Welcome to: "Basic scientific computing for drug discovery"

6/11/2018



The teaching team

Python/ Modeling



Dr M. M. Palm (Margriet)

R/Bioinformatics



Dr S. Wink (Steven)

Python | Cheminformatics



Brandon Bongers, Msc

Pharmacokinetics



Dr E.H.J. Krekels (Elke)

Python | Chemoinformatics



Dr G.J. P. van Westen (Gerard)

Organizer



Ivonne Koomen

ICI developer



Michael van Vliet

Session 1: Tuesday 6 November 2018			
What	Time	Lecture hall	Lecturer
Session 1: Python basic	09.00 – 13.00	DM021PC	Steven Wink (opening)
	13.00 - 14.15	DM009PC	Margriet Palm
	14.15 - 15.45	DM119	Brandon Bongers
	15.30 - 17.00	DM009PC	

Session 2: Thursday 8 November 2018			
What	Time	Lecture hall	Lecturer
Session 2: Python basic	09.00 - 17.00	DM021PC	Margriet Palm
			Brandon Bongers
			Gerard van Westen

Session 3: Monday 12 November 2018			
What	Time	Lecture hall	Lecturer
Session 3: R basic	09.00 – 17.00	DM021PC	Steven Wink Elke Krekels

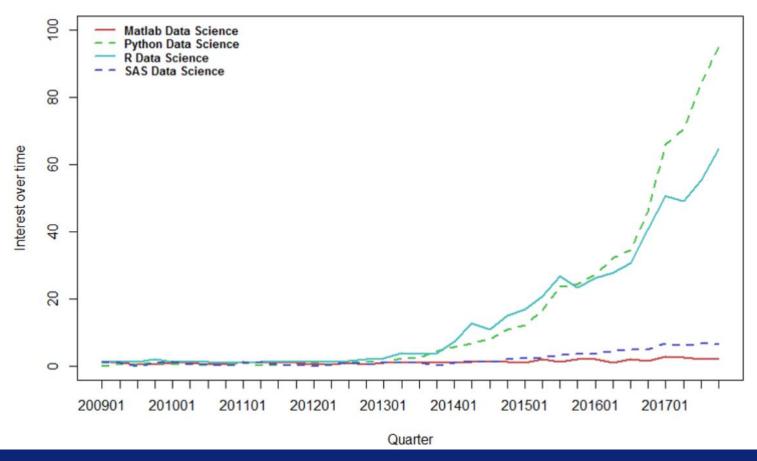
Session 4: Thursday 15 November 2018			
What	Time	Lecture hall	Lecturer
Session 4: R basic	09.00 – 17.00	DM017PC	Steven Wink Elke Krekels

R & Python popular data science languages.

For a nice article on what specific differences are:

https://www.digitalvidya.com/blog/r-vs-python/

Google Trends Keywords 2009 - 2017



R or Python for data science

Python

- Easier syntax
 - Bit easier learning curve
- Generic programming language
 - Web api's, database queries, pipeline development

R

- Developed by/for statisticians
 - Statistics books will often use R for implementation
- Tools for omics/biology (Bioconductor)
 - Microarray, annotation tools, RNAseq analysis development is done in R

How to choose: look at your work environment.

A lot of biologists and statisticians tend to use R.

Computational scientists/ software developers tend to use Python over R.

Computational applications

- In your feedback: what topics would you be interested in? Some examples are introductions into:
 - ODE modeling (R)
 - Machine learning (python or R)
 - Pharmacokinetic modeling (R)
 - Omics analysis? (RNA-seq, for metabolomics we would have to check) (R)
 - Statistics using linear modeling approaches or generalized additive models (R)

Good luck and have fun!

Rstudio (IDE)

Run lines with 'Ctrl + enter'



Documentation

- ?plot
 - R documentation, for arguments and examples
- help("plot")
 - Same as?
- ?'+'
 - For special symbols use backticks
- ??Mean
 - Fuzzy matching, for if you don't remember the exact function name
- www.stackoverflow.com
 - For finding answers to your coding problems, usually you are not the first!
 - After an extensive search for existing answers, you are encouraged to post your own question.

Documentation

aggregate {stats}

R Documentation

Compute Summary Statistics of Data Subsets

Description

Splits the data into subsets, computes summary statistics for each, and returns the result in a convenient form.

Usage

Arguments

x an R object.

by a list of grouping elements, each as long as the variables in the data frame

```
## Formulas, one ~ one, one ~ many, many ~ one, and many ~ many:
aggregate (weight ~ feed, data = chickwts, mean)
aggregate (breaks ~ wool + tension, data = warpbreaks, mean)
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, mean)
aggregate(cbind(ncases, ncontrols) ~ alcqp + tobqp, data = esoph,
## Dot notation:
aggregate(. ~ Species, data = iris, mean)
aggregate(len ~ ., data = ToothGrowth, mean)
## Often followed by xtabs():
ag <- aggregate(len ~ ., data = ToothGrowth, mean)
xtabs(len ~ ., data = ag)
## Compute the average annual approval ratings for American presid
aggregate (presidents, nfrequency = 1, FUN = mean)
## Give the summer less weight.
aggregate (presidents, nfrequency = 1,
          FUN = weighted.mean, w = c(1, 1, 0.5, 1))
                     [Package stats version 3.4.2 Index]
```

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• https://google.github.io/styleguide/Rguide.xml

Summary: R Style Rules

- 1. File Names: end in .R
- Identifiers: variable.name (Or variableName), FunctionName, kConstantName
- Line Length: maximum 80 characters
- Indentation: two spaces, no tabs
- Spacing
- 6. Curly Braces: first on same line, last on own line
- 7. else: Surround else with braces
- 8. Assignment: use <-, not =
- 9. Semicolons: don't use them
- 10. General Layout and Ordering
- 11. Commenting Guidelines: all comments begin with # followed by a space; inline com
- 12. Function Definitions and Calls
- 13. Function Documentation
- 14. Example Function
- 15. TODO Style: TODO (username)

Alternative:

Variable names separated with _

Function names start with small letter, then camel-case

Constants without the k in front.

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Write multiple R scripts each performing a certain definable or related task.

Not to long and not to short....

- Easier to understand
- Easier to debug
- Easier to extend / modify
- Easier to reuse
- Avoid using global variables as much as possible, use local variables inside functions instead.
- Name stuff in a way that makes sense to everyone.
- Save your workspace
- Save .Rdata R objects

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Example

```
source("s00_lockAndload.R")
source("s02_run_format_functions.R")
source("sD3_exploratory_plot.R")
source("s04_minmaxNorm.R")
source("s05_timeIDtoTime.R")
source("s06_makeDoseLevels.R")
options(stringsAsFactors = FALSE)
require(RColorBrewer )
require(qqplot2)
# als nieuwe r sessie om nieuwe packages te
#trace(utils:::unpackPkgZip, edit=TRUE)
#regel 140 pas sys.sleep aan naar 2 seconde
#raw_data <- load_data(rootdir = "J:/Workgr</pre>
                       debug = FALSE)
#rm(list=1s())
load("../tmp/raw_data.Rdata")
combined_data <- run_formats(raw_data)</pre>
head(combined_data)
dim(combined_data)
```

Name	Date modified	Туре
.RData	5-1-2018 10:52	RDATA File
Rhistory	5-1-2018 10:52	RHISTORY File
	20-11-2017 15:19	R File
	20-11-2017 15:19	R File
o s02_run_format_functions.R	20-11-2017 16:37	R File
o s03_exploratory_plot.R	23-11-2017 13:41	R File
💽 main.R	8-1-2018 12:17	R File
o s04_minmaxNorm.R	5-1-2018 10:10	R File
	23-11-2017 13:29	R File
	24-11-2017 15:59	R File
time6minEach.txt	5-1-2018 11:40	Text Document