DIY R PACKAGE: SIMPLIFY LIFE WITH R

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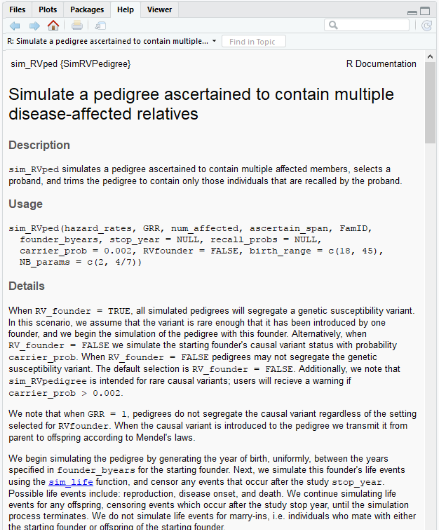
DETAILED FUNCTION DESCRIPTIONS

No more digging through old notes to figure out what you did months ago!
Store information where you use it: in R.



sim_RVped {SimRVPedigree}   R Documentation

Simulate a pedigree ascertained to contain multiple disease-affected relatives

Description

sim_RVped simulates a pedigree ascertained to contain multiple affected members, selects a proband, and trims the pedigree to contain only those individuals that are recalled by the proband.

Usage

```
sim_RVped(hazard_rates, GRR, num_affected, ascertain_span, FamID,
  founder_byears, stop_year = NULL, recall_probs = NULL,
  carrier_prob = 0.002, RVfounder = FALSE, birth_range = c(18, 45),
  NB_params = c(2, 4/7))
```

Details

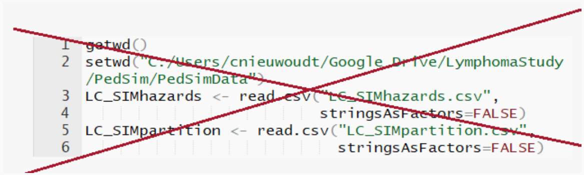
When RV_founder = TRUE, all simulated pedigrees will segregate a genetic susceptibility variant. In this scenario, we assume that the variant is rare enough that it has been introduced by one founder, and we begin the simulation of the pedigree with this founder. Alternatively, when RV_founder = FALSE we simulate the starting founder's causal variant status with probability carrier_prob. When RV_founder = FALSE pedigrees may not segregate the genetic susceptibility variant. The default selection is RV_founder = FALSE. Additionally, we note that sim_RVpedigree is intended for rare causal variants; users will recieve a warning if carrier_prob > 0.002.

We note that when GRR = 1, pedigrees do not segregate the causal variant regardless of the setting selected for RVfounder. When the causal variant is introduced to the pedigree we transmit it from parent to offspring according to Mendel's laws.

We begin simulating the pedigree by generating the year of birth, uniformly, between the years specified in founder_byears for the starting founder. Next, we simulate this founder's life events using the sim_life function, and censor any events that occur after the study stop_year. Possible life events include: reproduction, disease onset, and death. We continue simulating life events for any offspring, censoring events which occur after the study stop year, until the simulation process terminates. We do not simulate life events for marry-ins, i.e. individuals who mate with either the starting founder or offspring of the starting founder.

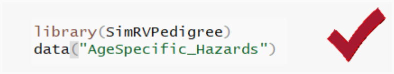
EASY DATA IMPORT

No more tedious, time-consuming data import!



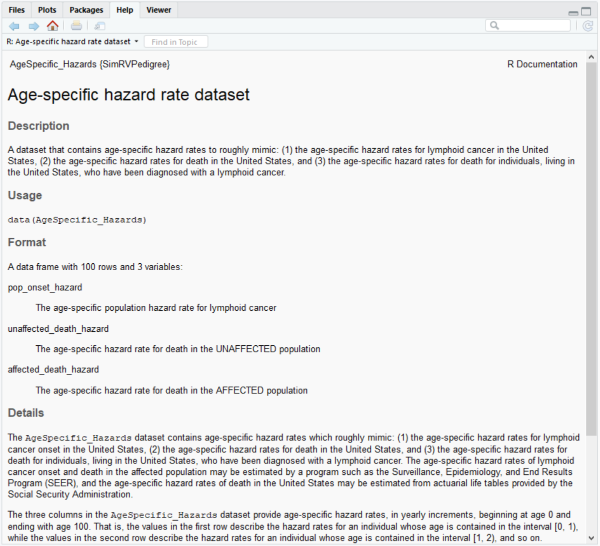
```r
getwd()
setwd("C:/Users/cnieuwoudt/Google Drive/LymphomaStudy
/PedSim/PedSimData")
LC_SIMhazards <- read.csv("LC_SIMhazards.csv",
                          stringsAsFactors=FALSE)
LC_SIMpartition <- read.csv("LC_SIMpartition.csv",
                            stringsAsFactors=FALSE)
```

Simply load the package and then the data.



```r
library(SimRVPedigree)
data("AgeSpecific_Hazards")
```

BONUS: You can clearly document your datasets, which may save you valuable time in the future.



AgeSpecific_Hazards {SimRVPedigree} R Documentation

Age-specific hazard rate dataset

Description

A dataset that contains age-specific hazard rates to roughly mimic: (1) the age-specific hazard rates for lymphoid cancer in the United States, (2) the age-specific hazard rates for death in the United States, and (3) the age-specific hazard rates for death for individuals, living in the United States, who have been diagnosed with a lymphoid cancer.

Usage

```
data(AgeSpecific_Hazards)
```

Format

A data frame with 100 rows and 3 variables:

pop_onset_hazard

The age-specific population hazard rate for lymphoid cancer

unaffected_death_hazard

The age-specific hazard rate for death in the UNAFFECTED population

affected_death_hazard

The age-specific hazard rate for death in the AFFECTED population

Details

The `AgeSpecific_Hazards` dataset contains age-specific hazard rates which roughly mimic: (1) the age-specific hazard rates for lymphoid cancer onset in the United States, (2) the age-specific hazard rates for death in the United States, and (3) the age-specific hazard rates for death for individuals, living in the United States, who have been diagnosed with a lymphoid cancer. The age-specific hazard rates of lymphoid cancer onset and death in the affected population may be estimated by a program such as the Surveillance, Epidemiology, and End Results Program (SEER), and the age-specific hazard rates of death in the United States may be estimated from actuarial life tables provided by the Social Security Administration.

The three columns in the `AgeSpecific_Hazards` dataset provide age-specific hazard rates, in yearly increments, beginning at age 0 and ending with age 100. That is, the values in the first row describe the hazard rates for an individual whose age is contained in the interval [0, 1), while the values in the second row describe the hazard rates for an individual whose age is contained in the interval [1, 2), and so on.

VERSION CONTROL

Track and Revert Changes

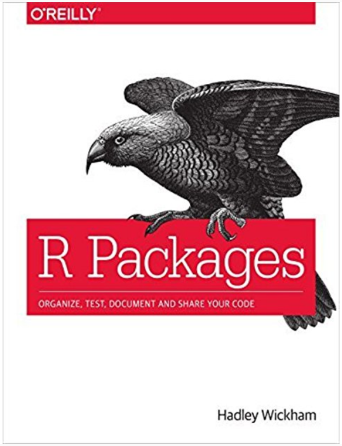
- Git
- Subversion

Useful links:

- https://support.rstudio.com/hc/en-us/articles/200532077-Version-Control-with-Git-and-SVN
- https://www.r-bloggers.com/version-control-with-git/

OMG, THANK YOU HADLEY WICKHAM!

Wickham, Hadley: *R Packages: Organize, Test, Document, and Share Your Code*. 1st Edition, O'Reilly Media (2015).



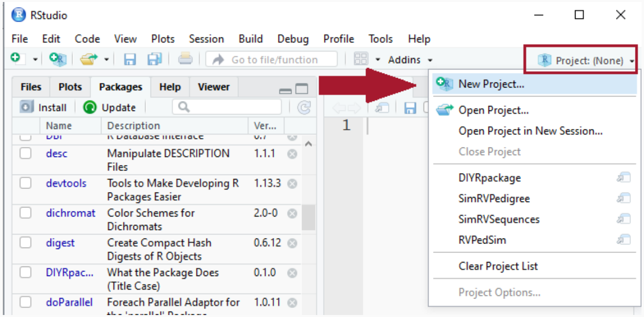
Available online http://r-pkgs.had.co.nz/

REQUIREMENTS

- Developer Tools (NOT R PACKAGES)
  - Windows:
    - Rtools: https://cran.r-project.org/bin/windows/Rtools/
  - Mac:
    - XCode: Available for free in App Store
    - Command Line Tools for Xcode: http://developer.apple.com/downloads
  - Linux: See HW's book.

- R packages:
  - devtools
  - roxygen2
  - knitr
  - testthat

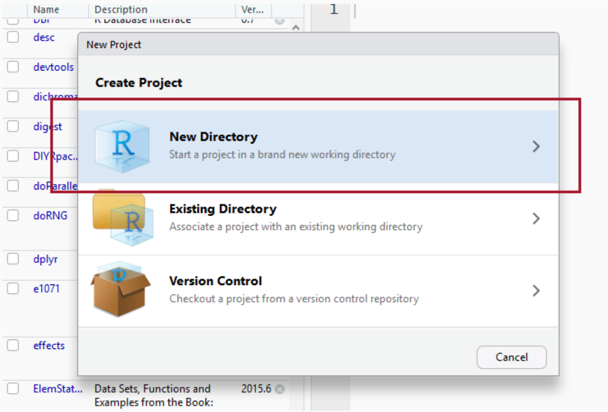
CREATE R PACKAGE



Name	Description	Ver...
desc	Manipulate DESCRIPTION Files	1.1.1
devtools	Tools to Make Developing R Packages Easier	1.13.3
dichromat	Color Schemes for Dichromats	2.0-0
digest	Create Compact Hash Digests of R Objects	0.6.12
DIYRpac...	What the Package Does (Title Case)	0.1.0
doParallel	Foreach Parallel Adaptor for	1.0.11

Click on the *Project* drop down menu and select *New Project*.

CREATE R PACKAGE



New Project

Create Project

New Directory
Start a project in a brand new working directory

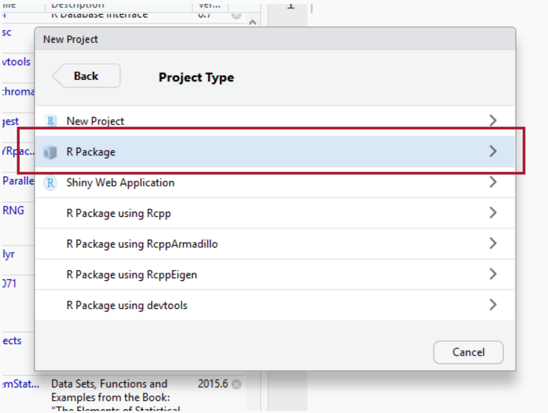
Existing Directory
Associate a project with an existing working directory

Version Control
Checkout a project from a version control repository

Cancel

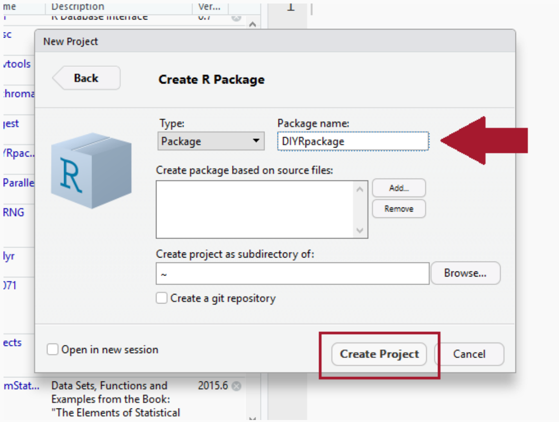
Select *New Directory* from the *New Project* options.

CREATE R PACKAGE



Choose *R Package* from the *Project Type* options.

CREATE R PACKAGE



Type: Package

Package name: DIYRpackage

Create package based on source files:

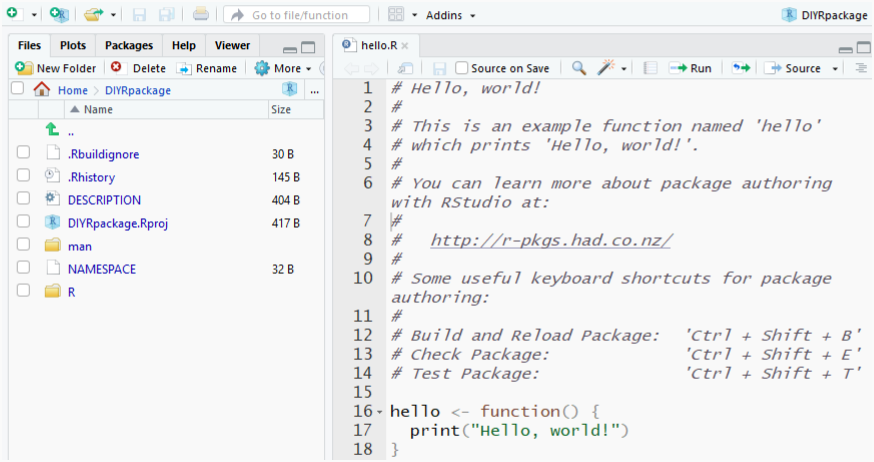
Create project as subdirectory of: ~

☐ Create a git repository

☐ Open in new session

Name the package and click *Create Project*.

CREATE R PACKAGE

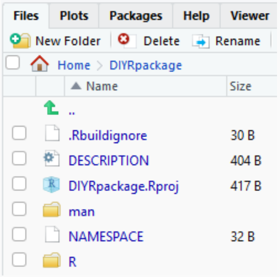


Name	Size
..	
.Rbuildignore	30 B
.Rhistory	145 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

```
# 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!")
}
```

R generates a new package with basic package files and a hello world function.

R PACKAGE FILES



Name	Size
..	
.Rbuildignore	30 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

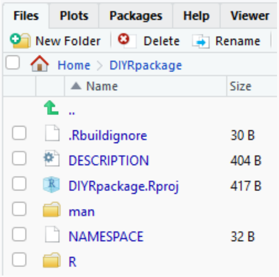
R package directory files:

- .Rproj file
- .Rbuildignore
- DESCRIPTION
- NAMESPACE
- \R
- \man

.Rproj file: a text file that stores project preferences.
.Rbuildignore: Important for CRAN packages, for more info check out Chapter 2 of HW's book.

Don't worry about them. You don't need to edit them by hand.

R PACKAGE FILES



Name	Size
..	
.Rbuildignore	30 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

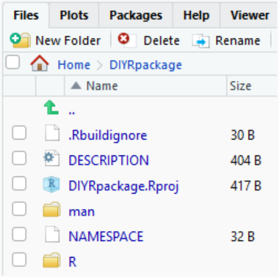
R package directory files:

- .Rproj file
- .Rbuildignore
- DESCRIPTION
- NAMESPACE
- \R
- \man

NAMESPACE

Important for CRAN packages.
Don't worry about it; `roxygen2` manages this for you.

R PACKAGE FILES



Name	Size
.Rbuildignore	30 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

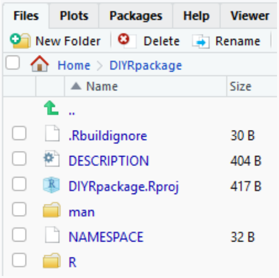
R package directory files:

- .Rproj file
- .Rbuildignore
- DESCRIPTION
- NAMESPACE
- \R
- \man

DESCRIPTION

Contains package metadata, more on this soon.

R PACKAGE FILES


Files Plots Packages Help Viewer
New Folder Delete Rename
Home > DIYRpackage

Name	Size
..	
.Rbuildignore	30 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

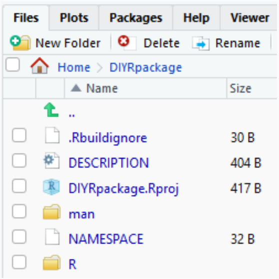
R package directory files:

- .Rproj file
- .Rbuildignore
- DESCRIPTION
- NAMESPACE
- \R
- \man

\R

All R code is stored here.

R PACKAGE FILES



Name	Size
.Rbuildignore	30 B
DESCRIPTION	404 B
DIYRpackage.Rproj	417 B
man	
NAMESPACE	32 B
R	

R package directory files:

- .Rproj file
- .Rbuildignore
- DESCRIPTION
- NAMESPACE
- \R
- \man

\man

This is where description files are stored.

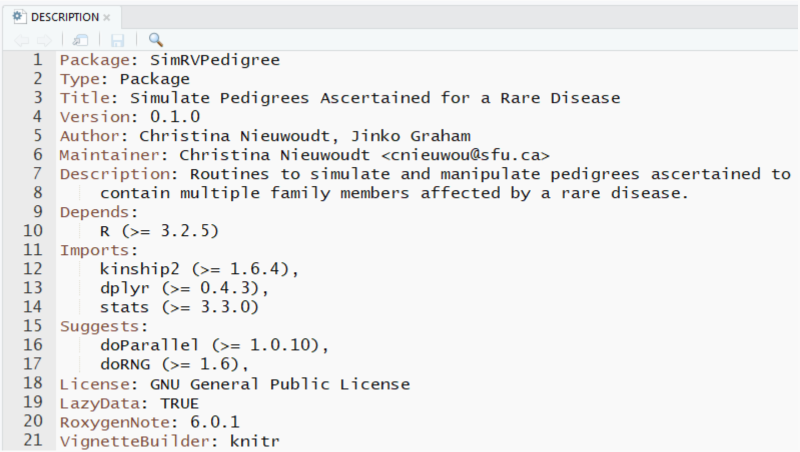
NEVER edit these by hand; `roxygen2` does all of the work for you.

ADDITIONAL FILES

Additionally, you may find the following files to be useful additions to your R package directory:

- `\data`
- `\vignettes`
- `\tests`

DESCRIPTION FILE



```
Package: SimRVPedigree
Type: Package
Title: Simulate Pedigrees Ascertained for a Rare Disease
Version: 0.1.0
Author: Christina Nieuwoudt, Jinko Graham
Maintainer: Christina Nieuwoudt <cnieuwou@sfu.ca>
Description: Routines to simulate and manipulate pedigrees ascertained to
    contain multiple family members affected by a rare disease.
Depends:
    R (>= 3.2.5)
Imports:
    kinship2 (>= 1.6.4),
    dplyr (>= 0.4.3),
    stats (>= 3.3.0)
Suggests:
    doParallel (>= 1.0.10),
    doRNG (>= 1.6),
License: GNU General Public License
LazyData: TRUE
RoxygenNote: 6.0.1
VignetteBuilder: knitr
```

For more information, refer to Chapter 4 of "*R Packages*"

ROXYGEN

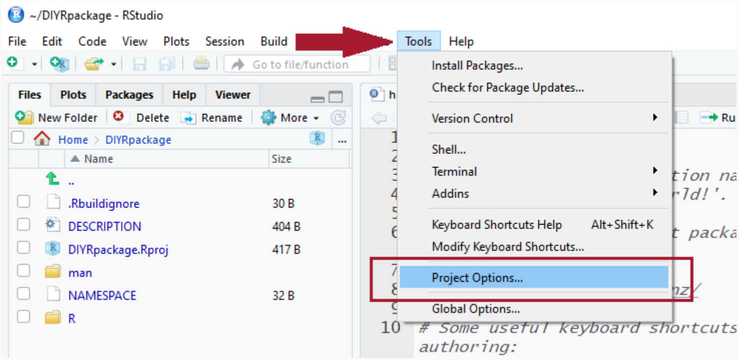
In conjunction with `devtools`, `roxygen2` is a really nice `R` package that will simplify development.

The `roxygen2` package:

- manages the NAMESPACE file,
- handles text formatting in documentation, and
- generates .Rd files in the \\`man` directory for documented functions.

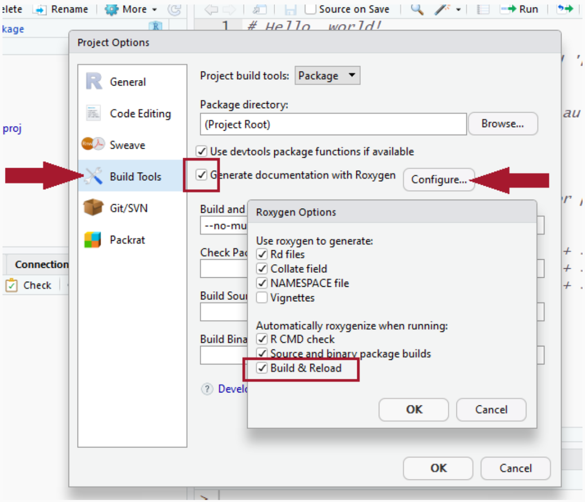
All this can be yours... but first, you must configure the project build tools to use `roxygen2`.

CONFIGURE ROXYGEN2



To configure, click on the *Tools* menu and select *Project Options...*.

CONFIGURE ROXYGEN2


Project Options

Project build tools: Package

Package directory: (Project Root)

☑ Use devtools package functions if available

☑ Generate documentation with Roxygen

Roxygen Options

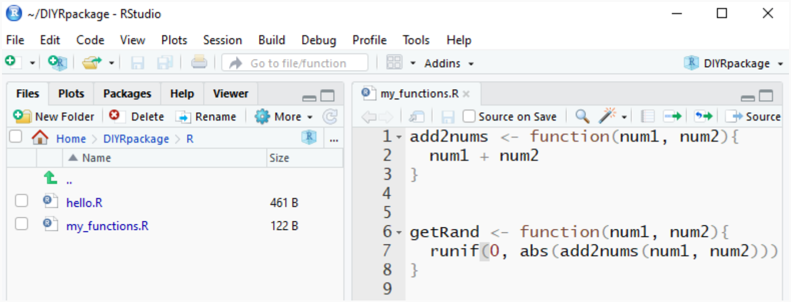
Use roxygen to generate:
☑ Rd files
☑ Collate field
☑ NAMESPACE file
☐ Vignettes

Automatically roxygenize when running:
☑ R CMD check
☑ Source and binary package builds
☑ Build & Reload

Under *Build Tools*, configure Roxygen as displayed above.

R FUNCTIONS

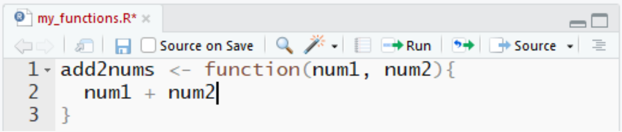
- R functions are stored in .R files in the \R directory.
- You may store and document multiple functions in the same script.


~/DIYRpackage - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
DIYRpackage
Files Plots Packages Help Viewer
New Folder Delete Rename More
Home > DIYRpackage > R
Name
Size
my_functions.R
Source on Save
Source

Name	Size
..	
hello.R	461 B
my_functions.R	122 B

```r
add2nums <- function(num1, num2){
  num1 + num2
}


getRand <- function(num1, num2){
  runif(0, abs(add2nums(num1, num2)))
}

```

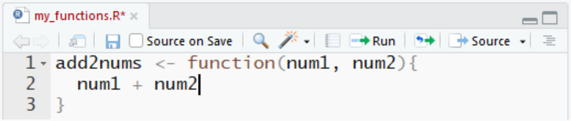
CREATE R FUNCTION AND DOCUMENTATION



```r
add2nums <- function(num1, num2){
  num1 + num2
}
```

Let's start by documenting this simple function, `add2num`, which returns the sum of `num1` and `num2`.

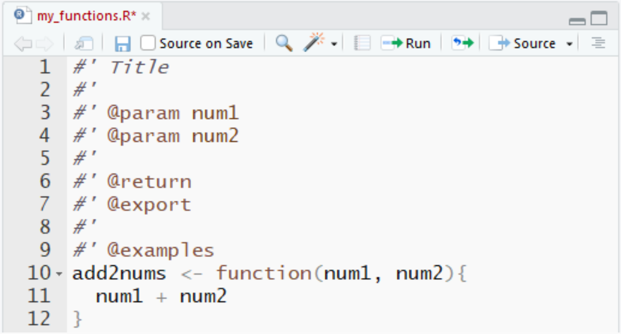
CREATE R FUNCTION AND DOCUMENTATION



```r
add2nums <- function(num1, num2){
  num1 + num2
}
```

- To generate a description skeleton with `roxygen2`:
  1. place cursor inside function definition
  2. hold: `Shift + Ctrl/Cmd + Alt + R`

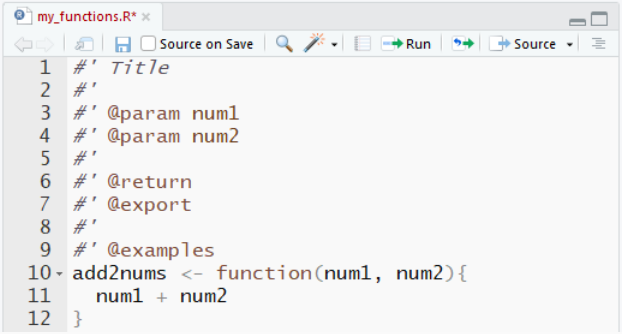
CREATE R FUNCTION AND DOCUMENTATION



```r
#' Title
#'
#' @param num1
#' @param num2
#'
#' @return
#' @export
#'
#' @examples
add2nums <- function(num1, num2){
  num1 + num2
}
```

Now we have a description skeleton generated by `roxygen2`.

CREATE R FUNCTION AND DOCUMENTATION



```r
#' Title
#'
#' @param num1
#' @param num2
#'
#' @return
#' @export
#'
#' @examples
add2nums <- function(num1, num2){
  num1 + num2
}
```

Quick Observations:

- all `roxygen2` comments start with #′, and
- `roxygen2` keywords start with `@`.

ROXYGEN2 KEYWORDS

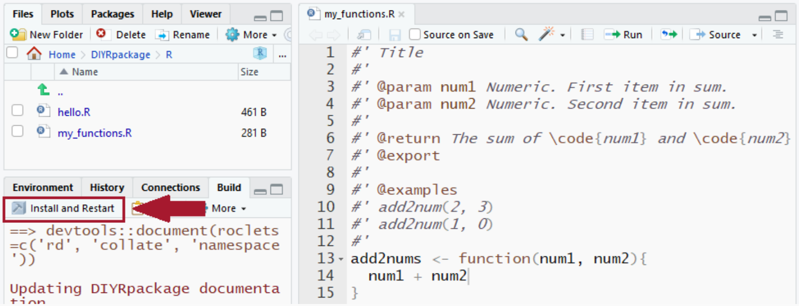
`@param`	documents function arguments.
`@return`	documents what the function returns to the user. This can be a single object or a list of objects.
`@export`	Tells R to make the function available to anyone using your package. For now, always include `@export`.
`@examples`	documents example R code.

Other useful keywords:

`@inheritParams`	inherit parameters of another function.
`@seealso`	provide links to other functions or resources.

UPDATE AND NAVIGATE TO DOCUMENTATION

To convert roxygen2 comments to .Rd files:
click on *Install and Restart*, under the *Build* tab.

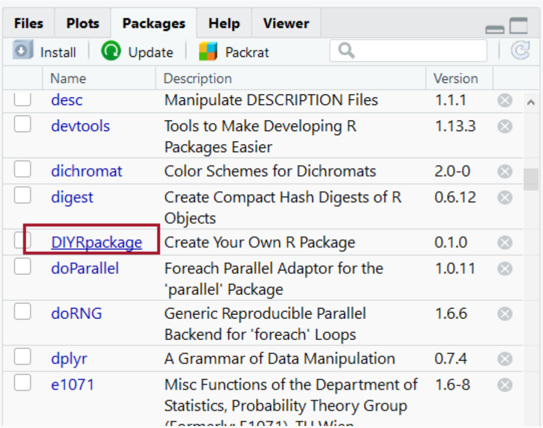


```
==> devtools::document(roclets
=c('rd', 'collate', 'namespace
'))

Updating DIYRpackage documenta
tion
```

```r
#' Title
#'
#' @param num1 Numeric. First item in sum.
#' @param num2 Numeric. Second item in sum.
#'
#' @return The sum of \code{num1} and \code{num2}
#' @export
#'
#' @examples
#' add2num(2, 3)
#' add2num(1, 0)
#'
add2nums <- function(num1, num2){
  num1 + num2
}
```

UPDATE AND NAVIGATE TO DOCUMENTATION

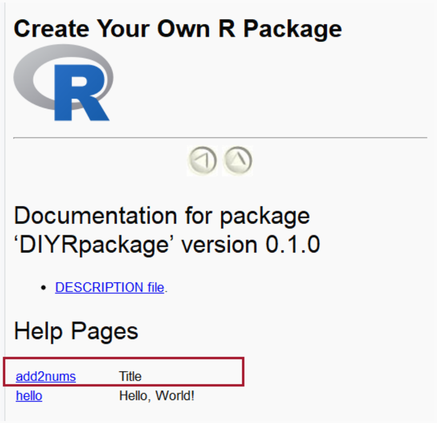
Find your package in the list of installed packages.



Name	Description	Version
desc	Manipulate DESCRIPTION Files	1.1.1
devtools	Tools to Make Developing R Packages Easier	1.13.3
dichromat	Color Schemes for Dichromats	2.0-0
digest	Create Compact Hash Digests of R Objects	0.6.12
DIYRpackage	Create Your Own R Package	0.1.0
doParallel	Foreach Parallel Adaptor for the 'parallel' Package	1.0.11
doRNG	Generic Reproducible Parallel Backend for 'foreach' Loops	1.6.6
dplyr	A Grammar of Data Manipulation	0.7.4
e1071	Misc Functions of the Department of Statistics, Probability Theory Group	1.6-8

UPDATE AND NAVIGATE TO DOCUMENTATION

Navigate to the documented function.



Create Your Own R Package

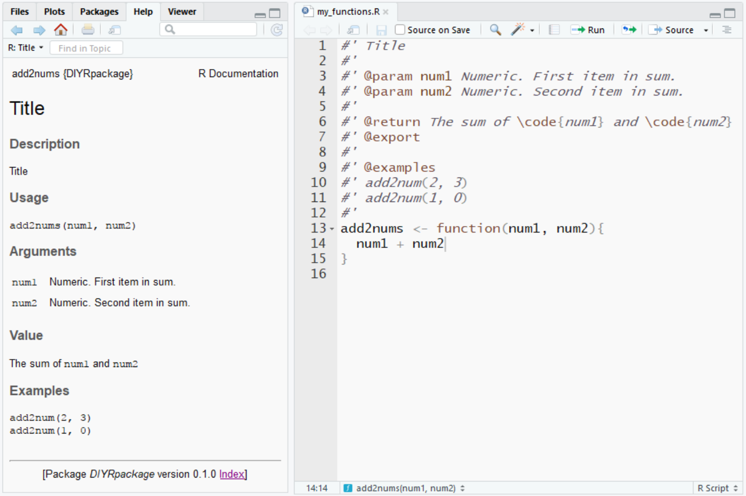
Documentation for package 'DIYRpackage' version 0.1.0

- DESCRIPTION file.

Help Pages

add2nums	Title
hello	Hello, World!

UPDATE AND NAVIGATE TO DOCUMENTATION



add2nums {DIYRpackage}   R Documentation

Title

Description

Title

Usage

```
add2nums(num1, num2)
```

Arguments

num1	Numeric. First item in sum.
num2	Numeric. Second item in sum.

Value

The sum of num1 and num2

Examples

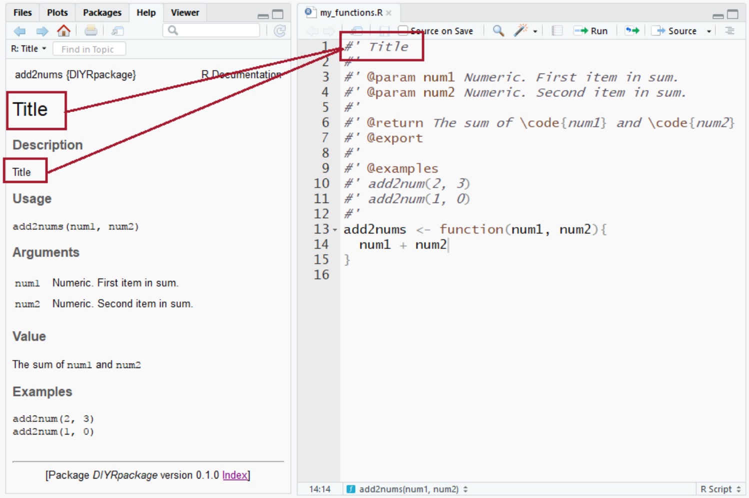
```
add2num(2, 3)
add2num(1, 0)
```

[Package *DIYRpackage* version 0.1.0 Index]

```r
#' Title
#'
#' @param num1 Numeric. First item in sum.
#' @param num2 Numeric. Second item in sum.
#'
#' @return The sum of \code{num1} and \code{num2}
#' @export
#'
#' @examples
#' add2num(2, 3)
#' add2num(1, 0)
#'
add2nums <- function(num1, num2){
  num1 + num2
}

```

CREATE DESCRIPTION AND DETAILS

If "*Description*" is not specified, "*Title*" is recycled and used again for "*Description*."



add2nums {DIYRpackage} R Documentation

Title

Description

Title

Usage

```
add2nums(num1, num2)
```

Arguments

num1	Numeric. First item in sum.
num2	Numeric. Second item in sum.

Value

The sum of num1 and num2

Examples

```
add2num(2, 3)
add2num(1, 0)
```

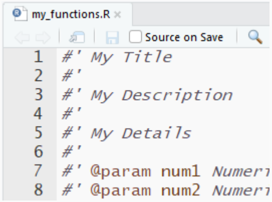
[Package *DIYRpackage* version 0.1.0 Index]

```r
#' Title
#'
#' @param num1 Numeric. First item in sum.
#' @param num2 Numeric. Second item in sum.
#'
#' @return The sum of \code{num1} and \code{num2}
#' @export
#'
#' @examples
#' add2num(2, 3)
#' add2num(1, 0)
#'
add2nums <- function(num1, num2){
  num1 + num2
}
```

14:14 add2nums(num1, num2) R Script

Create Description and Details

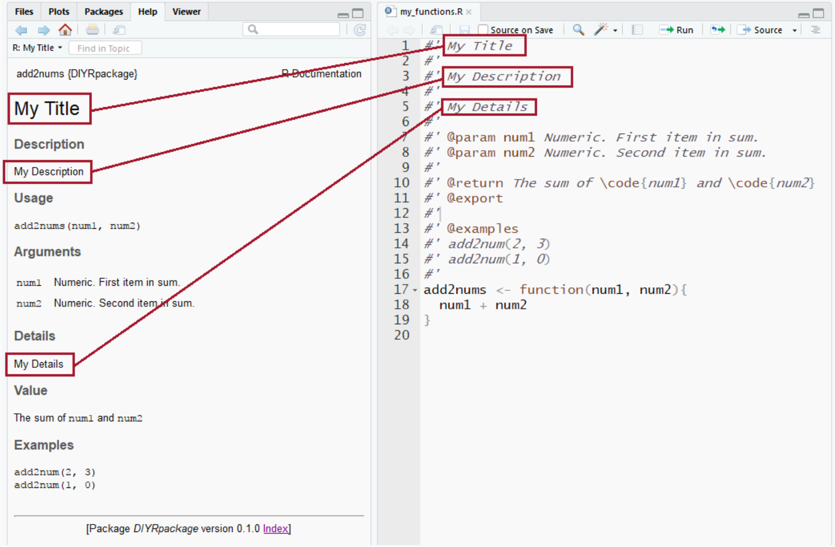
NOTE: There are no keyword specifiers for "*Title*", "*Description*", or "*Details*". To specify, simply separate text for each section by a blank line.



```
#' My Title
#'
#' My Description
#'
#' My Details
#'
#' @param num1 Numeri
#' @param num2 Numeri
```

`roxygen2` always treats the first chunk as "*Title*", the second chunk as "*Description*", and the third chunk as "*Details*".

CREATE DESCRIPTION AND DETAILS



add2nums {DIYRpackage} R Documentation

My Title

Description

My Description

Usage

```
add2nums(num1, num2)
```

Arguments

`num1`	Numeric. First item in sum.
`num2`	Numeric. Second item in sum.

Details

My Details

Value

The sum of `num1` and `num2`

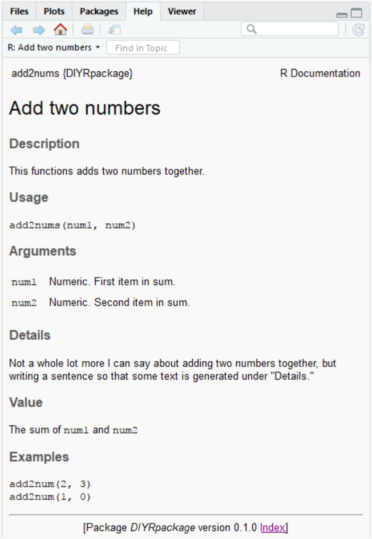
Examples

```
add2num(2, 3)
add2num(1, 0)
```

[Package *DIYRpackage* version 0.1.0 Index]

```r
#' My Title
#'
#' My Description
#'
#' My Details
#'
#' @param num1 Numeric. First item in sum.
#' @param num2 Numeric. Second item in sum.
#'
#' @return The sum of \code{num1} and \code{num2}
#' @export
#'
#' @examples
#' add2num(2, 3)
#' add2num(1, 0)
#'
add2nums <- function(num1, num2){
  num1 + num2
}
```

CREATE DESCRIPTION AND DETAILS



add2nums {DIYRpackage} R Documentation

Add two numbers

Description

This functions adds two numbers together.

Usage

```
add2nums(num1, num2)
```

Arguments

`num1`	Numeric. First item in sum.
`num2`	Numeric. Second item in sum.

Details

Not a whole lot more I can say about adding two numbers together, but writing a sentence so that some text is generated under "Details."

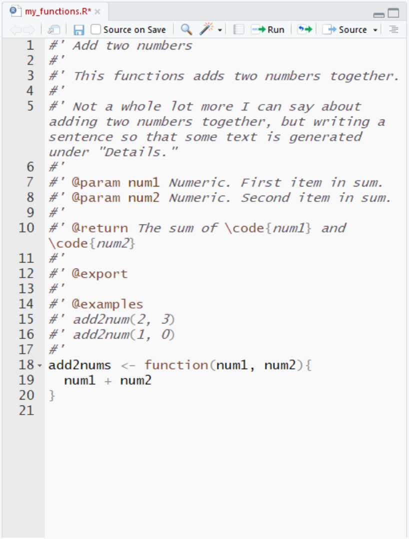
Value

The sum of `num1` and `num2`

Examples

```
add2num(2, 3)
add2num(1, 0)
```

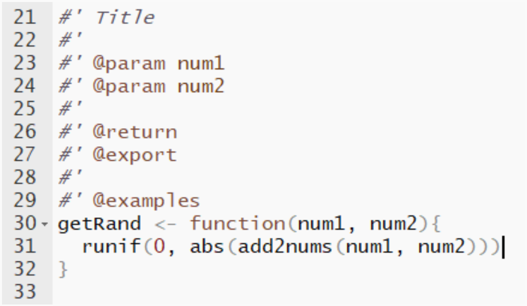
[Package *DIYRpackage* version 0.1.0 Index]



```
#' Add two numbers
#'
#' This functions adds two numbers together.
#'
#' Not a whole lot more I can say about
adding two numbers together, but writing a
sentence so that some text is generated
under "Details."
#'
#' @param num1 Numeric. First item in sum.
#' @param num2 Numeric. Second item in sum.
#'
#' @return The sum of \code{num1} and
\code{num2}
#'
#' @export
#'
#' @examples
#' add2num(2, 3)
#' add2num(1, 0)
#'
add2nums <- function(num1, num2){
  num1 + num2
}
```

Using @inheritParams and @importFrom

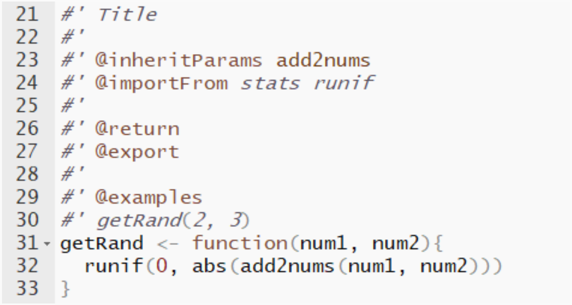
Let's use `roxygen2` to simplify documentation of `getRand`.



```r
#' Title
#'
#' @param num1
#' @param num2
#'
#' @return
#' @export
#'
#' @examples
getRand <- function(num1, num2){
  runif(0, abs(add2nums(num1, num2)))
}

```

USING @INHERITPARAMS AND @IMPORTFROM

To avoid re-documenting `num1` and `num2`, we replace `@param` with `@inheritParams`.

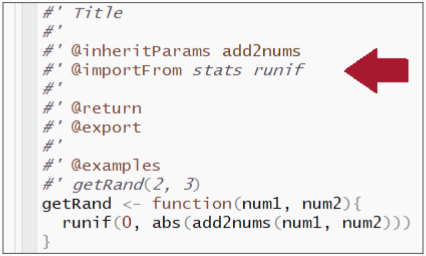


```r
#' Title
#'
#' @inheritParams add2nums
#' @importFrom stats runif
#'
#' @return
#' @export
#'
#' @examples
#' getRand(2, 3)
getRand <- function(num1, num2){
  runif(0, abs(add2nums(num1, num2)))
}
```

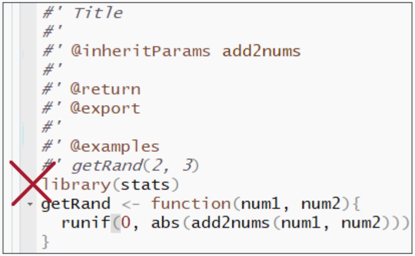
USING @INHERITPARAMS AND @IMPORTFROM

To import functions from other packages:

- Use `@importFrom <package> <function>`
- Do not use: `library(package)`



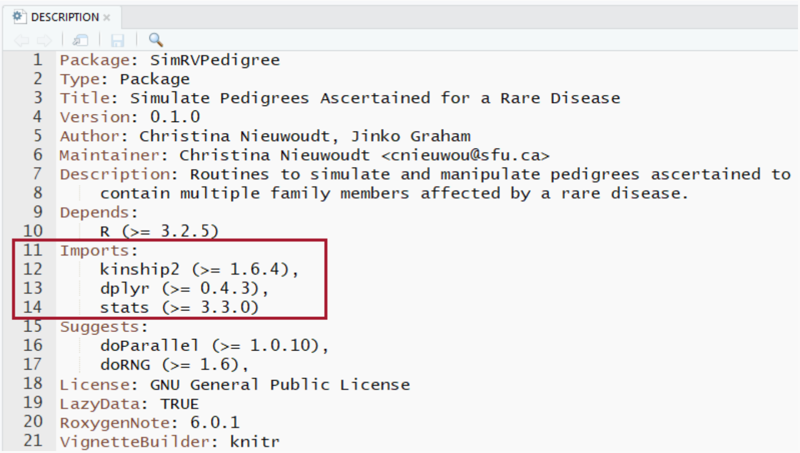
```
#' Title
#'
#' @inheritParams add2nums
#' @importFrom stats runif
#'
#' @return
#' @export
#'
#' @examples
#' getRand(2, 3)
getRand <- function(num1, num2){
  runif(0, abs(add2nums(num1, num2)))
}
```



```
#' Title
#'
#' @inheritParams add2nums
#'
#' @return
#' @export
#'
#' @examples
#' getRand(2, 3)
library(stats)
getRand <- function(num1, num2){
  runif(0, abs(add2nums(num1, num2)))
}
```

INCLUDE PACKAGES IN DESCRIPTION

Include any required packages in the `DESCRIPTION` file, under `Imports`, along with the version number of the package.

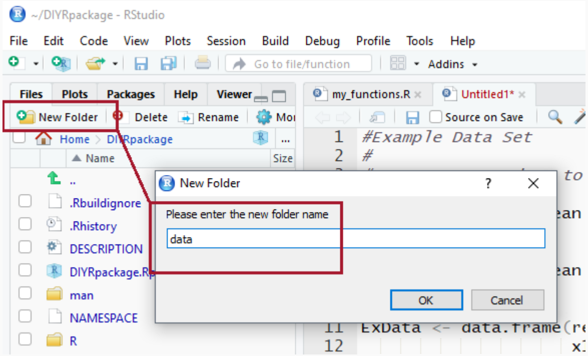


```
Package: SimRVPedigree
Type: Package
Title: Simulate Pedigrees Ascertained for a Rare Disease
Version: 0.1.0
Author: Christina Nieuwoudt, Jinko Graham
Maintainer: Christina Nieuwoudt <cnieuwou@sfu.ca>
Description: Routines to simulate and manipulate pedigrees ascertained to
    contain multiple family members affected by a rare disease.
Depends:
    R (>= 3.2.5)
Imports:
    kinship2 (>= 1.6.4),
    dplyr (>= 0.4.3),
    stats (>= 3.3.0)
Suggests:
    doParallel (>= 1.0.10),
    doRNG (>= 1.6),
License: GNU General Public License
LazyData: TRUE
RoxygenNote: 6.0.1
VignetteBuilder: knitr
```

CREATE AND STORE DATA SET

Data sets are stored in \data. We will need to create this directory.

1. Click on *New Folder* under *Files*
2. Name and create the data directory.



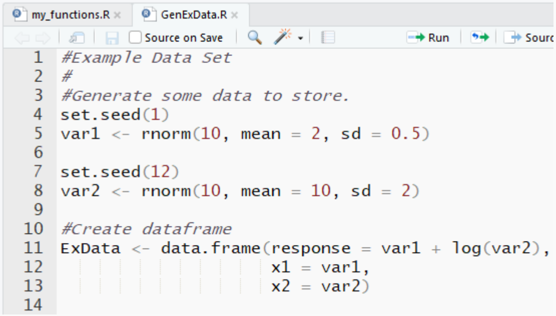
Please enter the new folder name

data

```
#Example Data Set
#
ExData <- data.frame(r
```

CREATE AND STORE DATA SET

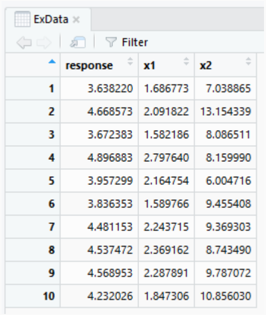
If you are following along, execute `GenExData.R`.



```
#Example Data Set
#
#Generate some data to store.
set.seed(1)
var1 <- rnorm(10, mean = 2, sd = 0.5)

set.seed(12)
var2 <- rnorm(10, mean = 10, sd = 2)

#Create dataframe
ExData <- data.frame(response = var1 + log(var2),
                     x1 = var1,
                     x2 = var2)

```

CREATE AND STORE DATA SET

Goal: store `ExData` in the \\`data` directory.

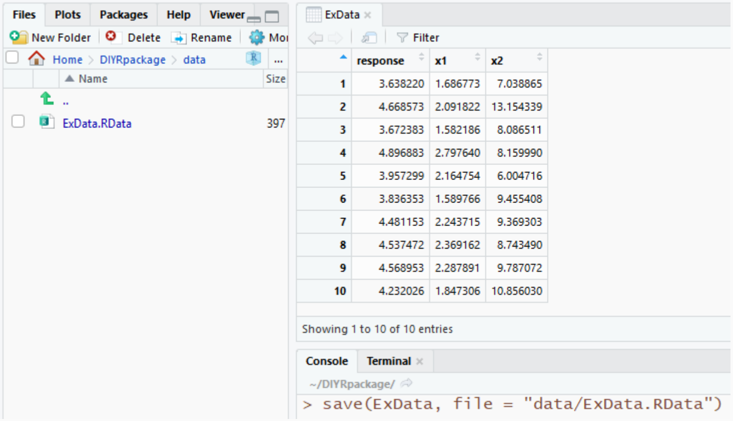


	response	x1	x2
1	3.638220	1.686773	7.038865
2	4.668573	2.091822	13.154339
3	3.672383	1.582186	8.086511
4	4.896883	2.797640	8.159990
5	3.957299	2.164754	6.004716
6	3.836353	1.589766	9.455408
7	4.481153	2.243715	9.369303
8	4.537472	2.369162	8.743490
9	4.568953	2.287891	9.787072
10	4.232026	1.847306	10.856030

In the console execute the command:

```
save(ExData, file = “data/ExData.RData”)
```

CREATE AND STORE DATA SET



	response	x1	x2
1	3.638220	1.686773	7.038865
2	4.668573	2.091822	13.154339
3	3.672383	1.582186	8.086511
4	4.896883	2.797640	8.159990
5	3.957299	2.164754	6.004716
6	3.836353	1.589766	9.455408
7	4.481153	2.243715	9.369303
8	4.537472	2.369162	8.743490
9	4.568953	2.287891	9.787072
10	4.232026	1.847306	10.856030

Showing 1 to 10 of 10 entries

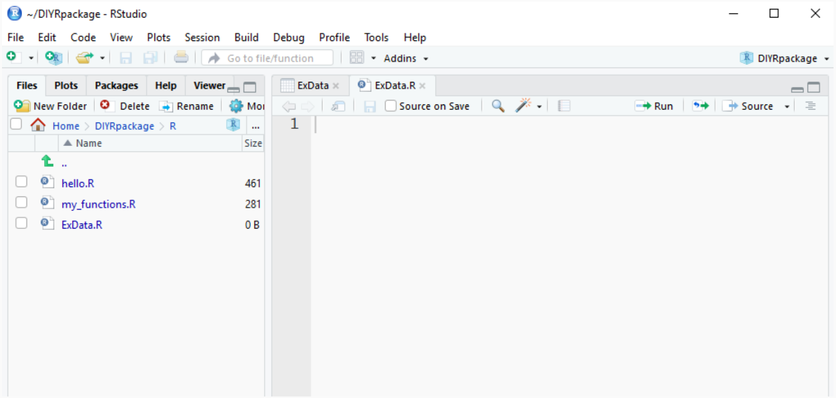
```
> save(ExData, file = "data/ExData.RData")
```

CREATE DATA DOCUMENTATION

- Documentation for a data set is created in an `.R` script, stored in the \\`R` directory, with the same name as data set stored in \\`data`.
- Each data set needs a separate documentation file.

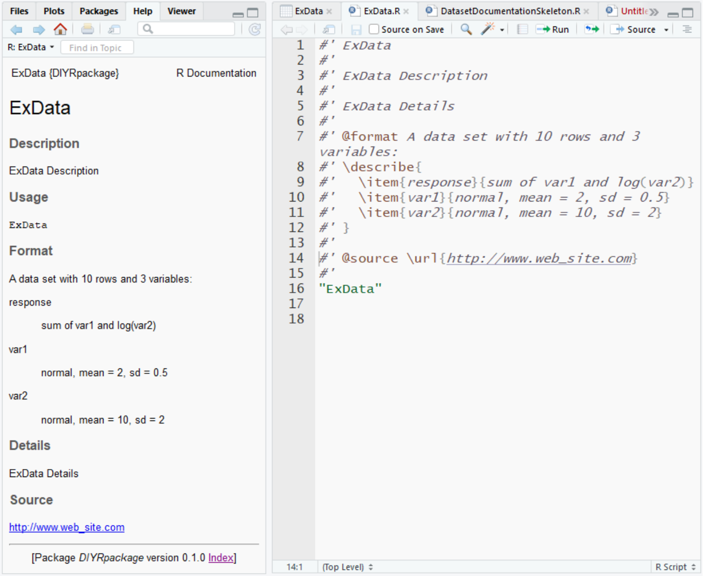
CREATE DATA DOCUMENTATION

1. Hold `Shift + Ctrl/Cmd + N` to create a new script.
2. Save as `ExData.R` in \R.



Name	Size
..	
hello.R	461
my_functions.R	281
ExData.R	0 B

CREATE DATA DOCUMENTATION



ExData {DIYRpackage} R Documentation

ExData

Description

ExData Description

Usage

```
ExData
```

Format

A data set with 10 rows and 3 variables:

response

sum of var1 and log(var2)

var1

normal, mean = 2, sd = 0.5

var2

normal, mean = 10, sd = 2

Details

ExData Details

Source

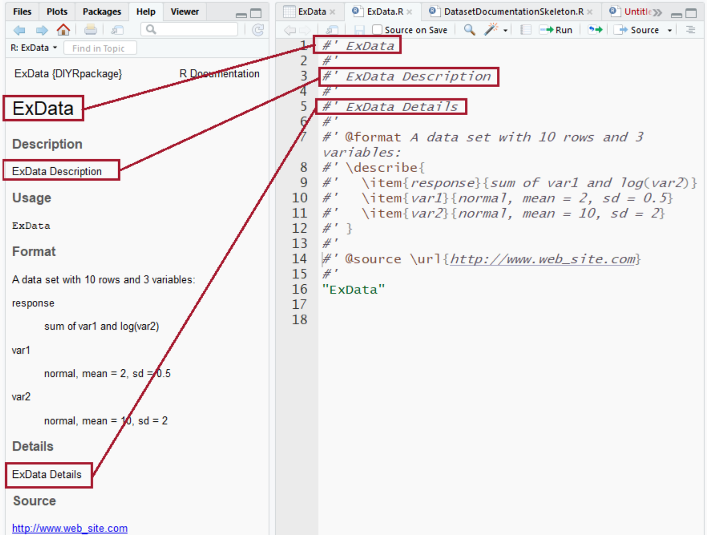
http://www.web_site.com

[Package *DIYRpackage* version 0.1.0 Index]

```
#' ExData
#'
#' ExData Description
#'
#' ExData Details
#'
#' @format A data set with 10 rows and 3
variables:
#' \describe{
#'   \item{response}{sum of var1 and log(var2)}
#'   \item{var1}{normal, mean = 2, sd = 0.5}
#'   \item{var2}{normal, mean = 10, sd = 2}
#' }
#'
#' @source \url{http://www.web_site.com}
#'
"ExData"
```

CREATE DATA DOCUMENTATION

As with function documentation, `roxygen2` treats the first chunk as "*Title*", the second chunk as "*Description*", and the third chunk as "*Details*".



ExData {DIYRpackage}   R Documentation

ExData

Description

ExData Description

Usage

`ExData`

Format

A data set with 10 rows and 3 variables:

response

    sum of var1 and log(var2)

var1

    normal, mean = 2, sd = 0.5

var2

    normal, mean = 10, sd = 2

Details

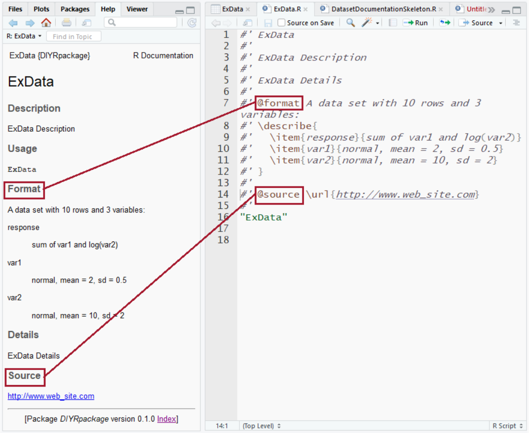
ExData Details

Source

http://www.web_site.com

```r
#' ExData
#'
#' ExData Description
#'
#' ExData Details
#'
#' @format A data set with 10 rows and 3 variables:
#' \describe{
#'   \item{response}{sum of var1 and log(var2)}
#'   \item{var1}{normal, mean = 2, sd = 0.5}
#'   \item{var2}{normal, mean = 10, sd = 2}
#' }
#'
#' @source \url{http://www.web_site.com}
#'
"ExData"
```

CREATE DATA DOCUMENTATION



ExData {DIYRpackage}   R Documentation

ExData

Description

ExData Description

Usage

ExData

Format

A data set with 10 rows and 3 variables:

response

sum of var1 and log(var2)

var1

normal, mean = 2, sd = 0.5

var2

normal, mean = 10, sd = 2

Details

ExData Details

Source

http://www.web_site.com

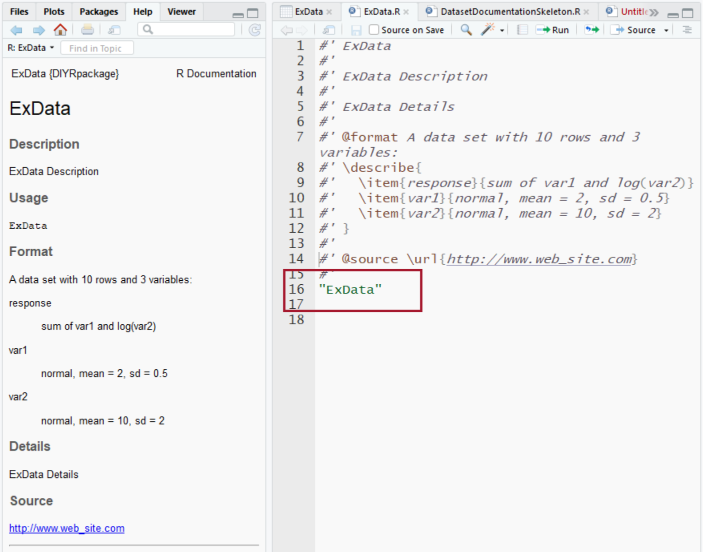
[Package *DIYRpackage* version 0.1.0 Index]

```
#' ExData
#'
#' ExData Description
#'
#' ExData Details
#'
#' @format A data set with 10 rows and 3 variables:
#' \describe{
#'    \item{response}{sum of var1 and log(var2)}
#'    \item{var1}{normal, mean = 2, sd = 0.5}
#'    \item{var2}{normal, mean = 10, sd = 2}
#' }
#'
#' @source \url{http://www.web_site.com}
#'
"ExData"
```

- `@format` is used to give an overview of the data
- `@source` is used to provide the data source. For multiple sources, use `@source` before each source.

CREATE DATA DOCUMENTATION

The last line is always the dataset name in quotation marks.
Note: this is not a `roxygen2` comment.



ExData {DIYRpackage} R Documentation

ExData

Description

ExData Description

Usage

```
ExData
```

Format

A data set with 10 rows and 3 variables:

response
    sum of var1 and log(var2)

var1
    normal, mean = 2, sd = 0.5

var2
    normal, mean = 10, sd = 2

Details

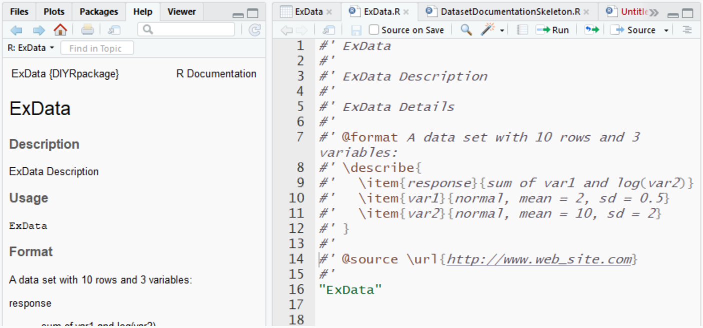
ExData Details

Source

http://www.web_site.com

```r
#' ExData
#'
#' ExData Description
#'
#' ExData Details
#'
#' @format A data set with 10 rows and 3
variables:
#' \describe{
#'   \item{response}{sum of var1 and log(var2)}
#'   \item{var1}{normal, mean = 2, sd = 0.5}
#'   \item{var2}{normal, mean = 10, sd = 2}
#' }
#'
#' @source \url{http://www.web_site.com}
#'
"ExData"


```

CREATE DATA DOCUMENTATION



ExData {DIYRpackage} R Documentation

ExData

Description

ExData Description

Usage

`ExData`

Format

A data set with 10 rows and 3 variables:

response

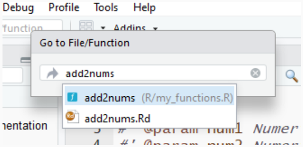
sum of var1 and log(var2)

```
#' ExData
#'
#' ExData Description
#'
#' ExData Details
#'
#' @format A data set with 10 rows and 3
variables:
#' \describe{
#'   \item{response}{sum of var1 and log(var2)}
#'   \item{var1}{normal, mean = 2, sd = 0.5}
#'   \item{var2}{normal, mean = 10, sd = 2}
#' }
#'
#' @source \url{http://www.web_site.com}
#'
"ExData"
```

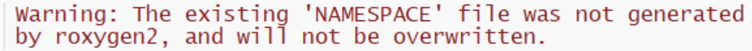
Never include `@export` in data documentation,
`@export` is used for functions only.

HELPFUL TRICKS

- To generate roxygen2 description skeleton:
  1. place cursor inside function definition
  2. hold: `Shift + Ctrl/Cmd + Alt + R`
- To jump to function definition:
  1. hold: `Ctrl/Cmd + .`
  2. type function name and choose from drop down list.



After clicking *Install and Reload*, if you receive the error message:



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

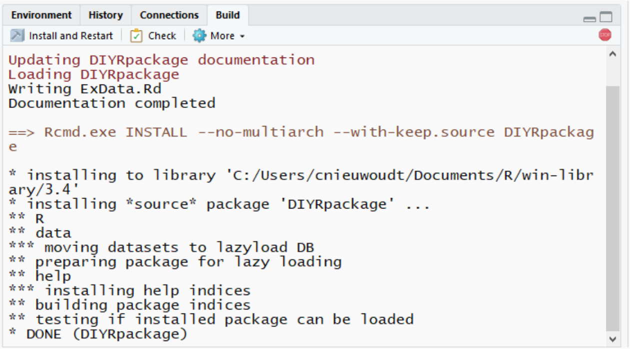
Try the following fix:

- Backup the NAMESPACE file (just in case)
- Delete the NAMESPACE file from the package directory
- In the console execute the command: `devtools::document()`.

Roxygen should create a new NAMESPACE file. If it works, you should not have to repeat this fix, again.

TROUBLESHOOTING

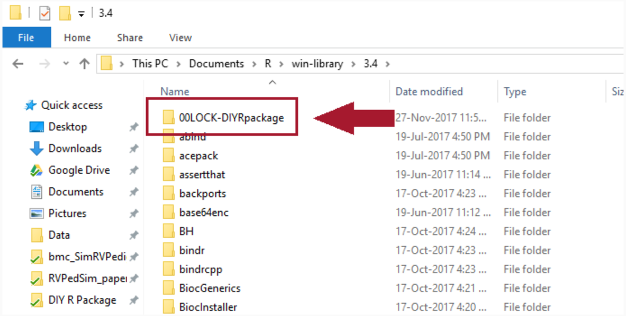
Occasionally, the package locks after clicking *Install and Reload*.



```
Updating DIYRpackage documentation
Loading DIYRpackage
Writing ExData.Rd
Documentation completed

==> Rcmd.exe INSTALL --no-multiarch --with-keep.source DIYRpackag
e

* installing to library 'C:/Users/cnieuwoudt/Documents/R/win-libr
ary/3.4'
* installing *source* package 'DIYRpackage' ...
** 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 (DIYRpackage)
```

You'll notice that after you hit *Install and Reload*, the `STOP` symbol does not go away and the library doesn't reload.

TROUBLESHOOTING

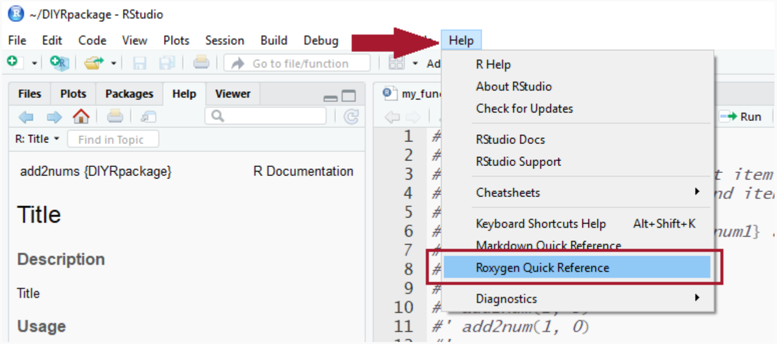


Name	Date modified	Type
00LOCK-DIYRpackage	27-Nov-2017 11:5...	File folder
abind	19-Jul-2017 4:50 PM	File folder
acepack	19-Jul-2017 4:50 PM	File folder
assertthat	19-Jun-2017 11:14 ...	File folder
backports	17-Oct-2017 4:23 ...	File folder
base64enc	19-Jun-2017 11:12 ...	File folder
BH	17-Oct-2017 4:24 ...	File folder
bindr	17-Oct-2017 4:23 ...	File folder
bindrcpp	17-Oct-2017 4:23 ...	File folder
BiocGenerics	17-Oct-2017 4:21 ...	File folder
BiocInstaller	17-Oct-2017 4:20 ...	File folder

- Navigate to the library with the same version number as your current installation of R.
- Locate the file entitled "*00LOCK-package_name*".
- Delete it.

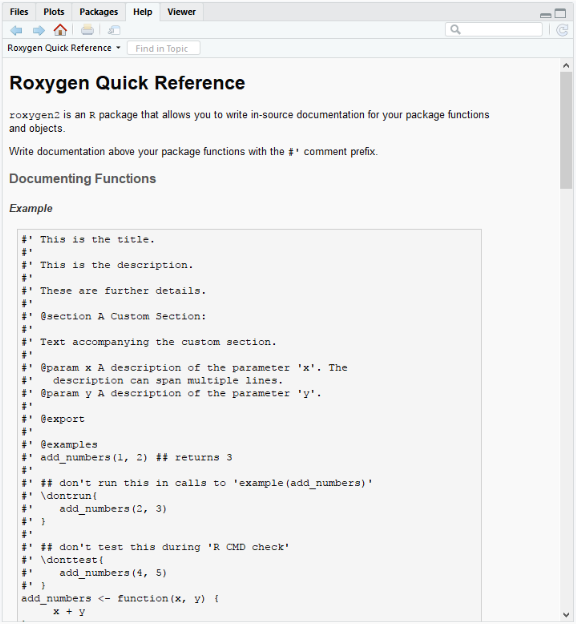
ROXYGEN QUICK REFERENCE

In `Rstudio`, additional information for `roxygen2` may be found by navigating to *Roxygen Quick Reference* in the *Help* menu



```
#' add2num(1, 0)
```

ROXYGEN QUICK REFERENCE



Roxygen Quick Reference

roxygen2 is an R package that allows you to write in-source documentation for your package functions and objects.

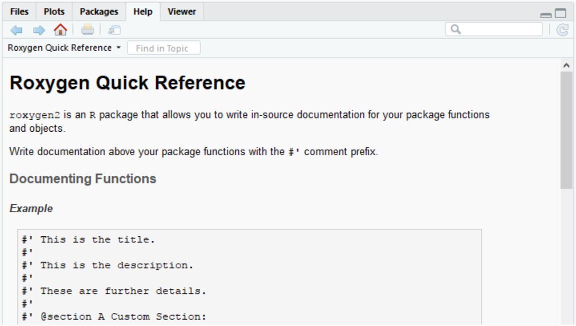
Write documentation above your package functions with the #' comment prefix.

Documenting Functions

Example

```
#' This is the title.
#'
#' This is the description.
#'
#' These are further details.
#'
#' @section A Custom Section:
#'
#' Text accompanying the custom section.
#'
#' @param x A description of the parameter 'x'. The
#'   description can span multiple lines.
#' @param y A description of the parameter 'y'.
#'
#' @export
#'
#' @examples
#' add_numbers(1, 2) ## returns 3
#'
#' ## don't run this in calls to 'example(add_numbers)'
#' \dontrun{
#'    add_numbers(2, 3)
#' }
#'
#' ## don't test this during 'R CMD check'
#' \donttest{
#'    add_numbers(4, 5)
#' }
add_numbers <- function(x, y) {
    x + y
```

ROXYGEN QUICK REFERENCE



Roxygen Quick Reference

roxygen2 is an R package that allows you to write in-source documentation for your package functions and objects.

Write documentation above your package functions with the #' comment prefix.

Documenting Functions

Example

```
#' This is the title.
#'
#' This is the description.
#'
#' These are further details.
#'
#' @section A Custom Section:
```

Additional references:

- https://cran.r-project.org/web/packages/roxygen2/vignettes/roxygen2.html
- Hadley Wickham's book "R Packages", Chapter 5
- ... the all-mighty and powerful Google.

HADLEY WICKHAM'S R PACKAGES

- Function Documentation: Chapter 5, pp. 49
- `roxygen2` introduction: Chapter 5
- Data Documentation: Chapter 9.1.1, pp. 107
- `.Rbuildignore`: Chapter 2
- `DESCRIPTION` file: Chapter 4