Computational Skills for Biostatistics I: Lecture 5

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November 8, 2017

R packages

Why write an R package?

- The best way to contribute to science
- Allow others to build on your advances
- Promote yourself and your work
- Pass this class

$$\text{package} = \text{code} + \text{other stuff}$$

This class will focus on the other stuff

Install versus load

Brief refresher: `install.packages()` downloads the package from CRAN, and `library()` loads the library

- Loads the library? `attach()`-es it
  - Adds it to search path

Attaching

Recall from homework 1 that you can `attach()` data frames

```
attach(women)
height
```

```
##  [1] 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72
```

```
height <- height*2.54
height
```

```
##  [1] 147.32 149.86 152.40 154.94 157.48 160.02 162.56 16
## [11] 172.72 175.26 177.80 180.34 182.88
```

```
women$height
```

```
##  [1] 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72
```

Attaching

Loading a library places its functions in the search path, but the global environment will always be in the first position

```
ggplot  <- function(...) "Ha! Overwritten!"
library(ggplot2)
ggplot(iris, aes(x = Sepal.Length, y = Petal.Width))
```

```
## [1] "Ha! Overwritten!"
```

Attach

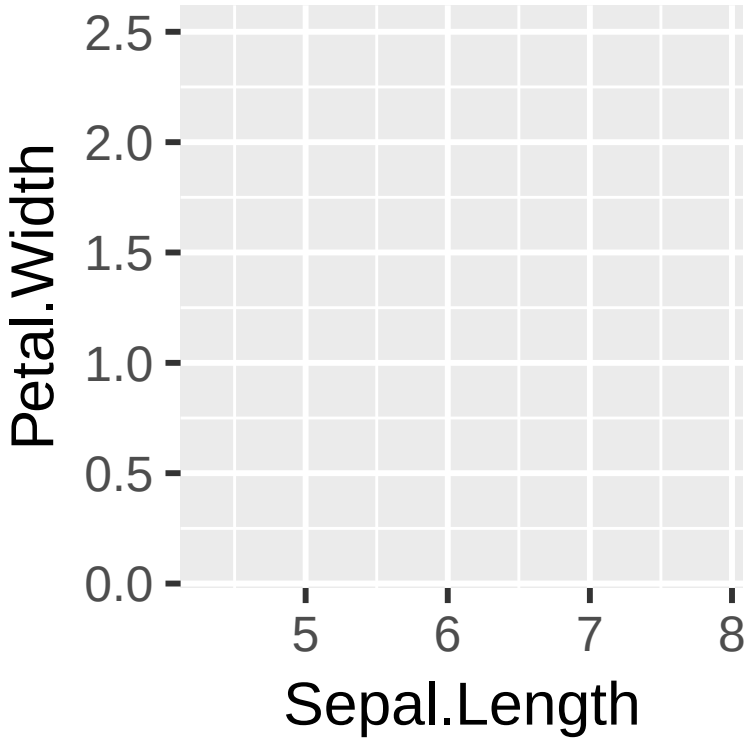
Moral of the story: Don't attach data frames, but it's fine to attach packages

If I ever used ‘require()‘ please forget it and use ‘library()‘ instead

Accessing functions in packages

The operator `x::y` means "the function `y` in the namespace of package `x`"

```
ggplot  <- function(...) "Ha! Overwritten!"
ggplot2::ggplot(iris, aes(x = Sepal.Length,
                          y = Petal.Width))
```



Namespaces

All packages have a `NAMESPACE` file: a collection of objects to be exported and imported

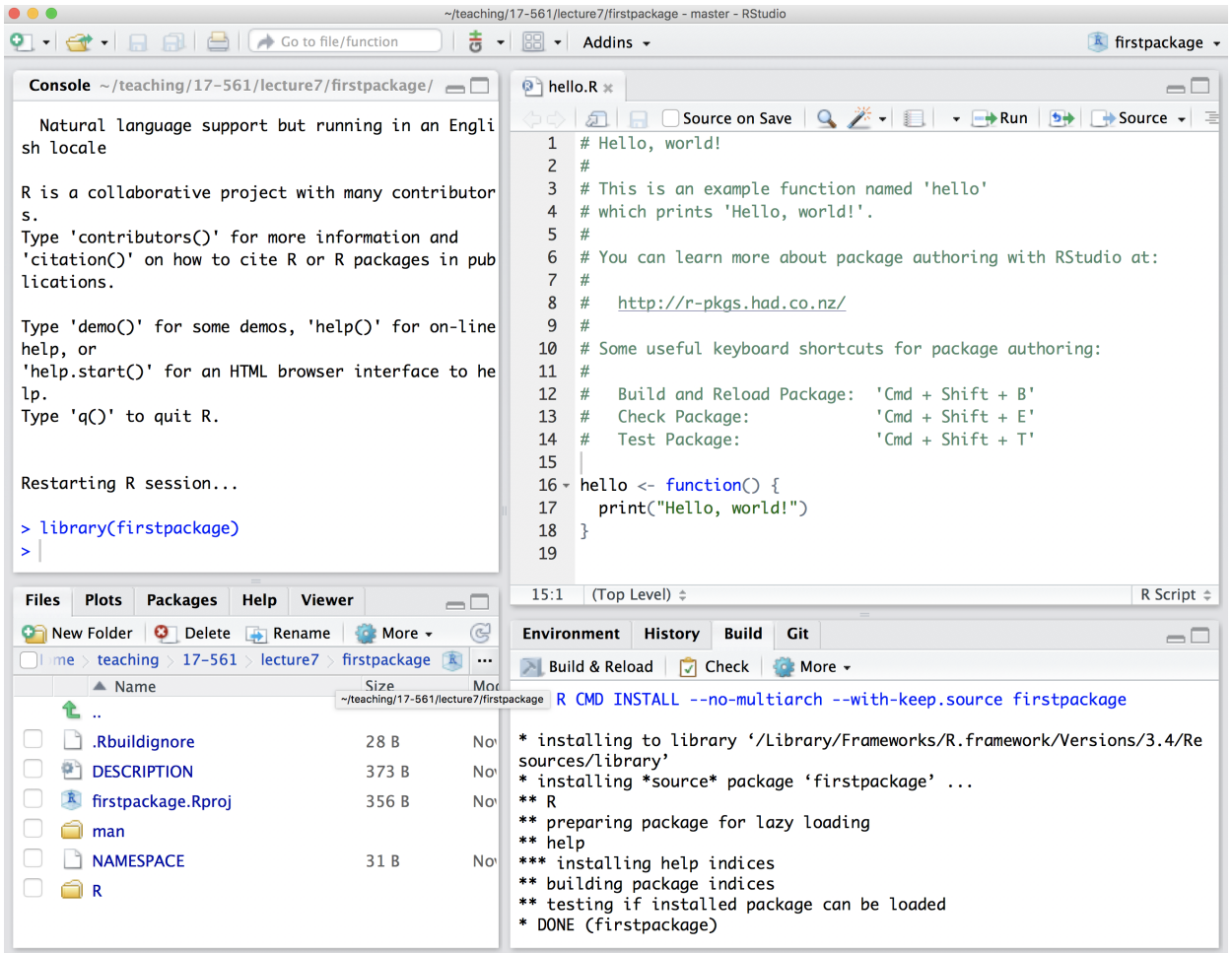
- To avoid overwriting users' variables
- To avoid ambiguity in function calls
- To ensure the package has everything it needs to run
- To encourage modular code

Your `NAMESPACE` is auto generated using *tags*; never directly modify your `NAMESPACE` file

Starting an R package

Ideally, create packages from scratch as soon as you begin on a project

- RStudio->File->New project->New Directory->R Package



Starting an R package: DESCRIPTION

Short-term: Keeps track of imports (dependencies)

Long-term: Help others find your package

hello.R | DESCRIPTION | NAMESPACE | hello.Rd

```
1  Package: firstpackage
2  Type: Package
3  Title: What the Package Does (Title Case)
4  Version: 0.1.0
5  Author: Who wrote it
6  Maintainer: The package maintainer <yourself@somewhere.net>
7  Description: More about what it does (maybe more than one line)
8      Use four spaces when indenting paragraphs within the Description.
9  License: What license is it under?
10 Encoding: UTF-8
11 LazyData: true
12 Imports:
13     dplyr,
14     ggplot
15 Suggests:
16     breakaway
17
```

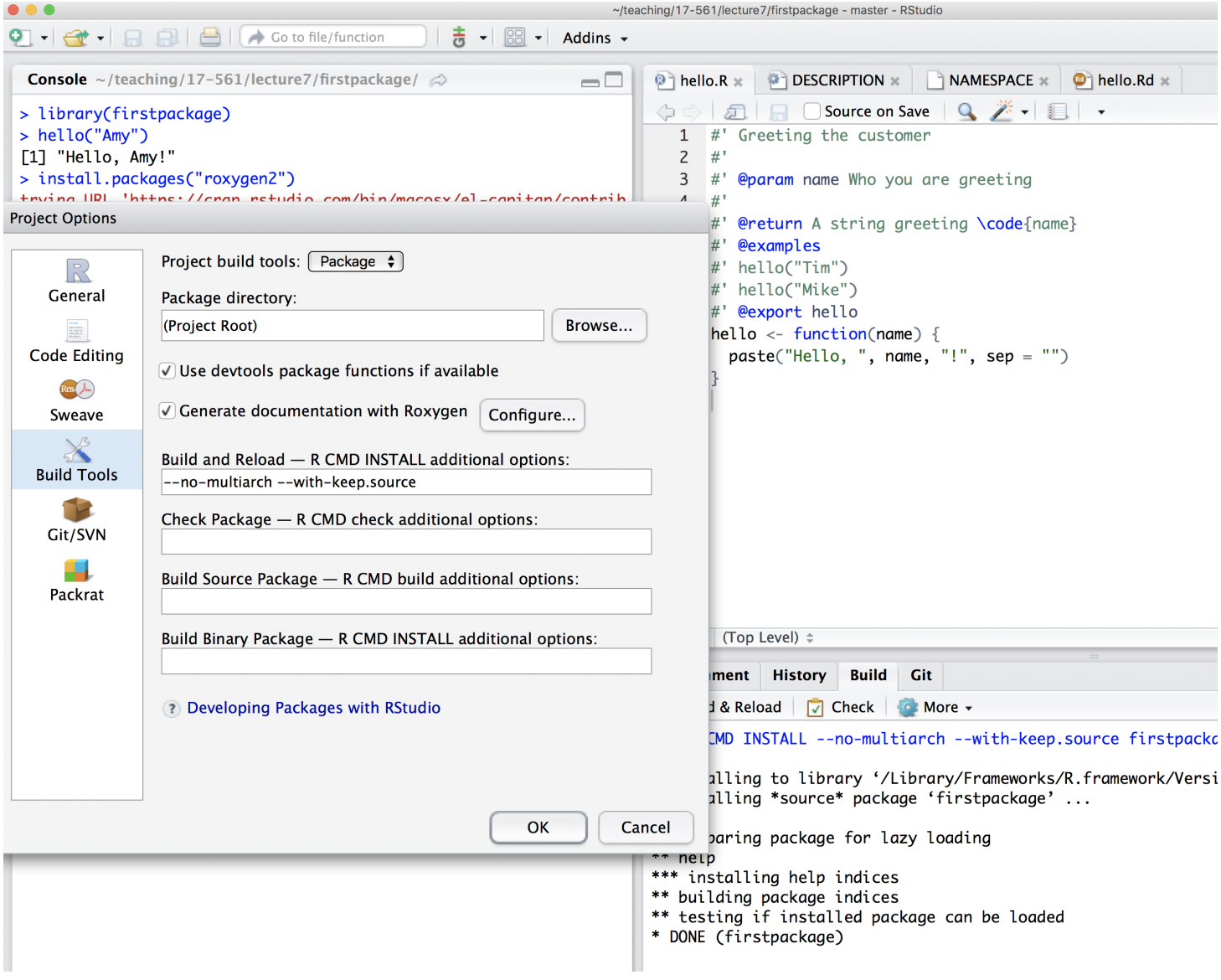
Writing R packages: documentation

`roxygen` documentation makes everything incredibly easy

```
install.packages("devtools")
devtools::install_github("hadley/devtools")
install.packages("roxygen2")
```

Writing R packages: documentation

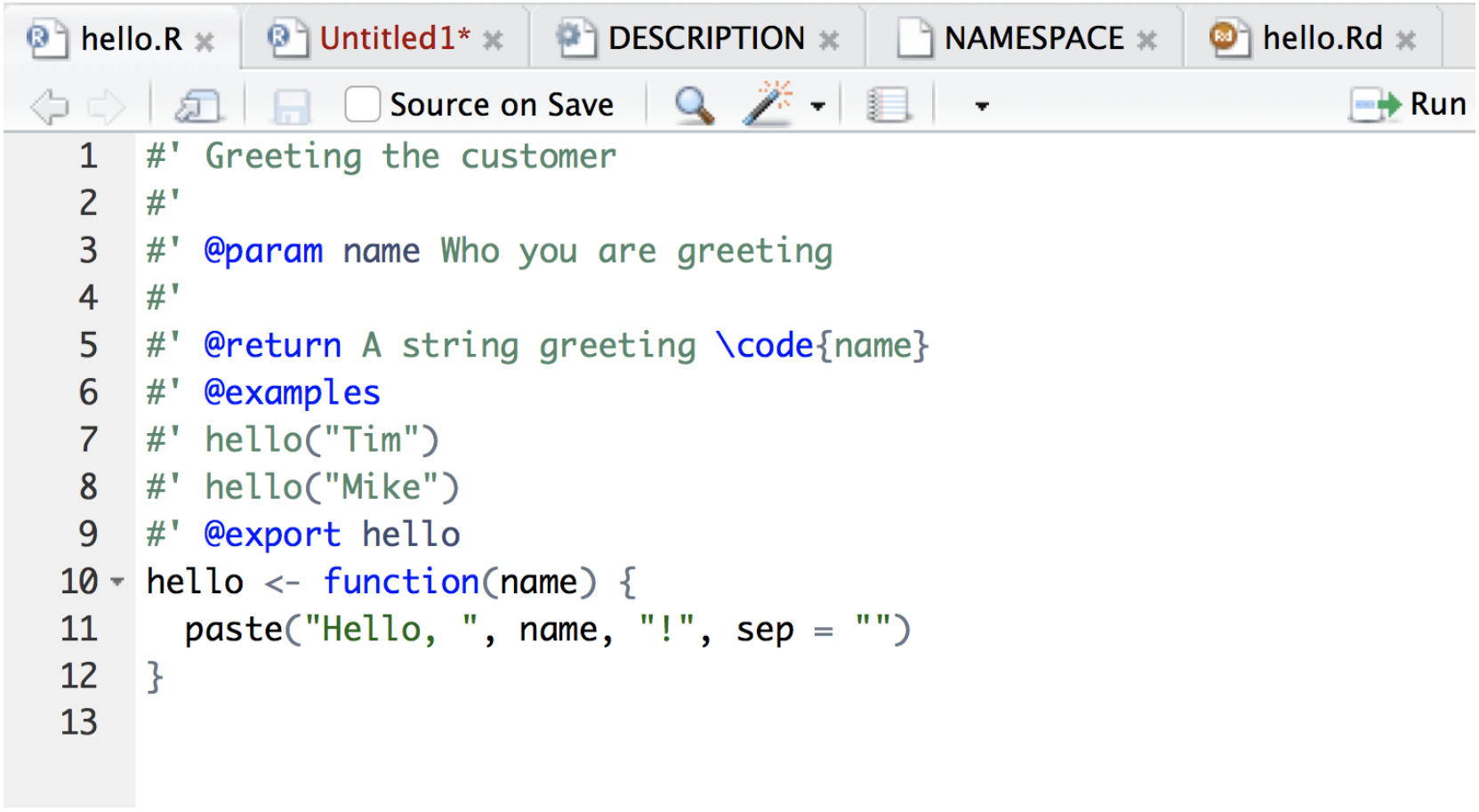
Under the `Build` tab, under Build tools, check `Generate documentation with Roxygen`



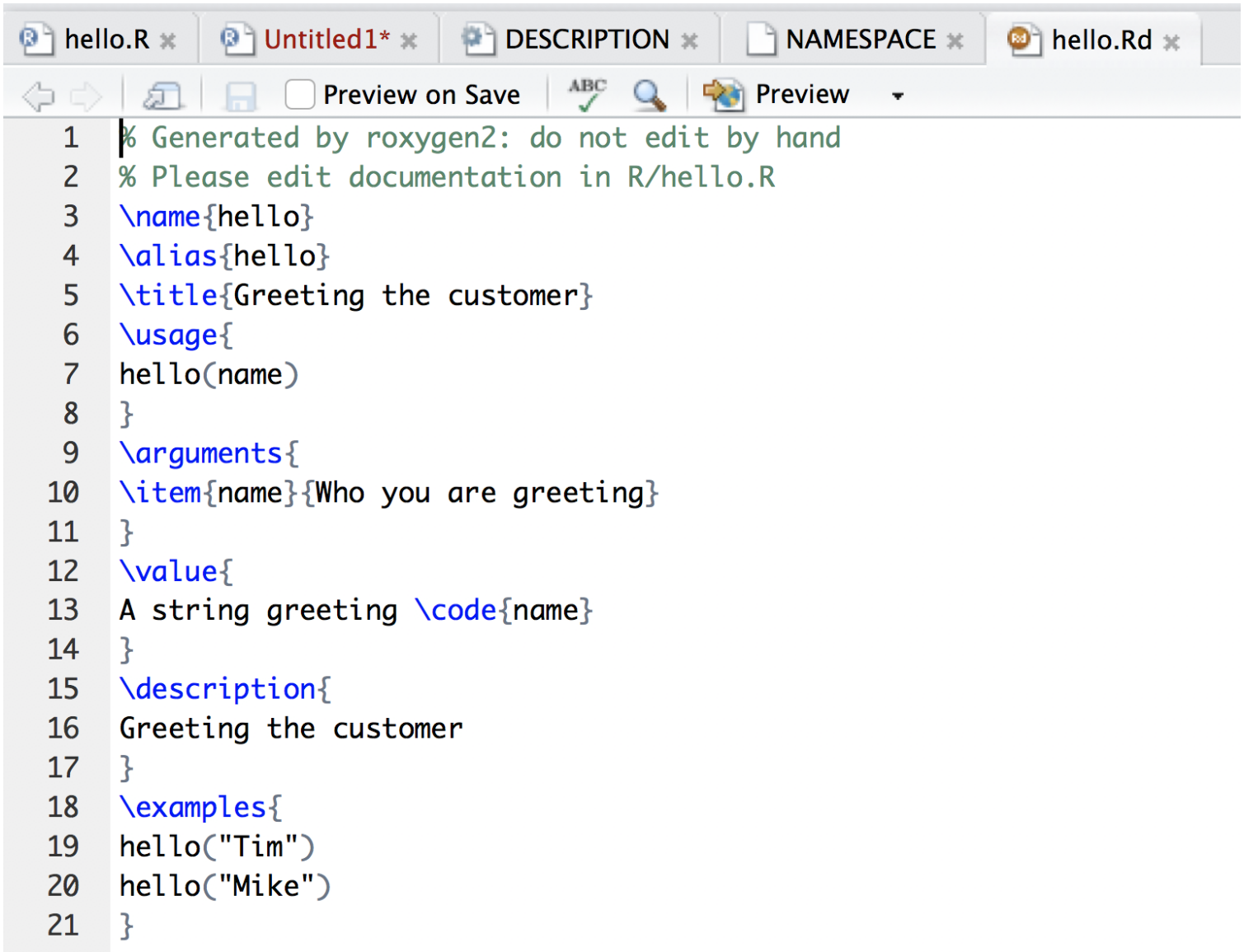
Writing R packages: documentation

1. Delete the default `NAMESPACE` file and the `man` folder
2. Write `roxygen` comments in your `.R` file
   - `roxygen` comments start with `#'`
3. `cmd/ctrl + shift + b` builds the package
4. `cmd/ctrl + shift + d` autogenerates documentation based on your roxygen comments

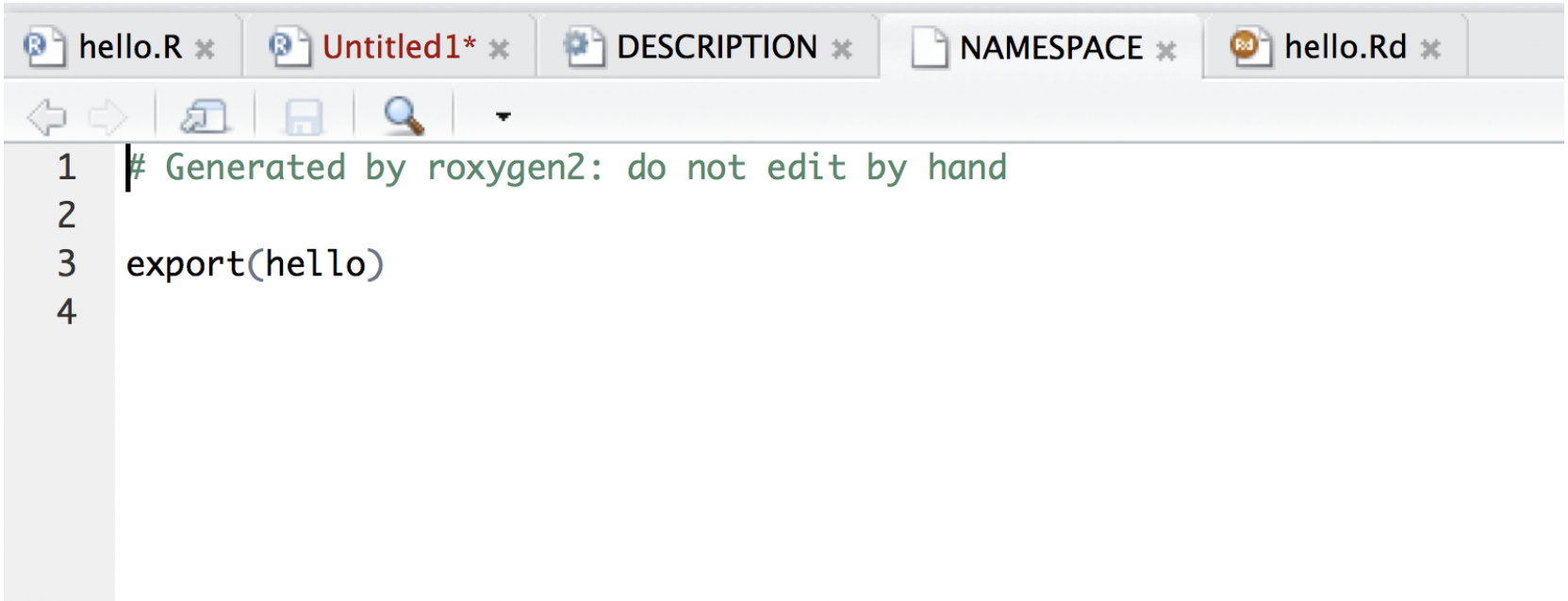
Writing R packages: documentation



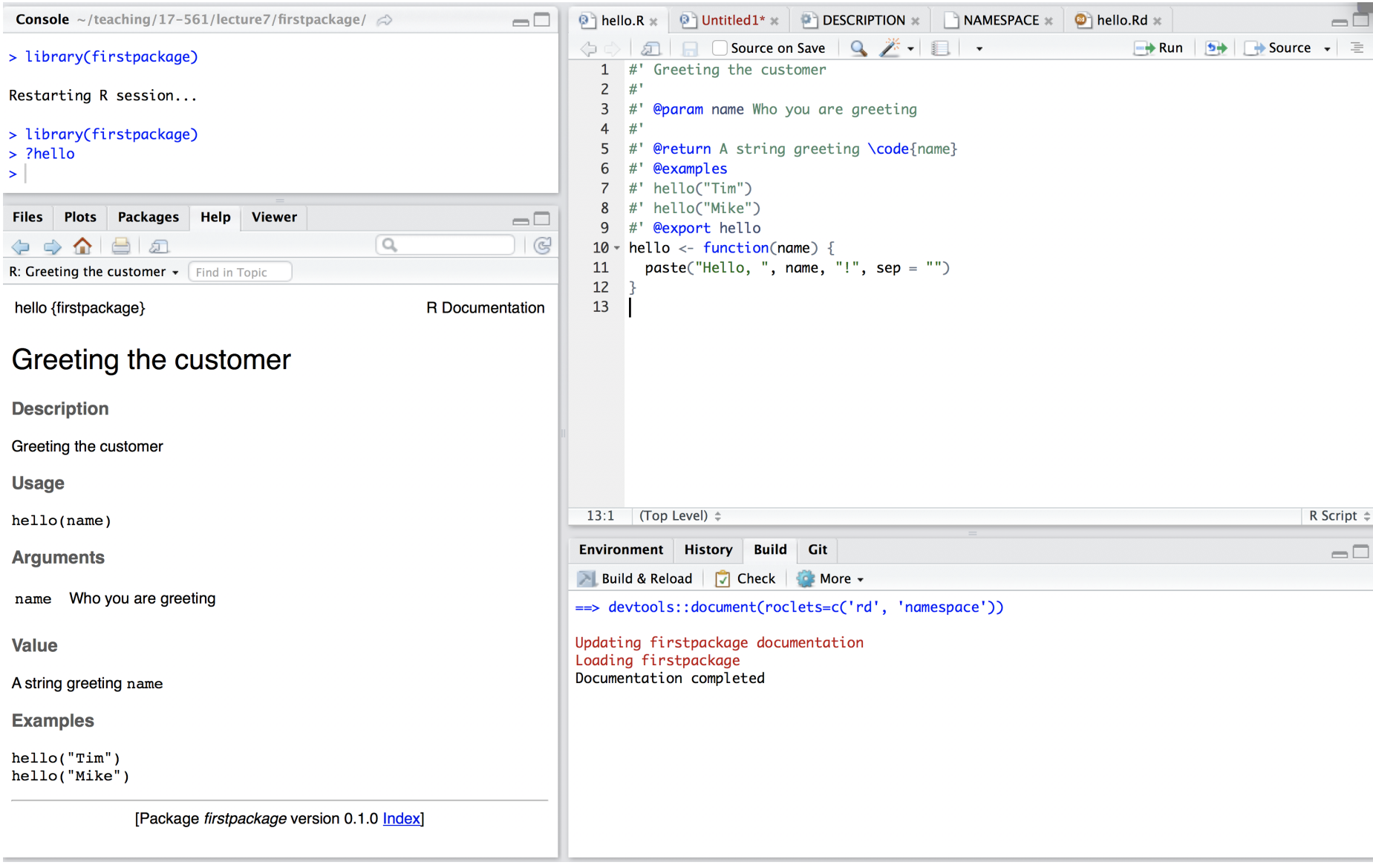
Writing R packages: documentation



Writing R packages: documentation



Writing R packages: documentation



Writing R packages: tags

```
#' \item{seest}{ The standard error in the diversity estimate.  } \item{full}{
#' The chosen nonlinear model for frequency ratios.  } \item{ci}{ An asymmetric
#' 95\% confidence interval for diversity.  }
#' @note \samp{breakaway} presents an estimator of species richness that is
#' well-suited to the high-diversity/microbial setting. However, many microbial
#' datasets display more diversity than the Kemp-type models can permit. In
#' this case, the log-transformed WLRM diversity estimator of Rocchetti et. al.
#' (2011) is returned. The authors' experience suggests that some datasets that
#' require the log-transformed WLRM contain ``false'' diversity, that is,
#' diversity attributable to sequencing errors (via an inflated singleton
#' count). The authors encourage judicious use of diversity estimators when the
#' dataset may contain these errors, and recommend the use of
#' \code{\link{breakaway_nof1}} as an exploratory tool in this case.
#' @author Amy Willis
#' @seealso \code{\link{breakaway_nof1}}; \code{\link{apples}}
#' @references Willis, A. and Bunge, J. (2015). Estimating diversity via
#' frequency ratios. \emph{Biometrics}, \bold{71}(4), 1042--1049.
#'
#' Rocchetti, I., Bunge, J. and Bohning, D. (2011). Population size estimation
#' based upon ratios of recapture probabilities. \emph{Annals of Applied
#' Statistics}, \bold{5}.
#' @keywords diversity microbial models nonlinear
#' @examples
#'
#' breakaway(apples)
#' breakaway(apples, plot = FALSE, output = FALSE, answers = TRUE)
#'
#'
#' @export breakaway
breakaway <- function(my_data, output=TRUE, plot=FALSE, answers=FALSE, force=FALSE, useAll=

  ## read in data
  if( !(is.matrix(my_data) || is.data.frame(my_data))) {
```

Writing R packages: documentation

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

export(betta)
export(betta_pic)
export(betta_points)
export(betta_random)
export(breakaway)
export(breakaway_clean)
export(breakaway_nof1)
export(build_frequency_count_tables)
export(chao1)
export(chao1_bc)
export(chao_bunge)
export(estimate_alpha_better)
export(frequency_count_or_proportion_or_column)
export(gini)
export(hill)
export(hill_better)
export(hill_pic)
export(inverse_simpson)
export(inverse_simpson_better)
export(make_frequency_count_table)
export(objective_bayes_geometric)
export(objective_bayes_mixedgeo)
export(objective_bayes_negbin)
export(objective_bayes_poisson)
export(plot_alpha)
export(proportions_instead)
export(resample_estimate)
export(rnbinomtable)
export(rztnbinomtable)
export(sample_size_estimate)
export(sample_size_figure)
export(shannon)
export(shannon_better)
export(simpson)
export(subsample_otu)
export(to_proportions)
export(wlrm_transformed)
export(wlrm_untransformed)
import(reshape2)
importFrom(MASS,mvrnorm)
importFrom(ggplot2,element_text)
importFrom(ggplot2,facet_wrap)
importFrom(ggplot2,geom_errorbar)
importFrom(plyr,is.discrete)
importFrom(stats,acf)
```

Building packages

Core "other stuff" for a package

- Code: written by you, goes into `R` folder (no subdirectories allowed)
- `DESCRIPTION`: written by you
- Documentation: autogenerated by `roxygen` comments, goes into `man` folder
- `NAMESPACE`: autogenerated by `roxygen` comments

documentation: vignettes

hello.R | breakaway.Rmd | DESCRIPTION | NAMESPACE | hello.Rd

Knit | Insert | Run

```
---
title: "Getting started with breakaway"
author: "Amy Willis"
date: "`r Sys.Date()`"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{getting-started}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---

`breakaway` is a package for species richness estimation and modelling. As the pac
grown and users have requested more functionality, it contains some basic generali
the statistical philosophy that underpins `breakaway` to the general alpha diversi
Because of the flexibility of the modelling strategies, most users of breakaway ar
microbial ecologists with very large OTU tables, however, nothing should exclude a
macroecologist from using the same tools. If you have a macroecology dataset and w
this package, I would love to hear from you so please feel free to contact me (ema
Github's Issues/Projects infrastructure).

## Vignette Info

This vignette will lead you through

- loading in your data and covariate information
- creating frequency tables
- using `breakaway` to estimate species richness
- using the objective bayes methods to estimate species richness
- estimating various alpha diversity indices and providing a very basic resample-b
method for ascribing variability to them
- using `betta` to model changes in alpha diversity with covariates

If there is something that you would like explained please feel free to request it

## Loading the package and data

Download the latest version of the package from github.

```{r}
### Run the first two lines at home! ####
# install.packages("devtools")
# devtools::install_github("adw96/breakaway")
library(breakaway)
data(toy_otu_table)
data(toy_metadata)
```
```

documentation: vignettes

277 lines (199 sloc) | 13.3 KB

Raw | Blame | History

title	author	date	output	vignette
Getting started with breakaway	Amy Willis	`r Sys.Date()`	rmarkdown::html_vignette	%\VignetteIndexEntry{getting-started} %\VignetteEngine{knitr::rmarkdown} %\VignetteEncoding{UTF-8}

`breakaway` is a package for species richness estimation and modelling. As the package has grown and users have requested more functionality, it contains some basic generalisations of the statistical philosophy that underpins `breakaway` to the general alpha diversity case. Because of the flexibility of the modelling strategies, most users of breakaway are microbial ecologists with very large OTU tables, however, nothing should exclude a macroecologist from using the same tools. If you have a macroecology dataset and want to use this package, I would love to hear from you so please feel free to contact me (email or via Github's Issues/Projects infrastructure).

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library(breakaway)
data(toy_otu_table)
data(toy_metadata)

## For historical reasons we going to call them:
otu_data <- toy_otu_table
meta_data <- toy_metadata
```

Other things to keep in mind

1. `testthat` is a H.W. package to write unit tests
2. Datasets take a special format
    - Don't release data in the same way as functions
3. `rm(list=ls(all=TRUE))` removes everything in the global environment
    - But not packages!
4. Consider making custom classes (S3 or S4)
5. `pkgdown` is a H.W. package that can autogenerate a website `build_site()`

Coming up

- New homework: your first R package
- Homework due Tuesday 21 November
  - Good luck with your 512 mid-term!
  - Move office hours from 3 p.m. Tuesday 14 November to 3 p.m. Friday 17 November?
- Next week: scripting + departmental computing with Brian Williamson