells are affected, the government will pass a law constraining well construction.
You sample 10 wells and find that 2 surpass the safety limit of arsenic concentration. What will you do?
To graph the uncertainty, you want to use the beta distribution.
You remember (from this class) that for a binomial trial, the two parameters can be defined as:
$\alpha - 1 =$ number of successes
$\beta - 1 =$ number of failures
What are the parameters in this case?

Beta distribution: motivating example

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$$\beta =$$

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What are the parameters in this case?

$$\alpha = 2 + 1 = 3$$
$$\beta = 10 - 2 + 1 = 9$$

Beta distribution: some theory + density plot

Beta distribution: some theory + density plot

- Continuous, values between 0 and 1

Beta distribution: some theory + density plot

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- Suitable for proportions and probabilities

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- Two parameters: a=alpha=`shape1` and b=beta=`shape2`.

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Exercise 37: Beta distribution density

1. Plot the beta distribution density (`dbeta`) for alpa=3 and beta=9.
2. If this describes the true distribution of contaminated well proportions across subregions of India, how likely is it to have a sample with 25% or more of the wells contaminated?
3. BONUS: Plot the distribution with `polygon`.

Two hints:

Beta distribution: some theory + density plot

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Two hints:

Hint 1: Create a vector from 0 to 1 with, say, 200 values.

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Two hints:

Hint 1: Create a vector from 0 to 1 with, say, 200 values.

Hint 2: Plot `dbeta(x)` over x using `type="l"`.

Solution to exercise 37: Beta density

```
proportion <- seq(0,1, len=200)
plot(proportion, dbeta(proportion, 3,9), type="l")
segments(x0=0.25, y0=-1, y1=3.097, col=2)
```

Solution to exercise 37: Beta density

```
proportion <- seq(0,1, len=200)
plot(proportion, dbeta(proportion, 3,9), type="l")
segments(x0=0.25, y0=-1, y1=3.097, col=2)
```

```
1-pbeta(0.25, 3,9)

## [1] 0.4552009
```

Beta parameters

Beta parameters

Large α: HDI (Highest Density Interval) more to the *left/right*?

Beta parameters

Large α: HDI (Highest Density Interval) more to the right

Beta parameters

Large α: HDI (Highest Density Interval) more to the right
Large β: HDI rather left, lower values

Beta parameters

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Large β: HDI rather left, lower values
Both large:

Beta parameters

Large α: HDI (Highest Density Interval) more to the right
Large β: HDI rather left, lower values
Both large: (*more samples*)

Beta parameters

Large α: HDI (Highest Density Interval) more to the right
Large β: HDI rather left, lower values
Both large: (*more samples*) narrow HDI

Beta parameters

Large α: HDI (Highest Density Interval) more to the right
Large β: HDI rather left, lower values
Both large: (*more samples*) narrow HDI

```
install.packages("berryFunctions")
```

Beta parameters

Large α: HDI (Highest Density Interval) more to the right
Large β: HDI rather left, lower values
Both large: (*more samples*) narrow HDI

```
install.packages("berryFunctions")
```

```
library(berryFunctions) # >= version 1.9.6 (2015-12-18)
betaPlot(shape1=alpha, shape2=beta, ...)
betaPlotComp()
```

Beta parameters

```
betaPlot(14, 2.4, ylim=lim0(5))
```

Beta parameters

```
betaPlot(6, 16, ylim=lim0(5))
```

Beta parameters

```
betaPlot(10, 10, ylim=lim0(5))
```

Beta parameters

```
betaPlot(3, 3, ylim=lim0(5))
```

Beta parameters

```
betaPlot(1, 1, ylim=lim0(5))
```

Beta parameters

```
betaPlot(0.8, 2, ylim=lim0(5))
```

Beta parameters

```
betaPlot(0.4, 0.4, ylim=lim0(5))
```

a = 0.5
a = 1
a = 2
a = 3
a = 4
a = 10
b = 0.5
b = 1
b = 2
b = 3
b = 4
b = 10
a=0.5, b=0.5
a=1, b=0.5
a=2, b=0.5
a=3, b=0.5
a=4, b=0.5
a=10, b=0.5
a=0.5, b=1
a=1, b=1
a=2, b=1
a=3, b=1
a=4, b=1
a=10, b=1
a=0.5, b=2
a=1, b=2
a=2, b=2
a=3, b=2
a=4, b=2
a=10, b=2
a=0.5, b=3
a=1, b=3
a=2, b=3
a=3, b=3
a=4, b=3
a=10, b=3
a=0.5, b=4
a=1, b=4
a=2, b=4
a=3, b=4
a=4, b=4
a=10, b=4
a=0.5, b=10
a=1, b=10
a=2, b=10
a=3, b=10
a=4, b=10
a=10, b=10
0
1
2
3
4
0.0
0.5
1.0

Beta distribution properties

Beta distribution properties

$$mean = \mu = \frac{a}{a+b}$$

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With these formulas, if a and b $\gg 1$, you can estimate an approximation to the normal distribution.

Beta distribution properties

$$mean = \mu = \frac{a}{a+b} \qquad variance = \sigma^2 = \frac{ab}{(a+b)^2 * (a+b+1)}$$

With these formulas, if a and b $\gg 1$, you can estimate an approximation to the normal distribution.

$$mode = density\ peak = m = \frac{a-1}{a+b-2} \qquad for\ a, b > 1$$

Beta distribution properties

$$mean = \mu = \frac{a}{a+b} \qquad variance = \sigma^2 = \frac{ab}{(a+b)^2 * (a+b+1)}$$

With these formulas, if a and b $\gg 1$, you can estimate an approximation to the normal distribution.

$$mode = density\ peak = m = \frac{a-1}{a+b-2} \qquad for\ a, b > 1$$

If you want to set the mode at a certain value, you can compute beta with

$$b = \frac{a-1}{m} - a + 2 \qquad \text{and alpha with} \qquad a = \frac{(2-b-1/m)*m}{m-1}$$

Beta distribution specification

Exercise 38: Beta distribution parameter determination

You want to specify a distribution with the peak at 90%, reached in a sample of 100.

1. What are the parameters?
2. What does the distribution look like? (Graph it)
3. BONUS: How does the HDI (highest density interval) width change for a sample size of 10?

Beta distribution parametrization solution

```
v <- seq(0,1, len=200)
plot(v, dbeta(v, 91,11), type="l", las=1)
lines(v, dbeta(v, 10,2), col=2)
points(qbeta(c(0.1, 0.9), 91,11), rep(-0.5,2), pch=3)
points(qbeta(c(0.1, 0.9), 10,2), rep(-0.5,2), pch=3, col=2)
```

Bayesian inference with beta distribution

Prior: weak knowledge that true proportion of cats among pets must be around 10 to 30%, but may also be more.

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Data: observation in survey: 35 of 100 households with a pet have a cat.

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Posterior beta parameters: a_prior + successes, b_prior + failures

Bayesian inference with beta distribution

Prior: weak knowledge that true proportion of cats among pets must be around 10 to 30%, but may also be more.
Data: observation in survey: 35 of 100 households with a pet have a cat.
Posterior beta parameters: a_prior + successes, b_prior + failures

```
betaPlot(3, 9, ylim=lim0(10), cum=F, mar=c(2,2,0,0), keeppar=T)
lines(x, dbeta(x, 3+35, 9+65), lwd=2, col=3)
```

Shift + scale values

If values do not lie between 0 and 1, but between m and n, you can transform the raw values (y) to the 0:1 space (y') with

$$y' = \frac{(y-m)}{(n-m)}$$

and beta values (y') to raw values (y) with

$$y = y' * (n - m) + m$$

Outlook: used for beta regression, see Liu and Kong (2015): zoib: An R Package for Bayesian Inference for Beta Regression and Zero/One Inflated Beta Regression. In: the R Journal Vol. 7/2, December 2015

Shift + scale values

```
x <- 400:580; m <- 120 ; n <- 570
plot(x, dbeta((x-m)/(n-m),30,4), type="l")
lines(x, dnorm((x-m)/(n-m),30/34, sd=sqrt(120/(34^2*35))), col=2)
```

Shift + scale values

```
m <- 120 ; n <- 570; set.seed(1)
x <- rbeta(800,30,4) * (n-m)+m
library(extremeStat) # github.com/brry/extremeStat
plotLfit(distLfit(x, quiet=T), breaks=30, nbest=11, legargs=c(x="left"))
```

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Simpson's Paradox

- Kievit et al (2015): Simpson's paradox in psychological science: a practical guide (Frontiers in Psychology)
- vudlab app
- Wikipedia entry
- 2016 example: development of crime rates in the USA

Simpson's Paradox: Kidney stone treatment success rate

	open surgery	small puncture
small stones large stones		
together	$\frac{273}{350} = 78\%$	$\frac{289}{350} = \mathbf{83\%}$

Wikipedia, Julious + Mullee (1994)

Simpson's Paradox: Kidney stone treatment success rate

	open surgery	small puncture
small stones	$\frac{81}{87} = \mathbf{93\%}$	$\frac{234}{270} = 87\%$
large stones		
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	open surgery	small puncture
small stones	$\frac{81}{87} = \mathbf{93\%}$	$\frac{234}{270} = 87\%$
large stones	$\frac{192}{263} = \mathbf{73\%}$	$\frac{55}{80} = 69\%$
together	$\frac{273}{350} = 78\%$	$\frac{289}{350} = \mathbf{83\%}$

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Simpson's Paradox: Kidney stone treatment success rate

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In less severe cases (small kidney stones), doctors favor percutaneous nephrolithotomy (which involves only a small puncture). Doctors tend to give the severe cases (large stones) the better treatment (open surgery). The success rate is more strongly influenced by the severity of the case than by the choice of treatment. When the less effective treatment (small puncture) is applied more frequently to less severe cases, it can appear to be a more effective treatment.

Simpson's Exercise

Exercise 39: Simpson

Visualize farming.txt, a fictional dataset measuring crop yield on 30 study fields after pesticide application.

Farming solution I

Farming solution II

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- Whether a dataset is normally distributed can be checked with a histogram (visually effective, but the class limits are subjective), with qqplots (I don't find them very intuitive), or with statistical tests.

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- This is an important assumption for many classical statistical methods.
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-

```
data <- rnorm(1000, mean=97, sd=8.9)
shapiro.test(data)
ks.test(data, "pnorm", mean(data), sd(data))
# if p > 0.05: accept Nullhypothesis that data are normally distributed.

if(!requireNamespace("nortest")) install.packages("nortest")
library(nortest)          # with Lilliefors-correction!
help(package="nortest")
lillie.test(data)  # Lilliefors (Kolmogorov-Smirnov) test for normality
ad.test(data)      # Anderson-Darling test for normality
cvm.test(data)     # Cramer-von Mises test for normality
pearson.test(data) # Pearson chi-square test for normality
sf.test(data)      # Shapiro-Francia test for normality
```

Normality Test: Kolmogorov-Smirnov

KS Hypothesis Test: Reject the null hypothesis (H0) that the values are drawn from a normal distribution if $D < \frac{k_\alpha}{\sqrt{n}}$.

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$D = max(\mid F_{(n)}(x) - F(x) \mid)$ *Difference between empirical and statistical (theoretical, population) Cumulated Density Function (CDF)*

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$D = max(\mid F_{(n)}(x) - F(x) \mid)$ *Difference between empirical and statistical (theoretical, population) Cumulated Density Function (CDF)*

$k_\alpha = \frac{\sqrt{-0.5 * ln(\frac{\alpha}{2})}}{\sqrt{n}}$ $(for\ n > 35)$ α often 0.05 (95% confidence)

Normality Test: Kolmogorov-Smirnov

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Background confidence intervals

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- About 70% of the values in a Gaussian distribution lie between mean-1sd and mean+1sd, as is shown by `pnorm(1) - pnorm(-1)`: `0.6826895`.

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- 95% of the values are between mean $\pm$ 1.96 sd, as is shown by `qnorm(0.975)`: `1.959964`. (As the bell curve is symmetrical, we want to know below what value 97.5% of the values are in the cumulated density).

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- This is the famous parameter in calculating the limits of confidence intervals (CI).

$$CI = \mu \pm p * \frac{sd}{\sqrt{n}}$$

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- This is the famous parameter in calculating the limits of confidence intervals (CI).

$$CI = \mu \pm p * \frac{sd}{\sqrt{n}}$$

$$p = \texttt{qt(1-alpha/2, df=n-1)}$$

Parameter confidence intervals

en.wikipedia.org/wiki/Student's_t-distribution#Table_of_selected_values
For a two-sided confidence interval with `qt(1-alpha/2, df=n-1)`:

	a=0.01	a=0.05	a=0.10
n=10	3.2498	2.2622	1.8331
n=30	2.7564	2.0452	1.6991
n=50	2.6800	2.0096	1.6766
n=100	2.6264	1.9842	1.6604
n=1000	2.5808	1.9623	1.6464

Parameter confidence intervals

en.wikipedia.org/wiki/Student's_t-distribution#Table_of_selected_values
For a two-sided confidence interval with `qt(1-alpha/2, df=n-1)`:

	a=0.01	a=0.05	a=0.10
n=10	3.2498	2.2622	1.8331
n=30	2.7564	2.0452	1.6991
n=50	2.6800	2.0096	1.6766
n=100	2.6264	1.9842	1.6604
n=1000	2.5808	1.9623	1.6464

code for generating this table:

```
alpha <- c(0.01, 0.05, 0.10)
n <- c(10, 30, 50, 100, 1000)
ttab <- t(sapply(n, function(x) qt(1-alpha/2 ,df=x-1)))
colnames(ttab) <- paste0("a=",alpha)
rownames(ttab) <- paste0("n=",n)
ttab
```

CI example

Exercise 40: Confidence intervals

1. Comment the code below.
2. plot the points along a number line and add the mean value with `points` and the confidence interval with `arrows` with `angle=90, code=3`. BONUS: plot the points as filled dots in a semitransparent color, see `rgb`.

```
values <- rnorm(80, 53, 4)
m <- mean(values)   ; m #
v <- var(values)    ; v #
n <- length(values) ; n #
p <- qnorm(0.975)   ; p #
p <- qt(0.975, df=n-1)  ; p #
cl <- m - p * sqrt(v/n) ; cl #
cu <- m + p * sqrt(v/n) ; cu #
```

CI in a faster way

Scripting this manually would take too long:

```
m <- mean(values)
v <- var(values)
n <- length(values)
p <- qt(0.975, df=n-1)

m + c(-1,1)* p * sqrt(v/n)

## [1] 52.34151 54.00713
```

CI in a faster way

Scripting this manually would take too long:

```
m <- mean(values)
v <- var(values)
n <- length(values)
p <- qt(0.975, df=n-1)

m + c(-1,1)* p * sqrt(v/n)

## [1] 52.34151 54.00713
```

You can use the side effect of `t.test`:

```
t.test(values, conf.level=.95)$conf.int

## [1] 52.34151 54.00713
## attr(,"conf.level")
## [1] 0.95
```

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    Simpsons Paradox
    Normality tests
    Confidence Intervals
    Linear regression
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Linear Regression

This section (linear models) was originally written by Matthias Seibert (GFZ).
It is excluded from this main document and can be obtained as pdf.

Storks Deliver Babies ($p = 0.008$)

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Task

Task

Your professor asks you to visually examine temperature and precipitation trends at certain meteorological stations in Germany. She hands you the files Potsdam.txt and Zugspitze.txt. How do you approach the project?

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Data selection, download, processing and saving:

```
library(rdwd) # github.com/brry/rdwd # not yet on CRAN
links <- selectDWD(c("Potsdam","Zugspitze"), current=TRUE,
                   res="monthly", var="kl", time="hist", outvec=TRUE)
clim <- dataDWD(links, dir="data")
write.table(clim[[1]], file="data/Potsdam.txt", row.names=F, quote=F)
write.table(clim[[2]], file="data/Zugspitze.txt", row.names=F, quote=F)
```

Task

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write.table(clim[[2]], file="data/Zugspitze.txt", row.names=F, quote=F)
```

```
potsdam$date <- as.Date(as.character(potsdam$MESS_DATUM_BEGINN), "%Y%m%d")
```

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Authorship note

This section (time series) was originally written by Matthias Seibert (GFZ). It is currently excluded from this main document but can be obtained as pdf.

```
library(xts)
```

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Kriging: Overview

Geostatistics: Kriging - spatial interpolation between points, using semivariance

1. Packages
2. read shapefile
3. Variogram
4. Kriging
5. Plotting

Kriging: packages

```r
install.packages("rgeos")
install.packages("sf")
install.packages("geoR")
```

```r
library(sf)    # for st_read (read shapefiles),
               # st_centroid, st_area, st_union
library(geoR) # as.geodata, variog, variofit,
               # krige.control, krige.conv, legend.krige
```

```
## Warning:  package 'sf' was built under R version 3.4.1
```

Kriging: read shapefile / few points for demonstration

```
x <- c(1,1,2,2,3,3,3,4,4,5,6,6,6)
y <- c(4,7,3,6,2,4,6,2,6,5,1,5,7)
z <- c(5,9,2,6,3,5,9,4,8,8,3,6,7)
plot(x,y, pch="+", cex=z/4)
```

Kriging: read shapefile II

```
GEODATA <- as.geodata(cbind(x,y,z))
plot(GEODATA)
```

Kriging: Variogram I

```
EMP_VARIOGRAM <- variog(GEODATA)

## variog: computing omnidirectional variogram

FIT_VARIOGRAM <- variofit(EMP_VARIOGRAM)

## variofit: covariance model used is matern
## variofit: weights used: npairs
## variofit: minimisation function used: optim

## Warning in variofit(EMP_VARIOGRAM): initial values not provided - running the
default search

## variofit: searching for best initial value ... selected values:
##                sigmasq phi    tausq kappa
## initial.value "9.19"  "3.65" "0"   "0.5"
## status        "est"   "est"  "est" "fix"
## loss value: 401.578968904954
```

Kriging: Variogram II

```
plot(EMP_VARIOGRAM)
lines(FIT_VARIOGRAM)
```

Kriging: Kriging

```
res <- 0.1
grid <- expand.grid(seq(min(x),max(x),res),
                    seq(min(y),max(y),res))
krico <- krige.control(type.krige="OK",
                       obj.model=FIT_VARIOGRAM)
krobj <- krige.conv(GEODATA,
                    locations=grid, krige=krico)

## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood

# KRigingObjekt
```

Kriging: Plotting I

```
image(krobj, col=rainbow2(100))
legend.krige(col=rainbow2(100),
             x.leg=c(6.2,6.7), y.leg=c(2,6),
             vert=T, off=-0.5,
             values=krobj$predict)
contour(krobj, add=T)
colPoints(x,y,z, col=rainbow2(100), legend=F)
points(x,y)
```

Kriging: Plotting II

Kriging: Plotting III

```
library("berryFunctions") # scatterpoints by color
colPoints(x,y,z, add=F, cex=2, legargs=list(y1=0.8,y2=1))
```

Kriging: Plotting IV

```
colPoints(grid[ ,1], grid[ ,2], krobj$predict, add=F,
          cex=2, col2=NA, legargs=list(y1=0.8,y2=1))
```

Time for a real dataset

Precipitation from ca 250 gauges in Brandenburg as Thiessen Polygons with steep gradients at edges:

Time for a real dataset

Exercise 41: Kriging

1. Load and plot the shapefile in PrecBrandenburg.zip with `sf::st_read`.
2. With `colPoints` in the package `berryFunctions`, add the precipitation values at the centroids of the polygons.
3. Calculate the variogram and fit a semivariance curve.
4. Perform kriging on a grid with a useful resolution (keep in mind that computing time rises exponentially with grid size).
5. Plot the interpolated values with `image` or an equivalent (Rclick 4.15) and add contour lines.
6. What went wrong? (if you used the defaults, the result will be dissatisfying.) How can you fix it?

Solution for exercise 41.1-2: Kriging Data

```
# Shapefile:
p <- sf::st_read("data/PrecBrandenburg/niederschlag.shp",
                 quiet=TRUE)
# Plot prep
pcol <- colorRampPalette(c("red","yellow","blue"))(50)
clss <- berryFunctions::classify(p$P1, breaks=50)$index
# Plot
par(mar = c(0,0,1.2,0))
plot(p, col=pcol[clss], max.plot=1) # P1: Precipitation
# kriging coordinates
cent <- sf::st_centroid(p)
berryFunctions::colPoints(cent$x, cent$y, p$P1, add=T, cex=0.7,
                          legargs=list(y1=0.8,y2=1), col=pcol)
points(cent$x, cent$y, cex=0.7)
```

Solution for exercise 41.3: Variogram

```
library(geoR)
# Semivariance:
geoprec <- as.geodata(cbind(cent$x,cent$y,p$P1))
vario <- variog(geoprec, max.dist=130000)

## variog: computing omnidirectional variogram

fit <- variofit(vario)

## variofit: covariance model used is matern
## variofit: weights used: npairs
## variofit: minimisation function used: optim

## Warning in variofit(vario):  initial values not provided - running the default
search

## variofit: searching for best initial value ... selected values:
##                sigmasq   phi        tausq kappa
## initial.value "1326.72" "19999.93" "0"   "0.5"
## status        "est"     "est"      "est" "fix"
## loss value: 107266266.76371
```

Solution for exercise 41.3: Variogram

```
plot(vario) ; lines(fit)
# distance to closest other point:
d <- sapply(1:nrow(cent), function(i) min(berryFunctions::distance(
                          cent$x[i], cent$y[i], cent$x[-i], cent$y[-i])))
hist(d/1000, breaks=20, main="distance to closest gauge [km]")
mean(d) # 8 km

## [1] 8165.633
```

Solution for exercise 41.4-5: Kriging

```
# Kriging:
res <- 1000 # 1 km, since stations are 8 km apart on average
grid <- expand.grid(seq(min(cent$x),max(cent$x),res),
                    seq(min(cent$y),max(cent$y),res))
krico <- krige.control(type.krige="OK", obj.model=fit)
krobj <- krige.conv(geoprec, locations=grid, krige=krico)

## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood

# Set values outside of Brandenburg to NA:
grid_sf <- sf::st_as_sf(grid, coords=1:2, crs=sf::st_crs(p))
isinp <- sapply(sf::st_within(grid_sf, p), length) > 0
krobj2 <- krobj
krobj2$predict[!isinp] <- NA
```

Solution for exercise 41.5: Kriging Visualization

```
geoR:::image.kriging(krobj2, col=pcol)
colPoints(cent$x, cent$y, p$P1, col=pcol, zlab="Prec", cex=0.7,
          legargs=list(y1=0.1,y2=0.8, x1=0.78, x2=0.87, horiz=F))
plot(p, add=T, col=NA, border=8)#; points(cent$x,cent$y, cex=0.7)
```

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R geo, further material

Use the sf, mapview, osmar and osmplotr packages!

Combine city names with geolocations:
blog.revolutionanalytics.com/2015/11/marriott.html

For this section (spatial data / GIS), a lot was originally written by Matthias Seibert (GFZ). With the advance of the `sf` package (late 2016), that material is mostly outdated. Until new material is created here, his slides can be obtained as pdf.

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Exercise 42: Final exercises to solve at home I

1. What is the difference between `c(5,3,-8)` and `vec <- c(5,3,-8)`?
2. What methods do you know to generate a vector?
3. What are object, element, command, argument, assignment, Workspace, Working Directory?
4. What data and object types do you know?
5. How do you call the help about the `lines` command?
6. How do you read a text file? What are the main arguments of the function?
7. How do you examine the imported table?
8. How do you obtain / change subsets of the table (column, row, element)?

Exercise 43: Final exercises to solve at home II

1. How often is Peter Pan mentioned in the E-book (peterpan.txt)? Exclude the meta data about the book!
2. Interpret the results from `pairs(iris)` and `cor(iris[ ,1:4])`. Why does `cor(iris)` not work?
3. What are the most important functions and arguments for creating graphics?
4. Write a for loop including a while statement to distribute points randomly, but with a certain minimal distance to each other, along a line (segment sampling design). A solution is in my RclickHandbuch Chapter 10.4.
5. What functions and packages are useful for dealing with time series?

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Exercise 44: Final exam

1. Download a long time series of weather data (e.g. DWD, NOAA), see slide 162.
2. Read the data into R and control the data types. Change the date (or time) to appropriate types with `as.Date`, `as.POSIXct` or `strptime`.
3. Write a subsection of the data (eg your birth year) to a tab-separated file so it's easy to copypaste this to Excel/Calc.
4. Plot the development of some aggregate (e.g. monthly 90% Quantile of windspeed, annual precipitation sum or temperature mean depending on hour of the day). Hints: `tapply`, `strftime`, `berryFunctions::monthLab`
5. Examine `cor`relations between variables.
6. Write a small report on your data analysis project with max 3 pages, including (beautiful) graphs. You can mail the code in a separate file.
   This is a requirement for the participation certificate with credit points.
7. BONUS 1: Write the report via Rnw, Rhtml, Rmd or Rpres (see slide 161).
8. BONUS 2: Make some interactive stuff (e.g. user can choose decade of analysis), e.g. via HTMLwidgets or Shiny (see more). This is a lot of initial effort, but you'll enable an awesome interactive graphical analyses!