Reproducible Research:

Writing an R Package

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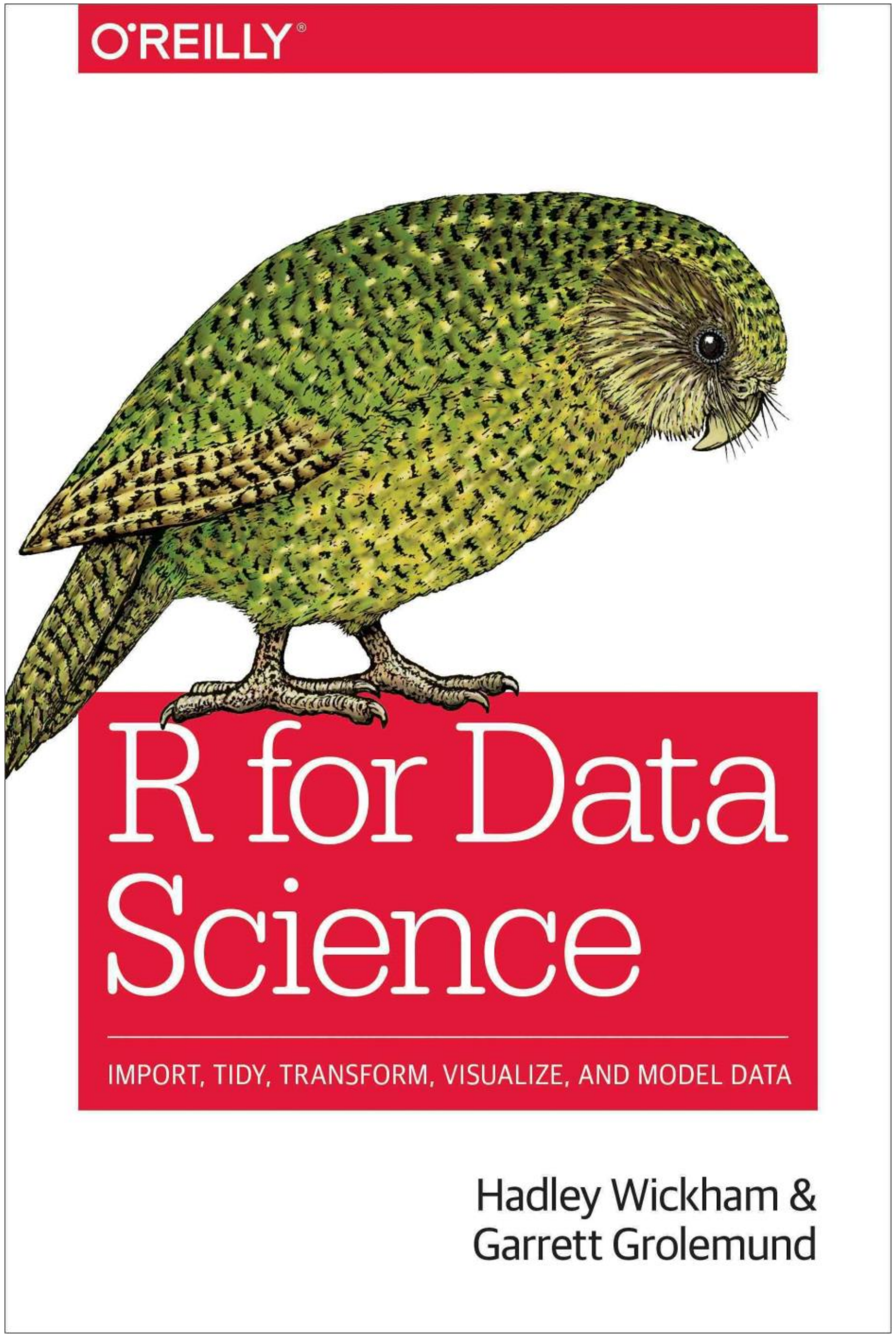
@jalapic

Materials will be available here:

- twitter.com/jalapic
- GitHub.com/jalapic/RPackage



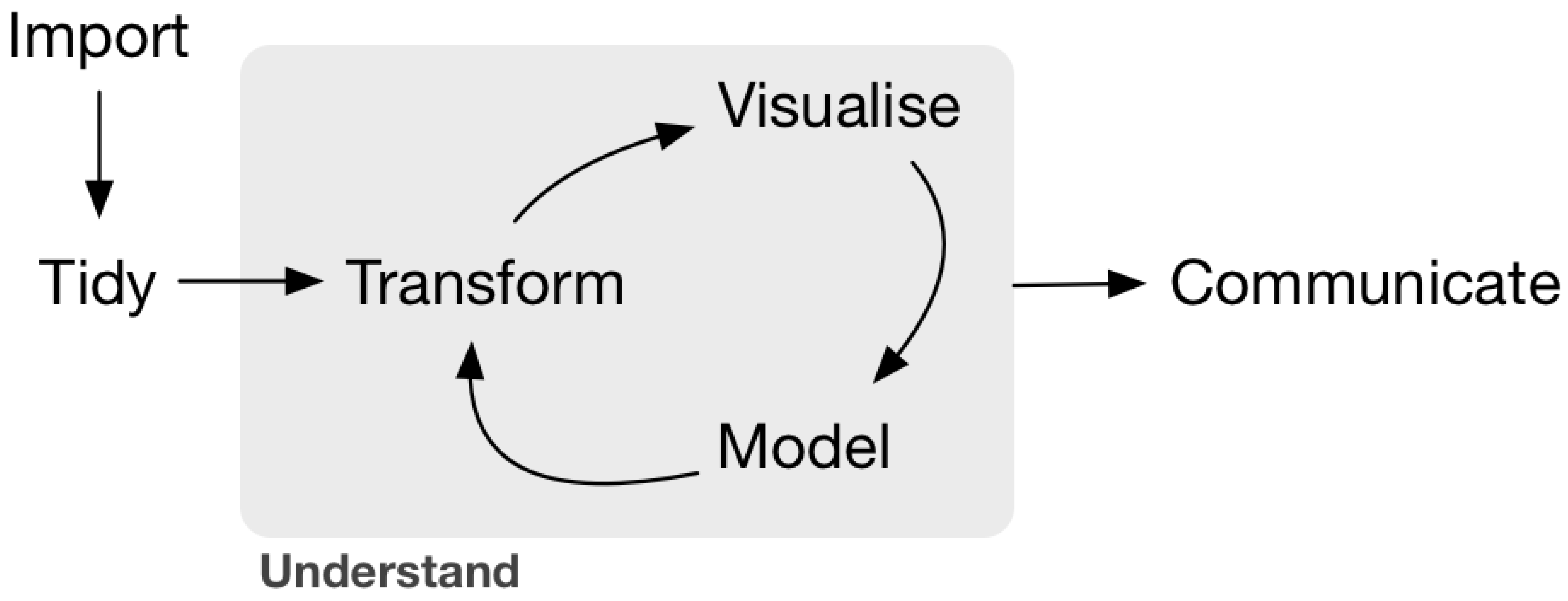
O'REILLY®

R for Data Science

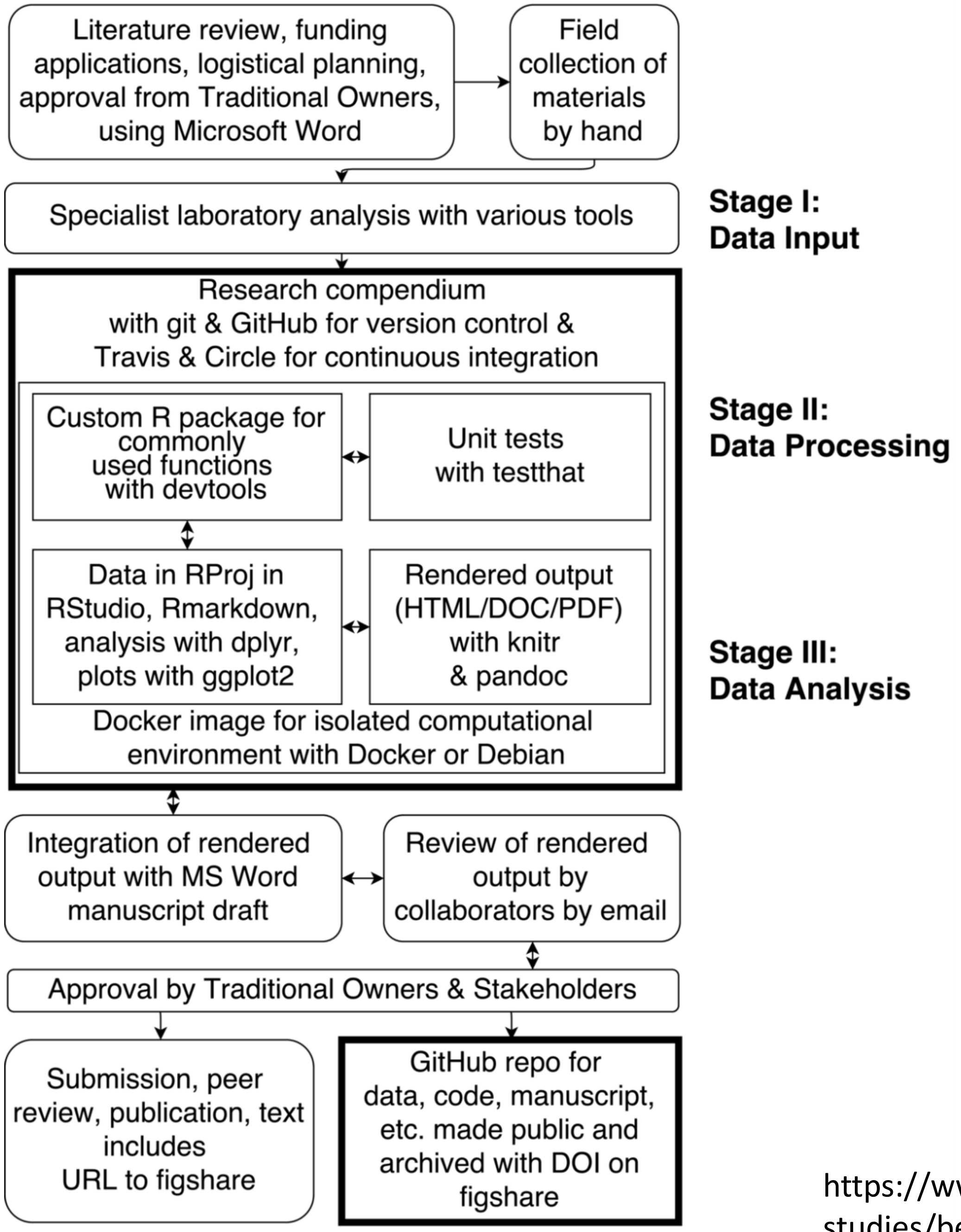
IMPORT, TIDY, TRANSFORM, VISUALIZE, AND MODEL DATA

Hadley Wickham &
Garrett Grolemund

Research Workflow – ideally automated and reproducible



Wickham & Grolemund / RStudio



Literature review, funding applications, logistical planning, approval from Traditional Owners, using Microsoft Word
Field collection of materials by hand
Specialist laboratory analysis with various tools
Stage I: Data Input
Research compendium with git & GitHub for version control & Travis & Circle for continuous integration
Custom R package for commonly used functions with devtools
Unit tests with testthat
Stage II: Data Processing
Data in RProj in RStudio, Rmarkdown, analysis with dplyr, plots with ggplot2
Rendered output (HTML/DOC/PDF) with knitr & pandoc
Stage III: Data Analysis
Docker image for isolated computational environment with Docker or Debian
Integration of rendered output with MS Word manuscript draft
Review of rendered output by collaborators by email
Approval by Traditional Owners & Stakeholders
Submission, peer review, publication, text includes URL to figshare
GitHub repo for data, code, manuscript, etc. made public and archived with DOI on figshare

Using R & Rstudio for Reproducible Research

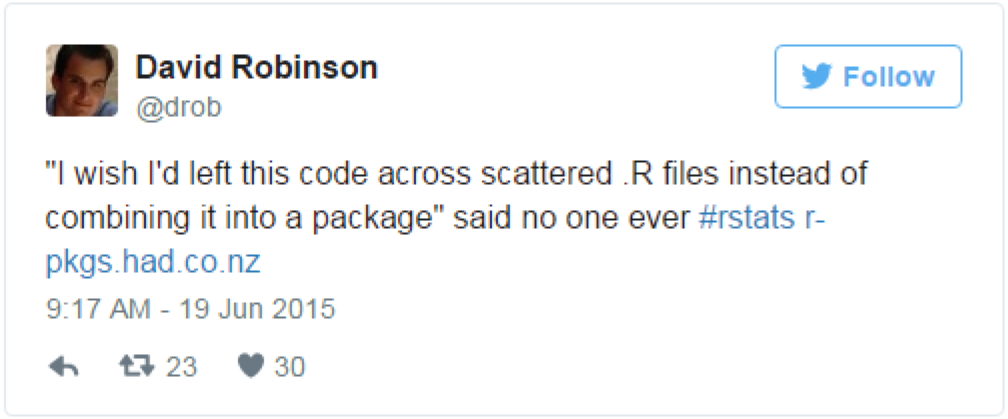
It can be overwhelming !

Let's start with one method –

Writing an R package

https://www.practicereproducibleresearch.org/case-studies/benmarwick.html

Inspiration for writing a R package


David Robinson
@drob

"I wish I'd left this code across scattered .R files instead of combining it into a package" said no one ever #rstats r-pkgs.had.co.nz

9:17 AM - 19 Jun 2015

Organization: Keep all .R files and data related to a project in the same place

Documentation: Helpful documentation enables you to remember how to use functions you've written – as well as your colleagues

Collaboration: Others will be able to follow your work and reproduce it – they may even collaborate to help improve the work

Credit: Producing an R package is added productivity and can is evidence of contribution to research. Especially if the package is available on CRAN it shows that you have worked up to a high standard in making the package.

References

Very helpful tutorials/blogs:

https://www.analyticsvidhya.com/blog/2017/03/create-packages-r-cran-github/

http://web.mit.edu/insong/www/pdf/rpackage_instructions.pdf

https://hilaryparker.com/2014/04/29/writing-an-r-package-from-scratch/

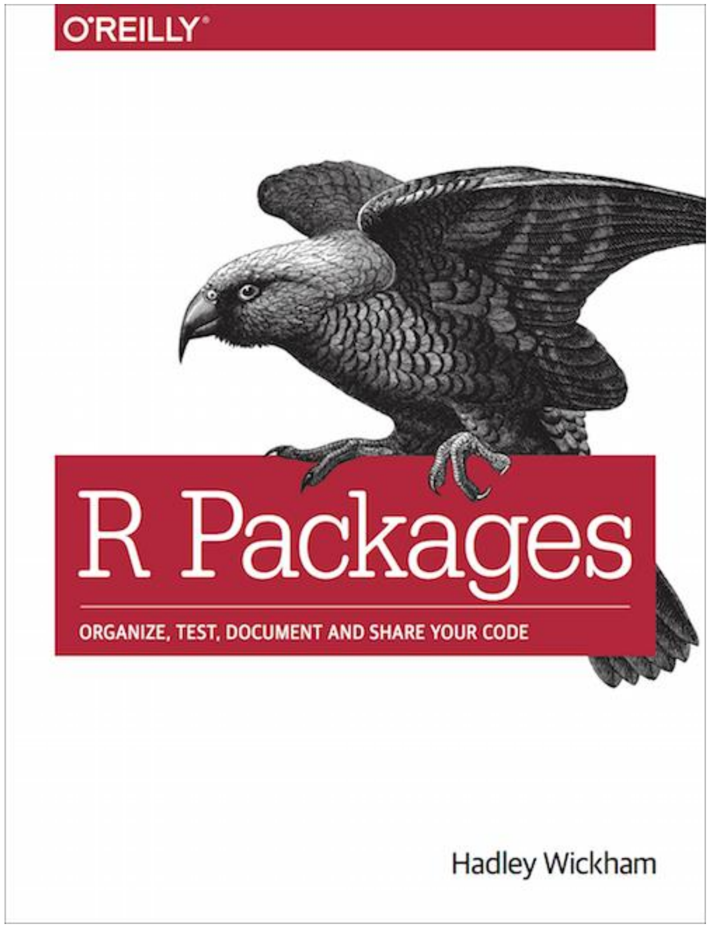
http://kbroman.org/pkg_primer/

http://stat545.com/packages00_index.html

http://tinyheero.github.io/jekyll/update/2015/07/26/making-your-first-R-package.html

If you're bold:

https://cran.r-project.org/doc/manuals/r-release/R-exts.html



The BEST resource
http://r-pkgs.had.co.nz/

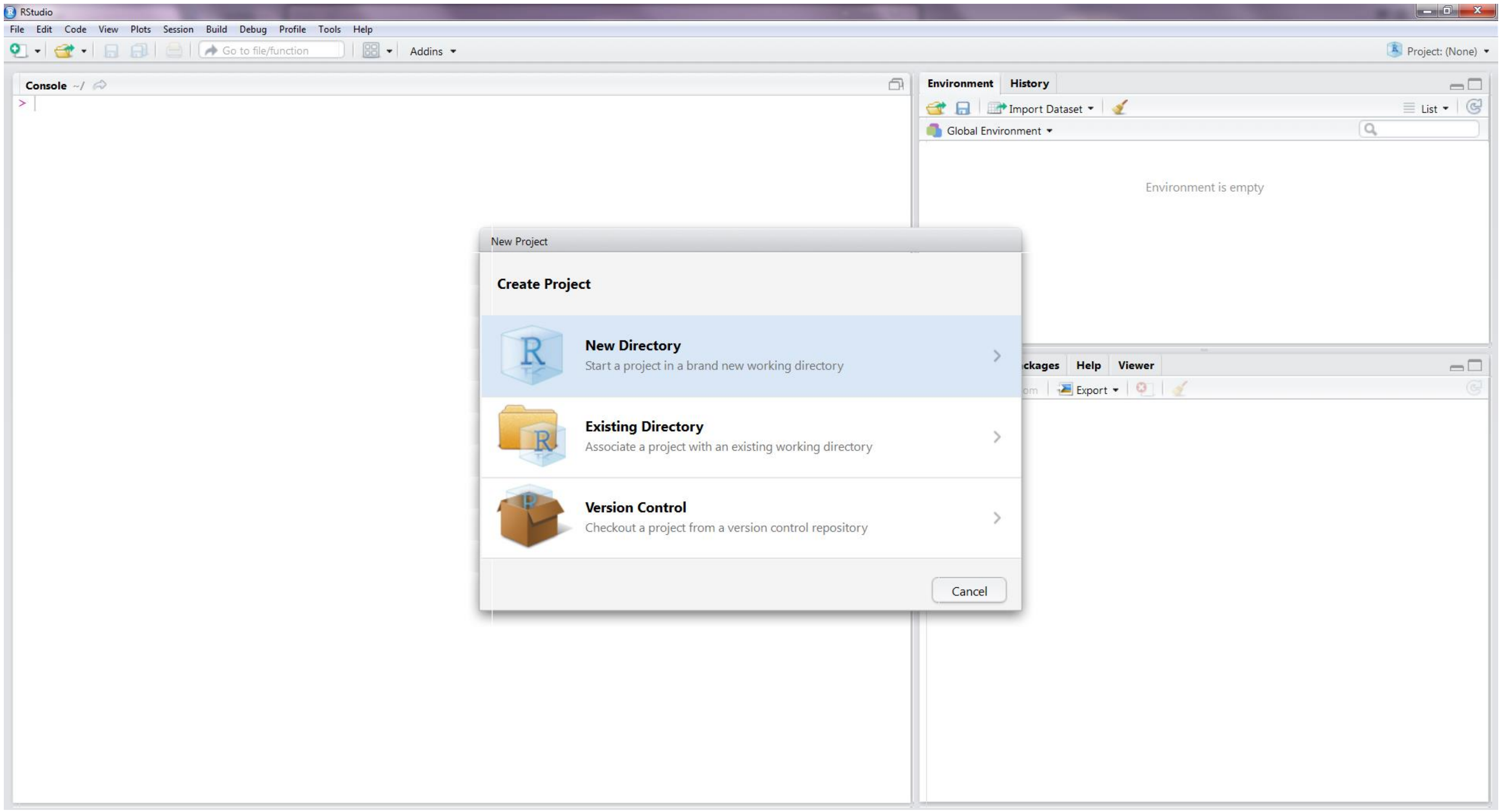
Writing our first basic R package

We will use Rstudio to build our package utilizing two packages:

devtools

roxygen2

Project > New Project or File > New Project



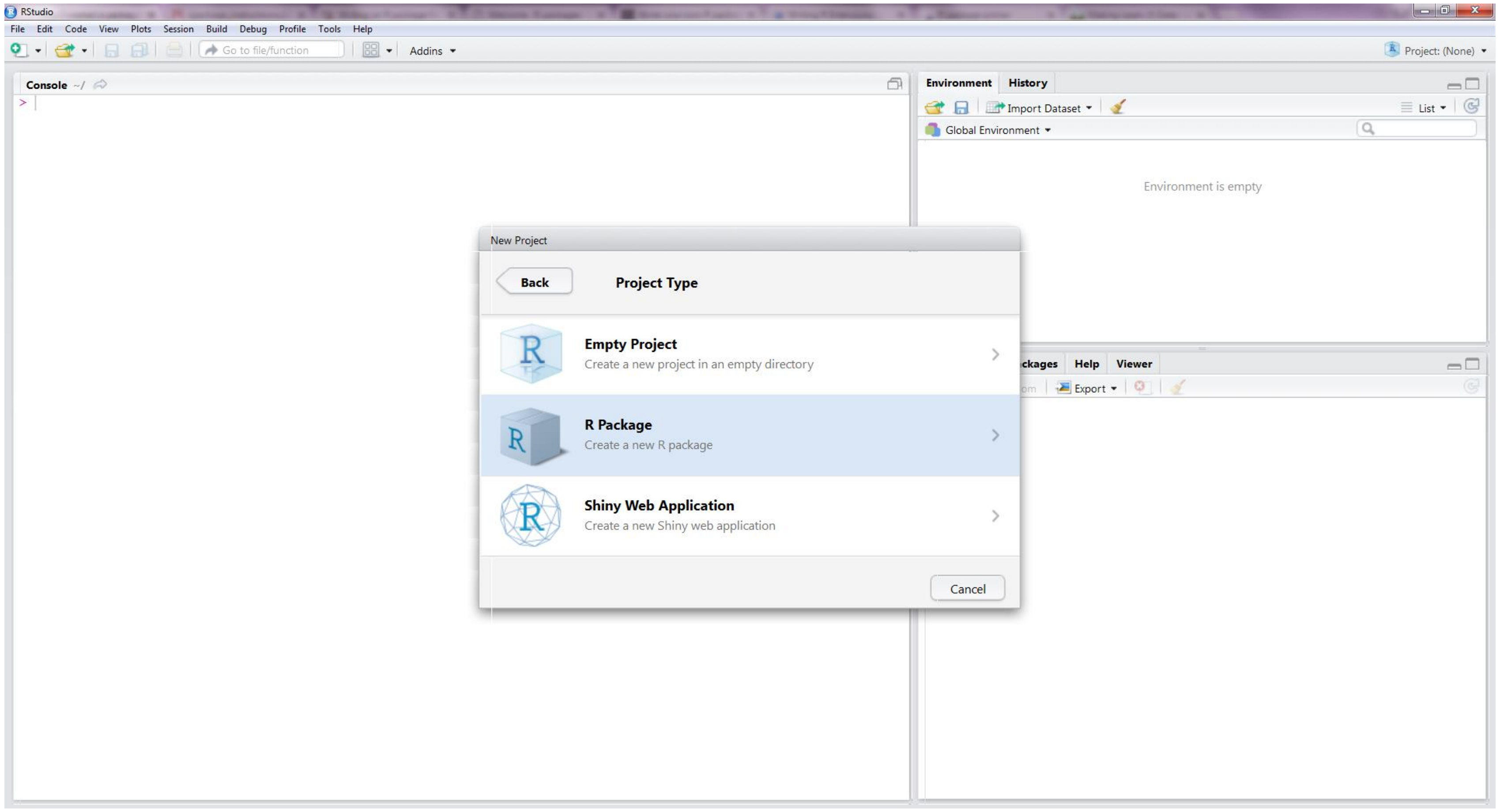
Create Project

New Directory
Start a project in a brand new working directory

Existing Directory
Associate a project with an existing working directory

Version Control
Checkout a project from a version control repository

New Directory > R Package



New Project

Back

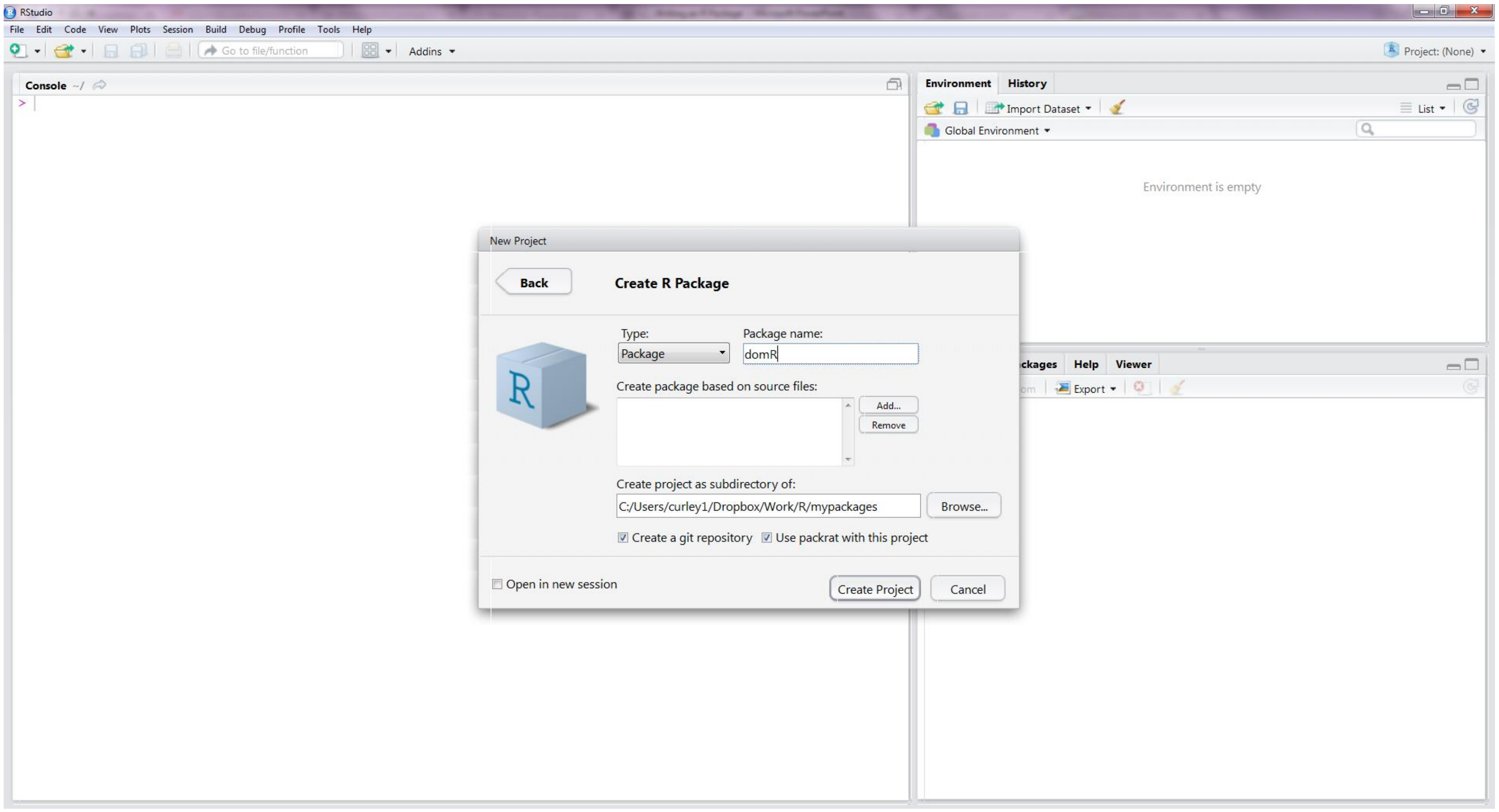
Project Type

Empty Project
Create a new project in an empty directory

R Package
Create a new R package

Shiny Web Application
Create a new Shiny web application

Choose a package name and a folder location



Type: Package

Package name: domR

Create package based on source files:

Add... Remove

Create project as subdirectory of: C:/Users/curley1/Dropbox/Work/R/mypackages

Browse...

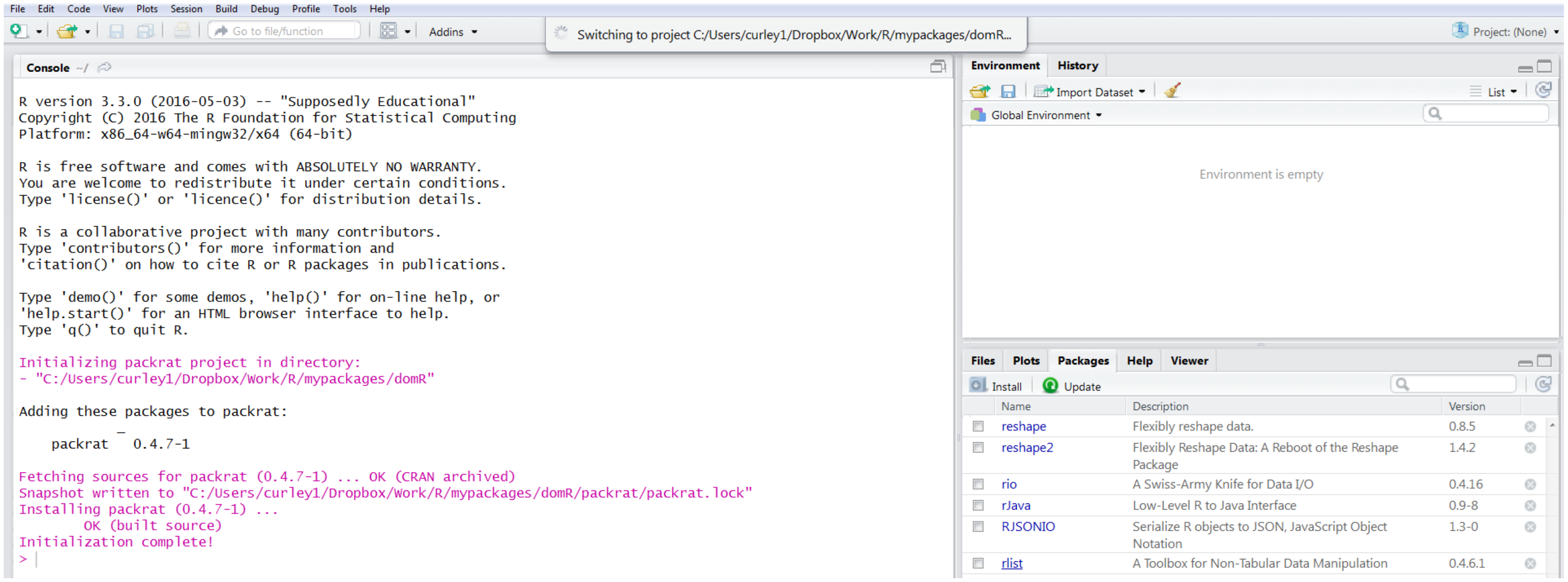
☑ Create a git repository ☑ Use packrat with this project

☐ Open in new session

Create Project Cancel

Why "packrat" ?

You should see this happen….

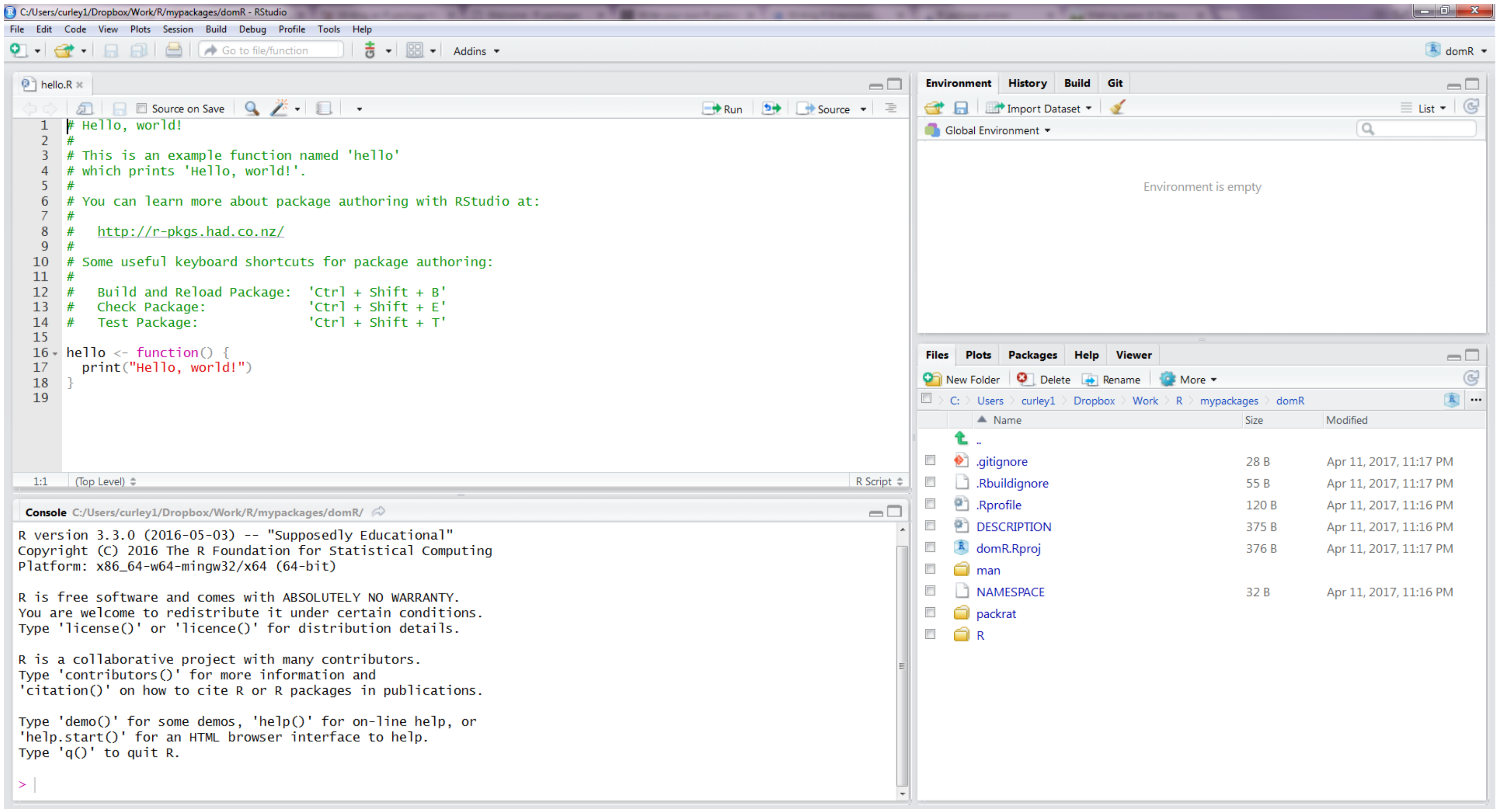


Switching to project C:/Users/curley1/Dropbox/Work/R/mypackages/domR...

```
R version 3.3.0 (2016-05-03) -- "Supposedly Educational"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

Initializing packrat project in directory:
- "C:/Users/curley1/Dropbox/Work/R/mypackages/domR"

Adding these packages to packrat:
            _
    packrat   0.4.7-1

Fetching sources for packrat (0.4.7-1) ... OK (CRAN archived)
Snapshot written to "C:/Users/curley1/Dropbox/Work/R/mypackages/domR/packrat/packrat.lock"
Installing packrat (0.4.7-1) ...
        OK (built source)
Initialization complete!
> 
```

Name	Description	Version
reshape	Flexibly reshape data.	0.8.5
reshape2	Flexibly Reshape Data: A Reboot of the Reshape Package	1.4.2
rio	A Swiss-Army Knife for Data I/O	0.4.16
rJava	Low-Level R to Java Interface	0.9-8
RJSONIO	Serialize R objects to JSON, JavaScript Object Notation	1.3-0
rlist	A Toolbox for Non-Tabular Data Manipulation	0.4.6.1

Several Files will be auto-generated in your folder like this: (I'll explain what these are)



```
# Hello, world!
#
# This is an example function named 'hello'
# which prints 'Hello, world!'.
#
# You can learn more about package authoring with RStudio at:
#
#   http://r-pkgs.had.co.nz/
#
# Some useful keyboard shortcuts for package authoring:
#
#   Build and Reload Package:  'Ctrl + Shift + B'
#   Check Package:             'Ctrl + Shift + E'
#   Test Package:              'Ctrl + Shift + T'

hello <- function() {
  print("Hello, world!")
}

```

Console C:/Users/curley1/Dropbox/Work/R/mypackages/domR/

```
R version 3.3.0 (2016-05-03) -- "Supposedly Educational"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
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'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

C: › Users › curley1 › Dropbox › Work › R › mypackages › domR

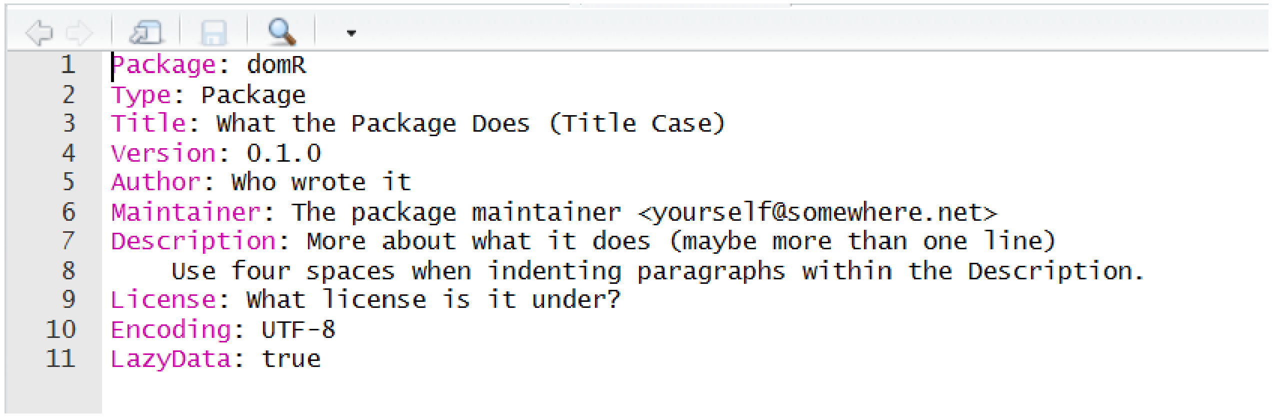
Name	Size	Modified
..		
.gitignore	28 B	Apr 11, 2017, 11:17 PM
.Rbuildignore	55 B	Apr 11, 2017, 11:17 PM
.Rprofile	120 B	Apr 11, 2017, 11:16 PM
DESCRIPTION	375 B	Apr 11, 2017, 11:16 PM
domR.Rproj	376 B	Apr 11, 2017, 11:17 PM
man		
NAMESPACE	32 B	Apr 11, 2017, 11:16 PM
packrat		
R		

C:/Users/curley1/Dropbox/Work/R/mypackages/domR - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
domR
hello.R
Source on Save
Run
Source
1:1
(Top Level)
R Script
Environment History Build Git
Import Dataset
List
Global Environment
Environment is empty
Files Plots Packages Help Viewer
New Folder Delete Rename More

Populate the DESCRIPTION file:

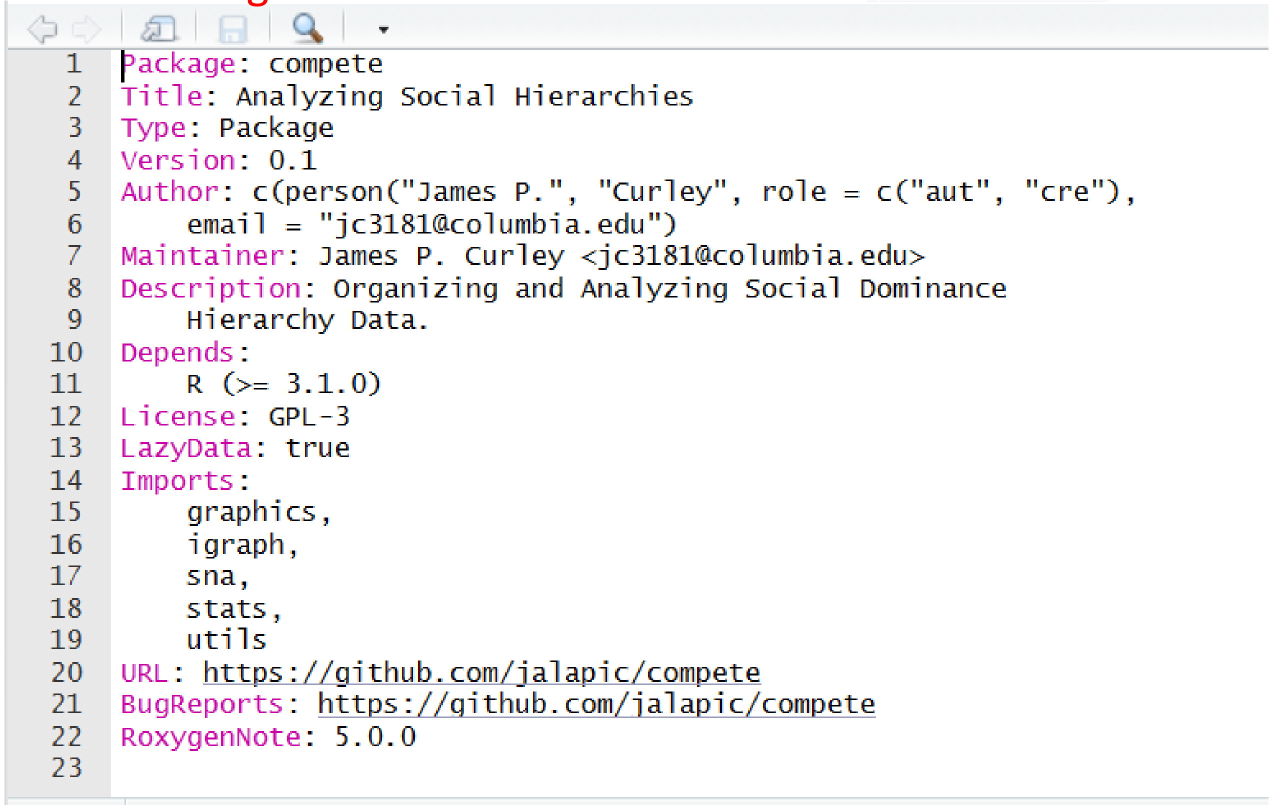
http://r-pkgs.had.co.nz/description.html

From this



```
Package: domR
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
```

To something like this

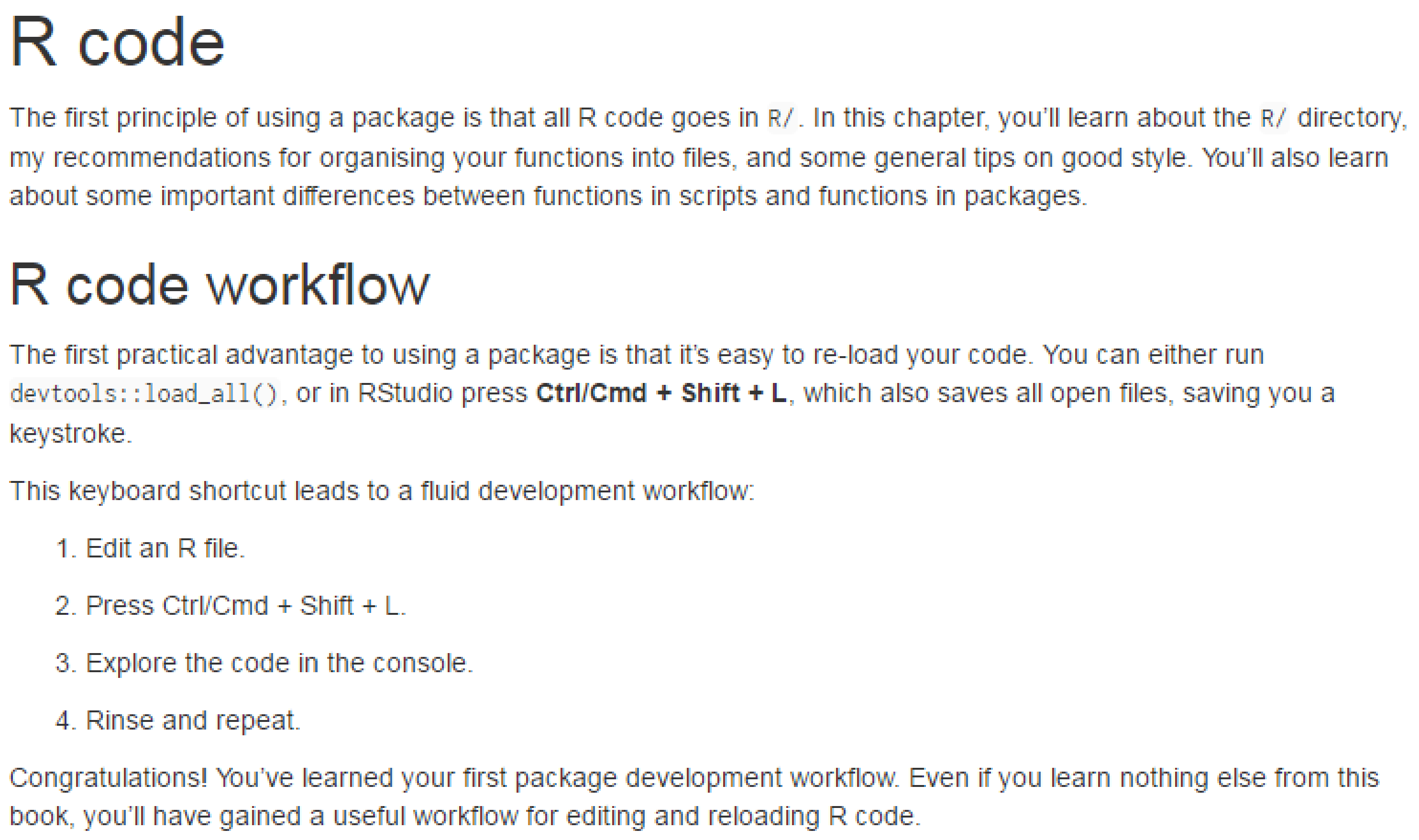


```
Package: compete
Title: Analyzing Social Hierarchies
Type: Package
Version: 0.1
Author: c(person("James P.", "Curley", role = c("aut", "cre"),
    email = "jc3181@columbia.edu")
Maintainer: James P. Curley <jc3181@columbia.edu>
Description: Organizing and Analyzing Social Dominance
    Hierarchy Data.
Depends:
    R (>= 3.1.0)
License: GPL-3
LazyData: true
Imports:
    graphics,
    igraph,
    sna,
    stats,
    utils
URL: https://github.com/jalapic/compete
BugReports: https://github.com/jalapic/compete
RoxygenNote: 5.0.0

```

If package uses functions from other packages, include them in the "Imports" section.

It's better in most cases to put them in "Imports" rather than "Depends"

Add .R functions to R folder



R code

The first principle of using a package is that all R code goes in `R/`. In this chapter, you'll learn about the `R/` directory, my recommendations for organising your functions into files, and some general tips on good style. You'll also learn about some important differences between functions in scripts and functions in packages.

R code workflow

The first practical advantage to using a package is that it's easy to re-load your code. You can either run `devtools::load_all()`, or in RStudio press **Ctrl/Cmd + Shift + L**, which also saves all open files, saving you a keystroke.

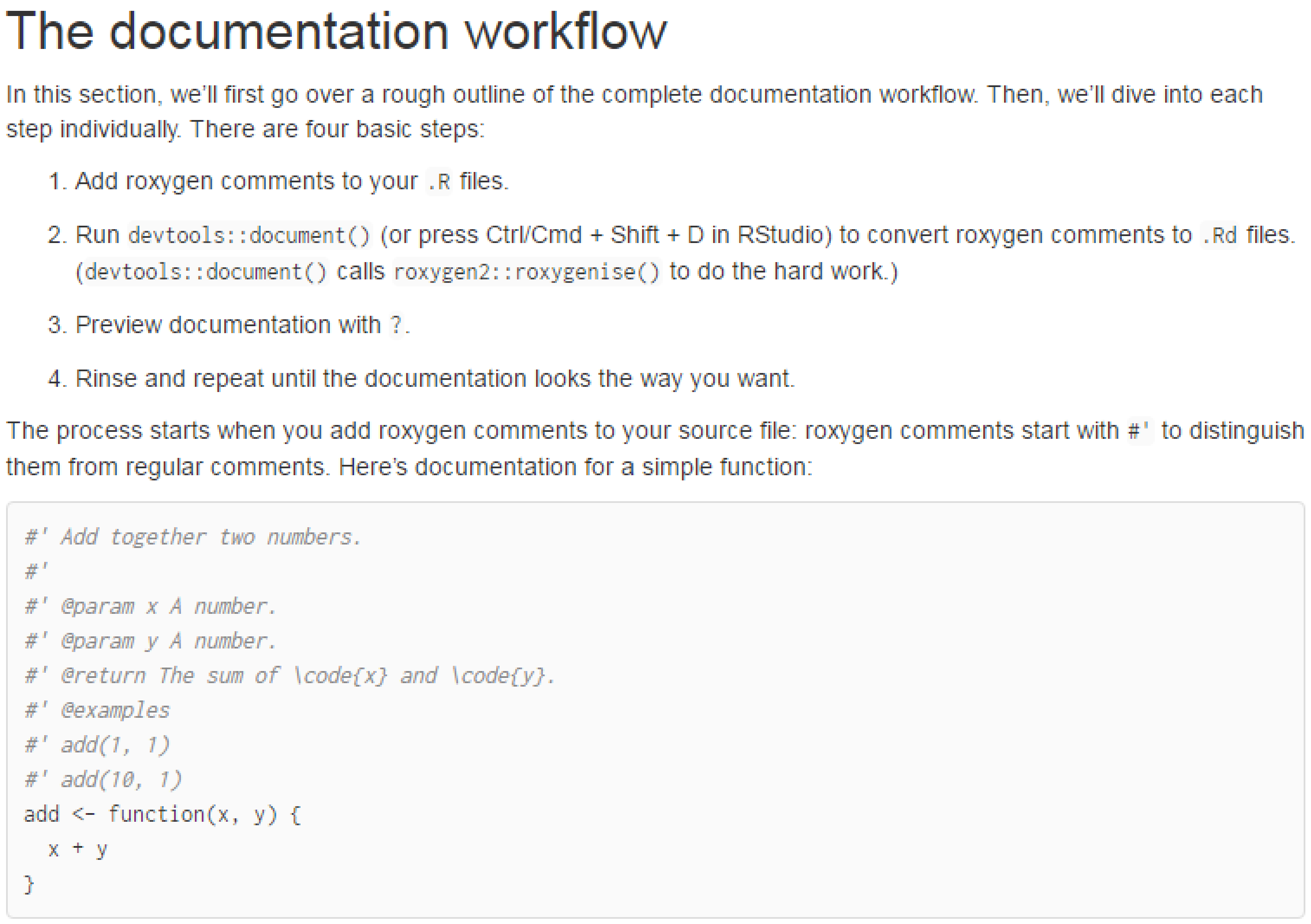
This keyboard shortcut leads to a fluid development workflow:

1. Edit an R file.
2. Press Ctrl/Cmd + Shift + L.
3. Explore the code in the console.
4. Rinse and repeat.

Congratulations! You've learned your first package development workflow. Even if you learn nothing else from this book, you'll have gained a useful workflow for editing and reloading R code.

See http://r-pkgs.had.co.nz/r.html for advice on code style and best practice

Add roxygen comments to top of .R functions script



The documentation workflow

In this section, we'll first go over a rough outline of the complete documentation workflow. Then, we'll dive into each step individually. There are four basic steps:

1. Add roxygen comments to your `.R` files.
2. Run `devtools::document()` (or press Ctrl/Cmd + Shift + D in RStudio) to convert roxygen comments to `.Rd` files. (`devtools::document()` calls `roxygen2::roxygenise()` to do the hard work.)
3. Preview documentation with `?`.
4. Rinse and repeat until the documentation looks the way you want.

The process starts when you add roxygen comments to your source file: roxygen comments start with `#'` to distinguish them from regular comments. Here's documentation for a simple function:

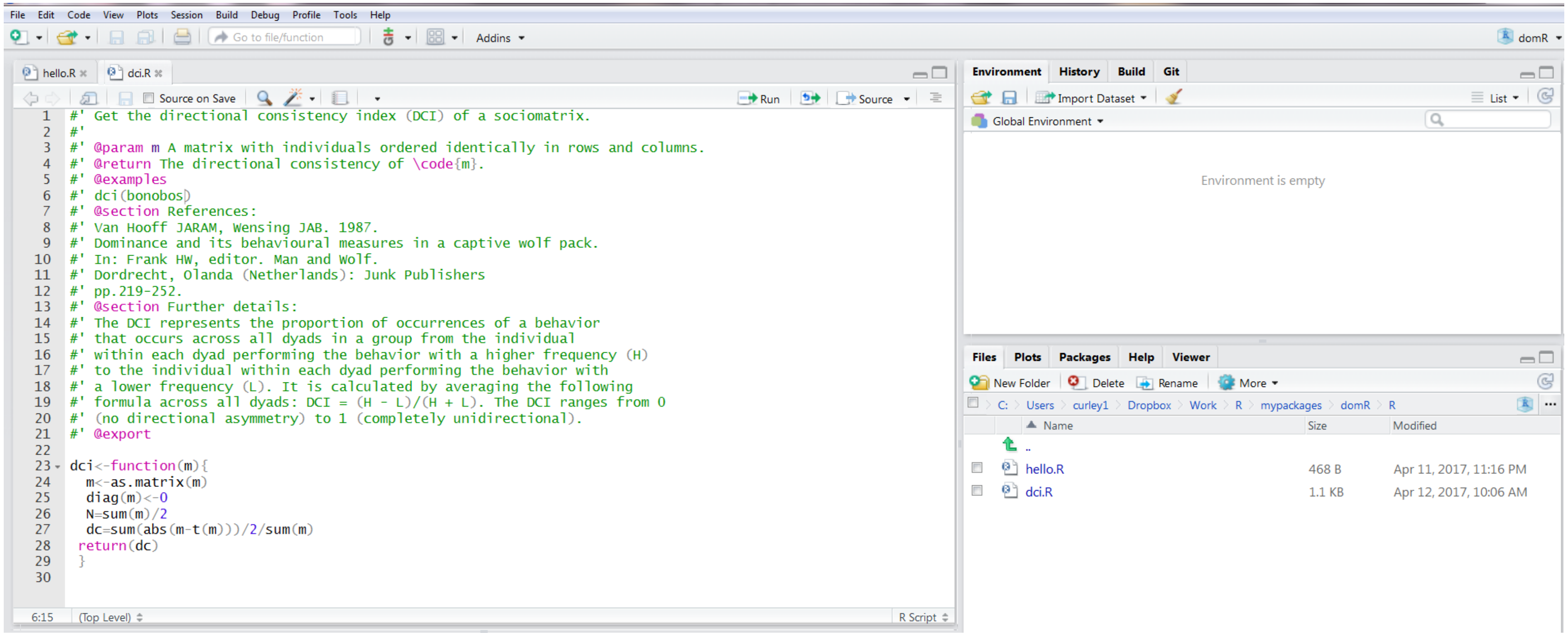
```r
#' Add together two numbers.
#'
#' @param x A number.
#' @param y A number.
#' @return The sum of \code{x} and \code{y}.
#' @examples
#' add(1, 1)
#' add(10, 1)
add <- function(x, y) {
  x + y
}
```

See http://r-pkgs.had.co.nz/man.html for style guide and best practice

roxygen comments

title	= title of the function.
description	= detailed explanation of what the package does.
param	= parameters/arguments in function. You can use multiple 'param' return = what object the function returns
importFrom	= functions you need from other packages
examples	= sample code (keep it small)
section	= anything else relevant that you might want to add
export	= function to export

Add .R functions to R folder and add roxygen comments



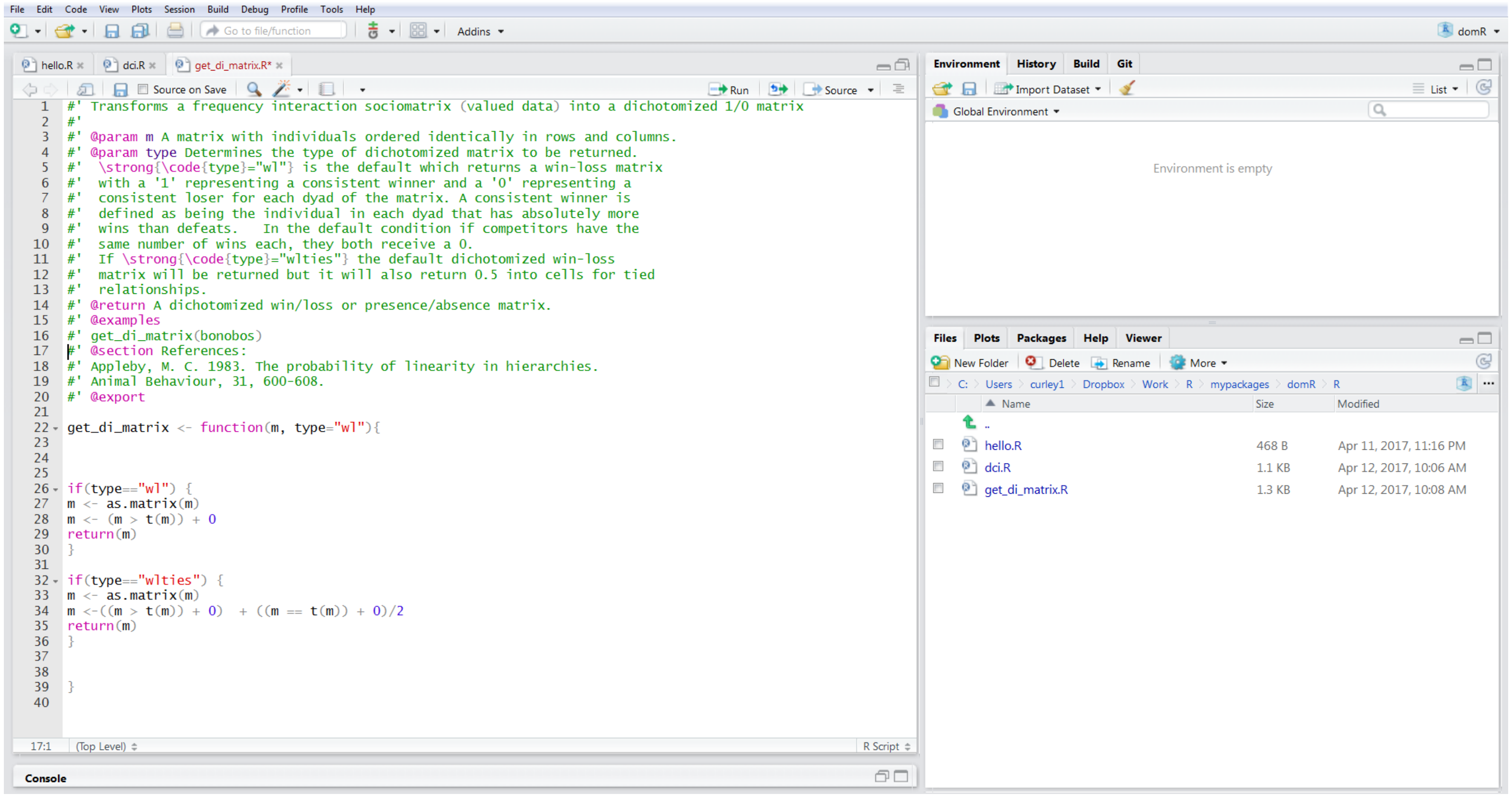
```r
#' Get the directional consistency index (DCI) of a sociomatrix.
#'
#' @param m A matrix with individuals ordered identically in rows and columns.
#' @return The directional consistency of \code{m}.
#' @examples
#' dci(bonobos)
#' @section References:
#' Van Hooff JARAM, Wensing JAB. 1987.
#' Dominance and its behavioural measures in a captive wolf pack.
#' In: Frank HW, editor. Man and Wolf.
#' Dordrecht, Olanda (Netherlands): Junk Publishers
#' pp.219-252.
#' @section Further details:
#' The DCI represents the proportion of occurrences of a behavior
#' that occurs across all dyads in a group from the individual
#' within each dyad performing the behavior with a higher frequency (H)
#' to the individual within each dyad performing the behavior with
#' a lower frequency (L). It is calculated by averaging the following
#' formula across all dyads: DCI = (H - L)/(H + L). The DCI ranges from 0
#' (no directional asymmetry) to 1 (completely unidirectional).
#' @export

dci<-function(m){
  m<-as.matrix(m)
  diag(m)<-0
  N=sum(m)/2
  dc=sum(abs(m-t(m)))/2/sum(m)
 return(dc)
 }
```

	Name	Size	Modified
	..		
	hello.R	468 B	Apr 11, 2017, 11:16 PM
	dci.R	1.1 KB	Apr 12, 2017, 10:06 AM

File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
domR
hello.R
dci.R
Source on Save
Run
Source
6:15
(Top Level)
R Script
Environment History Build Git
Import Dataset
List
Global Environment
Environment is empty
Files Plots Packages Help Viewer
New Folder Delete Rename More
C: > Users > curley1 > Dropbox > Work > R > mypackages > domR > R

Save functions with name of function

Do for next function …



```r
#' Transforms a frequency interaction sociomatrix (valued data) into a dichotomized 1/0 matrix
#'
#' @param m A matrix with individuals ordered identically in rows and columns.
#' @param type Determines the type of dichotomized matrix to be returned.
#'  \strong{\code{type}="wl"} is the default which returns a win-loss matrix
#'  with a '1' representing a consistent winner and a '0' representing a
#'  consistent loser for each dyad of the matrix. A consistent winner is
#'  defined as being the individual in each dyad that has absolutely more
#'  wins than defeats.   In the default condition if competitors have the
#'  same number of wins each, they both receive a 0.
#'  If \strong{\code{type}="wlties"} the default dichotomized win-loss
#'  matrix will be returned but it will also return 0.5 into cells for tied
#'  relationships.
#' @return A dichotomized win/loss or presence/absence matrix.
#' @examples
#' get_di_matrix(bonobos)
#' @section References:
#' Appleby, M. C. 1983. The probability of linearity in hierarchies.
#' Animal Behaviour, 31, 600-608.
#' @export

get_di_matrix <- function(m, type="wl"){



if(type=="wl") {
m <- as.matrix(m)
m <- (m > t(m)) + 0
return(m)
}

if(type=="wlties") {
m <- as.matrix(m)
m <-((m > t(m)) + 0)  + ((m == t(m)) + 0)/2
return(m)
}



}

```

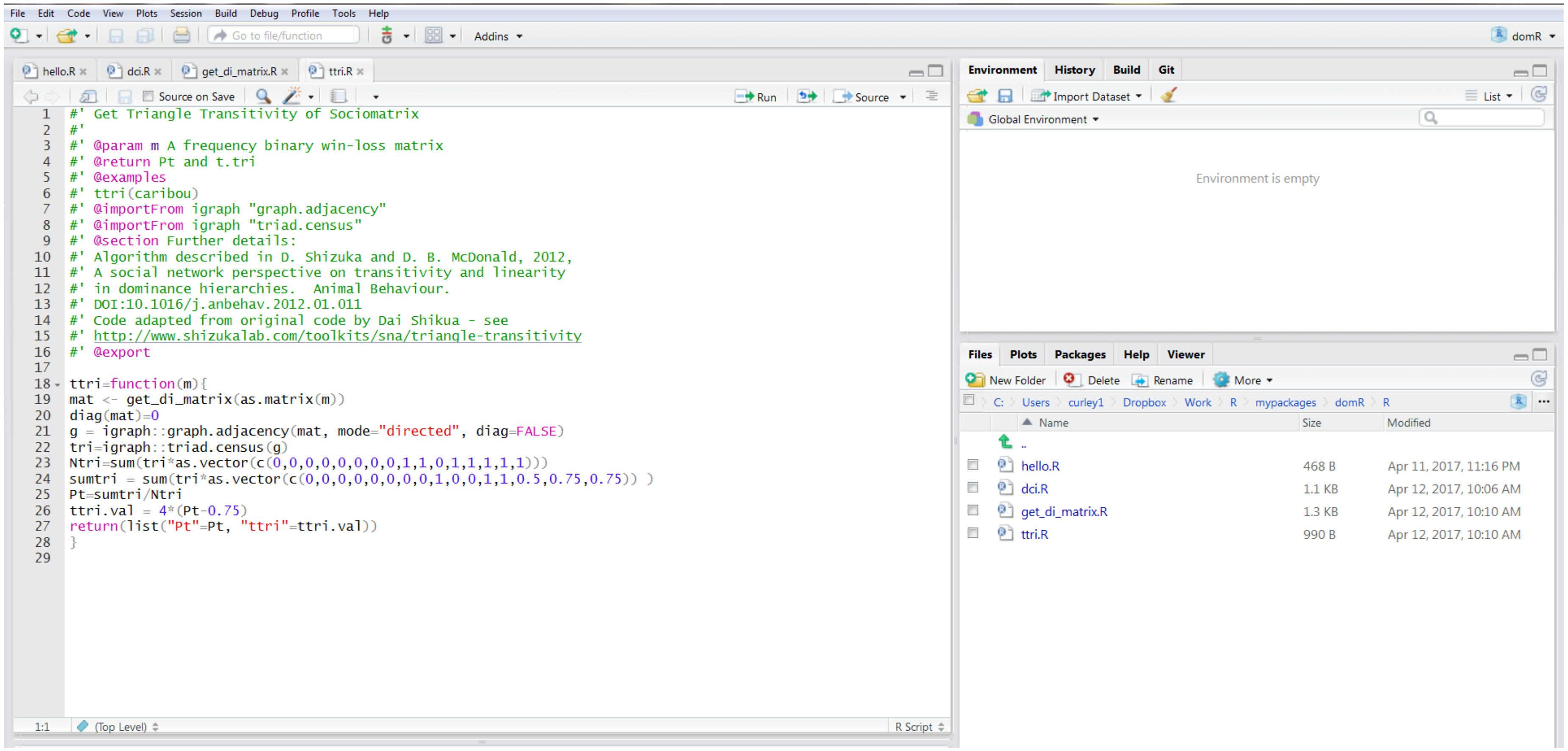
17:1 (Top Level) R Script

Environment is empty

C: › Users › curley1 › Dropbox › Work › R › mypackages › domR › R

Name	Size	Modified
..		
hello.R	468 B	Apr 11, 2017, 11:16 PM
dci.R	1.1 KB	Apr 12, 2017, 10:06 AM
get_di_matrix.R	1.3 KB	Apr 12, 2017, 10:08 AM

Keep going…



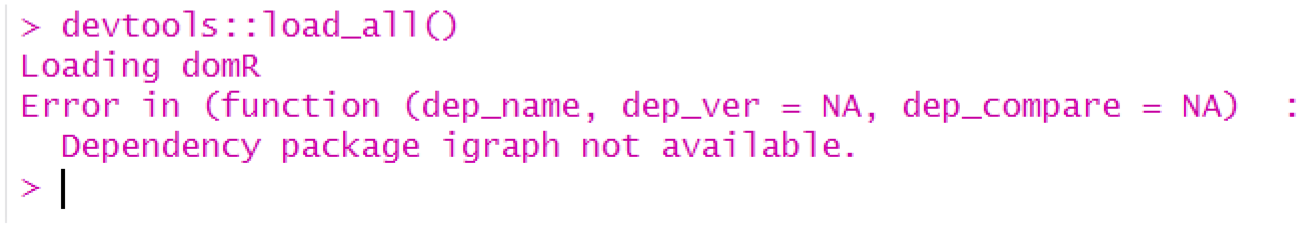
```r
#' Get Triangle Transitivity of Sociomatrix
#'
#' @param m A frequency binary win-loss matrix
#' @return Pt and t.tri
#' @examples
#' ttri(caribou)
#' @importFrom igraph "graph.adjacency"
#' @importFrom igraph "triad.census"
#' @section Further details:
#' Algorithm described in D. Shizuka and D. B. McDonald, 2012,
#' A social network perspective on transitivity and linearity
#' in dominance hierarchies.  Animal Behaviour.
#' DOI:10.1016/j.anbehav.2012.01.011
#' Code adapted from original code by Dai Shikua - see
#' http://www.shizukalab.com/toolkits/sna/triangle-transitivity
#' @export

ttri=function(m){
mat <- get_di_matrix(as.matrix(m))
diag(mat)=0
g = igraph::graph.adjacency(mat, mode="directed", diag=FALSE)
tri=igraph::triad.census(g)
Ntri=sum(tri*as.vector(c(0,0,0,0,0,0,0,0,1,1,0,1,1,1,1,1)))
sumtri = sum(tri*as.vector(c(0,0,0,0,0,0,0,0,1,0,0,1,1,0.5,0.75,0.75)) )
Pt=sumtri/Ntri
ttri.val = 4*(Pt-0.75)
return(list("Pt"=Pt, "ttri"=ttri.val))
}
```

Environment is empty

C: › Users › curley1 › Dropbox › Work › R › mypackages › domR › R

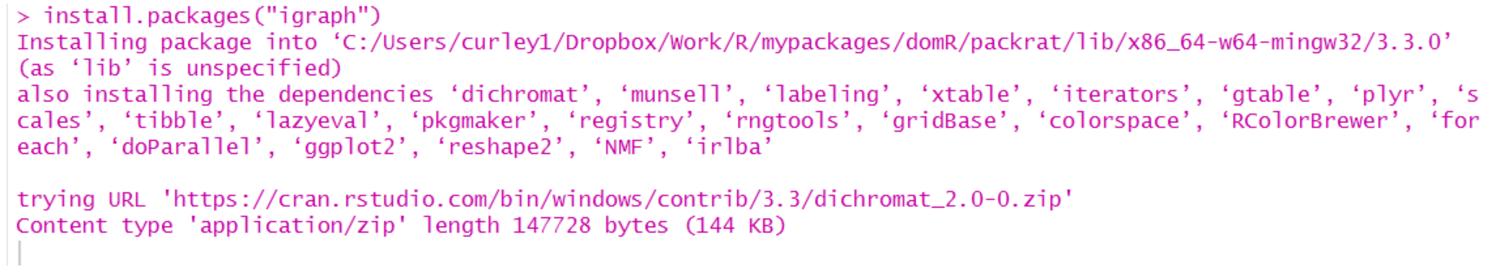
Name	Size	Modified
..		
hello.R	468 B	Apr 11, 2017, 11:16 PM
dci.R	1.1 KB	Apr 12, 2017, 10:06 AM
get_di_matrix.R	1.3 KB	Apr 12, 2017, 10:10 AM
ttri.R	990 B	Apr 12, 2017, 10:10 AM

Load .R files ...

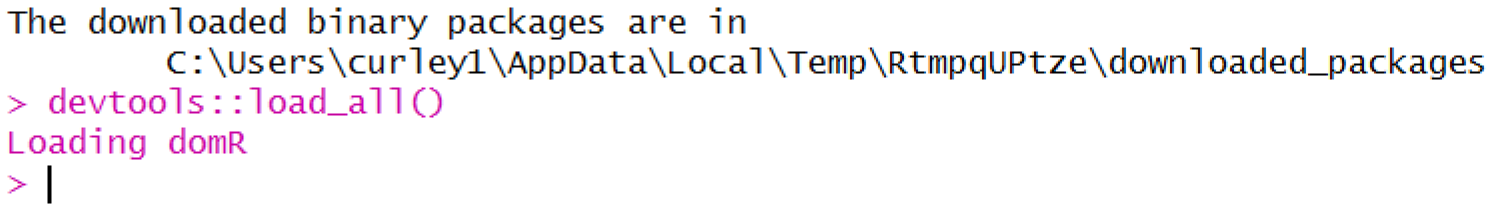


```
> devtools::load_all()
Loading domR
Error in (function (dep_name, dep_ver = NA, dep_compare = NA)  :
  Dependency package igraph not available.
> 
```

Fix error !



```
> install.packages("igraph")
Installing package into ‘C:/Users/curley1/Dropbox/Work/R/mypackages/domR/packrat/lib/x86_64-w64-mingw32/3.3.0’
(as ‘lib’ is unspecified)
also installing the dependencies ‘dichromat’, ‘munsell’, ‘labeling’, ‘xtable’, ‘iterators’, ‘gtable’, ‘plyr’, ‘s
cales’, ‘tibble’, ‘lazyeval’, ‘pkgmaker’, ‘registry’, ‘rngtools’, ‘gridBase’, ‘colorspace’, ‘RColorBrewer’, ‘for
each’, ‘doParallel’, ‘ggplot2’, ‘reshape2’, ‘NMF’, ‘irlba’

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.3/dichromat_2.0-0.zip'
Content type 'application/zip' length 147728 bytes (144 KB)
```

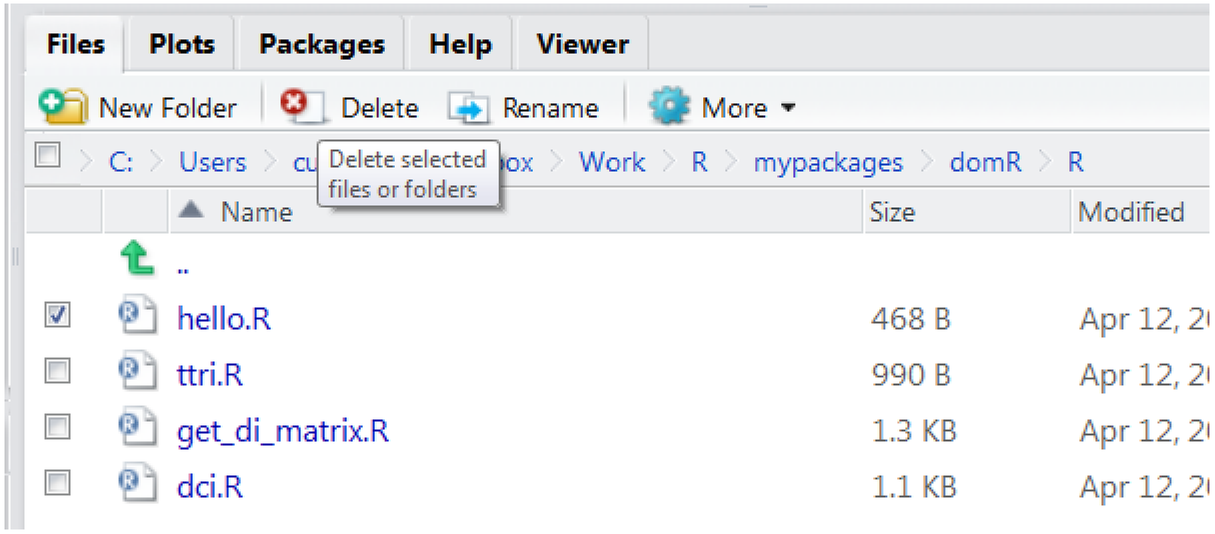


```
The downloaded binary packages are in
        C:\Users\curley1\AppData\Local\Temp\RtmpqUPtze\downloaded_packages
> devtools::load_all()
Loading domR
> 
```

We’re good

Deleting files

If we don't want a file – remove it's .R file and its .Rd file (if it exists).
Easiest way is with the Delete icon in Files window



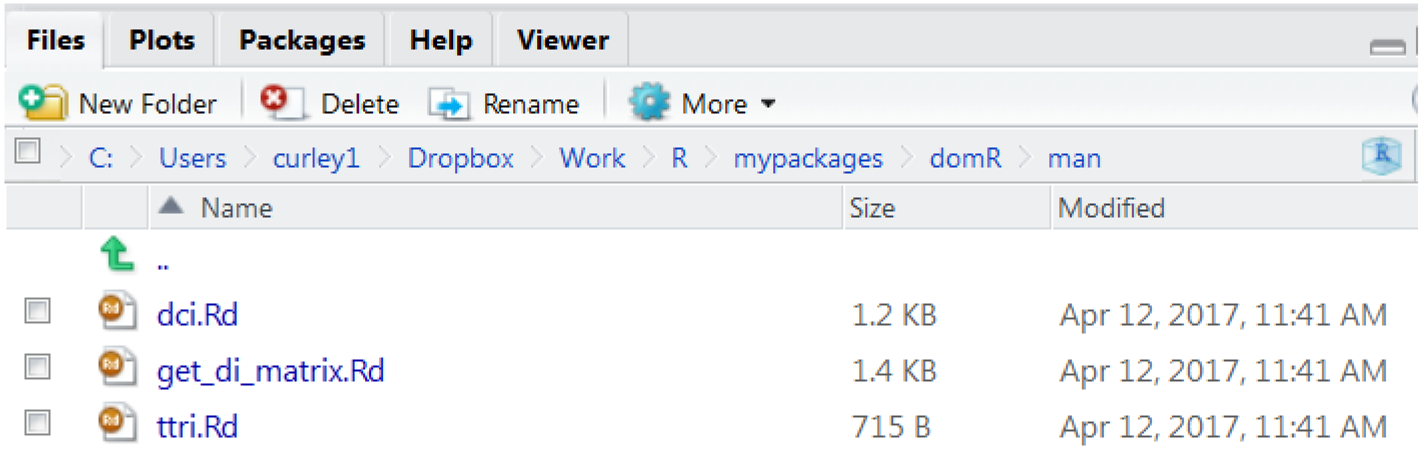
Files
Plots
Packages
Help
Viewer
New Folder
Delete
Rename
More
Delete selected files or folders
C: > Users > cu > ox > Work > R > mypackages > domR > R
Name
Size
Modified
..

	Name	Size	Modified
✓	hello.R	468 B	Apr 12, 2
	ttri.R	990 B	Apr 12, 2
	get_di_matrix.R	1.3 KB	Apr 12, 2
	dci.R	1.1 KB	Apr 12, 2

Add documentation
Man

devtools::document()

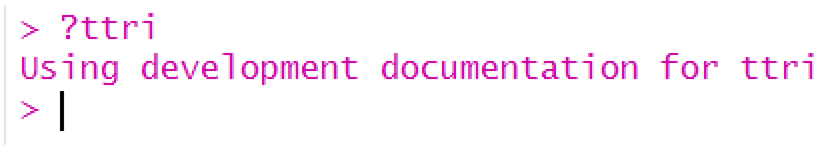
```
> devtools::document()
Updating domR documentation
Loading domR
First time using roxygen2. Upgrading automatically...
Warning: The existing 'NAMESPACE' file was not generated by roxygen2, and will not be overwritten.
Writing dci.Rd
Writing get_di_matrix.Rd
Writing ttri.Rd
>
```


Files
Plots
Packages
Help
Viewer
New Folder
Delete
Rename
More
C: > Users > curley1 > Dropbox > Work > R > mypackages > domR > man

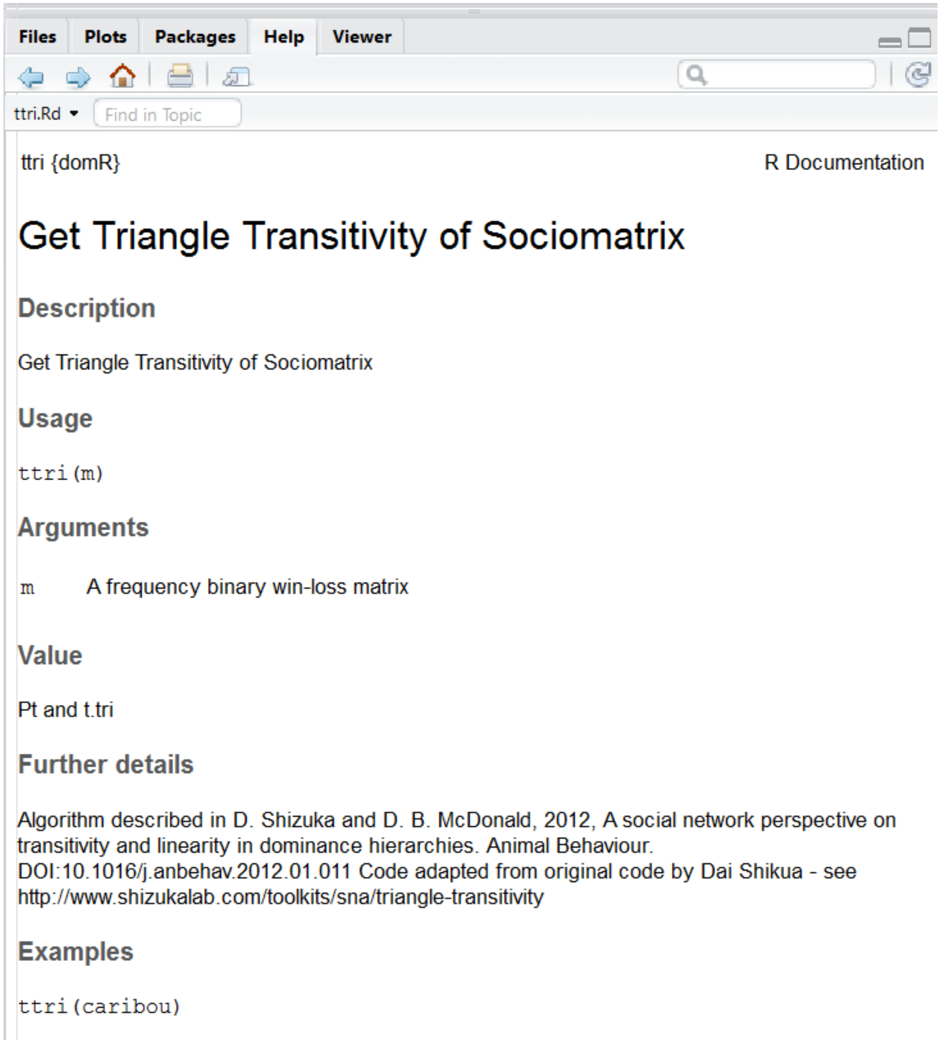
Name	Size	Modified
..		
dci.Rd	1.2 KB	Apr 12, 2017, 11:41 AM
get_di_matrix.Rd	1.4 KB	Apr 12, 2017, 11:41 AM
ttri.Rd	715 B	Apr 12, 2017, 11:41 AM

We now have docs !

Check them out with "?"



```
> ?ttri
Using development documentation for ttri
> 
```



ttri {domR}　　R Documentation

Get Triangle Transitivity of Sociomatrix

Description

Get Triangle Transitivity of Sociomatrix

Usage

```
ttri(m)
```

Arguments

m	A frequency binary win-loss matrix

Value

Pt and t.tri

Further details

Algorithm described in D. Shizuka and D. B. McDonald, 2012, A social network perspective on transitivity and linearity in dominance hierarchies. Animal Behaviour. DOI:10.1016/j.anbehav.2012.01.011 Code adapted from original code by Dai Shikua - see http://www.shizukalab.com/toolkits/sna/triangle-transitivity

Examples

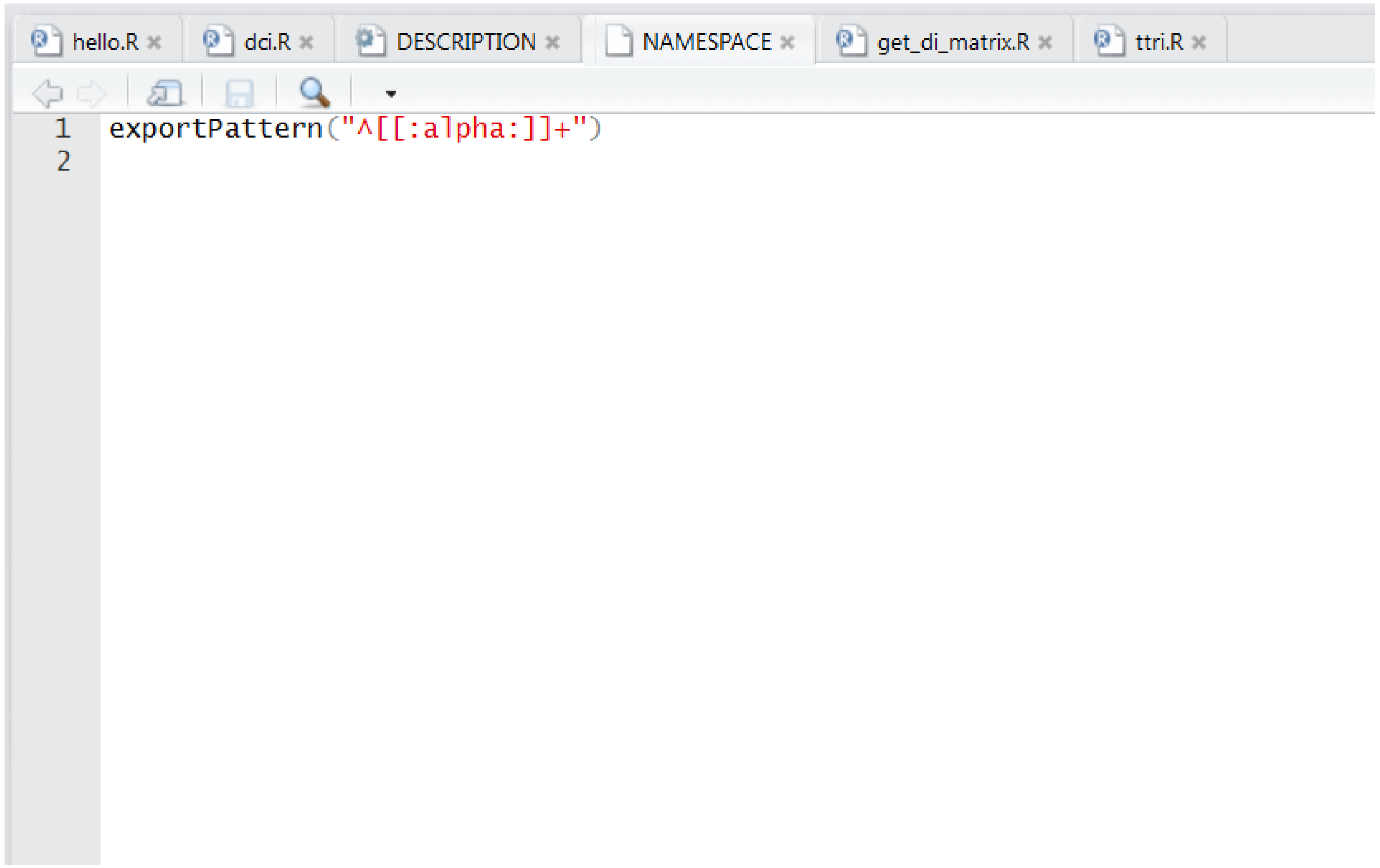
```
ttri(caribou)
```

```
Warning: The existing 'NAMESPACE' file was not generated by roxygen2, and will not be overwritten.
```

What does this mean ???

NAMESPACE

This is what the NAMESPACE looked like on initial package set up:

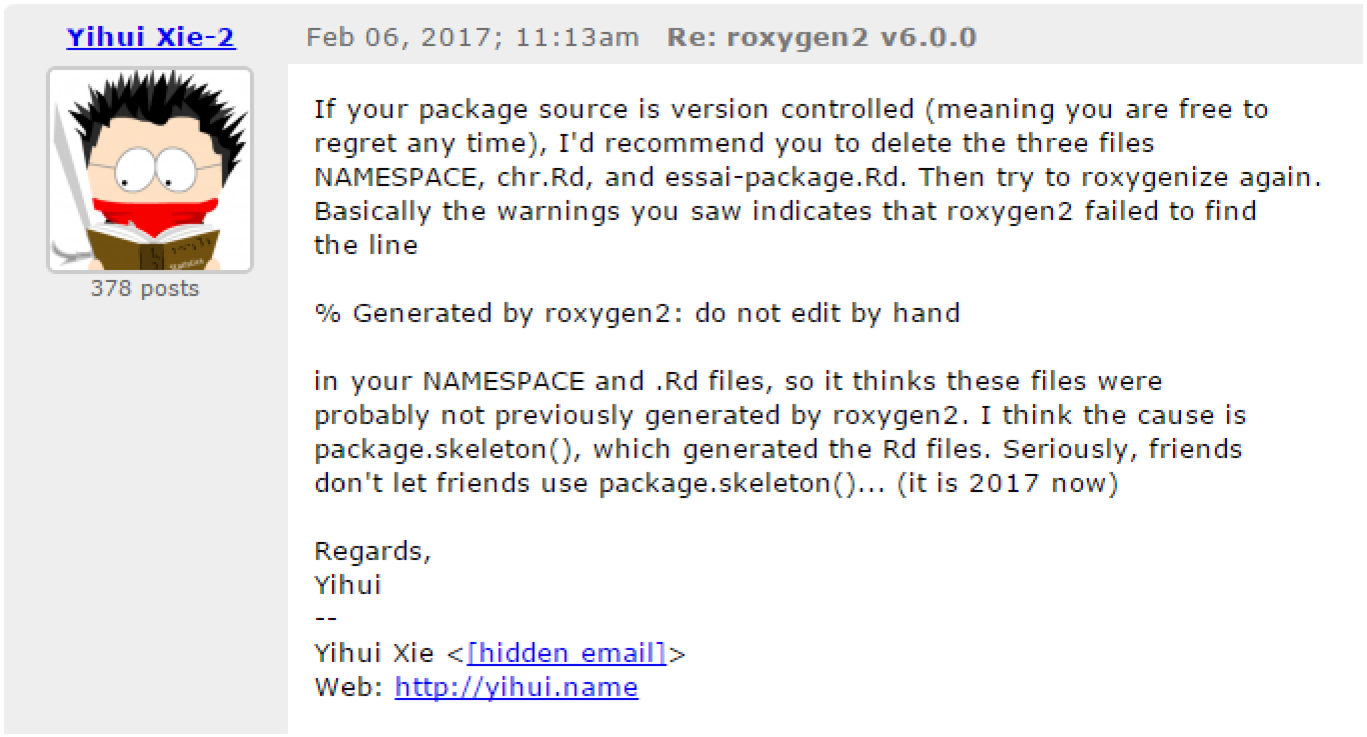


```
exportPattern("^[[:alpha:]]+")
```

NAMESPACE

Google it:

```
Warning: The existing 'NAMESPACE' file was not generated by roxygen2, and will not be overwritten.
```



Yihui Xie-2 Feb 06, 2017; 11:13am **Re: roxygen2 v6.0.0**

378 posts

If your package source is version controlled (meaning you are free to regret any time), I'd recommend you to delete the three files NAMESPACE, chr.Rd, and essai-package.Rd. Then try to roxygenize again. Basically the warnings you saw indicates that roxygen2 failed to find the line

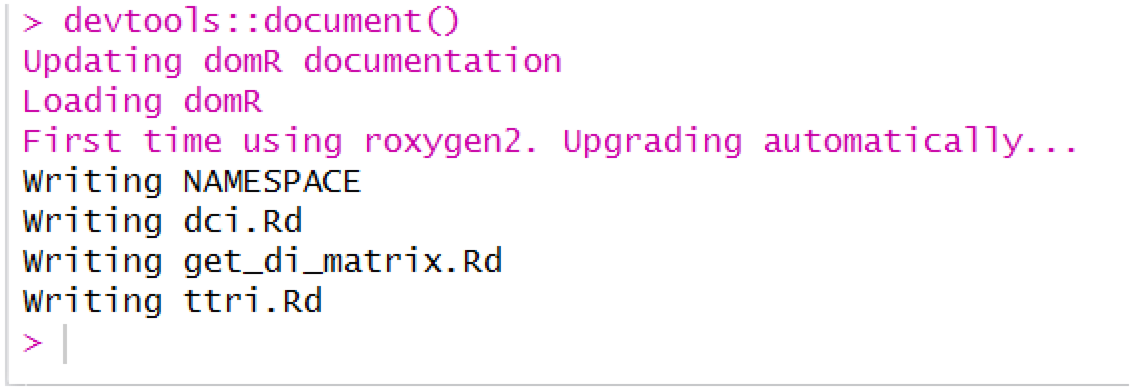
% Generated by roxygen2: do not edit by hand

in your NAMESPACE and .Rd files, so it thinks these files were probably not previously generated by roxygen2. I think the cause is package.skeleton(), which generated the Rd files. Seriously, friends don't let friends use package.skeleton()... (it is 2017 now)

Regards,
Yihui
--
Yihui Xie <[hidden email]>
Web: http://yihui.name

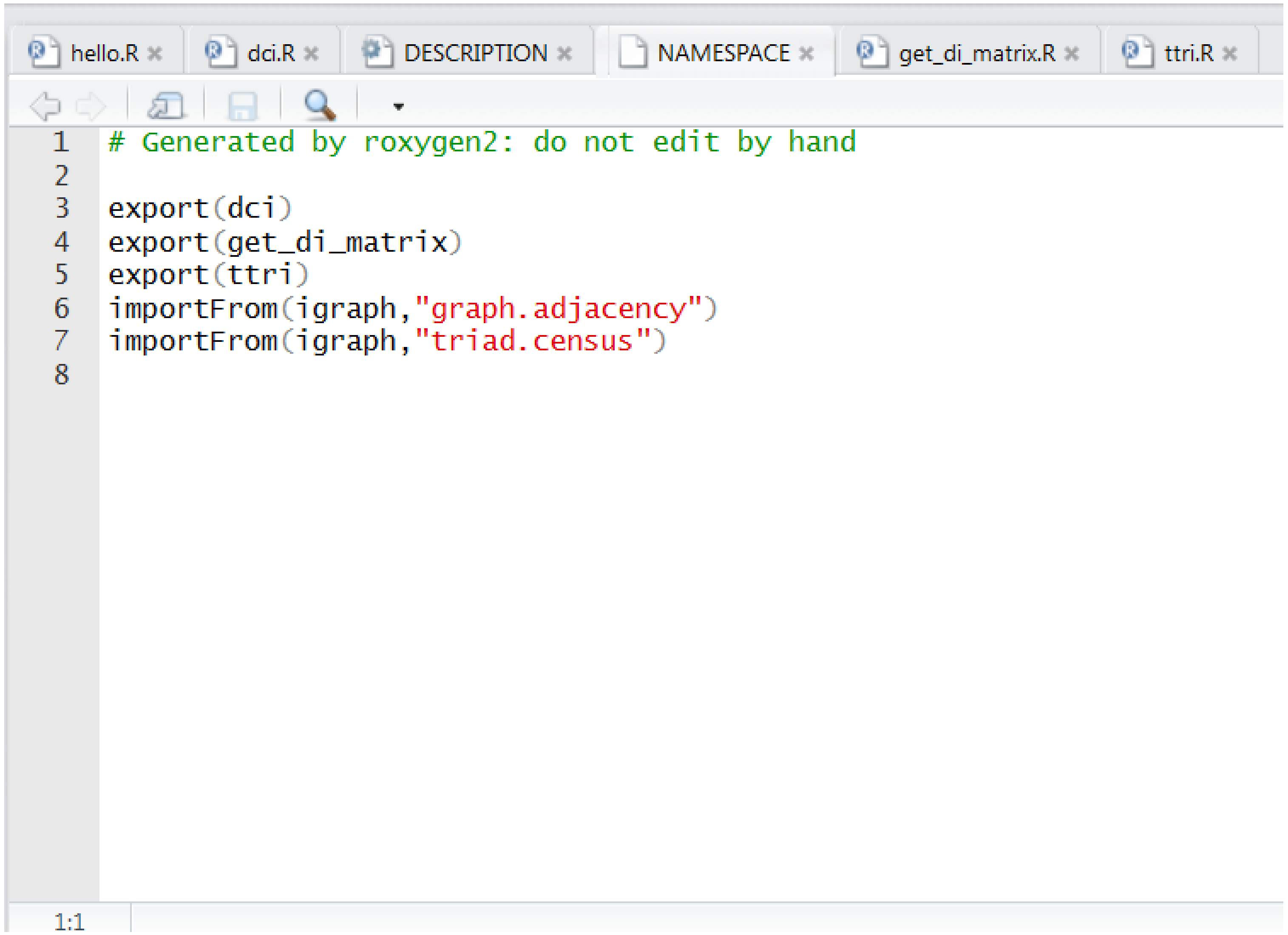
Do as Yihui says …

Delete .Rd files we just made, Delete the NAMESPACE, problem fixed !!!



```
> devtools::document()
Updating domR documentation
Loading domR
First time using roxygen2. Upgrading automatically...
Writing NAMESPACE
Writing dci.Rd
Writing get_di_matrix.Rd
Writing ttri.Rd
>
```

That's better – it should have the "do not edit by hand"



```
# Generated by roxygen2: do not edit by hand

export(dci)
export(get_di_matrix)
export(ttri)
importFrom(igraph,"graph.adjacency")
importFrom(igraph,"triad.census")
```

For every new .R file you will need to run:

```
devtools::document()
```

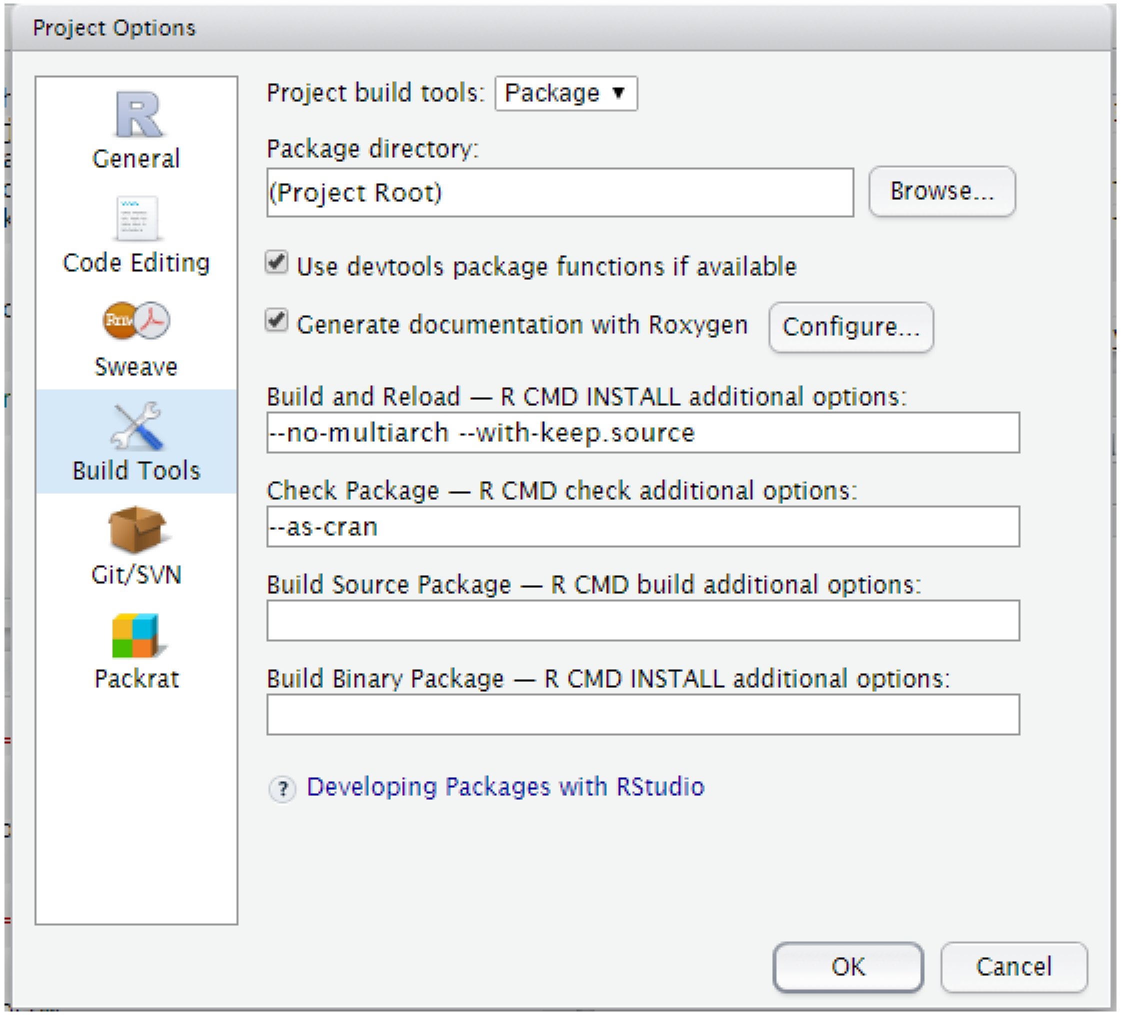
To generate your documentation.

You will also need to run it if you change the information in any .R file
- This often happens after you run CHECKS and realize you made some errors in the text.

BUILD!

Build > Configure Build Tools.

Now check the "Generate documentation with Roxygen" option and put "–as-cran" under Check Package space to simulate the CRAN package checking and testing.



Project Options

Project build tools: Package

Package directory:
(Project Root)

[✓] Use devtools package functions if available

[✓] Generate documentation with Roxygen

Build and Reload — R CMD INSTALL additional options:
--no-multiarch --with-keep.source

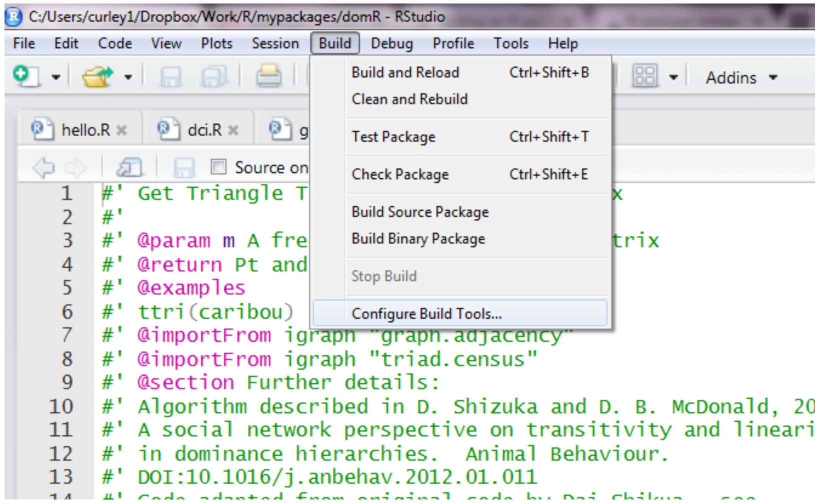
Check Package — R CMD check additional options:
--as-cran

Build Source Package — R CMD build additional options:

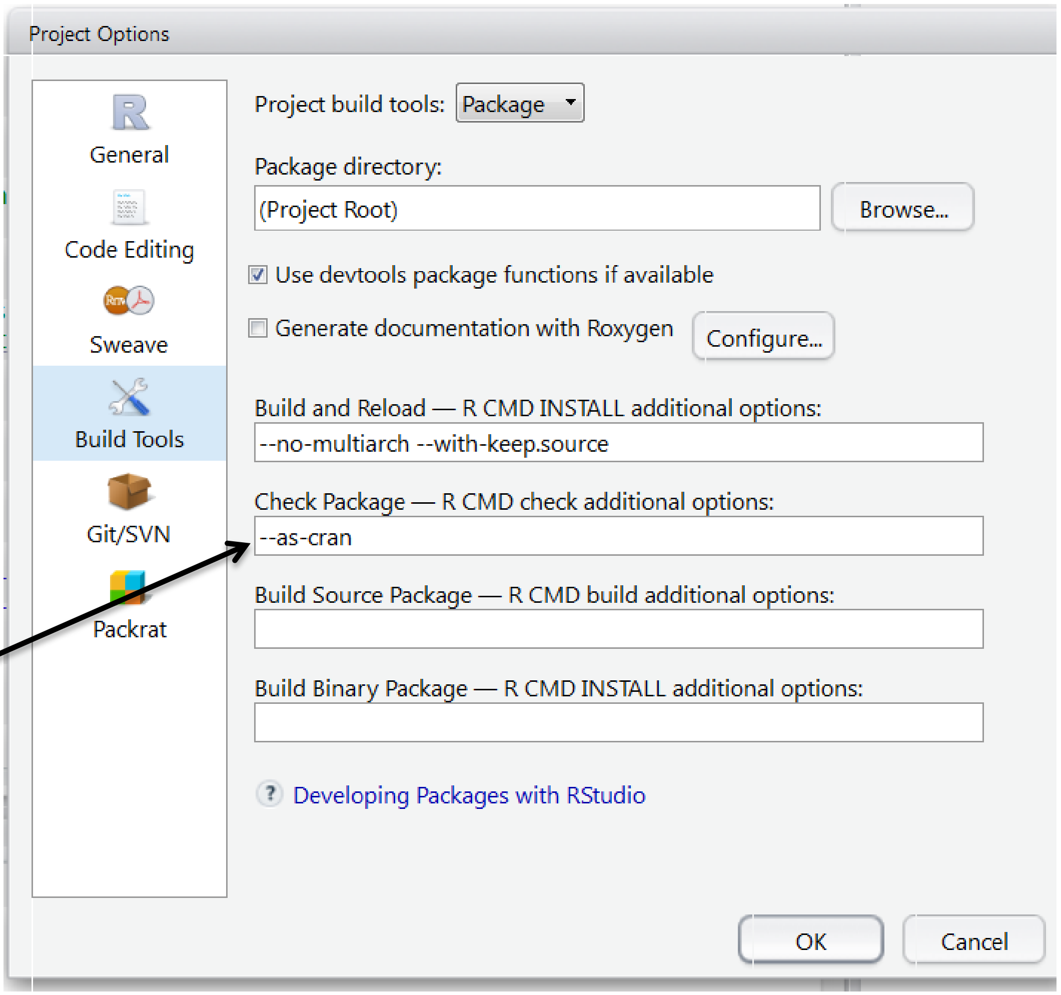
Build Binary Package — R CMD INSTALL additional options:

Developing Packages with RStudio

Configure Build Tools … (this is for CRAN checks so not entirely necessary for all)



```
#' Get Triangle T                                      x
#'
#' @param m A fre                                      trix
#' @return Pt and
#' @examples
#' ttri(caribou)
#' @importFrom igraph "graph.adjacency"
#' @importFrom igraph "triad.census"
#' @section Further details:
#' Algorithm described in D. Shizuka and D. B. McDonald, 20
#' A social network perspective on transitivity and lineari
#' in dominance hierarchies.  Animal Behaviour.
#' DOI:10.1016/j.anbehav.2012.01.011
```



Project build tools: Package

Package directory: (Project Root)

☑ Use devtools package functions if available

☐ Generate documentation with Roxygen

Build and Reload — R CMD INSTALL additional options: --no-multiarch --with-keep.source

Check Package — R CMD check additional options: --as-cran

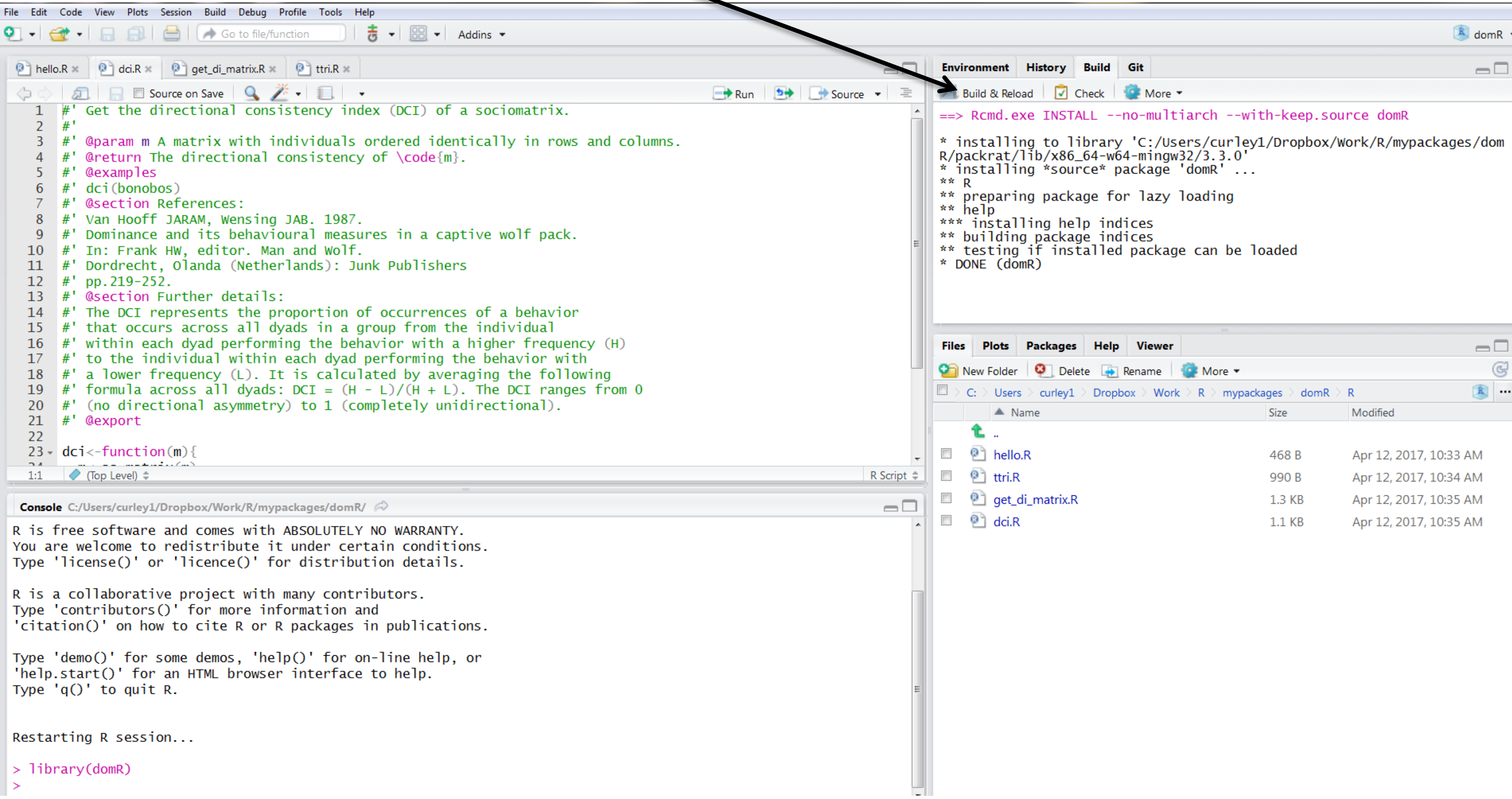
Build Source Package — R CMD build additional options:

Build Binary Package — R CMD INSTALL additional options:

Developing Packages with RStudio

Add: --as-cran

Build & Reload



```
#' Get the directional consistency index (DCI) of a sociomatrix.
#'
#' @param m A matrix with individuals ordered identically in rows and columns.
#' @return The directional consistency of \code{m}.
#' @examples
#' dci(bonobos)
#' @section References:
#' Van Hooff JARAM, Wensing JAB. 1987.
#' Dominance and its behavioural measures in a captive wolf pack.
#' In: Frank HW, editor. Man and Wolf.
#' Dordrecht, Olanda (Netherlands): Junk Publishers
#' pp.219-252.
#' @section Further details:
#' The DCI represents the proportion of occurrences of a behavior
#' that occurs across all dyads in a group from the individual
#' within each dyad performing the behavior with a higher frequency (H)
#' to the individual within each dyad performing the behavior with
#' a lower frequency (L). It is calculated by averaging the following
#' formula across all dyads: DCI = (H - L)/(H + L). The DCI ranges from 0
#' (no directional asymmetry) to 1 (completely unidirectional).
#' @export

dci<-function(m){
```

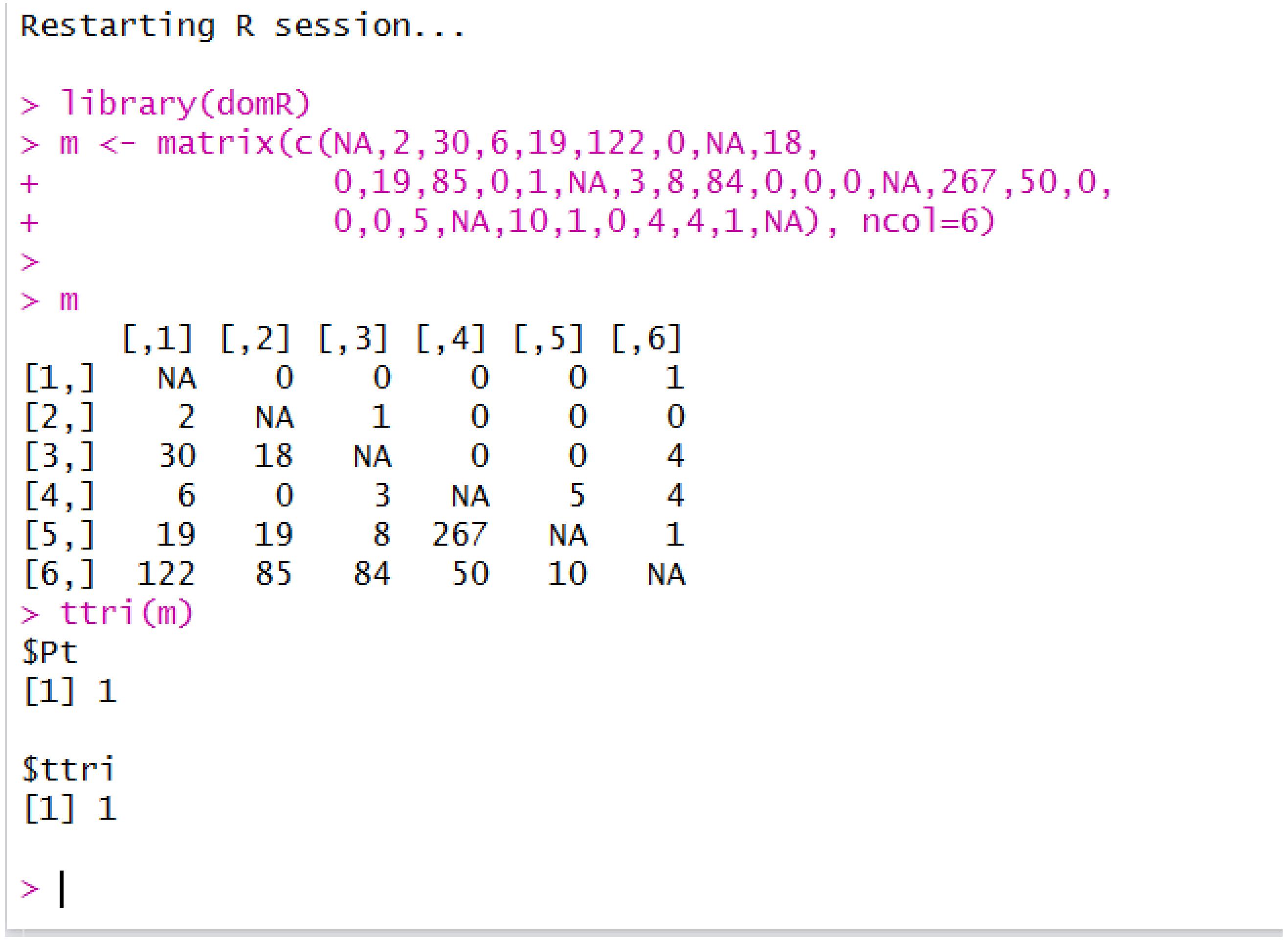
```
==> Rcmd.exe INSTALL --no-multiarch --with-keep.source domR

* installing to library 'C:/Users/curley1/Dropbox/Work/R/mypackages/dom
R/packrat/lib/x86_64-w64-mingw32/3.3.0'
* installing *source* package 'domR' ...
** R
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (domR)
```

	Name	Size	Modified
	..		
	hello.R	468 B	Apr 12, 2017, 10:33 AM
	ttri.R	990 B	Apr 12, 2017, 10:34 AM
	get_di_matrix.R	1.3 KB	Apr 12, 2017, 10:35 AM
	dci.R	1.1 KB	Apr 12, 2017, 10:35 AM

C: > Users > curley1 > Dropbox > Work > R > mypackages > domR > R

```
R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.


Restarting R session...

> library(domR)
>
```

You should be able to start using your functions now like a regular package:

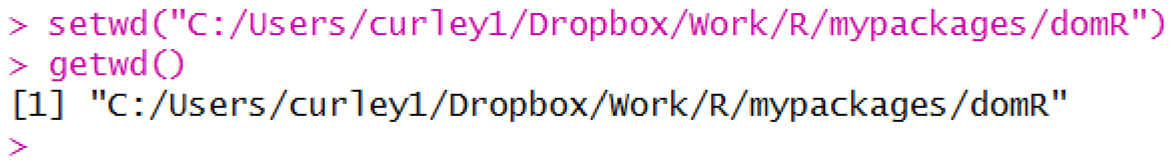


```
Restarting R session...

> library(domR)
> m <- matrix(c(NA,2,30,6,19,122,0,NA,18,
+                0,19,85,0,1,NA,3,8,84,0,0,0,NA,267,50,0,
+                0,0,5,NA,10,1,0,4,4,1,NA), ncol=6)
>
> m
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]   NA    0    0    0    0    1
[2,]    2   NA    1    0    0    0
[3,]   30   18   NA    0    0    4
[4,]    6    0    3   NA    5    4
[5,]   19   19    8  267   NA    1
[6,]  122   85   84   50   10   NA
> ttri(m)
$Pt
[1] 1

$ttri
[1] 1

> |
```

Often you will want to add data to the package:

- for examples
- for users
- for functions

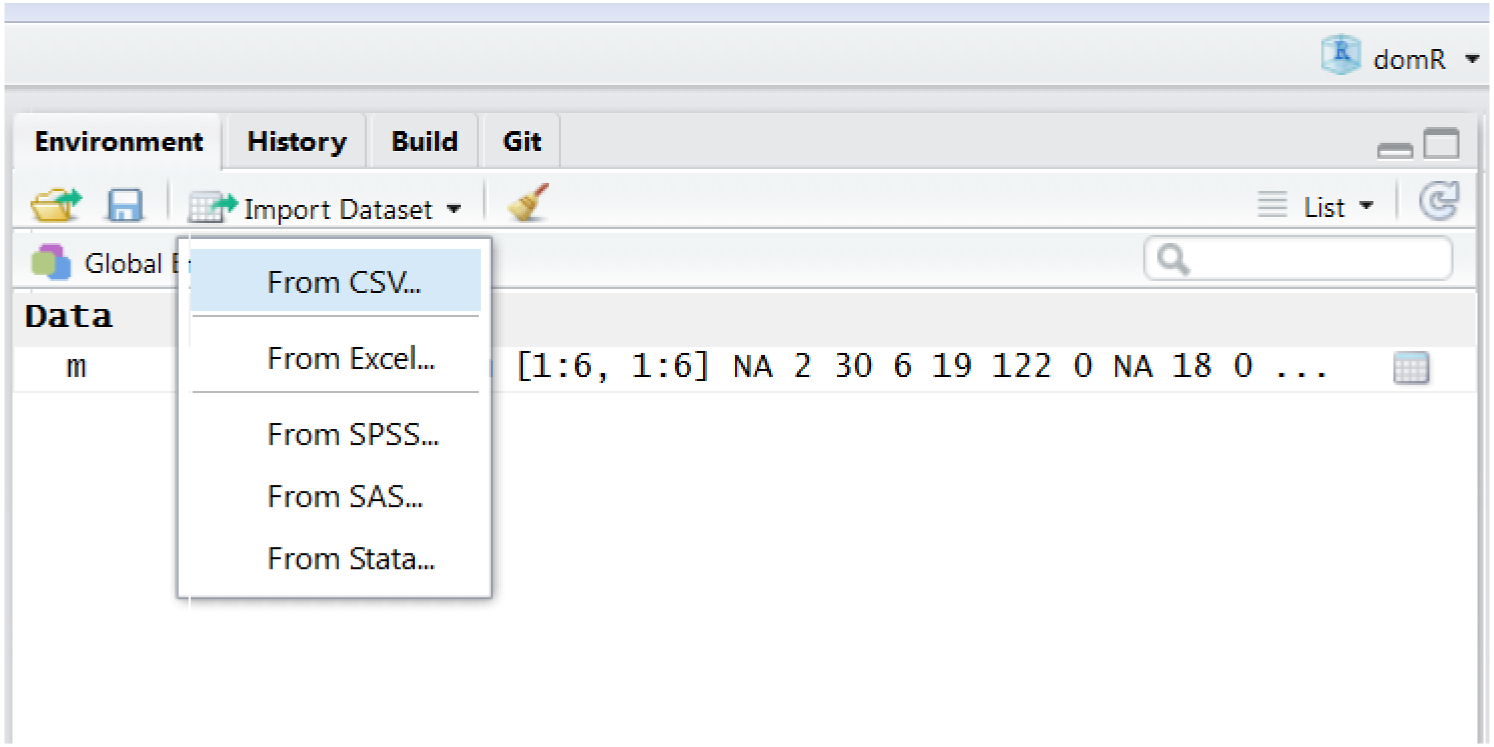
It’s worth checking that the working directory is your project at this point:



```
> setwd("C:/Users/curley1/Dropbox/Work/R/mypackages/domR")
> getwd()
[1] "C:/Users/curley1/Dropbox/Work/R/mypackages/domR"
> 
```

Here's how to make a data file available to users of your package

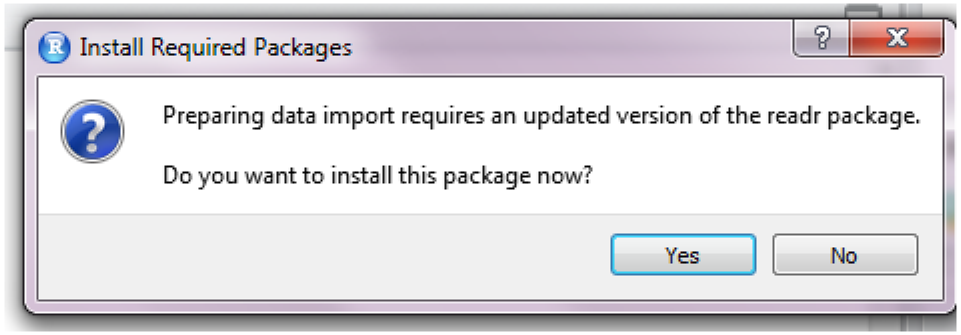
Example: Load "caribou.csv" into Global Environment



Data

m [1:6, 1:6] NA 2 30 6 19 122 0 NA 18 0 ...

If you're following this tutorial and using "packrat", and you import using the Rstudio dropdown menu you will get this prompt: Hit "YES"

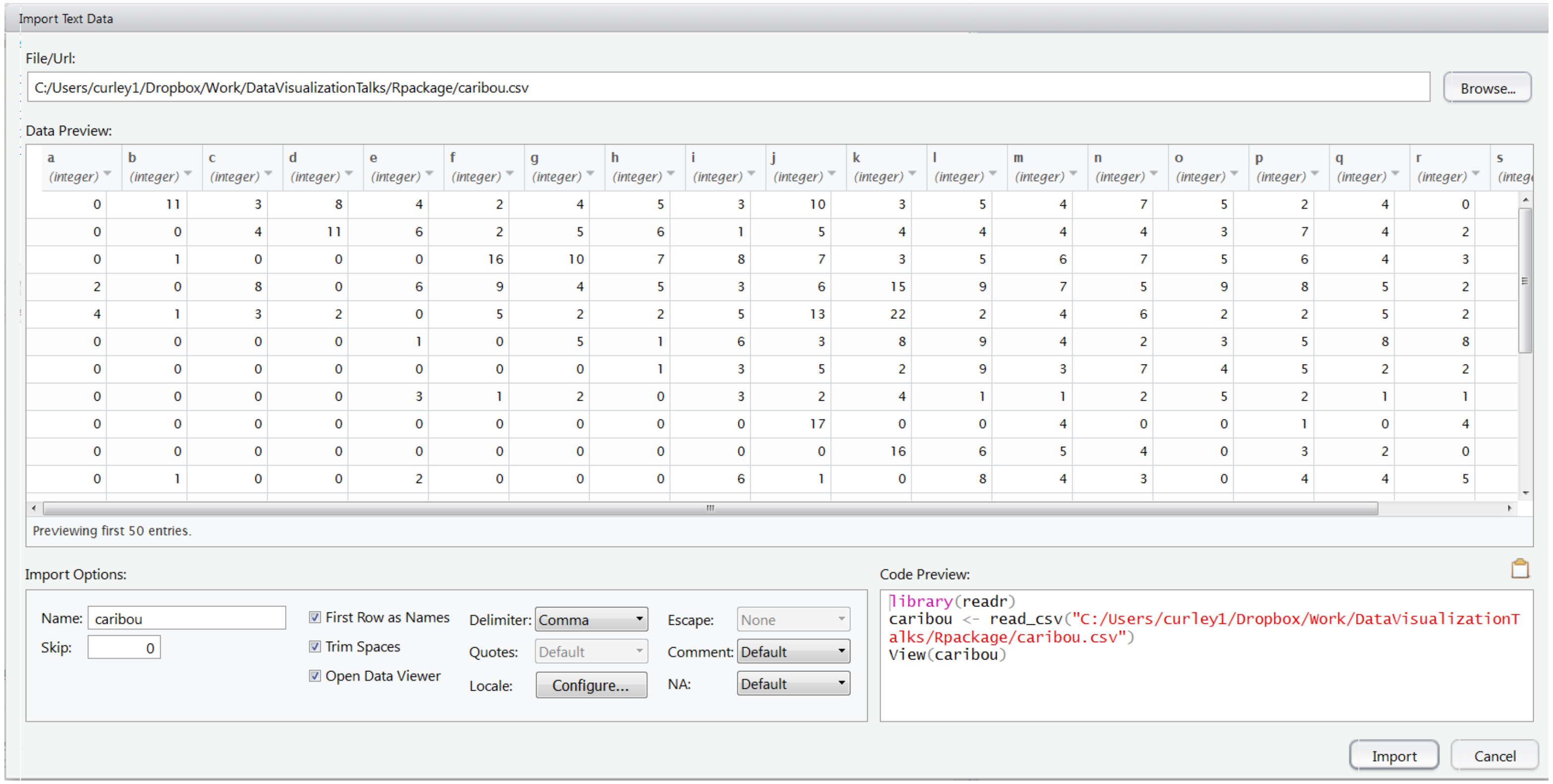


Preparing data import requires an updated version of the readr package.

Do you want to install this package now?

You could also import your data file in any other way to your working directory that you are comfortable with.

Importing …



Import Text Data

File/Url:

C:/Users/curley1/Dropbox/Work/DataVisualizationTalks/Rpackage/caribou.csv

Data Preview:

a (integer)	b (integer)	c (integer)	d (integer)	e (integer)	f (integer)	g (integer)	h (integer)	i (integer)	j (integer)	k (integer)	l (integer)	m (integer)	n (integer)	o (integer)	p (integer)	q (integer)	r (integer)	s (integ
0	11	3	8	4	2	4	5	3	10	3	5	4	7	5	2	4	0	
0	0	4	11	6	2	5	6	1	5	4	4	4	4	3	7	4	2	
0	1	0	0	0	16	10	7	8	7	3	5	6	7	5	6	4	3	
2	0	8	0	6	9	4	5	3	6	15	9	7	5	9	8	5	2	
4	1	3	2	0	5	2	2	5	13	22	2	4	6	2	2	5	2	
0	0	0	0	1	0	5	1	6	3	8	9	4	2	3	5	8	8	
0	0	0	0	0	0	0	1	3	5	2	9	3	7	4	5	2	2	
0	0	0	0	3	1	2	0	3	2	4	1	1	2	5	2	1	1	
0	0	0	0	0	0	0	0	0	17	0	0	4	0	0	1	0	4	
0	0	0	0	0	0	0	0	0	0	16	6	5	4	0	3	2	0	
0	1	0	0	2	0	0	0	6	1	0	8	4	3	0	4	4	5	

Previewing first 50 entries.

Import Options:

Name: caribou
Skip: 0

☑ First Row as Names
☑ Trim Spaces
☑ Open Data Viewer

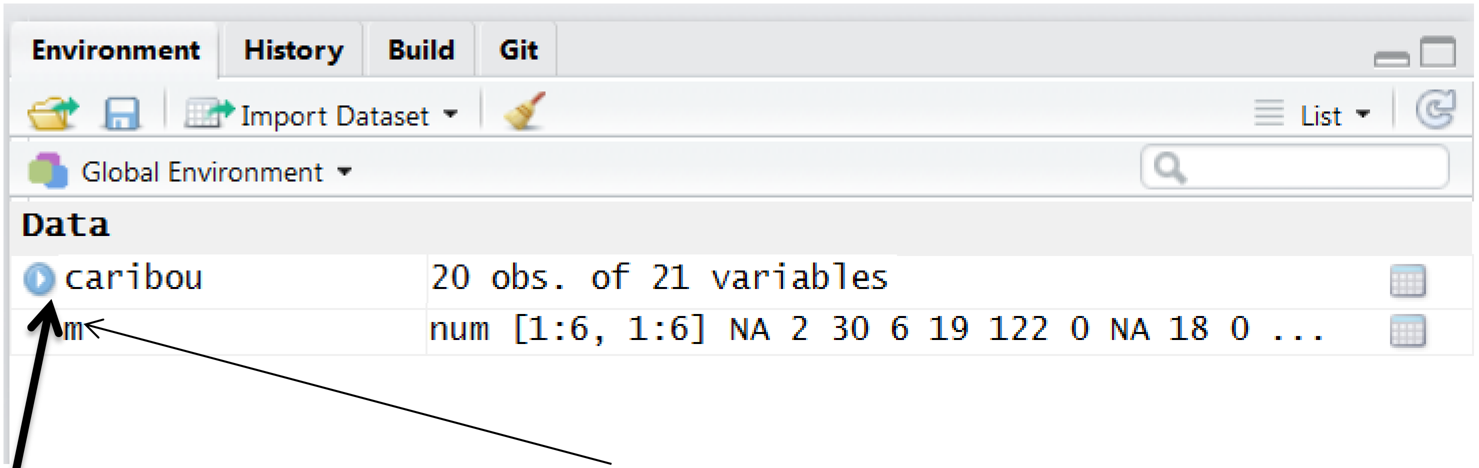
Delimiter: Comma
Quotes: Default
Locale: Configure...

Escape: None
Comment: Default
NA: Default

Code Preview:

```
library(readr)
caribou <- read_csv("C:/Users/curley1/Dropbox/Work/DataVisualizationT
alks/Rpackage/caribou.csv")
View(caribou)
```

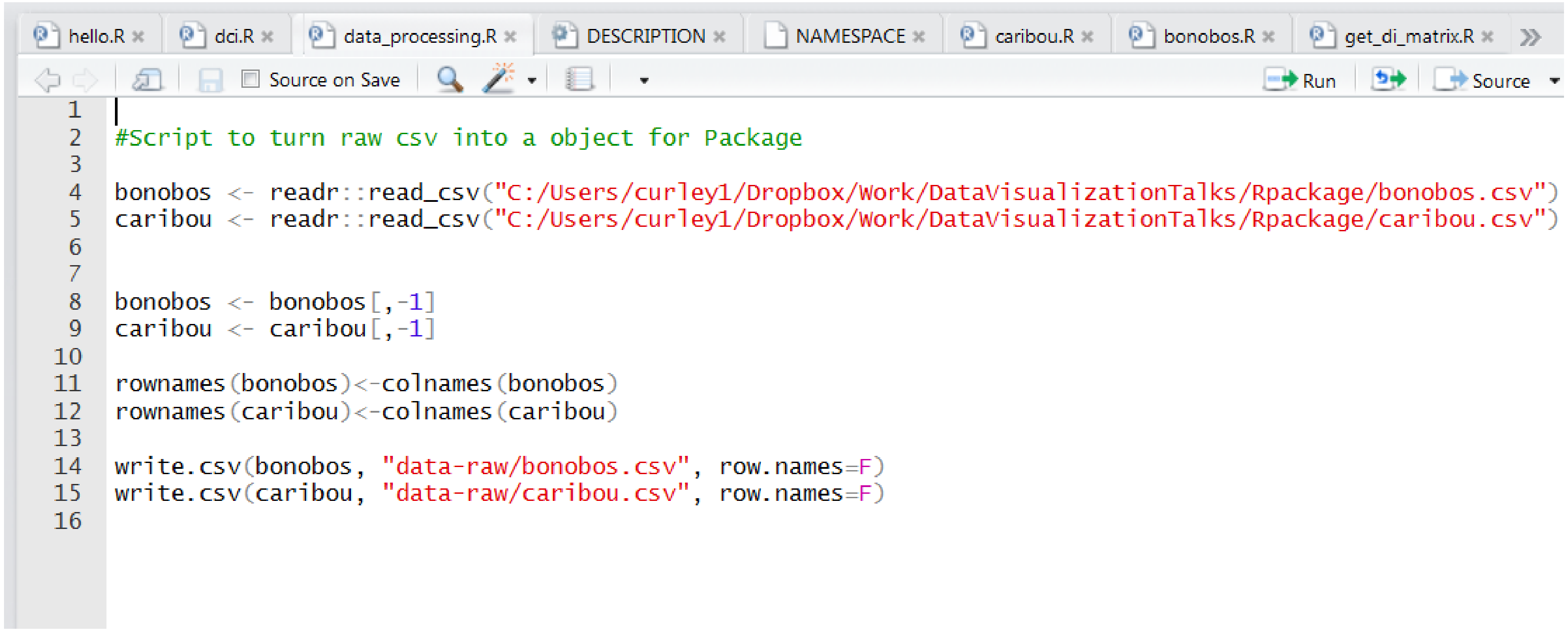
It should be in your Global Environment …



```
Data
caribou        20 obs. of 21 variables
m              num [1:6, 1:6] NA 2 30 6 19 122 0 NA 18 0 ...
```

The "m" is the object we used to test our function earlier

The data object should have the name that you want it to be called in your package.



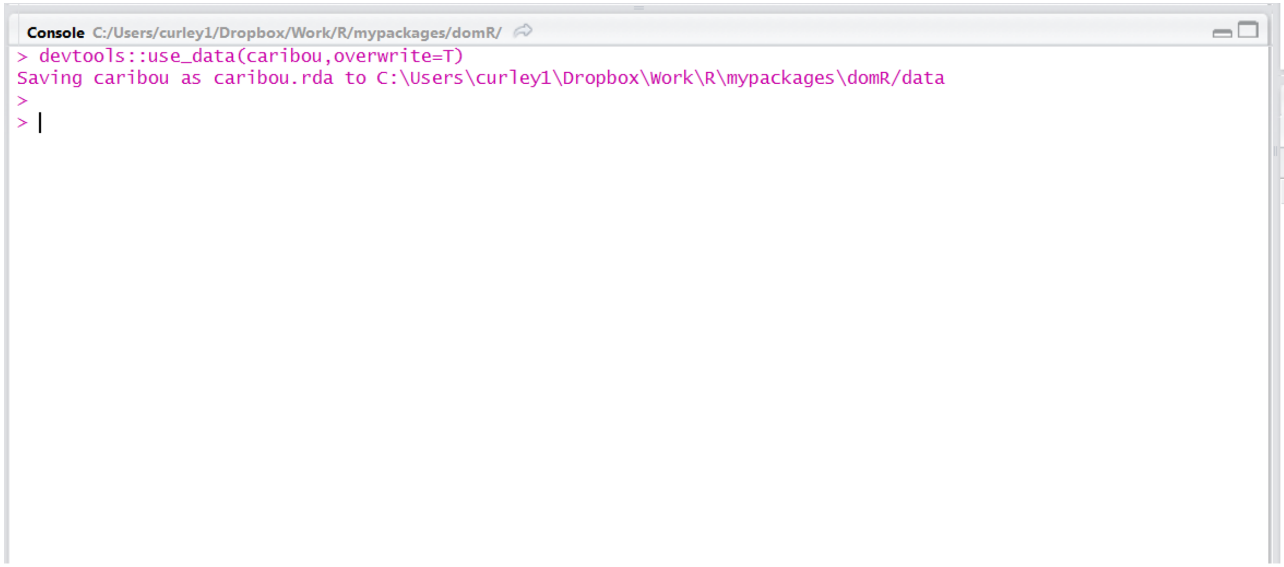
```r

#Script to turn raw csv into a object for Package

bonobos <- readr::read_csv("C:/Users/curley1/Dropbox/Work/DataVisualizationTalks/Rpackage/bonobos.csv")
caribou <- readr::read_csv("C:/Users/curley1/Dropbox/Work/DataVisualizationTalks/Rpackage/caribou.csv")


bonobos <- bonobos[,-1]
caribou <- caribou[,-1]

rownames(bonobos)<-colnames(bonobos)
rownames(caribou)<-colnames(caribou)

write.csv(bonobos, "data-raw/bonobos.csv", row.names=F)
write.csv(caribou, "data-raw/caribou.csv", row.names=F)

```

Creating our first data object

devtools::use_data()

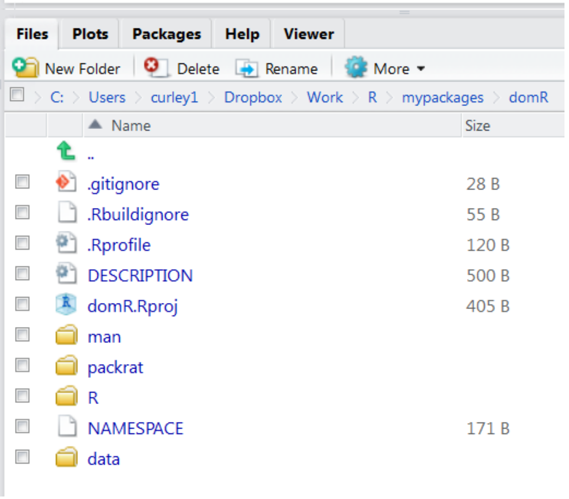
1. Will create a "DATA" folder
2. Will save the object as a ".rda" file in the DATA folder
3. Use "overwrite=T" to replace an existing file of same name (or just add file if no file of that name)

devtools::use_data(caribou,overwrite=T)



Console C:/Users/curley1/Dropbox/Work/R/mypackages/domR/

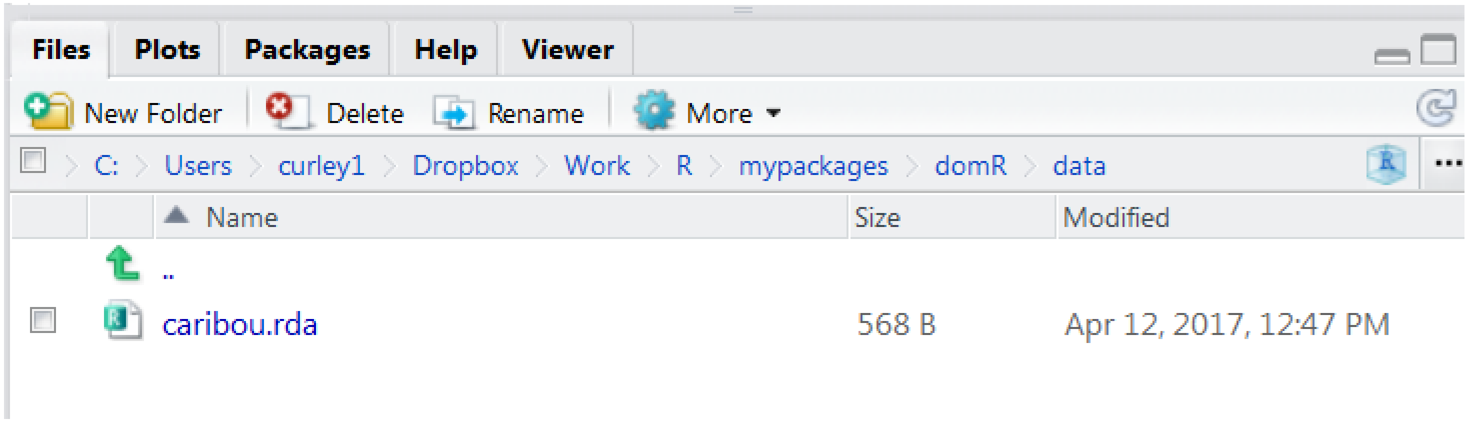
```
> devtools::use_data(caribou,overwrite=T)
Saving caribou as caribou.rda to C:\Users\curley1\Dropbox\Work\R\mypackages\domR/data
>
> |
```



Files
Plots
Packages
Help
Viewer
New Folder
Delete
Rename
More
C: > Users > curley1 > Dropbox > Work > R > mypackages > domR

Name	Size
..	
.gitignore	28 B
.Rbuildignore	55 B
.Rprofile	120 B
DESCRIPTION	500 B
domR.Rproj	405 B
man	
packrat	
R	
NAMESPACE	171 B
data	

The file should now be in the “DATA” folder:



C: › Users › curley1 › Dropbox › Work › R › mypackages › domR › data

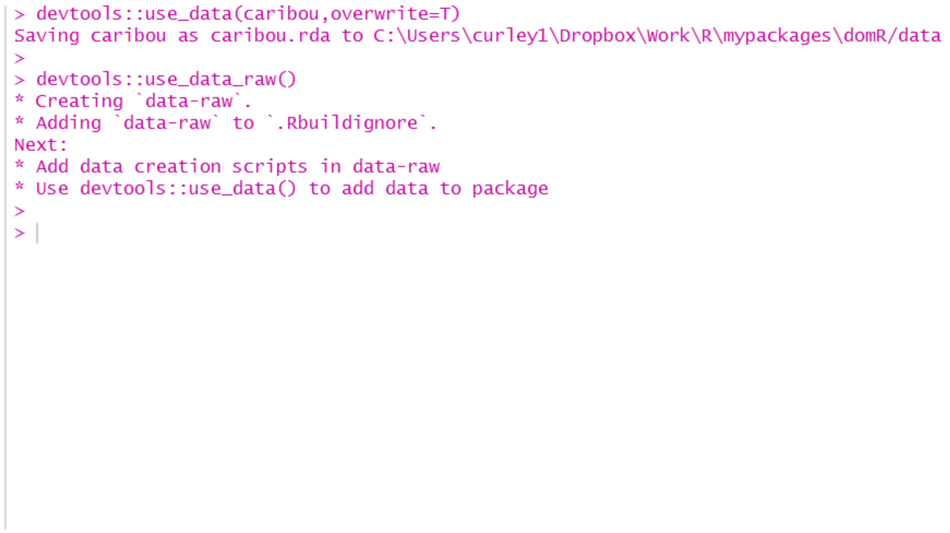
Name	Size	Modified
..		
caribou.rda	568 B	Apr 12, 2017, 12:47 PM

What about raw data ?

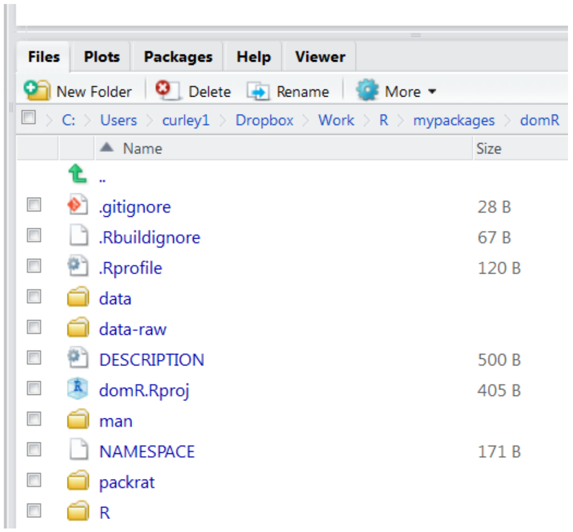
devtools::use_data-raw()

- best to keep this and any .R files used in processing data

- to enable anybody to go from raw data to final outcome, should be able to determine how data was processed



```
> devtools::use_data(caribou,overwrite=T)
Saving caribou as caribou.rda to C:\Users\curley1\Dropbox\Work\R\mypackages\domR/data
>
> devtools::use_data_raw()
* Creating `data-raw`.
* Adding `data-raw` to `.Rbuildignore`.
Next:
* Add data creation scripts in data-raw
* Use devtools::use_data() to add data to package
>
> |
```

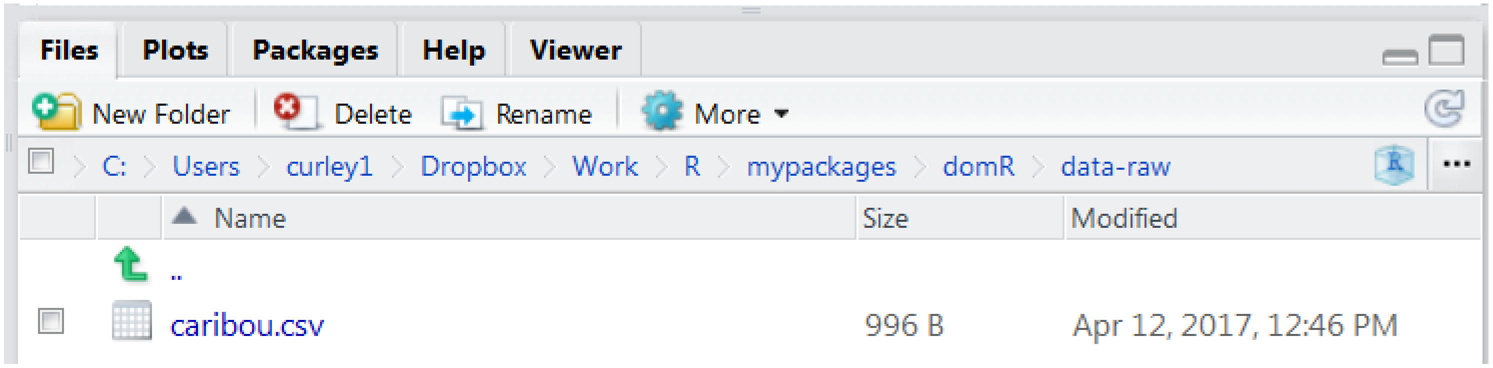


C: > Users > curley1 > Dropbox > Work > R > mypackages > domR

Name	Size
..	
.gitignore	28 B
.Rbuildignore	67 B
.Rprofile	120 B
data	
data-raw	
DESCRIPTION	500 B
domR.Rproj	405 B
man	
NAMESPACE	171 B
packrat	
R	

Files that you want to save into “data-raw” can be saved in any format:

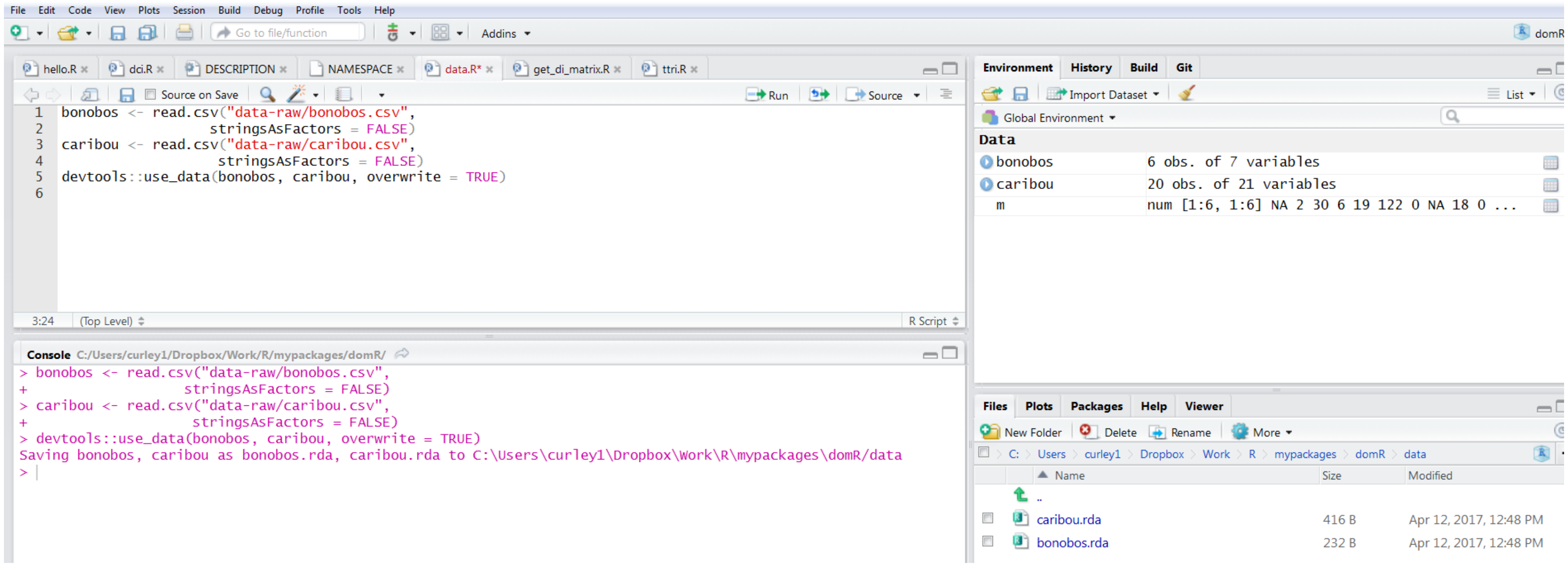
```
>
> write.csv(caribou, "data-raw/caribou.csv", row.names=F)
>
```



C: > Users > curley1 > Dropbox > Work > R > mypackages > domR > data-raw

Name	Size	Modified
..		
caribou.csv	996 B	Apr 12, 2017, 12:46 PM

Can do for multiple datasets



```
bonobos <- read.csv("data-raw/bonobos.csv",
                    stringsAsFactors = FALSE)
caribou <- read.csv("data-raw/caribou.csv",
                     stringsAsFactors = FALSE)
devtools::use_data(bonobos, caribou, overwrite = TRUE)
```

```
Console C:/Users/curley1/Dropbox/Work/R/mypackages/domR/
> bonobos <- read.csv("data-raw/bonobos.csv",
+                    stringsAsFactors = FALSE)
> caribou <- read.csv("data-raw/caribou.csv",
+                     stringsAsFactors = FALSE)
> devtools::use_data(bonobos, caribou, overwrite = TRUE)
Saving bonobos, caribou as bonobos.rda, caribou.rda to C:\Users\curley1\Dropbox\Work\R\mypackages\domR/data
> 
```

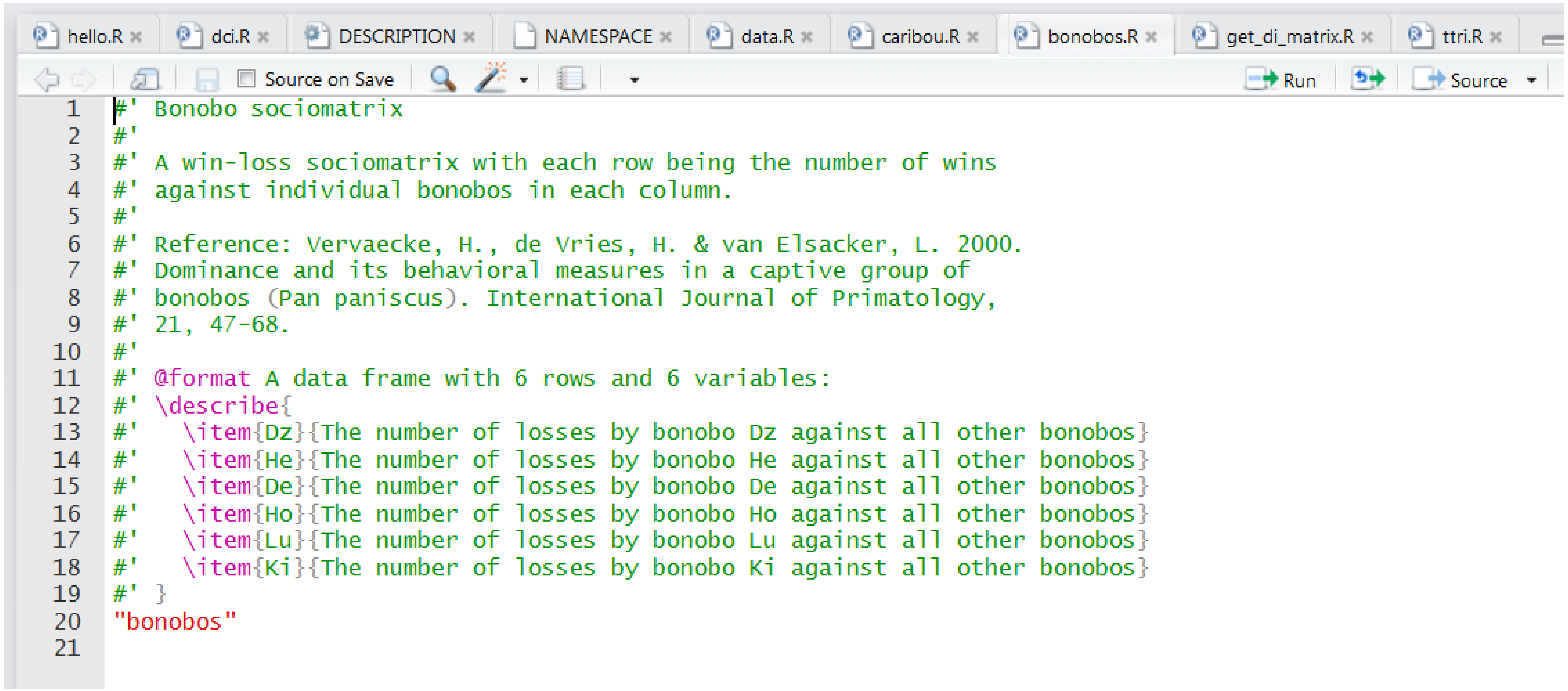
```
Data
bonobos     6 obs. of 7 variables
caribou     20 obs. of 21 variables
m           num [1:6, 1:6] NA 2 30 6 19 122 0 NA 18 0 ...
```

Name	Size	Modified
caribou.rda	416 B	Apr 12, 2017, 12:48 PM
bonobos.rda	232 B	Apr 12, 2017, 12:48 PM

Here, using a file called “data.R” that I will save in “data-raw” that contains the code to load files and save as “.rda” files in “data” folder.

I also added “data_processing.R” into “data-raw” folder

Add .R files to R folder for datasets

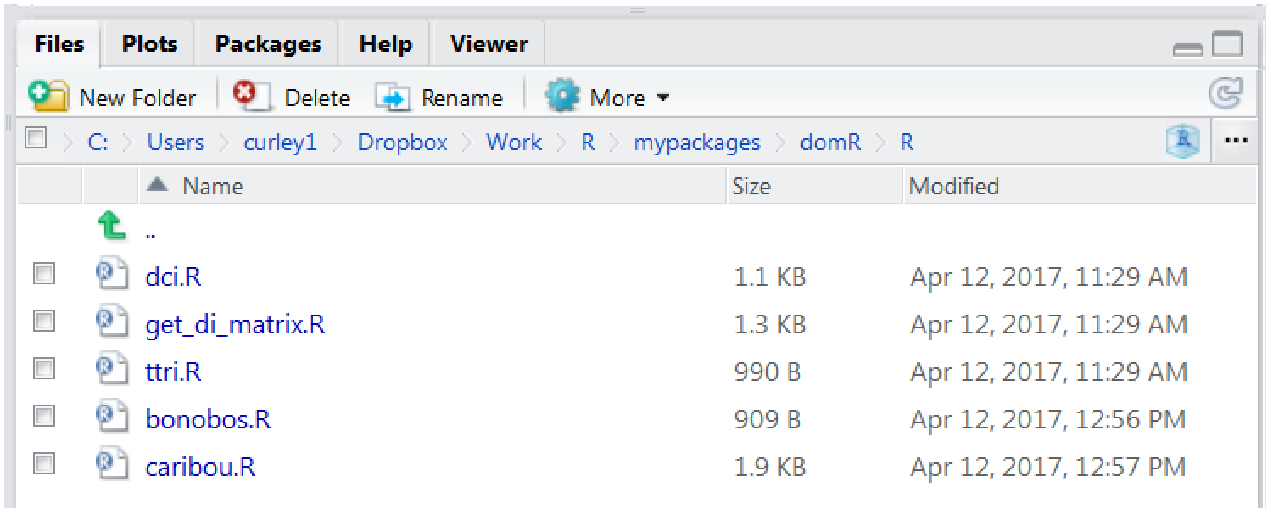


```
#' Bonobo sociomatrix
#'
#' A win-loss sociomatrix with each row being the number of wins
#' against individual bonobos in each column.
#'
#' Reference: Vervaecke, H., de Vries, H. & van Elsacker, L. 2000.
#' Dominance and its behavioral measures in a captive group of
#' bonobos (Pan paniscus). International Journal of Primatology,
#' 21, 47-68.
#'
#' @format A data frame with 6 rows and 6 variables:
#' \describe{
#'   \item{Dz}{The number of losses by bonobo Dz against all other bonobos}
#'   \item{He}{The number of losses by bonobo He against all other bonobos}
#'   \item{De}{The number of losses by bonobo De against all other bonobos}
#'   \item{Ho}{The number of losses by bonobo Ho against all other bonobos}
#'   \item{Lu}{The number of losses by bonobo Lu against all other bonobos}
#'   \item{Ki}{The number of losses by bonobo Ki against all other bonobos}
#' }
"bonobos"

```

Remember:

```
devtools::document()
```

Add .R files to R folder for datasets

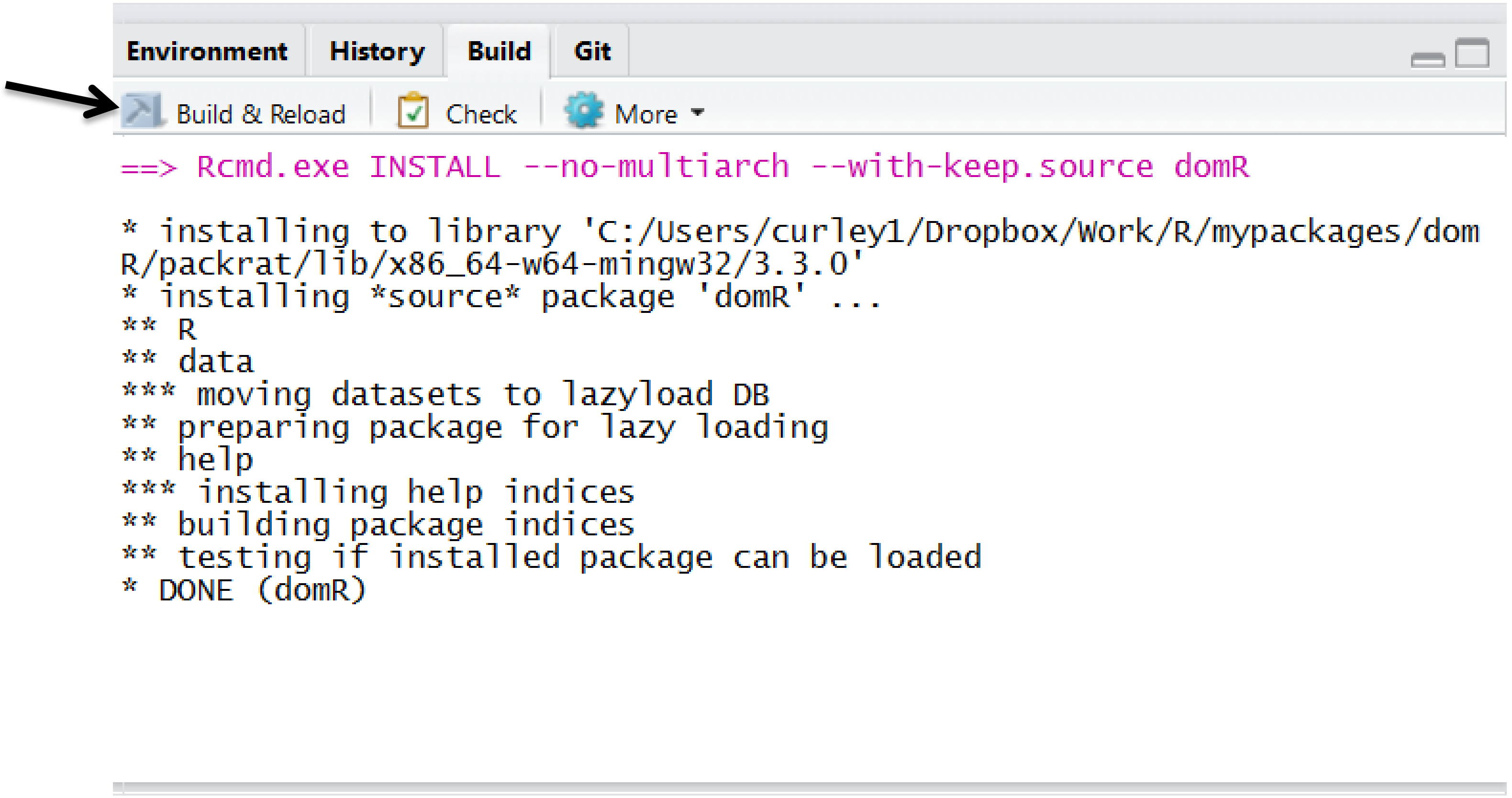


C: > Users > curley1 > Dropbox > Work > R > mypackages > domR > R

Name	Size	Modified
..		
dci.R	1.1 KB	Apr 12, 2017, 11:29 AM
get_di_matrix.R	1.3 KB	Apr 12, 2017, 11:29 AM
ttri.R	990 B	Apr 12, 2017, 11:29 AM
bonobos.R	909 B	Apr 12, 2017, 12:56 PM
caribou.R	1.9 KB	Apr 12, 2017, 12:57 PM

These .R files are needed when you run Checks.

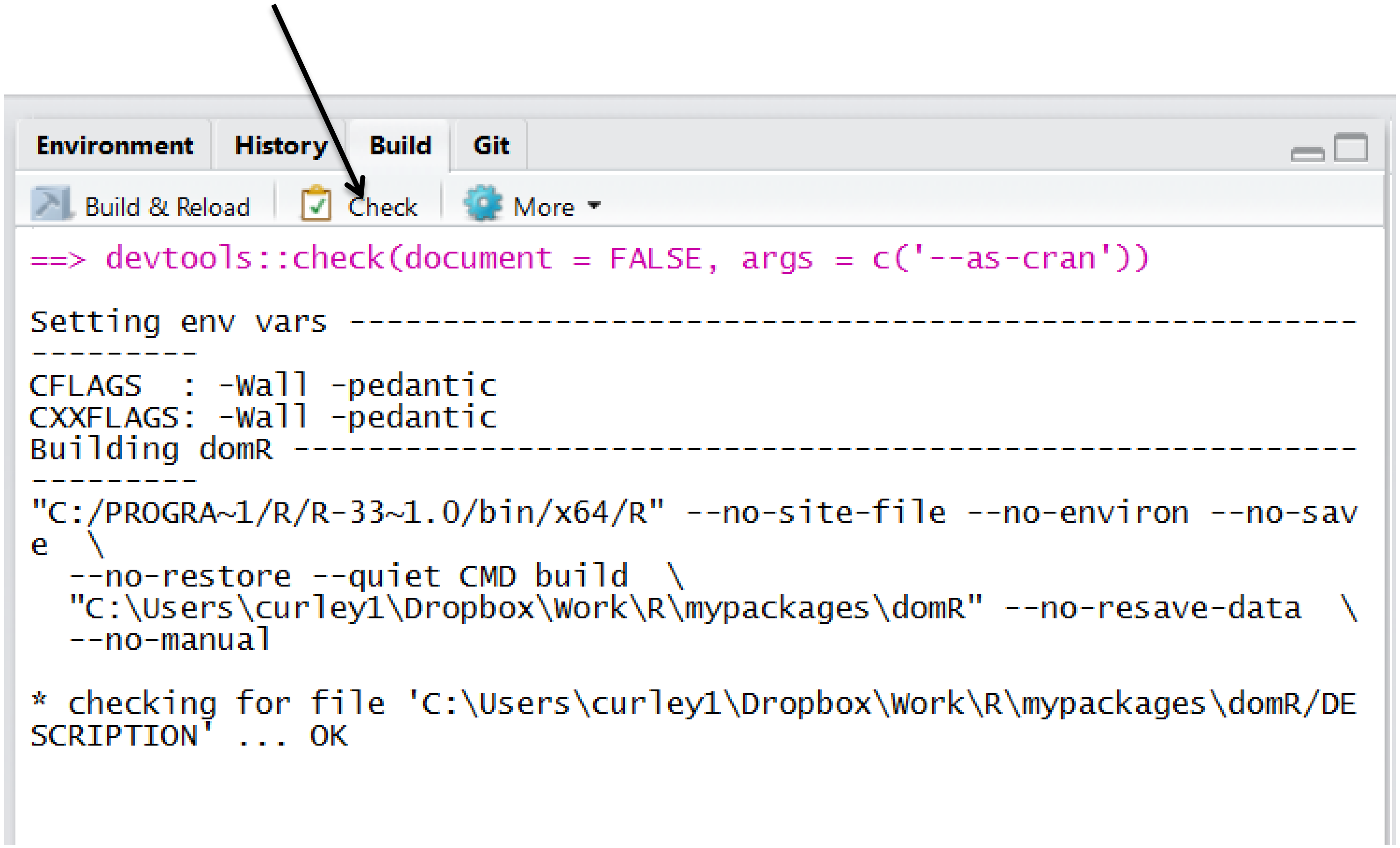
It’s always ok to rebuild



```
==> Rcmd.exe INSTALL --no-multiarch --with-keep.source domR

* installing to library 'C:/Users/curley1/Dropbox/Work/R/mypackages/dom
R/packrat/lib/x86_64-w64-mingw32/3.3.0'
* installing *source* package 'domR' ...
** R
** data
*** moving datasets to lazyload DB
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (domR)
```

Running a CRAN check

It starts by hitting this button



```
==> devtools::check(document = FALSE, args = c('--as-cran'))

Setting env vars ------------------------------------------------------
----------
CFLAGS  : -Wall -pedantic
CXXFLAGS: -Wall -pedantic
Building domR ---------------------------------------------------------
---------
"C:/PROGRA~1/R/R-33~1.0/bin/x64/R" --no-site-file --no-environ --no-sav
e  \
  --no-restore --quiet CMD build  \
  "C:\Users\curley1\Dropbox\Work\R\mypackages\domR" --no-resave-data  \
  --no-manual

* checking for file 'C:\Users\curley1\Dropbox\Work\R\mypackages\domR/DE
SCRIPTION' ... OK
```

Running a CRAN check

It then goes like this:

Running a CRAN check

The results will have at the bottom:

ERRORS	- you have to fix these immediately !
WARNINGS	- you really should fix these immediately !
NOTES	- you could not bother – but you should.

The point of this check is to ensure that your package will work consistently.

It can be hard to work out what the ERRORS/WARNINGS/NOTES are referring to, but it’s usually some error in the code or documentation that you’ve written. Persevere with it – Google it !!!

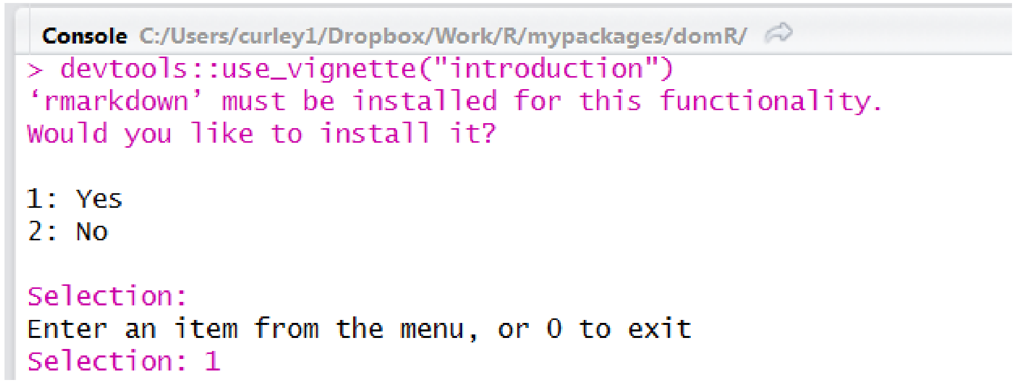
It can help to run checks after every new thing you add to the package – that way you know what went wrong immediately.

```
* DONE
Status: OK



R CMD check results
0 errors | 0 warnings | 0 notes

R CMD check succeeded
```

Adding vignettes

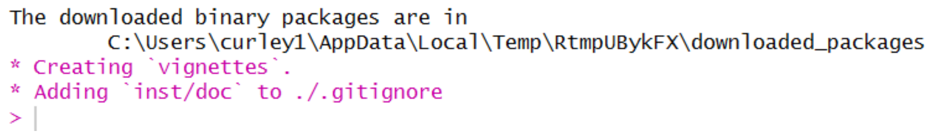
devtools::use_vignette()

For other colleagues, for peer-reviewers, for other users, for yourself !!!

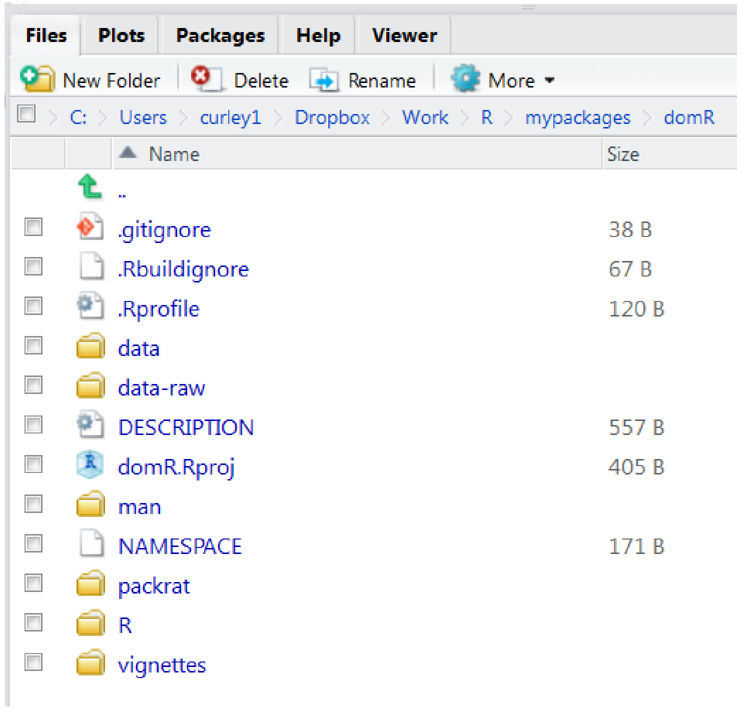


Console C:/Users/curley1/Dropbox/Work/R/mypackages/domR/

```
> devtools::use_vignette("introduction")
'rmarkdown' must be installed for this functionality.
Would you like to install it?

1: Yes
2: No

Selection:
Enter an item from the menu, or 0 to exit
Selection: 1
```



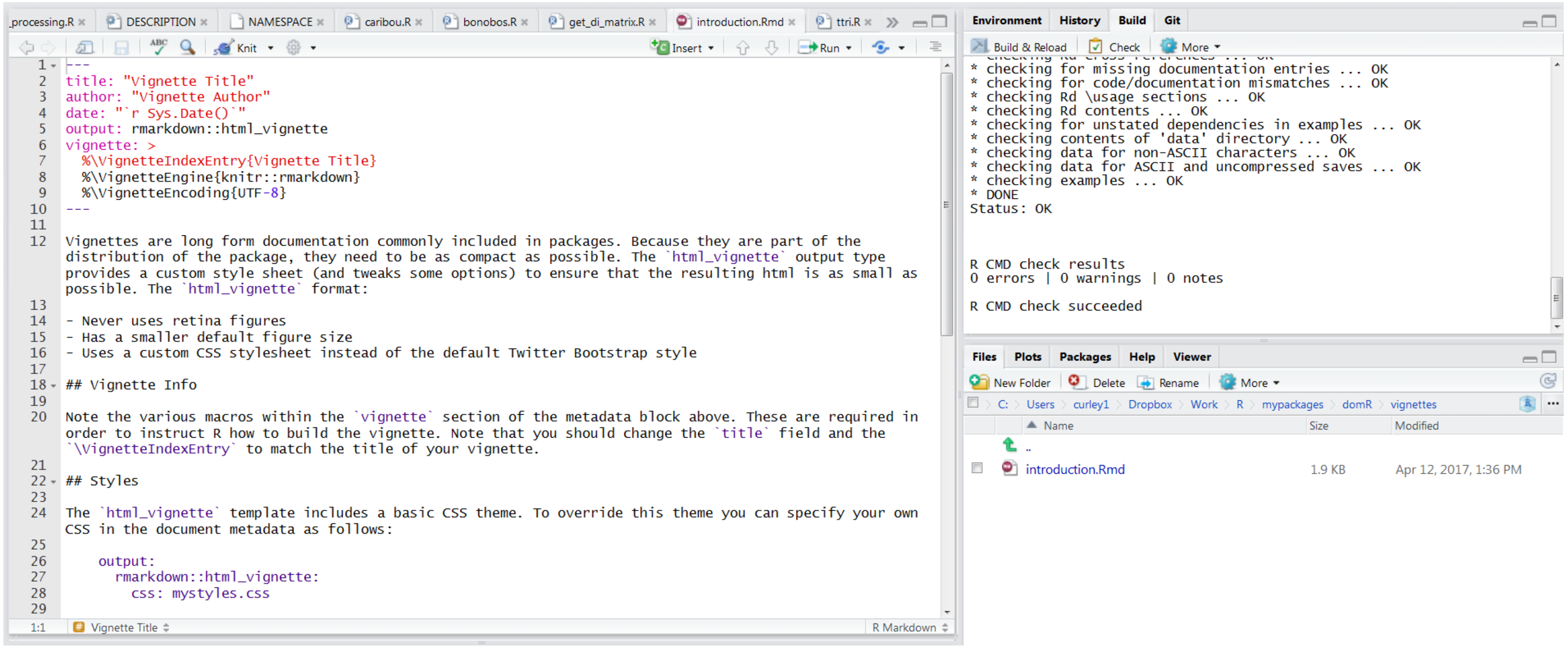
```
The downloaded binary packages are in
        C:\Users\curley1\AppData\Local\Temp\RtmpUBykFX\downloaded_packages
* Creating `vignettes`.
* Adding `inst/doc` to ./.gitignore
> |
```



C: > Users > curley1 > Dropbox > Work > R > mypackages > domR

Name	Size
..	
.gitignore	38 B
.Rbuildignore	67 B
.Rprofile	120 B
data	
data-raw	
DESCRIPTION	557 B
domR.Rproj	405 B
man	
NAMESPACE	171 B
packrat	
R	
vignettes	

You can now edit the vignette....



```
---
title: "Vignette Title"
author: "Vignette Author"
date: "`r Sys.Date()`"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---

Vignettes are long form documentation commonly included in packages. Because they are part of the
distribution of the package, they need to be as compact as possible. The `html_vignette` output type
provides a custom style sheet (and tweaks some options) to ensure that the resulting html is as small as
possible. The `html_vignette` format:

- 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 are required in
order to instruct R how to build the vignette. Note that you should change the `title` field and the
`\VignetteIndexEntry` to match the title of your vignette.

## Styles

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

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

```

```
* checking for missing documentation entries ... OK
* checking for code/documentation mismatches ... OK
* checking Rd \usage sections ... OK
* checking Rd contents ... OK
* checking for unstated dependencies in examples ... OK
* checking contents of 'data' directory ... OK
* checking data for non-ASCII characters ... OK
* checking data for ASCII and uncompressed saves ... OK
* checking examples ... OK
* DONE
Status: OK


R CMD check results
0 errors | 0 warnings | 0 notes

R CMD check succeeded
```

Name	Size	Modified
..		
introduction.Rmd	1.9 KB	Apr 12, 2017, 1:36 PM

Install your package into your R system library

```
devtools::install()
```

Your package should now be available on your machine whenever you need it.

Access it like you would any other package:

```
library(“domR”)
```

Publishing your package - GitHub

1. Create your repository on GitHub

2. Add the contents of your entire folder

3. Install/share from GitHub directly
   using the following:

```
devtools::install_github(“jalapic/domR”)
```

Publishing your package - CRAN

1. devtools::release()

2. Follow ALL of the instructions as they appear in the console

3. Add a file called “cran-comments.md” to the main folder.

4. This file should contain information based on the CRAN checks (see example).

5. Add this file to .Rbuildignore

See here: http://r-pkgs.had.co.nz/release.html

Things to cover in version 2 of this tutorial:

- Writing tests
- Writing a package website using “pkgdown”
- Further ‘how-to’ on CRAN submission
- Adding other data types e.g. internal only data into a package.