

Computing for Big Data (BST-262)

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Chapter 1

Introduction

1.1 Logistics

- Fall 2 course
- Tuesday and Thursday, 11:30am-1pm
- Contact info: Christine Choirat (cchoirat@iq.harvard.edu). Please use BST232 in the email title.
- TA's: Qian Di (qiandi@mail.harvard.edu) and Ben Sabath (mbsabath@hsph.harvard.edu)
- Office hours:
 - Ben: Tuesday 1:30-2:30pm
 - Qian: Thursday 10:30-11:30am
 - Christine: Tuesday 10:30-11:30am (office 437A)
- Course GitHub repository <https://github.com/cchoirat/bigdata17>
- Open file in folder `_book/index.html`
- These course notes are **work in progress**.

1.2 Prerequisites

For BST262 (Computing for Big Data), we assume familiarity with the material covered in BST260 (Introduction to Data Science).

We will use R to present concepts that are mostly language-agnostic. We could have used Python, as in BST261 (Data Science II).

1.3 Rationale

1. Available data grows at a much faster rate than available computing capacity.
2. Statistical software programs such as R were not designed to handle datasets of massive size.

1.4 Big data bottlenecks

As described by Lim and Tjhi (2015), there are three bottlenecks:

- CPU
- RAM

- I/O

Exercise 1.1. Can you identify points 1–7 in the following code snippet?

```
data <- read.csv("mydata.csv")
totals <- colSums(data)
write.csv(totals, "totals.csv")
```

1.5 Syllabus

Part I – Good code still matters (*even with lots of computing resources*)

Week 1 - Basic tools

- Lecture 1. Unix scripting, make
- Lecture 2. Version control: Git and GitHub (guest lecture: Ista Zhan)

Week 2 - Creating and maintaining R packages

- Lecture 3. Rationale, package structure, available tools
- Lecture 4. Basics of software engineering: unit testing, code coverage, continuous integration

Week 3 - Software optimization

- Lecture 5. Measuring performance: profiling and benchmarking tools
- Lecture 6. Improving performance: an introduction to C/C++, Rcpp

Part II – Scaling up (*don't use big data tools for small data*)

Week 4 – Databases

- Lecture 7. Overview of SQL (SQLite, PostgreSQL) and noSQL databases (HBase, MongoDB, Cassandra, BigTable, ...)
- Lecture 8. R database interfaces (in particular through dplyr and mongolite)

Week 5 - Analyzing data that does not fit in memory

- Lecture 9. Pure R solutions (sampling, `ff` and `bigmemory`, other interpreters). JVM solutions (h2o, Spark)
- Lecture 10. An introduction to parallel computing; clusters and cloud computing. “Divide and Conquer” (MapReduce approaches)

Week 6 – Visualization

- Lecture 11. Principles of visualization (guest lecture: James Honaker)
- Lecture 12. Maps and GIS: principles of GIS, using R as a GIS, PostGIS

Weeks 7 & 8 - Guest lectures (order and precise schedule TBD)

- Software project management (Danny Brooke)
- R and Spark (Ellen Kraffmiller and Robert Treacy)
- Advanced GIS and remote sensing (TBD)
- Cluster architecture (William J. Horka)

1.6 Evaluation

Grades will be based on **two mandatory problem sets**. Each problem set will correspond to 50% (= 50 points) of the final grade. The first problem set will be available by the end of week 3 and the second problem set by the end of week 6.

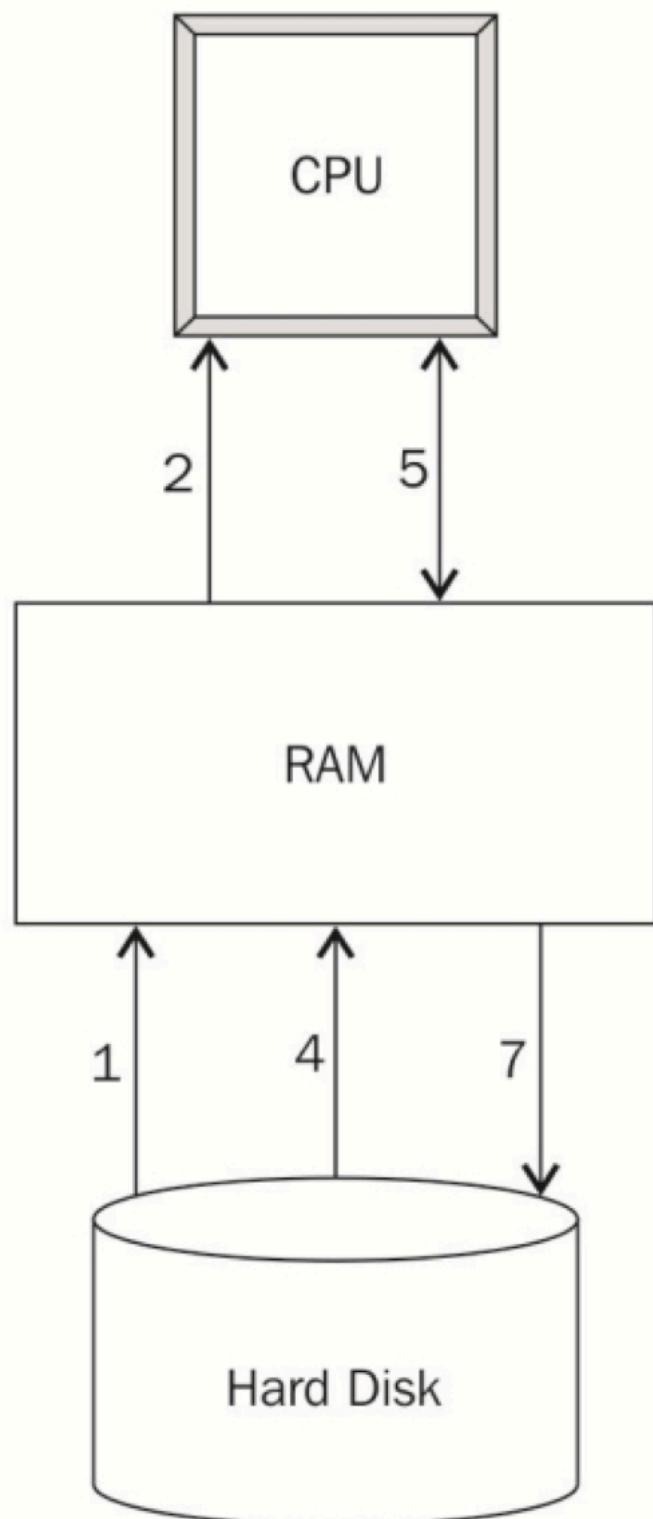


Figure 1.1: Steps to execute an R program, from @Lim2015, Chapter 1.

You will be required to submit problem set solutions within two weeks. Grades, and feedback when appropriate, will be returned two weeks after submission.

You will submit a markdown document that combines commented code for data analysis and detailed and structured explanations of the algorithms and software tools that you used.

1.7 Software tools and packages

We will mostly use R in this course. Some examples will be run in Python.

In general, we will use free and open-source software programs such as PostgreSQL / PostGIS or Spark.

1.8 Datasets

We have collected datasets to illustrate concepts. They are hosted on a Dropbox folder.

1.8.1 MovieLens

MovieLens by Harper and Konstan (2015, <https://grouplens.org/datasets/movielens/>) collects datasets from the website <https://movielens.org/>.

There are datasets of different sizes. We will use:

1. Small (1MB): <https://grouplens.org/datasets/movielens/latest/>
2. Benchmark (~190MB zipped): <https://grouplens.org/datasets/movielens/20m/>

1.8.2 Airlines data

The airlines dataset comes from the U.S. Department of Transportation and were used in the 2009 Data Expo of the American Statistical Association (ASA).

We will use a version curated by h2o: <https://github.com/h2oai/h2o-2/wiki/Hacking-Airline-DataSet-with-H2O>.

1.8.3 Insurance claims

Claims data contain Protected Health Information (PHI). There are strong privacy restrictions to store, use and share this type of data.

We will use synthetic data (Sample 1) from the Centers for Medicare and Medicaid Services (CMS).

1.8.4 Census

Census data is commonly merged with administrative claims data such as Medicare. We will use data from the Census Bureau.

1.8.5 PM_{2.5} exposure

We will use PM_{2.5} exposure data from the EPA Air Quality System (AQS) to illustrate GIS linkage concepts.

1.8.6 Methylation

If there is enough interest, we might present methylation examples.

1.9 Contributing with GitHub

If you have suggestions, you can open a GitHub issue at <https://github.com/cchoirat/bigdata17/issues>.

If you want to contribute, we welcome pull requests.

1.10 Before we start...

How much R do you know?

Introduction to R: <http://tutorials.iq.harvard.edu/R/Rintro/Rintro.html>

Regression models in R: <http://tutorials.iq.harvard.edu/R/Rstatistics/Rstatistics.html>

R graphics: <http://tutorials.iq.harvard.edu/R/Rgraphics/Rgraphics.html>

R programming: <http://tutorials.iq.harvard.edu/R/RProgramming/Rprogramming.html>

1.11 Style

Reading: <http://adv-r.had.co.nz/Style.html>

Chapter 2

Basic tools

In this Chapter, we present basic tools that will be important when interacting with big data systems: the command-line interface (CLI) in a Unix shell and several utilities (`less`, `awk`, `vi` and `make`).

2.1 Command line tools

We assume some familiarity with the Unix shell, for example as in <http://swcarpentry.github.io/shell-novice/>.

We also assume that you have access to a shell, either because you use Linux or OS X or because you have the right tools on Windows (for example Cygwin or the Bash shell in Windows 10).

2.1.1 Why use the command line?

- Batch processing
- Cluster and cloud computing

2.1.2 Basic Unix tools

2.1.3 Useful tools

2.1.3.1 `less`

`less` is a pager that lets you view one page at a time files that can be very large.

File `DE1_0_2008_to_2010_Carrier_Claims_Sample_1A.csv` in `Data17/SyntheticMedicare` is 1.2GB. Even if we have enough RAM to process the data, `less` helps get a very quick sense of the data (variable names, separators, etc.)

2.1.3.2 `awk`

`awk` is a text-processing programming language available on most Unix systems. It can be used for data extraction.

2.1.3.3 vi

vi is a screen-based text editor available on almost all Unix systems. Most versions are actually Vim (that stands for “Vi IMproved”).

There are many cheat sheets and tutorials available on-line (for example, the interactive <http://www.openvim.com/>). I invite you to learn basics vi commands.

2.1.4 Example

Let's apply some of the techniques described in Blackwell and Sen (2012) on Fisher's Iris data set saved in tab-delimited format. Of course, it is a small dataset easily processed with R:

```
iris <- read.table("~/Dropbox/Data17/iris/iris.tab")
head(iris, n = 5)

##   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
```

In a shell, we can use:

```
head -n 6 ~/Dropbox/Data17/iris/iris.tab
```

```
## "Sepal.Length"    "Sepal.Width"    "Petal.Length"    "Petal.Width"    "Species"
## "1"  5.1 3.5 1.4 0.2 "setosa"
## "2"  4.9 3   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   3.6 1.4 0.2 "setosa"
```

Suppose we only need to select two variables in our model, Sepal.Length and Species. In R, we can use:

```
iris_subset <- iris[, c("Sepal.Length", "Species")]
```

or

```
iris_subset <- iris[, c(1, 5)]
head(iris_subset)
```

```
##   Sepal.Length Species
## 1          5.1  setosa
## 2          4.9  setosa
## 3          4.7  setosa
## 4          4.6  setosa
## 5          5.0  setosa
## 6          5.4  setosa
```

With the tidyverse, we can use *pipes*. The %>% operator allows for performing chained operations.

```
suppressMessages(library(dplyr))

iris %>%
  select(1, 5) %>%
  head()
```

```
## Sepal.Length Species
## 1      5.1  setosa
## 2      4.9  setosa
## 3      4.7  setosa
## 4      4.6  setosa
## 5      5.0  setosa
## 6      5.4  setosa
```

In a shell, the pipe operator to combine shell commands is | and we can use:

```
cut -f 1,5 ~/Dropbox/Data17/iris/iris.tab | head -n 7
```

```
## "Sepal.Length"  "Species"
## "1"  0.2
## "2"  0.2
## "3"  0.2
## "4"  0.2
## "5"  0.2
## "6"  0.4
```

To keep observations with “Sepal.Length” greater than 5:

```
iris %>%
  filter(Sepal.Length > 5) %>%
  head()
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1      5.1      3.5      1.4      0.2  setosa
## 2      5.4      3.9      1.7      0.4  setosa
## 3      5.4      3.7      1.5      0.2  setosa
## 4      5.8      4.0      1.2      0.2  setosa
## 5      5.7      4.4      1.5      0.4  setosa
## 6      5.4      3.9      1.3      0.4  setosa
```

In the shell, we can use the AWK programming language. We start from row NR 2 (we could start from row 1, it contains variable names) and select rows such that the second variable (Sepal.Length) is greater than 5.

```
awk 'NR == 2 || $2 > 5' ~/Dropbox/Data17/iris/iris.tab | head
```

```
## "1"  5.1 3.5 1.4 0.2 "setosa"
## "6"  5.4 3.9 1.7 0.4 "setosa"
## "11" 5.4 3.7 1.5 0.2 "setosa"
## "15" 5.8 4.0 1.2 0.2 "setosa"
## "16" 5.7 4.4 1.5 0.4 "setosa"
## "17" 5.4 3.9 1.3 0.4 "setosa"
## "18" 5.1 3.5 1.4 0.3 "setosa"
## "19" 5.7 3.8 1.7 0.3 "setosa"
## "20" 5.1 3.8 1.5 0.3 "setosa"
## "21" 5.4 3.4 1.7 0.2 "setosa"
```

Exercise 2.1. The iris dataset is also saved in .csv format at ~/Dropbox/Data17/iris/iris.csv. Use AWK and tail to select the last 5 observations where Sepal.Width is larger than 3.5 and Petal.Length is smaller than 1.5.

2.2 Makefiles

`make` is a tool that helps put all the (interdependent) pieces of an analytic workflow together:

- data retrieving
- data cleaning
- analysis
- graphs
- reports
- ...

2.2.1 Simulate data in R

```
set.seed(123)

File simulate_data.R
# set.seed(123)
N <- 1000 # sample size

X1 <- rpois(n = N, lambda = 50)
X2 <- 10 + rbinom(n = N, prob = 0.8, size = 1)
Y <- 10 + 3 * X1 + -5 * X2 + 3 * rnorm(n = N)

write.csv(data.frame(Y = Y, X1 = X1, X2 = X2),
          "sample_data.csv", row.names = FALSE)

head(data.frame(Y = Y, X1 = X1, X2 = X2))

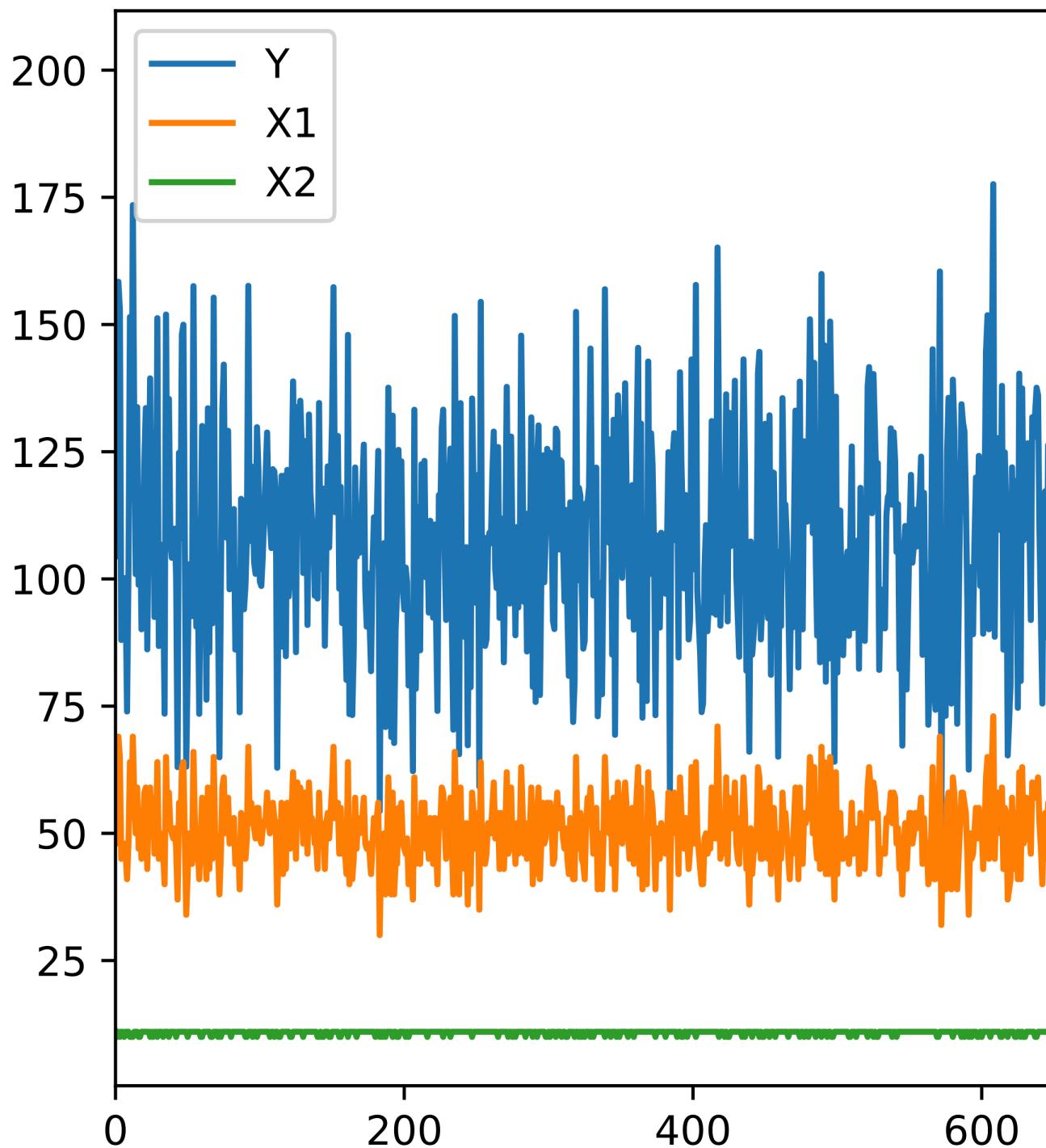
##           Y X1 X2
## 1 88.74430 46 11
## 2 125.77081 58 11
## 3 70.76396 38 10
## 4 110.32157 50 10
## 5 145.79546 62 11
## 6 109.45403 53 11
```

2.2.2 Create a plot in Python

```
File create_graph.py
import pandas as pd
import matplotlib.pyplot as plt

sim_data = pd.read_csv("sample_data.csv")

plt.figure()
sim_data.plot()
plt.savefig("plot.pdf", format = "pdf")
```



2.2.3 Run statistical model in R

We can estimate the model with R:

```
sim_data <- read.csv("sample_data.csv")
summary(lm(Y ~ X1 + X2, data = sim_data))

##
## Call:
## lm(formula = Y ~ X1 + X2, data = sim_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -8.3988 -1.9452 -0.0261  2.0216  9.1066 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 9.09087   2.54667   3.57  0.000374 ***
## X1          3.00531   0.01326 226.68 < 2e-16 ***
## X2         -4.94658   0.22876 -21.62 < 2e-16 ***  
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.936 on 997 degrees of freedom
## Multiple R-squared:  0.9811, Adjusted R-squared:  0.9811 
## F-statistic: 2.585e+04 on 2 and 997 DF,  p-value: < 2.2e-16
```

2.2.4 Run statistical model in R

To save the output, we use the `sink` function.

```
File estimate_model.R
sink("estimation_summary.txt")
summary(lm(Y ~ X1 + X2, data = sim_data))
sink()
```

2.2.5 Makefile syntax

- `make` is a *command* that runs on a text file often named `Makefile`.
- A `Makefile` contains one or several blocks with the following structure:

```
targetfile: sourcefile(s)
[tab] command
```

2.2.6 Naive version

File: `Makefile`

```
sample_data.csv: simulate_data.R
    R CMD BATCH simulate_data.R
```

```
plot.pdf: create_graph.py
```

```

python create_graph.py

estimation_summary.txt: estimate_model.R
  R CMD BATCH estimate_model.R

```

A simple call to `make` only builds the first target (`sample_data.csv`). To build the other targets, we have to use: `make plot.pdf` and `make estimation_summary.txt`.

2.2.7 Making all targets

```

File: Makefile

all: analysis

analysis: sample_data.csv plot.pdf estimation_summary.txt

sample_data.csv: simulate_data.R
  R CMD BATCH simulate_data.R

plot.pdf: create_graph.py
  python create_graph.py

estimation_summary.txt: estimate_model.R
  R CMD BATCH estimate_model.R

```

New data is simulated and saved in `sample_data.csv`. But `plot.pdf` and `estimation_summary.txt` are not updated.

2.2.8 Dealing with dependencies

- Problem `plot.pdf` and `estimation_summary.txt` depend on `sample_data.csv`.
- Solution: explicit dependencies.

```

File: Makefile

all: analysis

analysis: sample_data.csv plot.pdf estimation_summary.txt

sample_data.csv: simulate_data.R
  R CMD BATCH simulate_data.R

plot.pdf: sample_data.csv create_graph.py
  python create_graph.py

estimation_summary.txt: sample_data.csv estimate_model.R
  R CMD BATCH estimate_model.R

```

2.3 Git and GitHub

Guest lecture by Ista Zahn.

Chapter 3

Packages

We strongly recommend Wickham (2015).

We assume the following packages are installed:

```
install.packages(c("devtools", "roxygen2", "testthat", "knitr"))
```

3.1 Why?

- Organize your code
- Distribute your code
- Keep versions of your code

3.2 Package structure

- Folder hierarchy
 - NAMESPACE: package import / export
 - DESCRIPTION: metadata
 - R/: R code
 - man/: object documentation (with short examples)
 - tests/
 - data/
 - src/: compiled code
 - vignettes/: manual-like documentation
 - inst/: installed files
 - demo/: longer examples
 - exec, po, tools

3.3 Building steps

- R CMD build
- R CMD INSTALL
- R CMD check

3.3.1 R CMD build

```
R CMD build --help
```

Build R packages from package sources in the directories specified by ‘pkgdirs’

3.3.2 R CMD INSTALL

```
R CMD INSTALL --help
```

Install the add-on packages specified by pkgs. The elements of pkgs can be relative or absolute paths to directories with the package sources, or to gzipped package ‘tar’ archives. The library tree to install to can be specified via ‘–library’. By default, packages are installed in the library tree rooted at the first directory in .libPaths() for an R session run in the current environment.

3.3.3 R CMD check

```
R CMD check --help
```

<http://r-pkgs.had.co.nz/check.html>

Check R packages from package sources, which can be directories or package ‘tar’ archives with extension ‘tar.gz’, ‘tar.bz2’, ‘tar.xz’ or ‘tgz’.

A variety of diagnostic checks on directory structure, index and control files are performed. The package is installed into the log directory and production of the package PDF manual is tested. All examples and tests provided by the package are tested to see if they run successfully. By default code in the vignettes is tested, as is re-building the vignette PDFs.

3.3.4 Building steps with devtools

- `devtools::build`
- `devtools::install`
- `devtools::check`
- and many others: `load_all`, `document`, `test`, `run_examples`, ...

3.4 Create an R package

3.4.1 utils::package.skeleton

```
package.skeleton() # "in "clean" session ("anRpackage")
package.skeleton("pkgname") # in "clean" session

set.seed(02138)
f <- function(x, y) x+y
g <- function(x, y) x-y
d <- data.frame(a = 1, b = 2)
```



Figure 3.1: Submitting to CRAN. It's not that bad...

```
e <- rnorm(1000)
package.skeleton(list = c("f", "g", "d", "e"), name = "pkgname")
```

3.4.2 devtools::create

```
devtools::create("path/to/package/pkgname")
```

Also from RStudio ('File -> New Project').

3.4.3 Submit to CRAN

Reading: <http://r-pkgs.had.co.nz/release.html>

3.5 R packages on GitHub

Reading: <http://r-pkgs.had.co.nz/git.html>

- Version control
- Website, wiki, project management
- Easy install: `install_github` from `devtools`
- Collaboration
- Issue tracking

3.5.0.1 RStudio and GitHub integration

Command line

```
# git init # already run when creating package with RStudio
git add *
git commit -m "First commit"
git remote add origin https://github.com/cchoirat/Linreg
git push -u origin master
```

Create a new repository

A repository contains all the files for your project, including the revision history.

Owner **Repository name**

 **acchoirat** / Linreg ✓

Great repository names are short and memorable. Need inspiration? How about [upgrader](#)

Description (optional)

 **Public**
Anyone can see this repository. You choose who can commit.

 **Private**
You choose who can see and commit to this repository.

Initialize this repository with a README
This will let you immediately clone the repository to your computer. Skip this step if you don't want to.

Add .gitignore: **None** ▾ | Add a license: **None** ▾ 

Create repository

Figure 3.2: Create a new Linreg repository on GitHub

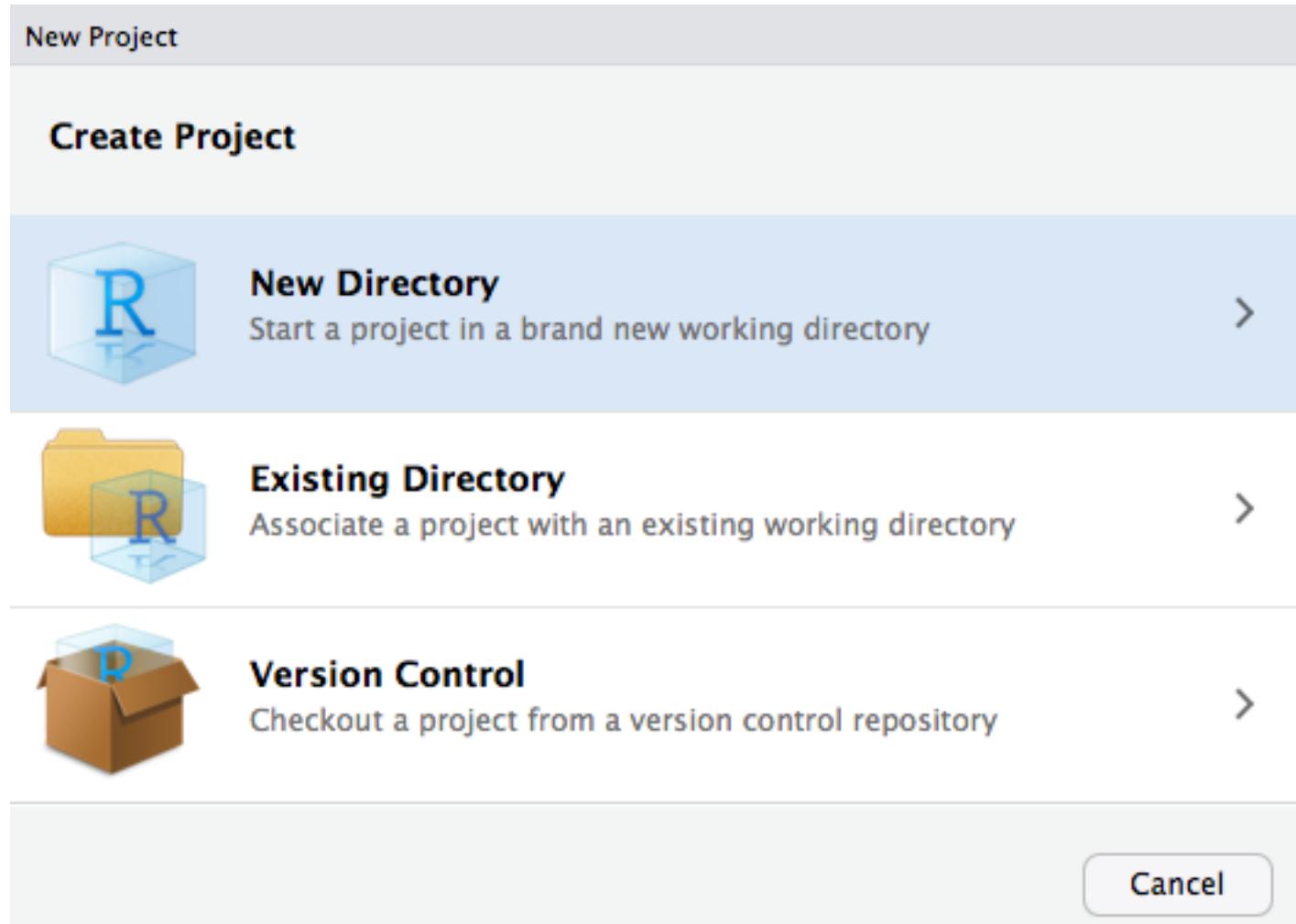


Figure 3.3: Create a new project in RStudio

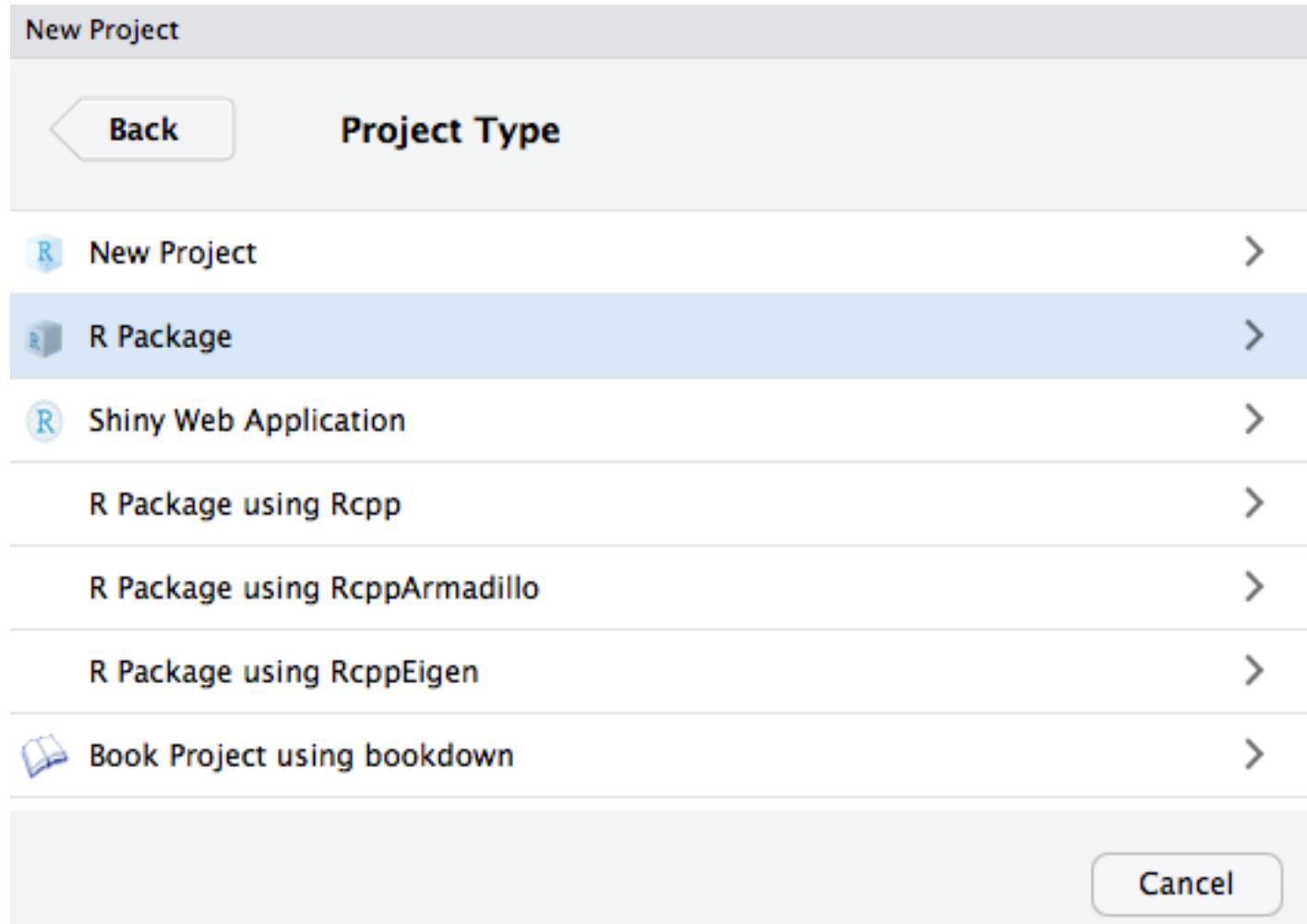


Figure 3.4: Select R package

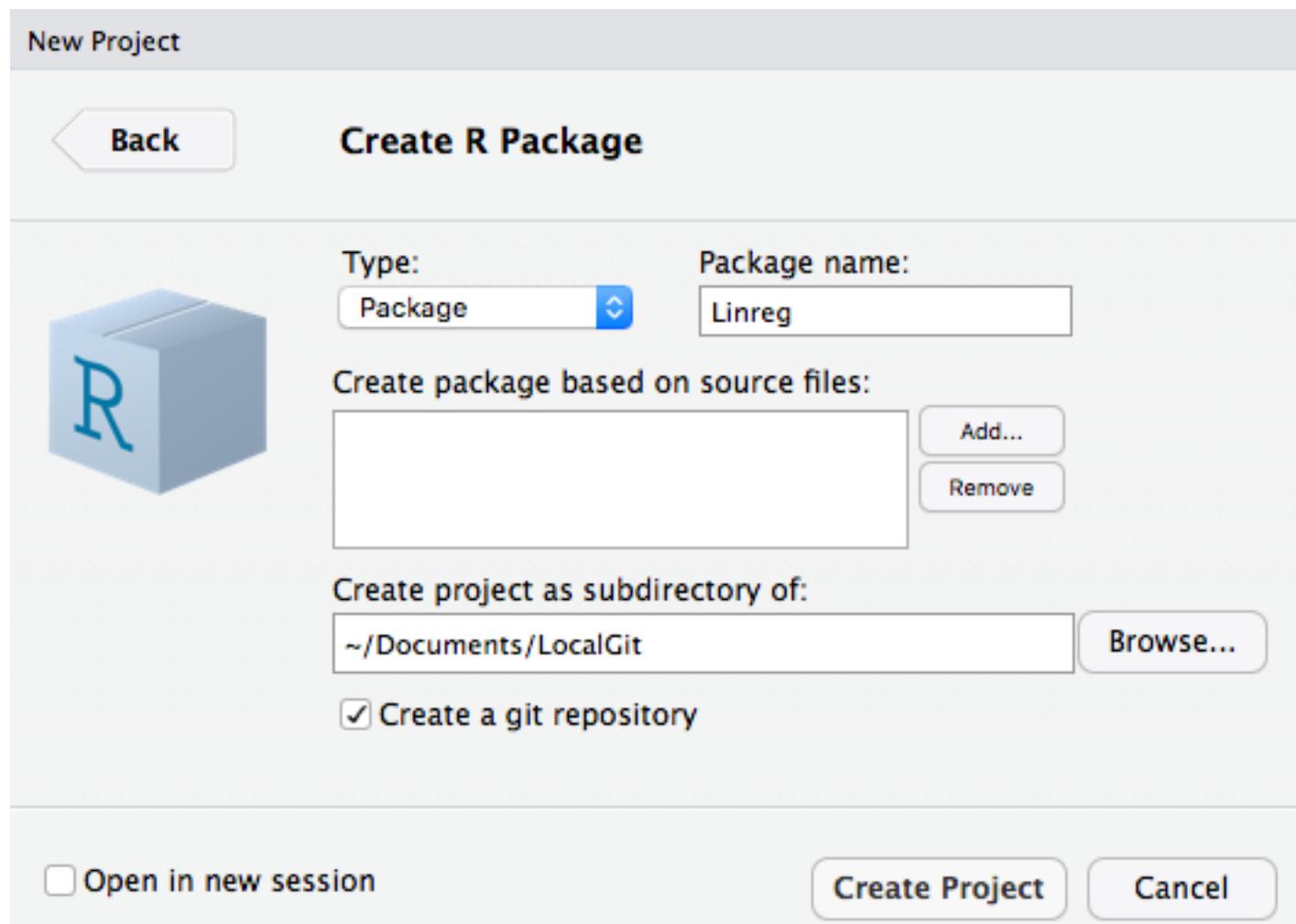


Figure 3.5: Create the Linreg R package as a Git repository

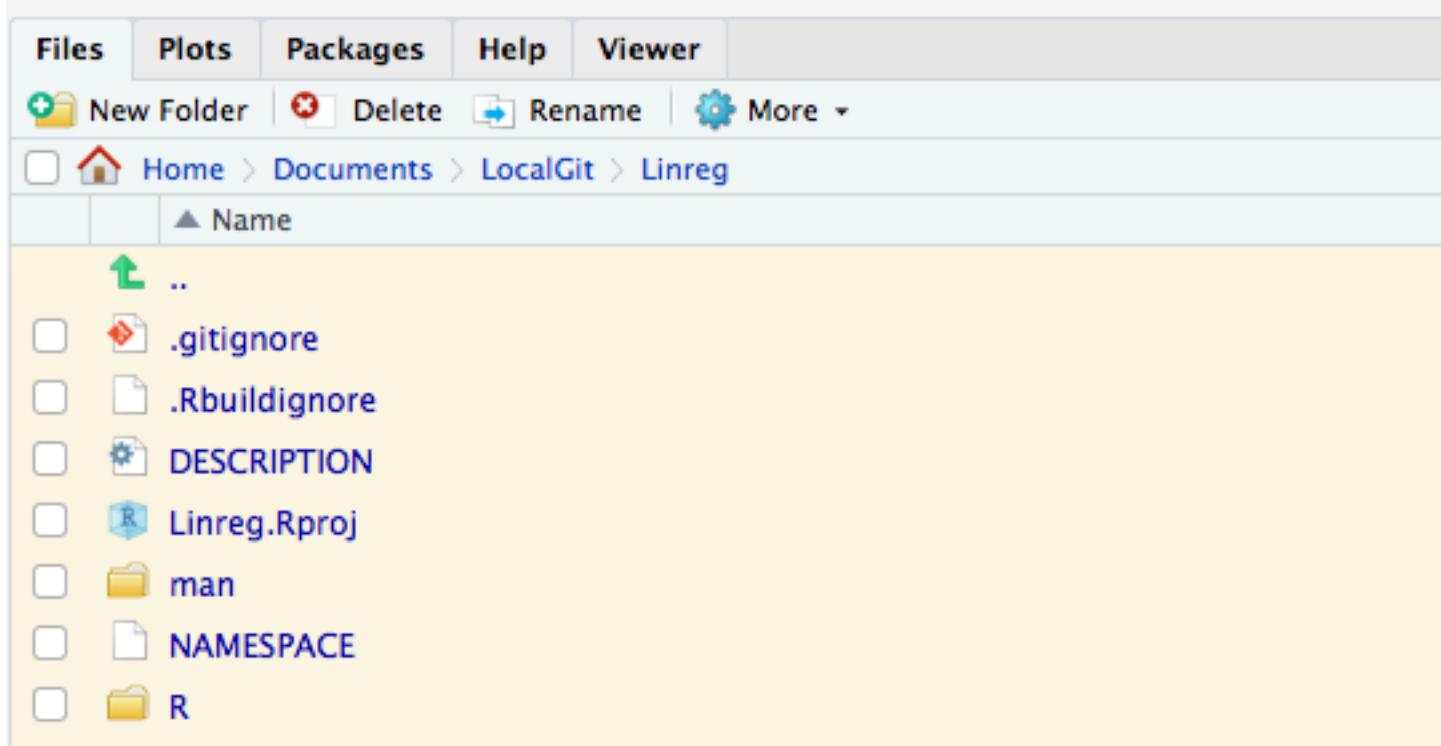


Figure 3.6: Automatically created files

```
==> R CMD INSTALL --no-multiarch --with-keep.source Linreg

* installing to library '/Library/Frameworks/R.framework/Versions/3.5/Resources/library'
* installing *source* package 'Linreg' ...
** R
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (Linreg)
```

Figure 3.7: Build tab in RStudio

The screenshot shows a GitHub repository page for 'cchoirat / Linreg'. At the top, there's a navigation bar with tabs for 'Code', 'Issues 0', 'Pull requests 0', 'Projects 0', 'Wiki', and 'Insights'. Below the navigation bar, there's a section titled 'Quick setup — if you've done this kind of thing before' with instructions for setting up the repository. It includes options to 'Set up in Desktop' or choose between 'HTTPS' and 'SSH' protocols, with 'SSH' being selected. It also recommends including a 'README', 'LICENSE', and '.gitignore'. Below this, there's a section titled '...or create a new repository on the command line' with a block of terminal commands for initializing a new repository. Further down, there's a section titled '...or push an existing repository from the command line' with another block of terminal commands for pushing an existing repository. At the bottom, there's a button labeled 'Import code'.

cchoirat / Linreg

Code Issues 0 Pull requests 0 Projects 0 Wiki Insights

Quick setup — if you've done this kind of thing before

Set up in Desktop or HTTPS SSH git@github.com:cchoirat/Linreg.git

We recommend every repository include a [README](#), [LICENSE](#), and [.gitignore](#).

...or create a new repository on the command line

```
echo "# Linreg" >> README.md  
git init  
git add README.md  
git commit -m "first commit"  
git remote add origin git@github.com:cchoirat/Linreg.git  
git push -u origin master
```

...or push an existing repository from the command line

```
git remote add origin git@github.com:cchoirat/Linreg.git  
git push -u origin master
```

...or import code from another repository

You can initialize this repository with code from a Subversion, Mercurial, or TFS project.

Import code

Figure 3.8: Github webpage

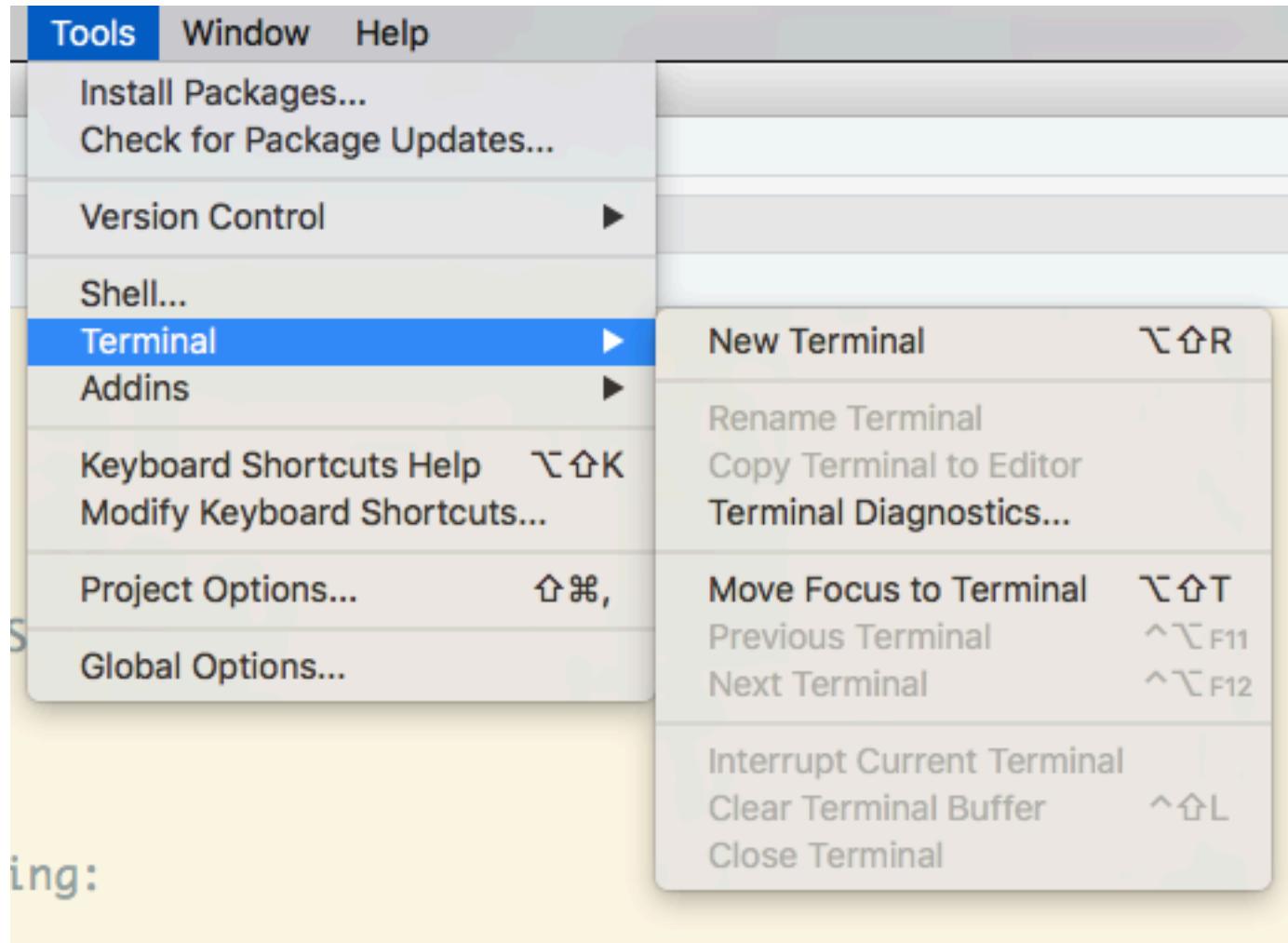


Figure 3.9: Open a terminal

The screenshot shows the GitHub repository page for `cchoirat / Linreg`. The top navigation bar includes links for Code, Issues (0), Pull requests (0), Projects (0), and Wiki. A message states, "No description, website, or topics provided." Below this, there is a link to "Add topics". Key statistics are displayed: 1 commit and 1 branch. A dropdown menu shows the current branch is "master". There is a button to "New pull request". The repository tree lists files and folders: `R`, `man`, `.Rbuildignore`, `.gitignore`, `DESCRIPTION`, `Linreg.Rproj`, and `NAMESPACE`. A note at the bottom encourages adding a README.

No description, website, or topics provided.

Add topics

1 commit 1 branch

Branch: master ▾ New pull request

A **cchoirat** First commit

- `R` First commit
- `man` First commit
- `.Rbuildignore` First commit
- `.gitignore` First commit
- `DESCRIPTION` First commit
- `Linreg.Rproj` First commit
- `NAMESPACE` First commit

Help people interested in this repository understand your project by adding a README

Figure 3.10: Github webpage is updated

3.5.1 .gitignore

RStudio default

```
.Rproj.user
.Rhistory
.RData
```

GitHub default

```
# History files
.Rhistory
.Rapp.history

# Example code in package build process
*-Ex.R

# RStudio files
.Rproj.user/

# produced vignettes
vignettes/*.html
vignettes/*.pdf
```

3.6 RStudio projects

- .Rproj file extension, in our example `Linreg.Rproj`
- A project has its own:
 - R session
 - .Rprofile (*e.g.*, to customize startup environment)
 - .Rhistory
- Default working directory is project directory
- Keeps track of project-specific recent files

3.6.1 Project options

```
Version: 1.0

RestoreWorkspace: Default
SaveWorkspace: Default
AlwaysSaveHistory: Default

EnableCodeIndexing: Yes
UseSpacesForTab: Yes
NumSpacesForTab: 2
Encoding: UTF-8

RnwWeave: knitr
LaTeX: pdfLaTeX
```

```
AutoAppendNewline: Yes
StripTrailingWhitespace: Yes

BuildType: Package
PackageUseDevtools: Yes
PackageInstallArgs: --no-multiarch --with-keep.source
```

3.6.2 Package documentation

- Functions and methods
- Vignettes
 - PDF
 - knitr

3.7 Package workflow example

Creating R Packages: A Tutorial (Friedrich Leisch, 2009)

Our example is adapted from <https://cran.r-project.org/doc/contrib/Leisch-CreatingPackages.pdf>.

3.7.1 Add linreg.R to R/ directory

```
linmodEst <- function(x, y) {
  ## CC: crossprod or a QR decomposition (as in the original version) are more efficient
  coef <- solve(t(x) %*% x) %*% t(x) %*% y
  print(coef)
  ## degrees of freedom and standard deviation of residuals
  df <- nrow(x) - ncol(x)
  sigma2 <- sum((y - x %*% coef)^ 2) / df
  ## compute sigma^2 * (x'x)^-1
  vcov <- sigma2 * solve(t(x) %*% x)
  colnames(vcov) <- rownames(vcov) <- colnames(x)
  list(
    coefficients = coef,
    vcov = vcov,
    sigma = sqrt(sigma2),
    df = df
  )
}
```

3.7.2 Run our function

```
data(cats, package = "MASS")
linmodEst(cbind(1, cats$Bwt), cats$Hwt)

##          [,1]
## [1,] -0.3566624
## [2,]  4.0340627
```

```
## $coefficients
##          [,1]
## [1,] -0.3566624
## [2,]  4.0340627
##
## $vcov
##          [,1]      [,2]
## [1,]  0.4792475 -0.17058197
## [2,] -0.1705820  0.06263081
##
## $sigma
## [1] 1.452373
##
## $df
## [1] 142
```

We can compare the output with `lm`.

```
lm1 <- lm(Hwt ~ Bwt, data = cats)
lm1

##
## Call:
## lm(formula = Hwt ~ Bwt, data = cats)
##
## Coefficients:
## (Intercept)      Bwt
## -0.3567       4.0341
coef(lm1)

## (Intercept)      Bwt
## -0.3566624    4.0340627
vcov(lm1)

##           (Intercept)      Bwt
## (Intercept)  0.4792475 -0.17058197
## Bwt        -0.1705820  0.06263081
summary(lm1)$sigma

## [1] 1.452373
```

3.7.3 Add ROxygen2 documentation

Reading: http://kbroman.org/pkg_primer/pages/docs.html

```
#' Linear regression
#'
#' Runs an OLS regression not unlike \code{\link{lm}}
#'
#' @param y response vector ( $1 \times n$ )
#' @param X covariate matrix ( $p \times n$ ) with no intercept
#'
#' @return A list with 4 elements: coefficients, vcov, sigma, df
#'
```

```

#' @examples
#' data(mtcars)
#' X <- as.matrix(mtcars[, c("cyl", "disp", "hp")])
#' y <- mtcars[, "mpg"]
#' linmodEst(y, X)
#'
#' @export
#'
linmodEst <- function(x, y) {
  ## CC: crossprod or a QR decomposition (as in the original version) are more efficient
  coef <- solve(t(x) %*% x) %*% t(x) %*% y
  print(coef)
  ## degrees of freedom and standard deviation of residuals
  df <- nrow(x) - ncol(x)
  sigma2 <- sum((y - x %*% coef)^2) / df
  ## compute sigma^2 * (x'x)^-1
  vcov <- sigma2 * solve(t(x) %*% x)
  colnames(vcov) <- rownames(vcov) <- colnames(x)
  list(
    coefficients = coef,
    vcov = vcov,
    sigma = sqrt(sigma2),
    df = df
  )
}

```

3.7.4 Configure Build Tools

3.7.5 man page

File ‘man/linmodEst.Rd’ contains:

```

% Generated by roxygen2: do not edit by hand
% Please edit documentation in R/linreg.R
\name{linmodEst}
\alias{linmodEst}
\title{Linear regression}
\usage{
linmodEst(x, y)
}
\arguments{
\item{y}{response vector (1 x n)}

\item{X}{covariate matrix (p x n) with no intercept}
}
\value{
A list with 4 elements: coefficients, vcov, sigma, df
}
\description{
Runs an OLS regression not unlike \code{\link{lm}}
}
\examples{
data(mtcars)
}
```

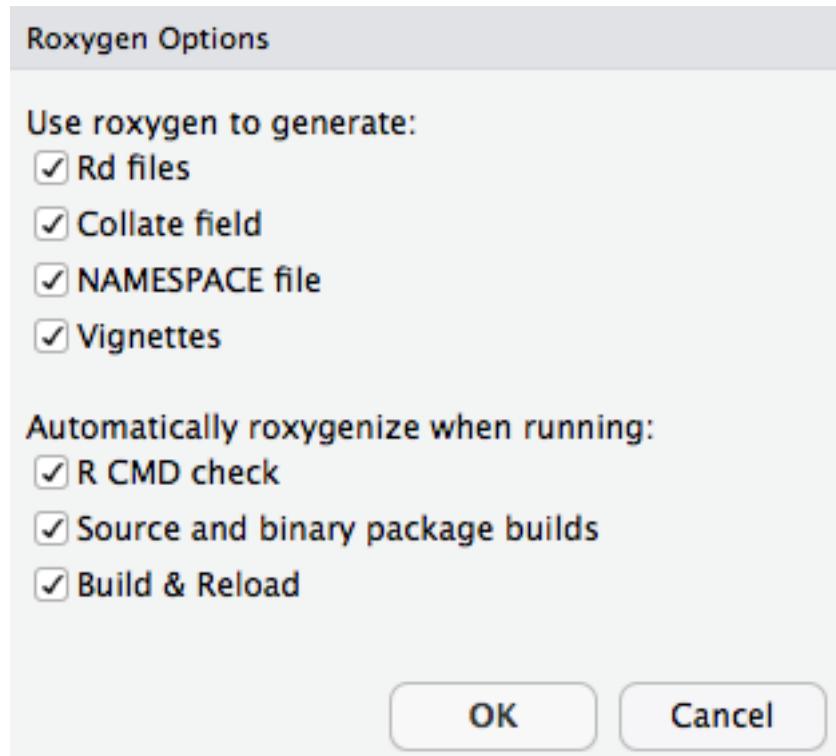


Figure 3.11: Roxygen options

```
X <- as.matrix(mtcars[, c("cyl", "disp", "hp")])
y <- mtcars[, "mpg"]
linmodEst(y, X)

}
```

3.7.6 Formatted output

3.7.7 DESCRIPTION

Reading: <http://r-pkgs.had.co.nz/description.html>

```
Package: Linreg
Type: Package
Title: What the Package Does (Title Case)
Version: 0.1.0
Author: Who wrote it
Maintainer: The package maintainer <yourself@somewhere.net>
Description: More about what it does (maybe more than one line)
  Use four spaces when indenting paragraphs within the Description.
License: What license is it under?
Encoding: UTF-8
LazyData: true
RoxygenNote: 6.0.1
```

```
linmodEst {Linreg}
```

Linear regression

Description

Runs an OLS regression not unlike [lm](#)

Usage

```
linmodEst(x, y)
```

Arguments

y response vector ($1 \times n$)

x covariate matrix ($p \times n$) with no intercept

Value

A list with 4 elements: coefficients, vcov, sigma, df

Examples

```
data(mtcars)
X <- as.matrix(mtcars[, c("cyl", "disp", "hp")])
y <- mtcars[, "mpg"]
linmodEst(y, X)
```



3.7.8 NAMESPACE

Reading: <http://r-pkgs.had.co.nz/namespaces.html>, in particular **Imports** vs **Suggests**

`export`'s automatically generated when parsing ROxygen2 snippets

```
export(linmodEst)
```

- A scary hack
- A scary tree

Reading: <https://git-scm.com/book/en/v2/Git-Branching-Basic-Branching-and-Merging>

3.7.9 S3 basics

Reading: <http://adv-r.had.co.nz/S3.html>

```
hello <- function() {
  s <- "Hello World!"
  class(s) <- "hi"
  return(s)
}

hello()

## [1] "Hello World!"
## attr(,"class")
## [1] "hi"

print.hi <- function(...) {
  print("Surprise!")
}

hello()

## [1] "Surprise!"
```

3.7.10 S3 and S4 generics

Reading: <http://adv-r.had.co.nz/S4.html>

```
linmod <- function(x, ...)
  UseMethod("linmod")
```





```
linmod.default <- function(x, y, ...) {
  x <- as.matrix(x)
  y <- as.numeric(y)
  est <- linmodEst(x, y)
  est$fitted.values <- as.vector(x %*% est$coefficients)
  est$residuals <- y - est$fitted.values
  est$call <- match.call()
  class(est) <- "linmod"
  return(est)
}
```

3.7.11 print

```
print.linmod <- function(x, ...) {
  cat("Call:\n")
  print(x$call)
  cat("\nCoefficients:\n")
  print(x$coefficients)
}
```

```
x <- cbind(Const = 1, Bwt = cats$Bwt)
y <- cats$Hw
mod1 <- linmod(x, y)
```

```
##          [,1]
## Const -0.3566624
## Bwt    4.0340627
```

```
mod1

## Call:
## linmod.default(x = x, y = y)
##
## Coefficients:
##              [,1]
## Const -0.3566624
## Bwt    4.0340627
```

3.7.12 Other methods

- `summary.linmod`
- `print.summary.linmod`
- `predict.linmod`
- `plot.linmod`
- `coef.linmod, vcov.linmod, ...`

Exercise 3.1. Write two functions that implement the `coef.linmod` and `vcov.linmod` methods.

3.7.13 Formulas and model frames

Reading: http://genomicsclass.github.io/book/pages/expressing_design_formula.html

`model.frame` (a generic function) and its methods return a `data.frame` with the variables needed to use formula and any ... arguments.

`model.matrix` creates a design (or model) matrix, e.g., by expanding factors to a set of dummy variables (depending on the contrasts) and expanding interactions similarly.

`model.response` returns the response of a model frame passed as optional arguments to `model.frame`.

Exercise 3.2. What is `model.extract`?

```
linmod.formula <- function(formula, data = list(), ...) {
  mf <- model.frame(formula = formula, data = data)
  x <- model.matrix(attr(mf, "terms"), data = mf)
  y <- model.response(mf)
  est <- linmod.default(x, y, ...)
  est$call <- match.call()
  est$formula <- formula
  return(est)
}
```

```
linmod(Hwt ~ -1 + Bwt * Sex, data = cats)
```

Call:

```
linmod.formula(formula = Hwt ~ -1 + Bwt * Sex, data = cats)
```

Coefficients:

Bwt	SexF	SexM	Bwt:SexM
2.636414	2.981312	-1.184088	1.676265

3.8 Unit testing

3.8.1 Unit tests and `testthat`

Reading: <http://r-pkgs.had.co.nz/tests.html>

In package directory:

```
devtools::use_testthat()
```

pre-populates `test/testthat/`

Test files should start with `test` to be processed.

3.8.2 `test_coef.R`

```
data(cats, package = "MASS")
l1 <- linmod(Hwt ~ Bwt * Sex, data = cats)
l2 <- lm(Hwt ~ Bwt * Sex, data = cats)

test_that("same estimated coefficients as lm function", {
  expect_equal(round(l1$coefficients, 3), round(l2$coefficients, 3))
})

> devtools::test()
Loading Linreg
Loading required package: testthat
Testing Linreg
.
DONE =====
```

3.9 Continuous integration

Readings: - <http://r-pkgs.had.co.nz/check.html#travis> - <https://juliasilge.com/blog/beginners-guide-to-travis/>

Website: <https://travis-ci.org/>

First step is to create a Travis account and link it to your GitHub account.

Travis will list all your public GitHub repositories for you to select the ones you want to test.

Calling

```
devtools::use_coverage(pkg = ".", type = c("codecov"))
```

creates the `.travis.yml` file:

```
# R for travis: see documentation at https://docs.travis-ci.com/user/languages/r

language: R
sudo: false
cache: packages
```

and pushing `Linreg` code to GitHub will automatically trigger a Travis build... which fails!

To be continued...

We're only showing your public repositories. You can add more.

1 Flick the repository switch on

2 Add .travis.yml to your repository

```
language: ruby
rvm:
  - "1.8.7"
  - "1.9.2"
  - "1.9.3"
  - jruby-18mode
  - jruby-19mode
  - rbx
# uncomment this line
script: bundle install
```



cchoirat/Linreg



cchoirat / Linreg (master)

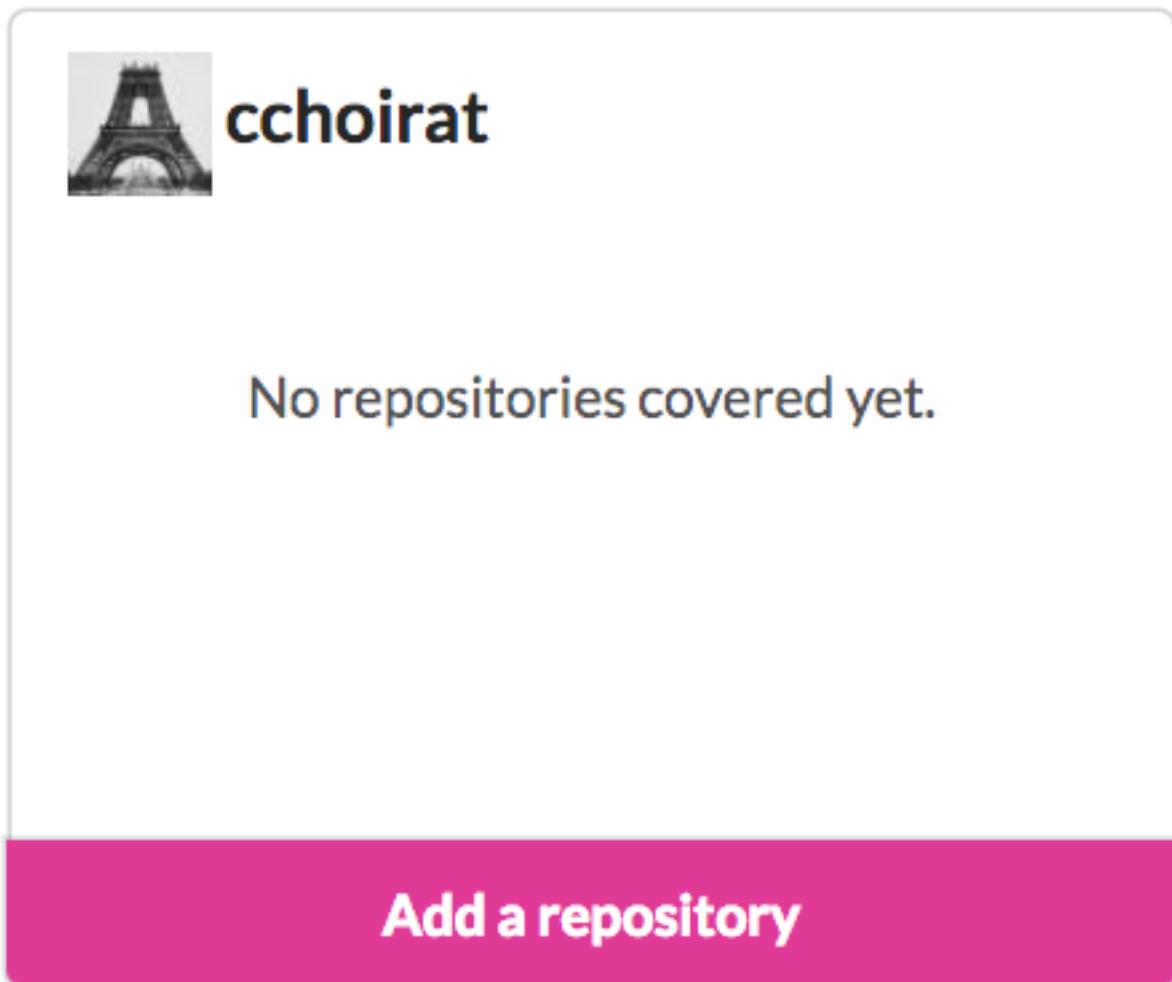


Build #1 failed.



cchoirat

Trying to trigger a build



3.10 Code coverage

Reading: <https://walczak.org/2017/06/how-to-add-code-coverage-Codecov-to-your-R-package/>

Website: <https://codecov.io/>

Like Travis, codecov has to be linked to a GitHub account:

```
devtools::use_coverage(pkg = ".", type = c("codecov"))
```

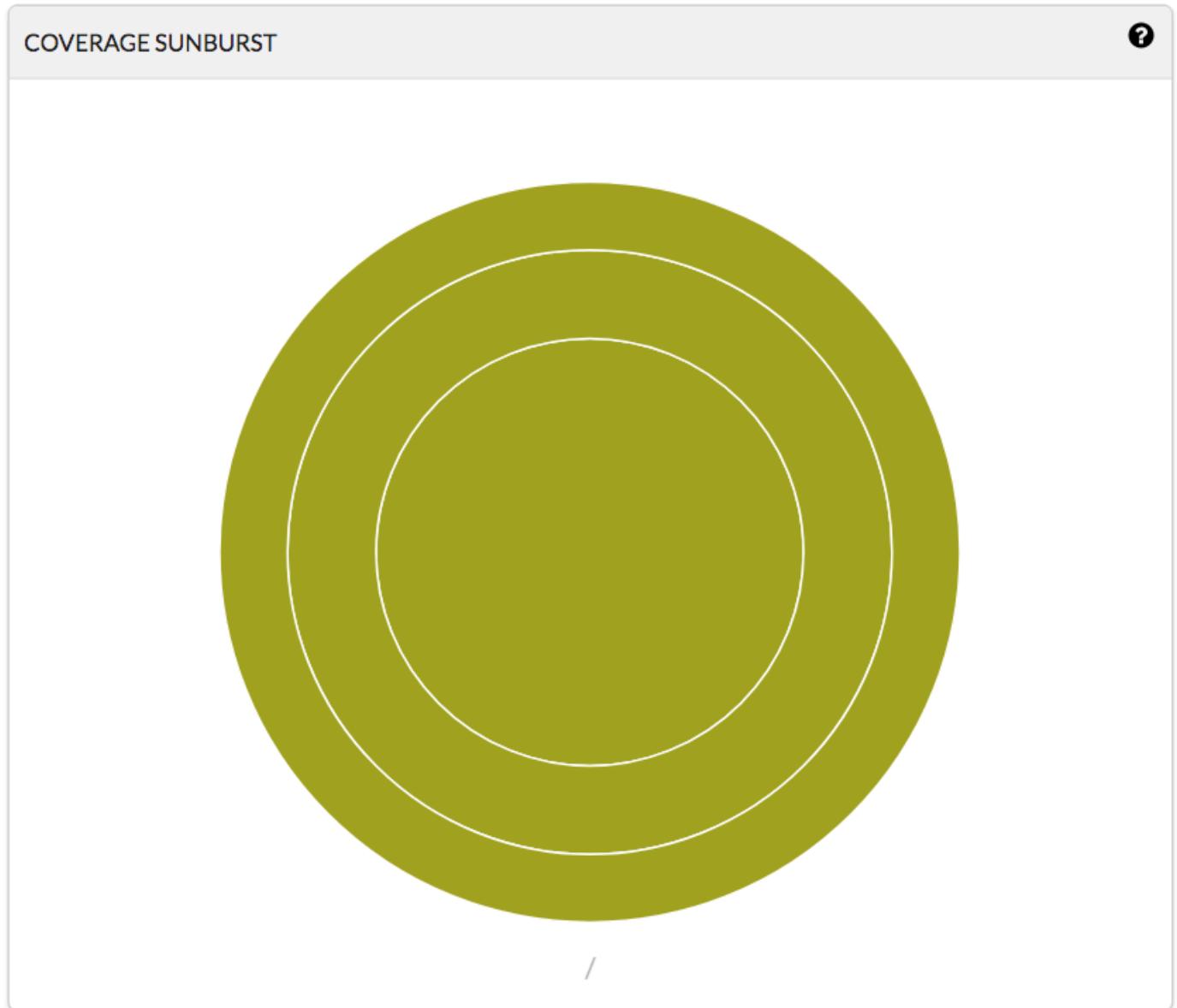
creates the `codecov.yml` file:

```
comment: false
```

A call to

```
covr::codecov(token = "YOUR_TOKEN")
```

will give you code coverage information:



Files	
	R/linreg.R
Project Totals	(1 files)



3.11 Back to GitHub

Badges can be added to README.md:

```
<!-- Badges -->
[![Travis (LINUX) Build Status](https://travis-ci.org/cchoirat/Linreg.svg?branch=master)](https://travis-ci.org/cchoirat/Linreg)
[![codecov](https://codecov.io/gh/cchoirat/Linreg/branch/master/graph/badge.svg)](https://codecov.io/gh/cchoirat/Linreg)

## `Linreg` package template

Based on "Creating R Packages: A Tutorial" (Friedrich Leisch, 2009)
- https://cran.r-project.org/doc/contrib/Leisch-CreatingPackages.pdf
```

are automatically displayed on GitHub:

3.12 Vignettes

Reading: <http://r-pkgs.had.co.nz/vignettes.html>

Reading: http://kbroman.org/pkg_primer/pages/vignettes.html

Even if all the functions and datasets of your package are documented, it is still useful to have a more detailed illustration on how to use your package. A *vignette* is the right place to explain a workflow and a statistical method.

Running:

```
devtools::use_vignette("my-linear-regression")
```

creates a `vignettes` folder and provide a template in RMarkdown format `my-linear-regression.Rmd`:

<https://github.com/cchoirat/Linreg/blob/master/vignettes/my-linear-regression.Rmd>

It also indicates in `DESCRIPTION` that vignettes should be built with `knitr`.

```
VignetteBuilder: knitr
```

The vignette is built into a HTML document with

```
devtools::build_vignettes()
```

Building Linreg vignettes

Moving `my-linear-regression.html`, `my-linear-regression.R` to `inst/doc/`

Copying `my-linear-regression.Rmd` to `inst/doc/`

The vignette is accessible with

```
vignette("my-linear-regression")
vignette("my-linear-regression", package = "Linreg")
```

Vignette Title

Vignette Author

2017-10-21

Vignettes are long form documentation commonly included in packages. Because they are distributed with the package, they need to be as compact as possible. The `html_vignette` custom style sheet (and tweaks some options) to ensure that the resulting HTML is as small as possible:

- Never uses retina figures
- Has a smaller default figure size
- Uses a custom CSS stylesheet instead of the default Twitter Bootstrap style

Vignette Info

Note the various macros within the `vignette` section of the metadata block above. These instruct R how to build the vignette. Note that you should change the `title` field and match the title of your vignette.

Styles

The `html_vignette` template includes a basic CSS theme. To override this theme you can do so in the document metadata as follows:

```
output:  
  rmarkdown::html_vignette:  
    css: mystyles.css
```

Chapter 4

Optimization

In this Chapter, we will see how to measure and improve code performance.

4.1 Measuring performance

4.1.1 Benchmarking

Reading: <http://adv-r.had.co.nz/Performance.html#microbenchmarking>

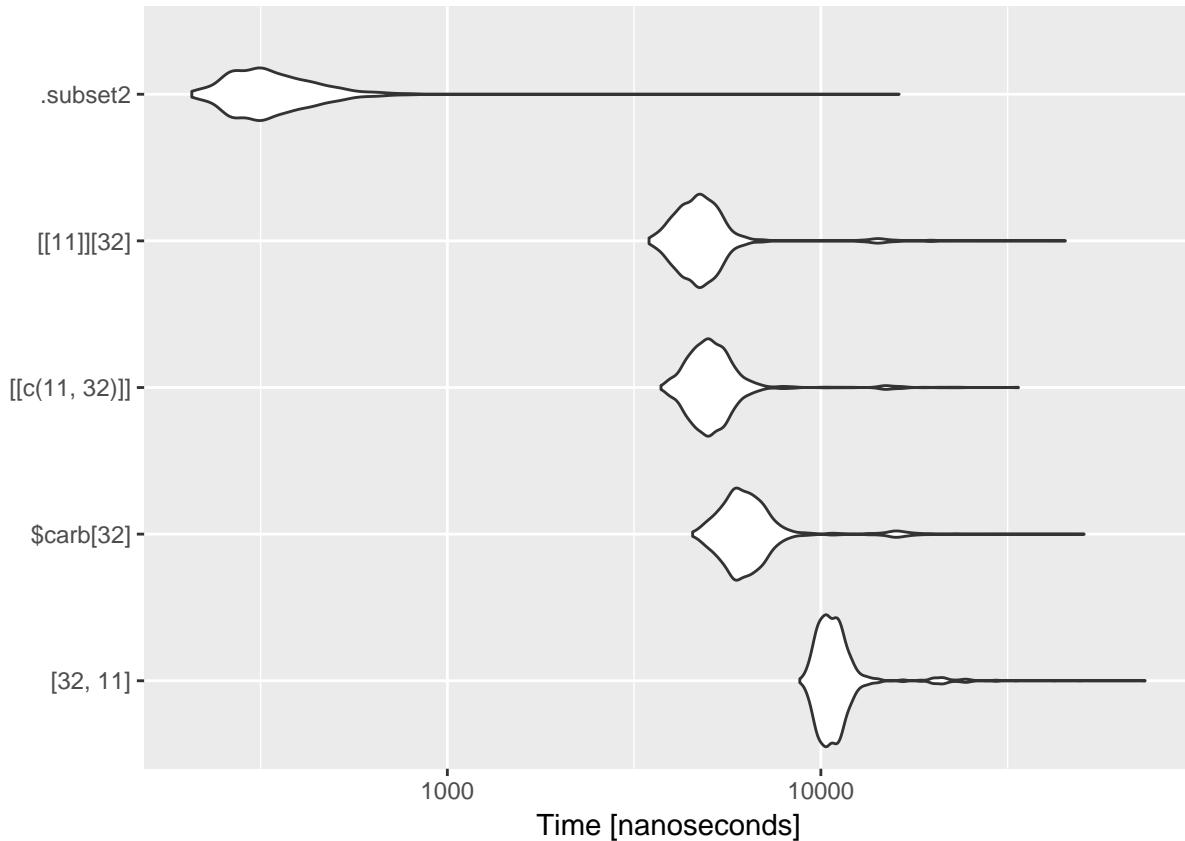
There are several ways to benchmark code (see http://www.alexejgossmann.com/benchmarking_r/) from `system.time` to dedicated packages such as `rbenchmark` (Kusnirczyk (2012)) or `microbenchmark` (Mersmann (2015)).

Let's start with an example from Wickham (2014).

```
library(microbenchmark)
m <- microbenchmark(
  times = 1000, # default is 100
  "[32, 11]"     = mtcars[32, 11],
  "$carb[32]"    = mtcars$carb[32],
  "[[c(11, 32)]]" = mtcars[[c(11, 32)]],
  "[[11]][32]"   = mtcars[[11]][32],
  ".subset2"      = .subset2(mtcars, 11)[32]
)
m

## Unit: nanoseconds
##           expr  min    lq    mean   median    uq    max neval
## [32, 11] 8783 10046.0 11326.018 10673.5 11362.5 73789 1000
## $carb[32] 4536  5697.5  6763.718  6214.0  6865.0 50683 1000
## [[c(11, 32)]] 3732  4628.5  5377.422  5029.5  5507.0 33802 1000
## [[11]][32] 3467  4287.5  5093.947  4712.5  5166.5 45145 1000
## .subset2  207   275.0   378.369   323.0   394.5 16201 1000

ggplot2::autoplot(m)
```



4.1.2 Profiling and optimization

Reading: <http://adv-r.had.co.nz/Profiling.html#measure-perf>

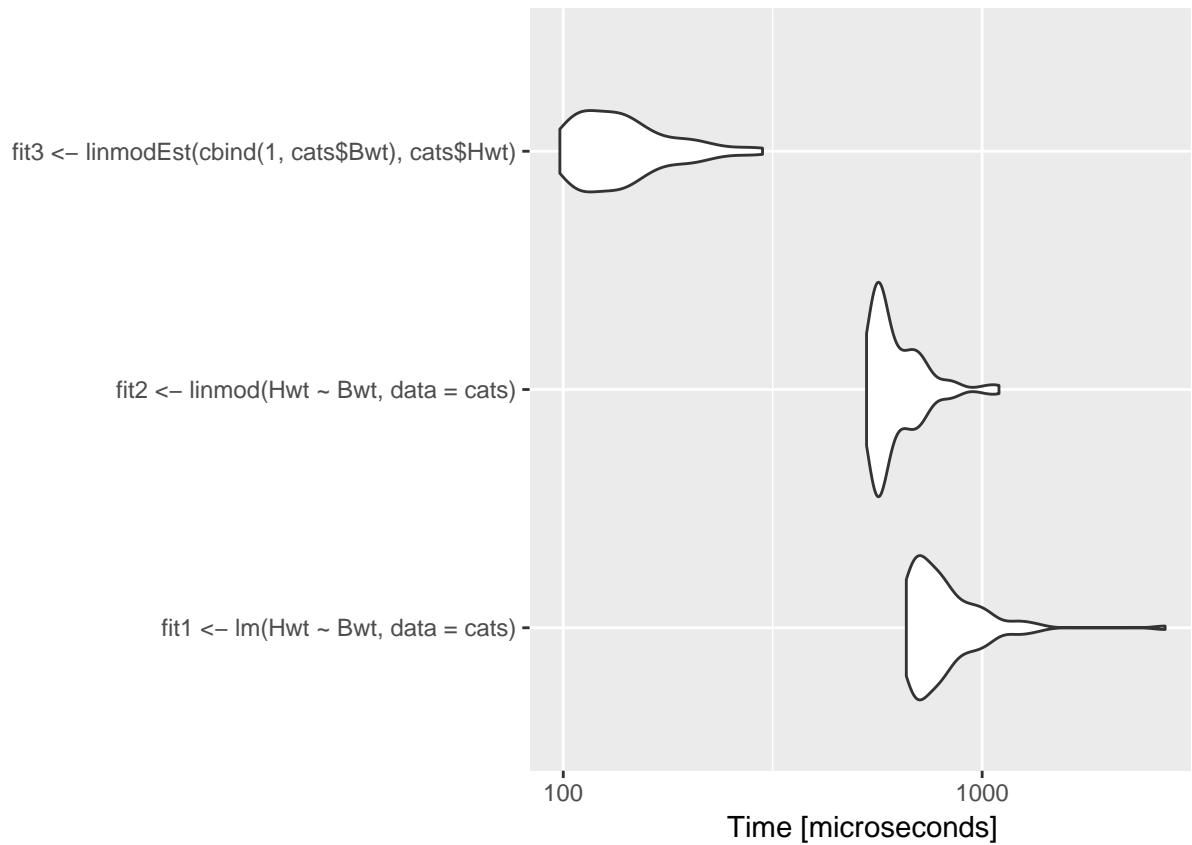
Let's compare three ways of estimating a linear regression: with built-in `lm` and with two functions we defined in package `Linreg` in Chapter 3.

```
library(Linreg)
data(cats, package = "MASS")
fit1 <- lm(Hwt ~ Bwt, data = cats)
fit2 <- linmod(Hwt ~ Bwt, data = cats)
fit3 <- linmodEst(cbind(1, cats$Bwt), cats$Hwt)

##           [,1]
## [1,] -0.3566624
## [2,]  4.0340627
all.equal(round(coef(fit1), 5), round(coef(fit2), 5))

## [1] "names for target but not for current"
## [2] "Attributes: < names for current but not for target >"
## [3] "Attributes: < Length mismatch: comparison on first 0 components >"
## [4] "target is numeric, current is matrix"
all.equal(round(coef(fit1), 5), round(fit3$coefficients, 5), check.names = FALSE)

## [1] "Attributes: < names for current but not for target >"
## [2] "Attributes: < Length mismatch: comparison on first 0 components >"
```

4.2 Improving performance

- Vectorize
- Parallelize
- Use a faster language (C/C++, Fortran, ...)
- Use different tools (as in Chapter 6)

4.3 Vectorization

Let's take an example from a blog post (that seems to be gone). It's used in Wickham (2014, Section Case studies).

```
vacc1a <- function(age, female, ily) {
  p <- 0.25 + 0.3 * 1 / (1 - exp(0.04 * age)) + 0.1 * ily
  p <- p * if (female) 1.25 else 0.75
  p <- max(0, p)
  p <- min(1, p)
  p
}

set.seed(1959)
n <- 1000
```

```

age <- rnorm(n, mean = 50, sd = 10)
female <- sample(c(T, F), n, rep = TRUE)
ily <- sample(c(T, F), n, prob = c(0.8, 0.2), rep = TRUE)

vacc1a(age[1], female[1], ily[1])

## [1] 0.1667005
vacc1a(age[2], female[2], ily[2])

## [1] 0.4045439
vacc1a(age[3], female[3], ily[3])

## [1] 0.2699324

vacc1a is not designed for vector inputs
vacc1a(age, female, ily)

## Warning in if (female) 1.25 else 0.75: the condition has length > 1 and
## only the first element will be used

## [1] 0.2526293

It should be called
vacc1a(age[1], female[1], ily[1])

## [1] 0.1667005
vacc1a(age[2], female[2], ily[2])

## [1] 0.4045439
vacc1a(age[3], female[3], ily[3])

## [1] 0.2699324

```

We can use a loop:

```

out <- numeric(n)
for (i in 1:n)
  out[i] <- vacc1a(age[i], female[i], ily[i])

```

or one of the apply functions:

```

vacc0<- function(age, female, ily) {
  sapply(1:n, function(i) vacc1a(age[i], female[i], ily[i]))
}

out0 <- vacc0(age, female, ily)

all.equal(out, out0)

## [1] TRUE

```

But, it's convenient for the function to support vector inputs, instead of relying on users writing their own wrappers. We can loop inside the function body.

```

vacc1 <- function(age, female, ily) {
  n <- length(age)
  out <- numeric(n)

```

```

for (i in seq_len(n)) {
  out[i] <- vacc1(age[i], female[i], ily[i])
}
out
}

```

or we can rely on base R functions that accept vector inputs

```

vacc2 <- function(age, female, ily) {
  p <- 0.25 + 0.3 * 1 / (1 - exp(0.04 * age)) + 0.1 * ily
  p <- p * ifelse(female, 1.25, 0.75)
  p <- pmax(0, p)
  p <- pmin(1, p)
  p
}

```

4.4 Parallelization

```

library(parallel)
cores <- detectCores()
cores

## [1] 4

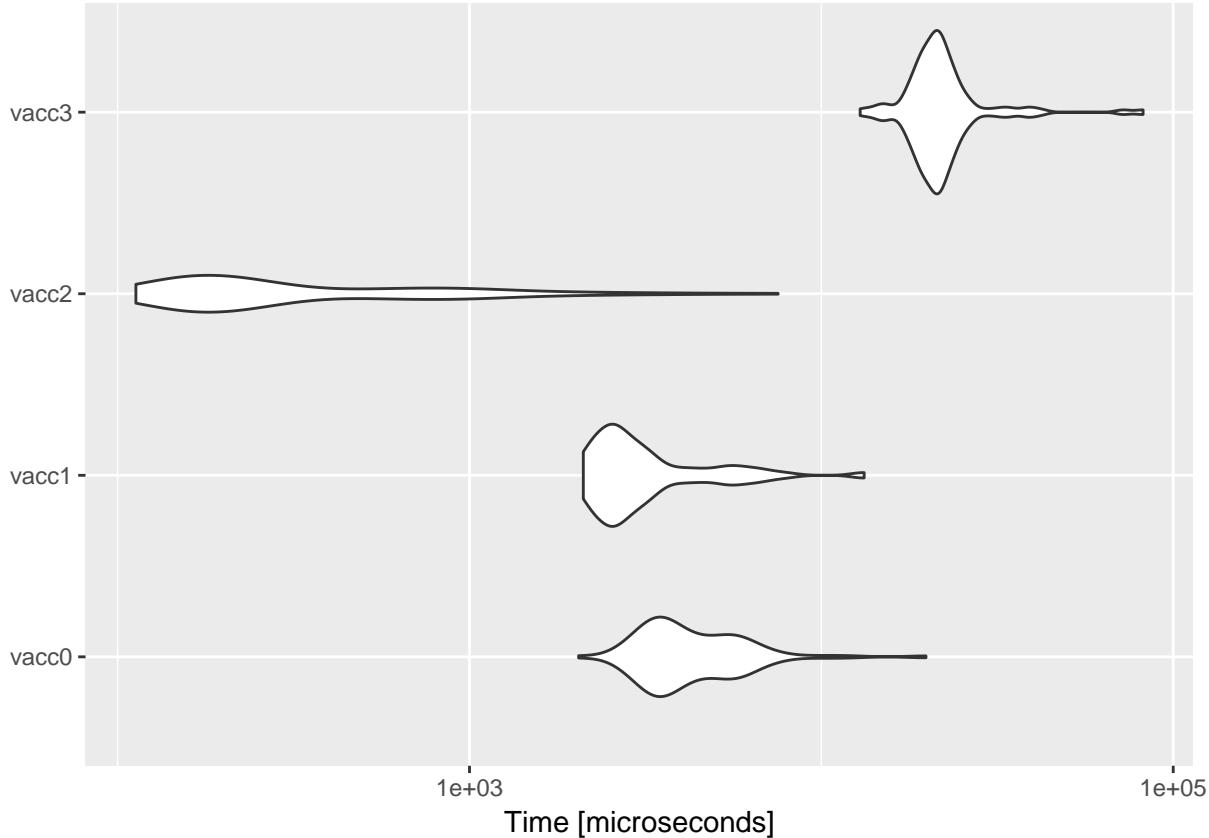
vacc3 <- function(age, female, ily) {
  mcmapply(function(i) vacc1(age[i], female[i], ily[i]), 1:n, mc.cores = cores - 1)
}

out3 <- vacc3(age, female, ily)

library(microbenchmark)
m <- microbenchmark(
  vacc0 = vacc0(age, female, ily),
  vacc1 = vacc1(age, female, ily),
  vacc2 = vacc2(age, female, ily),
  vacc3 = vacc3(age, female, ily)
)
m

## Unit: microseconds
##   expr      min       lq      mean     median       uq      max neval
##   vacc0 2042.355 3349.736 4552.8067 3803.228 5320.949 19835.006   100
##   vacc1 2106.299 2475.339 3477.1346 2762.795 3389.323 13232.481   100
##   vacc2   112.700 160.636  546.3875  221.698  614.314  7536.343   100
##   vacc3 12891.545 19432.145 22898.9777 21261.046 23412.436 82110.084   100
ggplot2::autoplot(m)

```



So, what's going on?

We will talk more about parallelization tools and techniques in Chapter ‘?(bigdata).

4.5 Introduction to C++

- C++ is a very powerful object-oriented language.
- Many tutorials are available on-line, for example <http://www.cplusplus.com/doc/tutorial/>.
- R is *interpreted*, C++ is *compiled* and typically much faster (in loops for examples).
- Our introduction to C++ is from an R perspective. Python (and most interpreted languages) can be extended with C++ too.

4.5.1 Rcpp

Reading: <http://adv-r.had.co.nz/Rcpp.html>

- Rcpp Eddelbuettel (2013) makes it very easy to use C++ code in R (for example to speed up a function or to wrap methods already implemented in C++).
- Rcpp provides “syntactic sugar” that makes it easy to leverage C++ even without a deep knowledge of it.
- To use Rcpp, you need a C++ compiler:
 - Windows: Rtools

- OS X: Xcode
- Linux: `r-base-dev` from package manager

4.5.2 Hello World!

```
library(Rcpp)
cppFunction('void hello(){
  Rprintf("Hello, world!");
}')
hello

## function ()
## invisible(.Primitive(".Call"))(<pointer: 0x11081dcc0>)
hello()

## Hello, world!
```

`Rprintf` is the counterpart of C++ `printf` function.

Let's take the first example of Wickham (2014), Section Getting started with C++.

```
cppFunction('int add(int x, int y, int z) {
  int sum = x + y + z;
  return sum;
}')
```

We have to specify the input type and the output type. As expected

```
add(1, 2, 3)
```

returns 6. How about?

```
add(1.1, 2.2, 3.3)
```

```
cppFunction('double addd(double x, double y, double z) {
  double sum = x + y + z;
  return sum;
}')
```

With `addd` we do get 6.6:

```
addd(1.1, 2.2, 3.3)
```

4.5.3 sourceCpp

When C++ code takes more than a couple of lines, it's more convenient to create a stand-alone C++ source file.

From the RStudio default template:

```
#include <Rcpp.h>
using namespace Rcpp;

NumericVector timesTwo(NumericVector x) {
  return x * 2;
}
```

```
/** R
timesTwo(42)
*/
```

From R, we can use `sourceCpp` to access `timesTwo` in R:

```
sourceCpp("src/times-two.cpp")
timesTwo(100)
```

4.5.4 Data types

```
int double bool string
NumericVector LogicalVector IntegerVector CharacterVector
NumericMatrix IntegerMatrix LogicalMatrix CharacterMatrix
NA_REAL NA_INTEGER NA_STRING NA_LOGICAL
List DataFrame Function
...
```

4.5.5 Sugar

Reading: <http://adv-r.had.co.nz/Rcpp.html#rcpp-sugar>.

- Vectorization of `+`, `*`, `-`, `/`, `pow`, `<`, `<=`, `>`, `>=`, `==`, `!=`, ...
- Vectorization of R-like functions: `abs()`, `exp()`, `factorial()`, ...

Exercise 4.1. Can you write an Rcpp function similar to `addd` but accepting vector arguments?

```
cppFunction('NumericVector addv(NumericVector x, NumericVector y, NumericVector z) {
  NumericVector sum = x + y + z;
  return sum;
}')
```

4.5.6 Example (continued)

```
#include <Rcpp.h>
using namespace Rcpp;

double vacc3a(double age, bool female, bool ily){
  double p = 0.25 + 0.3 * 1 / (1 - exp(0.04 * age)) + 0.1 * ily;
  p = p * (female ? 1.25 : 0.75);
  p = std::max(p, 0.0);
  p = std::min(p, 1.0);
  return p;
}

// [[Rcpp::export]]
NumericVector vacc3(NumericVector age, LogicalVector female,
                    LogicalVector ily) {
  int n = age.size();
```

```

NumericVector out(n);

for(int i = 0; i < n; ++i) {
    out[i] = vacc3a(age[i], female[i], ily[i]);
}

return out;
}

```

4.5.7 Back to Linreg

- `armadillo` is a very powerful C++ linear algebra library: <http://arma.sourceforge.net/>
- It can be used in `Rcpp` via the `RcppArmadillo` package.

Exercise 4.2. Can you write an `Rcpp` function similar to `linmodEst`?

```

linmodEst <- function(x, y) {
  ## CC: crossprod or a QR decomposition (as in the original version) are more efficient
  coef <- solve(t(x) %*% x) %*% t(x) %*% y
  ## degrees of freedom and standard deviation of residuals
  df <- nrow(x) - ncol(x)
  sigma2 <- sum((y - x %*% coef)^ 2) / df
  ## compute sigma^2 * (x'x)^-1
  vcov <- sigma2 * solve(t(x) %*% x)
  colnames(vcov) <- rownames(vcov) <- colnames(x)
  list(
    coefficients = coef,
    vcov = vcov,
    sigma = sqrt(sigma2),
    df = df
  )
}

```

4.6 Rcpp packages

Readings: - <https://cran.r-project.org/web/packages/Rcpp/vignettes/Rcpp-package.pdf> - <http://adv-r.had.co.nz/Rcpp.html#rcpp-package>

4.7 Getting serious about C++

4.7.1 STL

STL: Standard Template Library

Reading: <http://adv-r.had.co.nz/Rcpp.html#stl>

4.8 Profiling

Reading: <https://rstudio.github.io/profvis/>

```
library(profvis)

profvis({
  data(diamonds, package = "ggplot2")

  plot(price ~ carat, data = diamonds)
  m <- lm(price ~ carat, data = diamonds)
  abline(m, col = "red")
})
```

Chapter 5

Databases

5.1 What is SQL?

SQL (Structured Query Language) is a standard way of specifying the information you want to receive from a database. There are a number of variations on the language, and a number of online resources available for learning their various complexities. However, the general structure of all SQL queries is consistent across implementations.

SQL is an imperative computer language. This means that it describes the output desired without actually describing the calculations required to get the output described. This allows for the verbs and structures of the language to be used across database systems, as well as in other areas of data handling.

5.1.1 What is a database?

A database is simply an organized structure for storing and accessing data on disk. There are a number of structures used to store data on disk, each with their own languages. However, despite the variations in structure, the goals (and song) remain the same. The process of data storage on disk is controlled by the database management system (DBMS).

5.1.2 Relational Databases (SQL)

The most common type of DBMS is a relational database (RDBMS). A Relational Database stores information in the form of entities and the relationships between them. Entities are typically nouns and relationships are typically verbs. For example, if we wanted to store information about class enrollment at a university, the entities would consist of objects like a student, class, and professor. The relationships would consist of takes and teaches. Relationships can be one to one, many to many, or one to many.

5.1.3 Types of Relational Databases

- Commercial
 - Oracle Database
 - Microsoft
 - SQL Server
 - ...
- Open-source
 - MySQL

- PostgreSQL
- SQLite
- ...
- SQLite is the easiest way to start: unlike the others, it's not a client-server DB. The whole DB can live in a (portable) folder. All the required tools are included in `dplyr`.

5.1.4 SQL

In relational databases, entities and relationships are represented by tables, where each row or record in a table represents a particular instance of that general object. Continuing the class example, students would be stored in `Student`, classes in `Class`, and professors in `Professor`. The table containing the relationships between students and classes would be likely named `StudentClass` and the

The three key parts of a SQL query are the `SELECT` clause, the `FROM` clause, and the `WHERE` clause. The `SELECT` clause specifies the pieces of information you want about an individual record, the `FROM` clause specifies the tables that will be used

To get all information about all students we would type the following:

```
SELECT * FROM STUDENT
```

To Select the name and birthday of all students in classes taught by Dr. Choirat would be a more complex query, which would likely look something like this:

```
SELECT Name,
       DOB
  FROM Student s
    inner join StudentClass sc on
      s.ID = sc.studentid
    inner join ProfessorClass pc on
      sc.classid = pc.classid
    inner join Professor p on
      pc.profid = p.id
 WHERE p.lastname = "Choirat"
```

5.2 SQLite: An Exercise

Create an in memory DB

```
sqlite3
```

5.2.1 Make a Table

```
CREATE TABLE table1(x,y,z);
```

5.2.2 Insert Values

```
INSERT INTO table1 VALUES (1,2,3),(4,5,6),(7,8,9);
```

5.2.3 Select Values

Select All Values

```
SELECT * FROM table1;
```

Select specific values

```
SELECT z from table1 WHERE x = 4;
```

5.3 SQL and R

There are a number of R packages for interfacing directly with RDBs. RODBC is one such example that allows for queries to be submitted to previously set up database connections with the results being returned as a data frame for further analysis in R. There's a large amount of documentation available online for these methods. Each system has its own idiosyncracies.

5.3.1 Data: oscars and movies again: 2016 Oscars Nominations

```
library(readr)
library(dplyr)

db <- src_sqlite("db.sqlite3", create = TRUE)

oscars <-
name,movie,category
Adam McKay,The Big Short,Best Director
Alejandro González Iñárritu,The Revenant,Best Director
Lenny Abrahamson,Room,Best Director
Tom McCarthy,Spotlight,Best Director
George Miller,Mad Max: Fury Road,Best Director
Bryan Cranston,Trumbo,Best Actor
Matt Damon,The Martian,Best Actor
Michael Fassbender,Steve Jobs,Best Actor
Leonardo DiCaprio,The Revenant,Best Actor
Eddie Redmayne,The Danish Girl,Best Actor
Cate Blanchett,Carol,Best Actress
Brie Larson,Room,Best Actress
Jennifer Lawrence,Joy,Best Actress
Charlotte Rampling,45 Years,Best Actress
 Saoirse Ronan,Brooklyn,Best Actress
"
oscars <- read_csv(oscars, trim_ws = TRUE, skip = 1)

movies <-
movie,length_mins
The Big Short,130
Star Wars: The Force Awakens,135
Brooklyn,111
Mad Max: Fury Road,120
Room,118
The Martian,144
```

```
The Revenant,156
Spotlight,128
"
movies <- read_csv(movies, trim_ws = TRUE, skip = 1)

oscars_table <- copy_to(db, oscars)
movies_table <- copy_to(db, movies)

db
```

5.4 Non-Relational Databases (noSQL)

5.4.1 Drawbacks of Relational Databases

- Looking up all information about one entity can be expensive
- Require a large amount of overhead
- Difficult to distribute across multiple disks
- Considered to by some to be inflexible

5.4.2 Common Types of NoSQL Databases

- Graph Databases
 - Neo4j
 - OrientDB
- Document Databases
 - MongoDB
 - JSON Databases
 - XML Databases

5.5 References

The Oscar movie example comes from this lecture by Rafa Irizarry: <https://github.com/datascienceclabs/2016/blob/master/lectures/wrangling/data-wrangling-with-dplyr.Rmd>

5.6 NoSQL: MongoDB

5.6.1 JSON format

JSON: JavaScript Object Notation.

Readings:

- <http://www.json.org/>
- <http://json.org/example.html>
- <https://cran.r-project.org/web/packages/jsonlite/vignettes/json-aquickstart.html>

```
library(jsonlite)
l <- fromJSON(
  '{
```

```

"GLOSSARY": {
    "title": "example glossary",
    "GLOSSDIV": {
        "title": "S",
        "GLOSSLIST": {
            "GLOSSENTRY": {
                "ID": "SGML",
                "SortAs": "SGML",
                "GLOSSTERM": "Standard Generalized Markup Language",
                "ACRONYM": "SGML",
                "ABBREV": "ISO 8879:1986",
                "GLOSSDEF": {
                    "para": "A meta-markup language, used to create markup languages such as DocBook.",
                    "GLOSSSEEALSO": ["GML", "XML"]
                },
                "GLOSSSEE": "markup"
            }
        }
    }
}
l$GLOSSARY$title

## [1] "example glossary"
l$GLOSSARY$GLOSSDIV$GLOSSLIST$GLOSSENTRY$GLOSSDEF

## $para
## [1] "A meta-markup language, used to create markup languages such as DocBook."
##
## $GLOSSSEEALSO
## [1] "GML" "XML"
l <- fromJSON("src/example.json")

```

5.6.2 Reading a JSON file

```
l <- fromJSON("~/Dropbox/Data17/citibike/stations_2017-11-25.json")
```

5.6.3 RESTful APIs

REST: Representational State Transfer

Readings:

- <https://spring.io/understanding/REST>
- https://en.wikipedia.org/wiki/Representational_state_transfer#Applied_to_Web_services
- <https://cran.r-project.org/web/packages/jsonlite/vignettes/json-apis.html>

5.6.4 Back and forth

```

l <- list(
  a = data.frame(v1 = 1:5, v2 = letters[1:5]),
  b = list(el1 = 4, el2 = "hello")
)
l

## $a
##   v1 v2
## 1  1  a
## 2  2  b
## 3  3  c
## 4  4  d
## 5  5  e
##
## $b
## $b$el1
## [1] 4
##
## $b$el2
## [1] "hello"
toJSON(l)

## [{"a": [{"v1": 1, "v2": "a"}, {"v1": 2, "v2": "b"}, {"v1": 3, "v2": "c"}, {"v1": 4, "v2": "d"}, {"v1": 5, "v2": "e"}], "b": [
  {"el1": 4, "el2": "hello"}]}
toJSON(l, pretty = TRUE)

## [
##   "a": [
##     {
##       "v1": 1,
##       "v2": "a"
##     },
##     {
##       "v1": 2,
##       "v2": "b"
##     },
##     {
##       "v1": 3,
##       "v2": "c"
##     },
##     {
##       "v1": 4,
##       "v2": "d"
##     },
##     {
##       "v1": 5,
##       "v2": "e"
##     }
##   ],
##   "b": [
##     {
##       "el1": 4,
##       "el2": "hello"
##     }
##   ]
## ]

```

```
##    }
## }
l1 <- fromJSON(toJSON(l1))
```

5.6.5 MongoDB

Reading: <https://docs.mongodb.com/manual/administration/install-community/>

With homebrew on OS X:

```
brew update
brew install mongodb
brew tap homebrew/services # once
brew services start mongodb
```

5.6.6 Querying data

Reading: <https://jeroen.github.io/mongolite/query-data.html>

5.6.7 Example: mHealth data

```
system("mongoimport --db mhealth --collection sleep --drop --file ~/Dropbox/Data17/mHealth/sleep-duration.csv")
library(mongolite)
mhealth <- mongo(db = "mhealth")
sleep <- mongo(collection = "sleep", db = "mhealth")
sleep$count() # 52 records
alldata <- sleep$find({})
alldata
sleep$find()
```


Chapter 6

Big data

6.1 How to deal with (very / too) large datasets?

1. Use more RAM / processors / drive space...
2. Use less data: (re)sample, ...
3. Use a database
4. Use specific R packages (`ff`, `bigmemory`)
5. Use other tools

6.2 How big is big?

1. Fits in RAM and on drive (but slow)
2. Doesn't fit in RAM but fits on drive
3. Doesn't fit in RAM and doesn't fit on drive

6.3 List of tools

Reading: Varian (2014) (PDF available)

Spark? h2o? More? Let's go back to the bottlenecks

- CPU
- RAM
- I/O

6.4 Data that fits in memory

6.4.1 Faster I/O

Reading: <https://cran.r-project.org/web/packages/data.table/vignettes/datatable-intro.html>

`data.table` provides an enhanced of a `data.frame` and faster I/O with `fread` and `fwrite`.

To read the 0.5GB ratings file from MovieLens

Tools for Manipulating Big Data

<i>Google name</i>	<i>Analog</i>	<i>Description</i>
Google File System	Hadoop File System	This system supports files stored in a distributed across hundred of computers.
Bigtable	Cassandra	This is a table of data that can stretch across multiple servers. It too can stretch out horizontally.
MapReduce	Hadoop	This is a system for accessing data in large data structures. MapReduce allows you to access data by specifying the data you are interested in. This is distributed to the machines and is then aggregated back to the different shards of the data. The results are then combined ("reduced") into a summary table you are interested in.
Sawzall	Pig	This is a language for creating data processing pipelines.
Go	None	Go is flexible open-source, statically typed computer language that makes parallel data processing.
Dremel, BigQuery	Hive, Drill, Impala	This is a tool that allows data to be queried in a simplified form of Structured Query Language (SQL). With Dremel it is possible to query on a petabyte of data in a few seconds.

Table 6.1: I/O comparison

package	function.	speed	output
base	read.csv	slow	data.frame
data.table	fread	very fast	data.table
readr	read_csv	fast	tibble

```
library(data.table)
system.time(ratings <- fread("~/Dropbox/Data17/ml-20m/ratings.csv"))
```

takes

```
Read 20000263 rows and 4 (of 4) columns from 0.497 GB file in 00:00:05
  user  system elapsed
 4.007   0.229   4.244
```

while

```
system.time(ratings <- read.csv("~/Dropbox/Data17/ml-20m/ratings.csv"))
```

takes

```
  user  system elapsed
85.199   2.711  90.997
```

There are ways to improve the speed of `read.csv` (for example, by specifying column types). But in general `fread` is much faster.

```
library(readr) # in tidyverse
system.time(ratings <- read_csv("~/Dropbox/Data17/ml-20m/ratings.csv"))
```

```
  user  system elapsed
10.290   3.037  18.450
```

also tends to perform better than `read.csv`.

6.4.2 Reference vs copy

Reading: <http://adv-r.had.co.nz/memory.html> Reading: <https://jangorecki.gitlab.io/data.table/library/data.table/html/assign.html>

```
library(pryr)
library(data.table)

d <- read.csv("~/Dropbox/Data17/ml-latest-small/ratings.csv")
D <- fread("~/Dropbox/Data17/ml-latest-small/ratings.csv")

object_size(d)
object_size(D)

mem_change(d$Idx <- 1:nrow(d))
mem_change(D[, Idx:= 1:N])

object_size(d$Idx)
object_size(D$Idx)
```

```
d <- read.csv("~/Dropbox/Data17/ml-latest-small/ratings.csv")
D <- fread("~/Dropbox/Data17/ml-latest-small/ratings.csv")

.Internal(inspect(d))
d$Idx <- 1:nrow(d)
.Internal(inspect(d))

.Internal(inspect(D))
D[, Idx:= 1:N]
.Internal(inspect(D))
```

6.4.3 data.table: another data manipulation grammar

Reading: <https://cran.r-project.org/web/packages/data.table/vignettes/datatable-intro.html>

Exercise 6.1. Benchmark adding a column to a large data frame vs a large data table.

6.5 Data that doesn't fit in memory (but fits on drive)

Let's try to work with a 12GB file and 4/8 GB of memory...

6.6 Pure R solutions

6.6.1 A regressions example

```
library(data.table)
airlines <- fread("/Users/cchoirat/Dropbox/Data17/AirFlights/allyears2k.csv")
rfit <- lm(ArrDelay ~ Distance, data = airlines)
summary(rfit)
```

6.6.2 Sampling

- Read the data (even line by line)
- Select a sample of rows
- Run your model on the random sample

6.6.3 bigmemory

<https://cran.r-project.org/web/packages/bigmemory/index.html>

Reading: <https://cran.r-project.org/web/packages/bigmemory/vignettes/Overview.pdf>

bigmemory: Manage Massive Matrices with Shared Memory and Memory-Mapped Files

Create, store, access, and manipulate massive matrices. Matrices are allocated to shared memory and may use memory-mapped files. Packages ‘biganalytics’, ‘bigtabulate’, ‘synchronicity’, and ‘bigalgebra’ provide advanced functionality.

(+) pure R solution from a user perspective

(-) mostly for numeric data matrices, mostly to speed up computations on data of +/- RAM size

```
library(bigmemory)
library(biganalytics)
# library(bigtabulate)
# library(biglm)

flights <- read.big.matrix(
  "/Users/cchoirat/Dropbox/Data17/AirFlights/allyears2k.csv",
  header = TRUE,
  backingfile = "allyears2k.bin",
  backingpath = "/Users/cchoirat/Dropbox/Data17/AirFlights/",
  descriptorfile = "allyears2k.desc",
  shared = TRUE)

air_flights <- attach.big.matrix("/Users/cchoirat/Dropbox/Data17/AirFlights/allyears2k.desc")
dim(air_flights)
colnames(air_flights)
mean(air_flights[, "ArrDelay"], na.rm = TRUE)

fit <- biglm.big.matrix(ArrDelay ~ Distance, data = air_flights)
fit
summary(fit)
```

6.6.4 Database connections and lazy evaluation

```
library(data.table)
D <- fread("~/Dropbox/Data17/ml-20m/ratings.csv")

library(sqlite)
read.csv.sql(file = "~/Dropbox/Data17/ml-20m/ratings.csv",
             sql = c("ATTACH 'ratings.sqlite3' AS NEW"))
read.csv.sql(file = "~/Dropbox/Data17/ml-20m/ratings.csv",
             sql = "CREATE TABLE ratings_table AS SELECT * FROM file",
             dbname = "ratings.sqlite3")

library(dplyr)
library(DBI)

con <- DBI::dbConnect(RSQLite::SQLite(), dbname = "ratings.sqlite3")

ratings_db <- tbl(con, "ratings_table")
ratings_db %>%
  select(ends_with("Id")) %>%
  filter(movieId < 100)

# Source: lazy query [?? x 2]
# Database: sqlite 3.19.3
#   [/Users/cchoirat/Documents/LocalGit/bigdata17/ratings.sqlite3]
  userId movieId
    <int>   <int>
 1       1       2
 2       1      29
```

```

3     1     32
4     1     47
5     1     50
6     2     3
7     2     62
8     2     70
9     3     1
10    3     24
# ... with more rows
# ... with more rows

ratings_db %>%
  select(ends_with("Id")) %>%
  filter(movieId < 100) %>%
  collect()

# A tibble: 790,226 x 2
  userId movieId
  <int>   <int>
1     1       2
2     1      29
3     1      32
4     1      47
5     1      50
6     2       3
7     2     62
8     2     70
9     3       1
10    3     24
# ... with 790,216 more rows

```

6.7 Scaling up

6.8 Parallel computing and clusters

6.9 Cloud computing

More soon with the Odyssey guest lecture (<https://www.rc.fas.harvard.edu/odyssey/>).

6.10 h2o: “Fast Scalable Machine Learning”

<http://www.h2o.ai/>

<http://www.r-bloggers.com/scalable-machine-learning-for-big-data-using-r-and-h2o/>

<http://venturebeat.com/2014/11/07/h2o-funding/> <https://www.h2o.ai/driveless-ai/> <https://www.infoworld.com/article/3236048/machine-learning/review-h2oai-automates-machine-learning.html>

6.10.1 Ecosystem

Readings:

- <http://docs.h2o.ai/h2o/latest-stable/h2o-docs/welcome.html>
- <http://www.h2o.ai/download/h2o/r>
- <https://cran.r-project.org/web/packages/h2o/index.html>

To build H2O or run H2O tests, the 64-bit JDK is required.

To run the H2O binary using either the command line, R, or Python packages, only 64-bit JRE is required.

```
if ("package:h2o" %in% search()) { detach("package:h2o", unload=TRUE) }
if ("h2o" %in% rownames(installed.packages())) { remove.packages("h2o") }
install.packages("h2o")
```

6.11 Running h2o locally within R

```
library(h2o)
localH2O <- h2o.init(min_mem_size = "32g")

# h2o.init(ip = "localhost", port = 54321, startH2O = TRUE,
#           forceDL = FALSE, enable_assertions = TRUE, license = NULL,
#           nthreads = -2, max_mem_size = NULL, min_mem_size = NULL,
#           ice_root = tempdir(), strict_version_check = TRUE,
#           proxy = NA_character_, https = FALSE, insecure = FALSE,
#           username = NA_character_, password = NA_character_)
```

Connection successful!

R is connected to the H2O cluster:

H2O cluster uptime:	19 days 12 hours
H2O cluster version:	3.14.0.3
H2O cluster version age:	1 month and 24 days
H2O cluster name:	H2O_started_from_R_cchoirat_bgt310
H2O cluster total nodes:	1
H2O cluster total memory:	30.67 GB
H2O cluster total cores:	8
H2O cluster allowed cores:	8
H2O cluster healthy:	TRUE
H2O Connection ip:	localhost
H2O Connection port:	54321
H2O Connection proxy:	NA
H2O Internal Security:	FALSE
H2O API Extensions:	XGBoost, Algos, AutoML, Core V3, Core V4
R Version:	R version 3.4.2 (2017-09-28)

6.12 JVM (from Wikipedia)

A Java virtual machine (JVM) is an abstract computing machine that enables a computer to run a Java program. There are three notions of the JVM: specification, implementation, and instance. The specification is a document that formally describes what is required of a JVM implementation.

(https://en.wikipedia.org/wiki/Java_virtual_machine)

6.13 Which languages? (from Wikipedia)

This list of JVM Languages comprises notable computer programming languages that are used to produce software that runs on the Java Virtual Machine (JVM). Some of these languages are interpreted by a Java program, and some are compiled to Java bytecode and JIT-compiled during execution as regular Java programs to improve performance.

6.14 Which languages?

https://en.wikipedia.org/wiki/List_of_JVM_languages

- Java
- Scala, an object-oriented and functional programming language
- Jython
- R (an implementation of R: [https://en.wikipedia.org/wiki/R_\(programming_language\)](https://en.wikipedia.org/wiki/R_(programming_language)))
- ...

6.15 State of the h2o JVM

```
h2o.clusterInfo()

R is connected to the H2O cluster:
H2O cluster uptime:      19 days 13 hours
H2O cluster version:     3.14.0.3
H2O cluster version age: 1 month and 24 days
H2O cluster name:        H2O_started_from_R_cchoirat_bgt310
H2O cluster total nodes: 1
H2O cluster total memory: 30.67 GB
H2O cluster total cores: 8
H2O cluster allowed cores: 8
H2O cluster healthy:     TRUE
H2O Connection ip:       localhost
H2O Connection port:     54321
H2O Connection proxy:    NA
H2O Internal Security:   FALSE
H2O API Extensions:     XGBoost, Algos, AutoML, Core V3, Core V4
R Version:               R version 3.4.2 (2017-09-28)
```

Let's check <http://localhost:54321/flow/index.html>.



Flow ▾

Cell ▾

Data ▾

Model ▾

Score

Untitled Flow



CS

assist

?

Assistance

<i>Routine</i>	<i>Description</i>
importFiles	Import file(s) into H ₂ O
getFrames	Get a list of frames in H ₂ O
splitFrame	Split a frame into two or more frames
mergeFrames	Merge two frames into one
getModels	Get a list of models in H ₂ O
getGrids	Get a list of grid search results in H ₂ O
getPredictions	Get a list of predictions in H ₂ O
getJobs	Get a list of jobs running in H ₂ O
buildModel	Build a model
runAutoML	Automatically train and tune many models
importModel	Import a saved model
predict	Make a prediction

● Ready

6.15.1 Importing data into h2o from the R session

```
data(cars)
cars_to_h2o <- as.h2o(cars, destination_frame = "cars_from_r")
is.data.frame(cars_to_h2o) # FALSE
class(cars_to_h2o) # H2OFrame
```

(No persistence beyond the R session when h2O is started from R.)

6.15.2 h2o functions

```
summary(cars_to_h2o) # actually calls h2o:::summary.H2OFrame(cars_to_h2o)
```

Approximated quantiles computed! If you are interested in exact quantiles, please pass the `exact_quantiles` argument.

	Min.	Min.	1st Qu.	1st Qu.	Median	Median	Mean	Mean	3rd Qu.	3rd Qu.	Max.	Max.
	: 4.0	: 2.00	: 12.0	: 26.00	: 15.0	: 36.00	: 15.4	: 42.98	: 19.0	: 56.00	: 25.0	: 120.00

6.15.3 Let's check from the h2o JVM

From the browser: ‘Data’ -> ‘List All Frames’

The screenshot shows the H2O FLOW interface. At the top, there is a navigation bar with tabs: "H₂O FLOW" (highlighted in yellow), "Flow", "Cell", "Data" (highlighted in yellow), and "Model". Below the navigation bar, the title "Untitled Flow" is displayed. A toolbar with various icons follows. The main content area shows a message: "Deleted" with a trash can icon, indicating that the following keys were deleted from your flow:

- airlines_from_r

On the left, a sidebar shows a "getFrames" step under the "cs" workspace. The "Frames" section lists two frames:

- Type ID
- cars_from_r**

With "cars_from_r" selected, three buttons are available: "Build Model...", "Predict...", and "Inspect". At the bottom, two additional buttons are shown: "Predict on selected frames..." and "Delete selected frames".

6.15.4 Importing data into h2o from disk

```
airlines_path <- "/Users/cchoirat/Dropbox/Data17/AirFlights/allyears2k.csv" # full path
airlines_to_h2o <- h2o.importFile(path = airlines_path,
                                    destination_frame = "airlines_from_r")
summary(airlines_to_h2o)
```

6.15.5 Running a statistical model

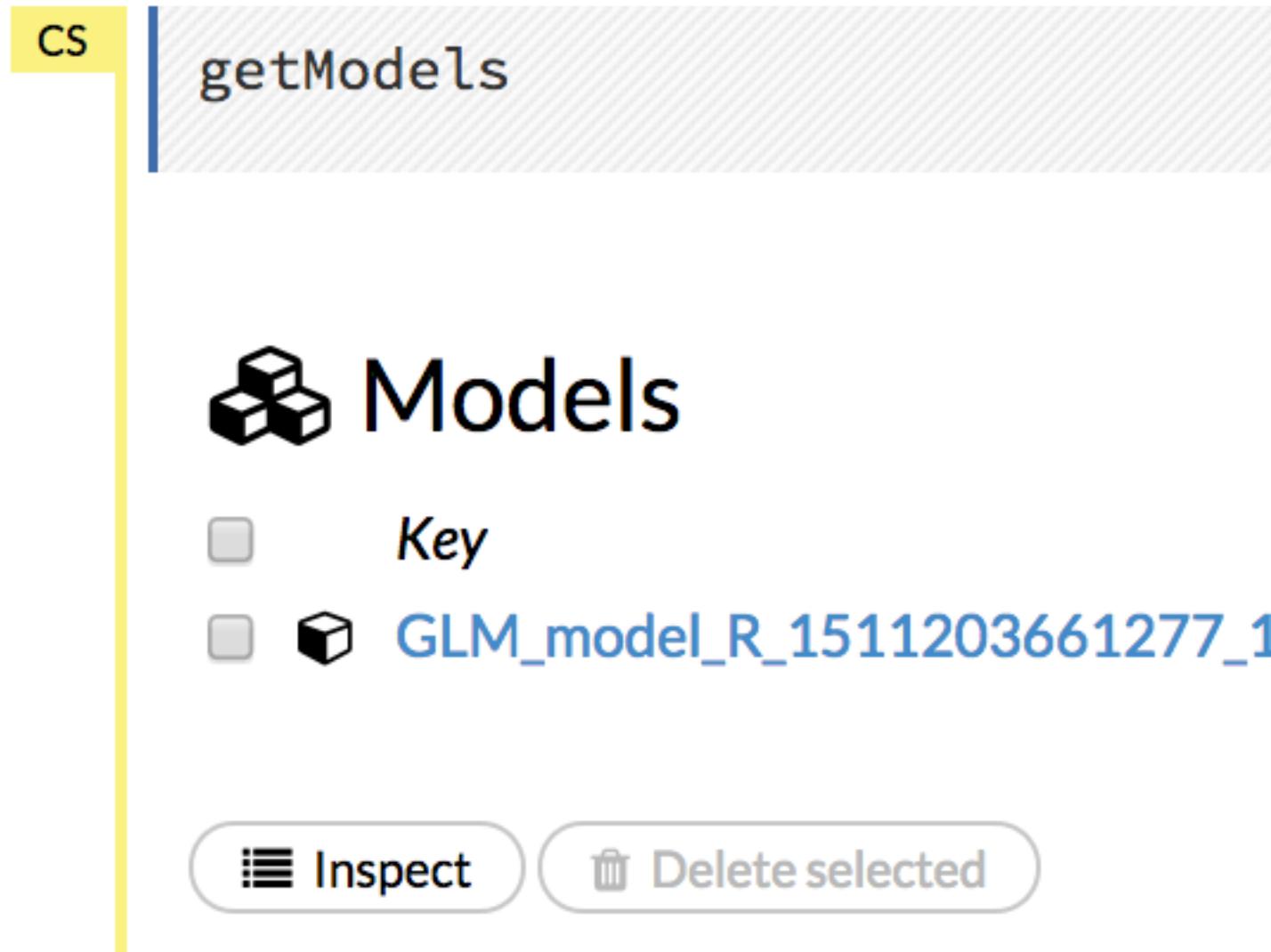
```
h2ofit <- h2o.glm(y = "ArrDelay", x = "Distance",
                     training_frame = airlines_to_h2o,
                     intercept = TRUE, # default is TRUE
                     family = "gaussian")
h2ofit
summary(h2ofit)

Coefficients: glm coefficients
              names coefficients standardized_coefficients
1 Intercept     7.702657                  9.308665
2 Distance      0.002199                 1.272253

airlines <- read.csv("~/Dropbox/Data17/AirFlights/allyears2k.csv")
rfit <- lm(ArrDelay ~ Distance, data = airlines)
summary(rfit)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 7.7011553  0.2326198 33.106  <2e-16 ***
Distance    0.0022045  0.0002487  8.865  <2e-16 ***
```

6.15.6 h2o models



6.15.7 Closing the h2o session

```
h2o.shutdown()
```

6.15.8 Available algorithms

- Deep learning
- Distributed random forest
- Gradient boosting method
- Generalized linear modeling
- Generalized low rank modeling

- K-means
- Naive Bayes
- Principal component analysis

6.15.9 How to incorporate new models in h2o?

(+) built-in models behave very much like R and are scalable

(-) not easy to extend (*e.g.*, GLM <https://github.com/h2oai/h2o-3/blob/master/h2o-algos/src/main/java/hex/glm/GLM.java>)

Exercise 6.2. Run the same analysis with the whole dataset `allyears.csv`.

6.16 Spark

Reading: <https://spark.rstudio.com/>

```
library(sparklyr)
spark_install(version = "2.1.0")

conf <- spark_config()
conf$`sparklyr.shell.driver-memory` <- "32G"
conf$spark.memory.fraction <- 0.5
sc <- spark_connect(master = "local")

library(dplyr)
iris_tbl <- copy_to(sc, iris)
flights_tbl <- copy_to(sc, nycflights13::flights, "flights")
batting_tbl <- copy_to(sc, Lahman::Batting, "batting")
src_tbls(sc)

[1] "batting" "flights" "iris"
```

You can use SQL:

```
library(DBI)
iris_preview <- dbGetQuery(sc, "SELECT * FROM iris LIMIT 10")
```

Like h2o, you can open a web interface:

```
spark_web(sc)

top_rows <- read.csv("~/Dropbox/Data17/AirFlights/allyears.csv", nrows = 5)
file_columns <- top_rows %>%
  purrr::map(function(x)"character")
rm(top_rows)

sp_flights <- spark_read_csv(sc,
  name = "flights2",
  path = "~/Dropbox/Data17/AirFlights/allyears.csv",
  memory = FALSE,
  columns = file_columns,
  infer_schema = FALSE)

# Source:   table<flights2> [?? x 31]
# Database: spark_connection
```

```

Year Month DayofMonth DayOfWeek DepTime CRSDepTime ArrTime CRSArrTime UniqueCarrier
<chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
1 1987 10 14 3 741 730 912 849 PS
2 1987 10 15 4 729 730 903 849 PS
3 1987 10 17 6 741 730 918 849 PS
4 1987 10 18 7 729 730 847 849 PS
5 1987 10 19 1 749 730 922 849 PS
6 1987 10 21 3 728 730 848 849 PS
7 1987 10 22 4 728 730 852 849 PS
8 1987 10 23 5 731 730 902 849 PS
9 1987 10 24 6 744 730 908 849 PS
10 1987 10 25 7 729 730 851 849 PS
# ... with more rows, and 22 more variables: FlightNum <chr>, TailNum <chr>,
# ActualElapsedTime <chr>, CRSElapsedTime <chr>, AirTime <chr>, ArrDelay <chr>,
# DepDelay <chr>, Origin <chr>, Dest <chr>, Distance <chr>, TaxiIn <chr>,
# TaxiOut <chr>, Cancelled <chr>, CancellationCode <chr>, Diverted <chr>,
# CarrierDelay <chr>, WeatherDelay <chr>, NASDelay <chr>, SecurityDelay <chr>,
# LateAircraftDelay <chr>, IsArrDelayed <chr>, IsDepDelayed <chr>

flights_table <- sp_flights %>%
  mutate(DepDelay = as.numeric(DepDelay),
         ArrDelay = as.numeric(ArrDelay),
         Distance = as.numeric(Distance),
         SchedDeparture = as.numeric(CRSDepTime)) %>%
  select(Origin, Dest, SchedDeparture, ArrDelay, DepDelay, Month, DayofMonth, Distance)

flights_table %>% head

```

Cache data:

```

sp_flights %>%
  tally # takes a looooong time

```

123534969...

```

# might take a while...
subset_table <- flights_table %>%
  compute("flights_subset")

subset_table %>%
  tally # a bit faster.

```

123534969 as well!

6.16.1 Run a statistical model

```

# small_flights <- spark_read_csv(sc,
#                                     name = "flights2",
#                                     path = "~/Dropbox/Data17/AirFlights/allyears2k.csv",
#                                     memory = FALSE,
#                                     columns = file_columns,
#                                     infer_schema = FALSE)

# small_flights_table <- small_flights %>%

```

```
#   mutate(DepDelay = as.numeric(DepDelay),
#          ArrDelay = as.numeric(ArrDelay),
#          Distance = as.numeric(Distance),
#          SchedDeparture = as.numeric(CRSDepTime)) %>%
#  select(Origin, Dest, SchedDeparture, ArrDelay, DepDelay, Month, DayofMonth, Distance)
#
# small_flights_table %>% head

# lm(arr_delay ~ distance, data = flights_tbl)
ml_linear_regression(flights_table, response = "ArrDelay", features = "Distance")

Coefficients:
(Intercept)      Distance
6.9707048955  0.0001100521
```

6.16.2 Deployment

Reading: <https://spark.rstudio.com/deployment.html>

6.17 Sparkling Water

Reading: <https://spark.rstudio.com/h2o.html>

6.18 Adding new models to h2o and spark

6.19 More?

GPU

6.20 Amazon Web Services (AWS)

AWS Management Console: <https://aws.amazon.com/console/>

- Amazon EC2

Amazon Elastic Compute Cloud (Amazon EC2) is a web service that provides secure, resizable compute capacity in the cloud. It is designed to make web-scale cloud computing easier for developers.

Let's launch an Amazon Linux instance (t2.micro free tier eligible) and configure a security group (Custom TCP, port 8787).

To connect:

```
chmod 400 ~/Downloads/bst262-demo.pem
ssh -i "~/Downloads/bst262-demo.pem" ec2-user@ec2-18-217-97-206.us-east-2.compute.amazonaws.com
```

--| --|_
| / Amazon Linux AMI

Stages for All Jobs

Active Stages: 1

Pending Stages: 1

Completed Stages: 13

Active Stages (1)

Stage Id ▾	Description	+details	(kill)
13	count at LinearRegression.scala:683	+details	(kill)

Pending Stages (1)

Stage Id ▾	Description	+details
14	count at LinearRegression.scala:683	+details

Completed Stages (13)

Stage Id ▾	Description	+details
12	sum at RegressionMetrics.scala:71	+details
11	aggregate at RegressionMetrics.scala:57	+details
10	treeAggregate at WeightedLeastSquares.scala:100	+details
9	treeAggregate at WeightedLeastSquares.scala:100	+details

Edit inbound rules

Type <small>i</small>	Protocol <small>i</small>	Port Range <small>i</small>	Source <small>i</small>
SSH	TCP	22	Custom
Custom TCP I	TCP	8787	Anywhere

Add Rule

NOTE: Any edits made on existing rules will result in the edited rule being deleted and the rule to be dropped for a very brief period of time until the new rule can be created.

	i-0ddfe7a3952a7cfab	t2.micro	us-east-2b
---	---------------------	----------	------------

```
___| \___| ___|
```

We install R

```
sudo yum update
sudo yum list R-* 
sudo yum install R
```

and Rstudio server (# <https://www.rstudio.com/products/rstudio/download-server/>)

```
wget https://download2.rstudio.org/rstudio-server-rhel-1.1.383-x86_64.rpm
sudo yum install --nogpgcheck rstudio-server-rhel-1.1.383-x86_64.rpm
```

We need to add user and password:

```
sudo useradd rserver
sudo passwd rserver
```

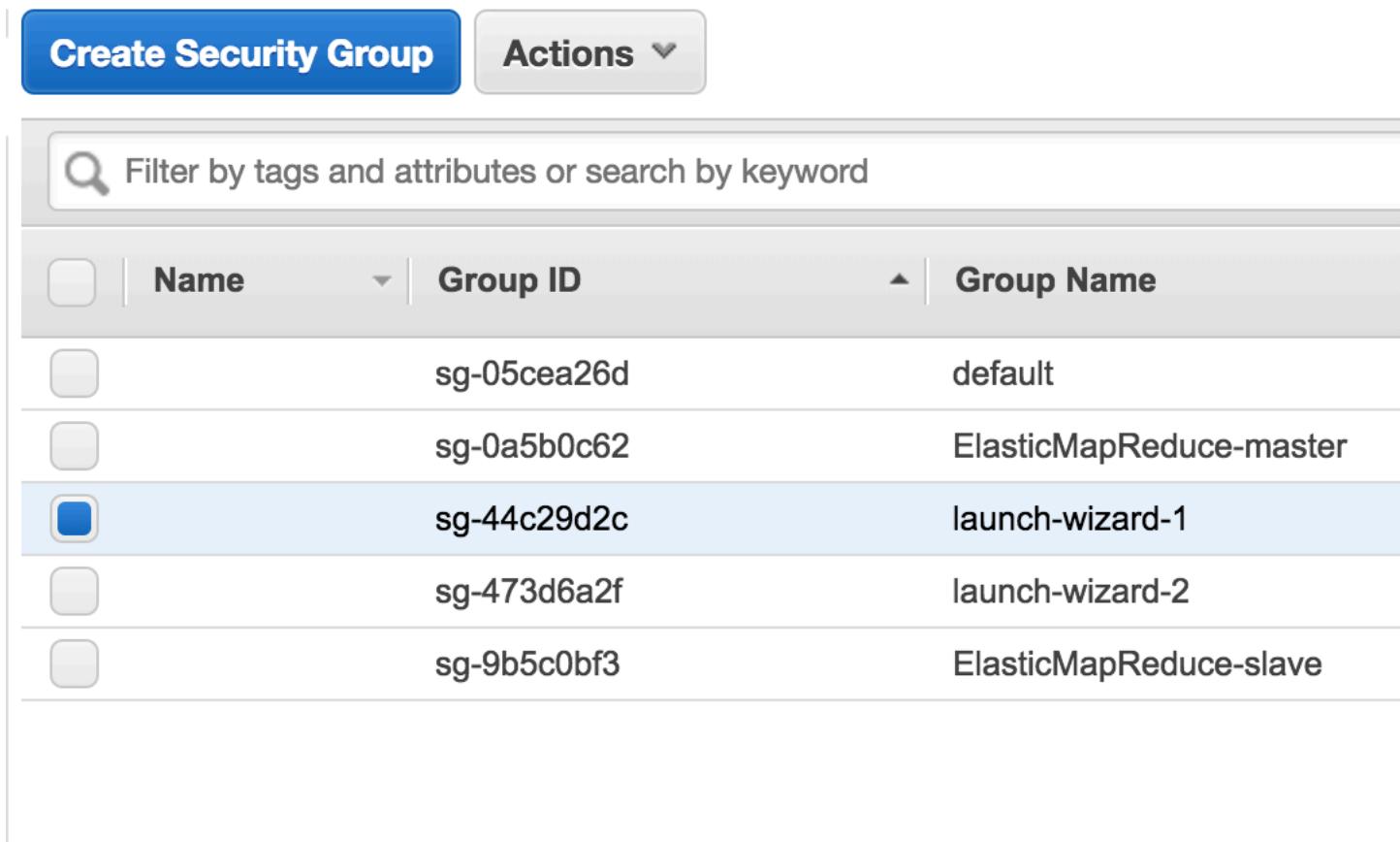
RStudio server uses port 8787. Let's fix the security groups:

We can now connect to RStudio server:

```
http://ec2-18-217-97-206.us-east-2.compute.amazonaws.com:8787/
```

6.21 Spark on AWS: Amazon Elastic MapReduce (EMR)

<https://aws.amazon.com/emr/>



The screenshot shows the AWS Management Console interface for managing security groups. At the top, there is a blue button labeled "Create Security Group" and a dropdown menu labeled "Actions". Below these, a search bar contains the placeholder text "Filter by tags and attributes or search by keyword". The main area displays a table of security groups with the following columns: "Name" (with a dropdown arrow), "Group ID", and "Group Name". The table lists five entries:

Name	Group ID	Group Name
<input type="checkbox"/>	sg-05cea26d	default
<input type="checkbox"/>	sg-0a5b0c62	ElasticMapReduce-master
<input checked="" type="checkbox"/>	sg-44c29d2c	launch-wizard-1
<input type="checkbox"/>	sg-473d6a2f	launch-wizard-2
<input type="checkbox"/>	sg-9b5c0bf3	ElasticMapReduce-slave

Sign in to RStudio

Username:

Password:

Stay signed in

Sign In

<https://aws.amazon.com/blogs/big-data/running-sparklyr-rstudios-r-interface-to-spark-on-amazon-emr/>

6.21.1 Amazon S3

GUI or CLI

6.21.2 Amazon CLI

<https://aws.amazon.com/cli/>

Chapter 7

Visualization

7.1 Maps and GIS

7.1.1 Longitudes, latitudes and CRS

7.1.2 Shapefiles

7.1.3 Backends

7.1.3.1 gdal

7.1.3.2 geos

7.1.4 R packages

7.1.4.1 sp

7.1.4.2 sf

7.1.4.3 ggmap

7.1.4.4 leaflet

7.1.4.5 Shiny

7.2 Principles of visualization

Guest lecture (James Honaker)

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