Rmarkdown
R Packages
R Shiny

Paul W. Egeler, MS
Spectrum Health
Office of Research and Education

Powered By SASS
Scholarly Activity and Scientific Support

Spectrum Health

What we'll cover...

What is it?

Why is it used?

How can I use it?

Rmarkdown

Spectrum Health

Powered by SASS

Motivating concepts

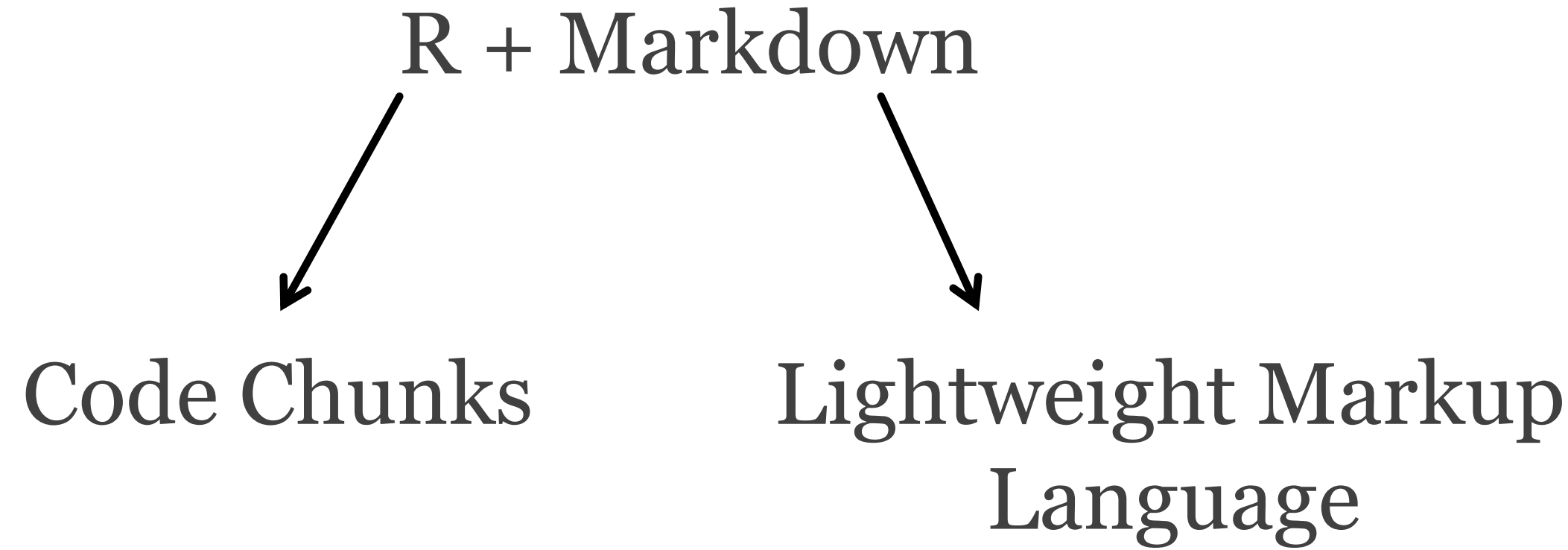
Literate programming
Reproducible research
Automated document generation

What is it?

R + Markdown

What is it?

R + Markdown



Code Chunks

Lightweight Markup Language

What is it?

R + Markdown

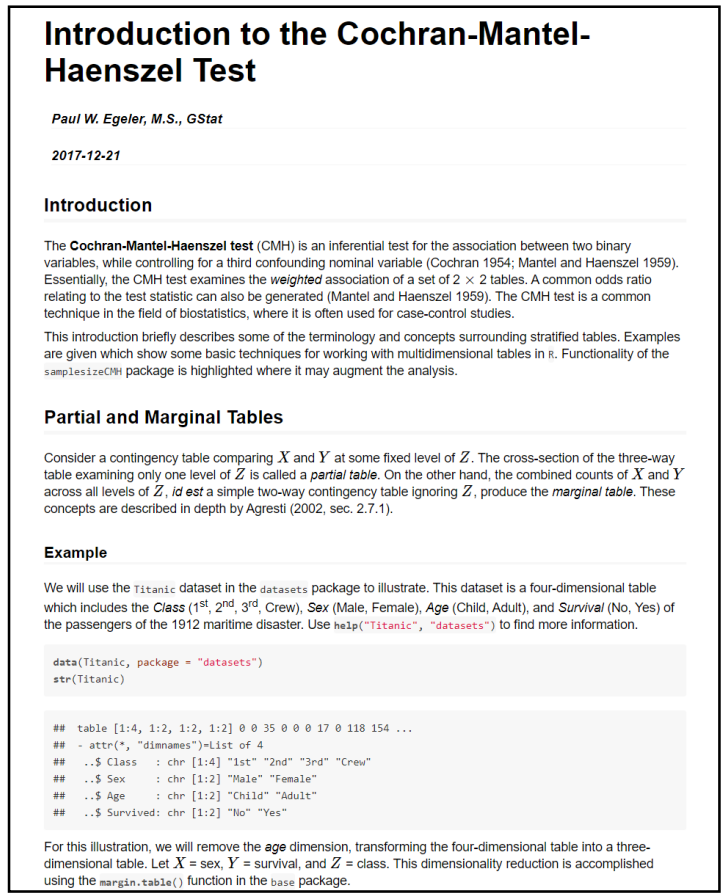
Document metadata (YAML)

Text (markdown)

Code (R)

Text (markdown)

Code (python)



Introduction to the Cochran-Mantel-Haenszel Test

Paul W. Egeler, M.S., GStat

2017-12-21

Introduction

The **Cochran-Mantel-Haenszel test** (CMH) is an inferential test for the association between two binary variables, while controlling for a third confounding nominal variable (Cochran 1954; Mantel and Haenszel 1959). Essentially, the CMH test examines the *weighted* association of a set of 2×2 tables. A common odds ratio relating to the test statistic can also be generated (Mantel and Haenszel 1959). The CMH test is a common technique in the field of biostatistics, where it is often used for case-control studies.

This introduction briefly describes some of the terminology and concepts surrounding stratified tables. Examples are given which show some basic techniques for working with multidimensional tables in `R`. Functionality of the `samplesizeCMH` package is highlighted where it may augment the analysis.

Partial and Marginal Tables

Consider a contingency table comparing X and Y at some fixed level of Z. The cross-section of the three-way table examining only one level of Z is called a *partial table*. On the other hand, the combined counts of X and Y across all levels of Z, *id est* a simple two-way contingency table ignoring Z, produce the *marginal table*. These concepts are described in depth by Agresti (2002, sec. 2.7.1).

Example

We will use the `Titanic` dataset in the `datasets` package to illustrate. This dataset is a four-dimensional table which includes the *Class* (1st, 2nd, 3rd, Crew), *Sex* (Male, Female), *Age* (Child, Adult), and *Survival* (No, Yes) of the passengers of the 1912 maritime disaster. Use `help("Titanic", "datasets")` to find more information.

```
data(Titanic, package = "datasets")
str(Titanic)
```

```
##  table [1:4, 1:2, 1:2, 1:2] 0 0 35 0 0 0 17 0 118 154 ...
##  - attr(*, "dimnames")=List of 4
##   ..$ Class   : chr [1:4] "1st" "2nd" "3rd" "Crew"
##   ..$ Sex     : chr [1:2] "Male" "Female"
##   ..$ Age     : chr [1:2] "Child" "Adult"
##   ..$ Survived: chr [1:2] "No" "Yes"
```

For this illustration, we will remove the *age* dimension, transforming the four-dimensional table into a three-dimensional table. Let X = sex, Y = survival, and Z = class. This dimensionality reduction is accomplished using the `margin.table()` function in the `base` package.

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What is it?

R Markdown Reference Guide

Learn more about R Markdown at rmarkdown.rstudio.com
Learn more about Interactive Docs at shiny.rstudio.com/articles

Contents:

1. **Markdown Syntax**
2. Knitr chunk options
3. Pandoc options

Syntax

```
Plain text

End a line with two spaces
to start a new paragraph.

*italics* and _italics_

**bold** and __bold__

superscript^2^

~~strikethrough~~

[link](www.rstudio.com)

# Header 1

## Header 2

### Header 3

#### Header 4

##### Header 5

###### Header 6

endash: --

emdash: ---

ellipsis: ...

inline equation: $A = \pi*r^{2}$

image: ![](path/to/smallorb.png)

horizontal rule (or slide break):
```

Becomes

Plain text

End a line with two spaces to start a new paragraph.

italics and *italics*

bold and **bold**

superscript^2

~~strikethrough~~

link

Header 1

Header 2

Header 3

Header 4

Header 5

Header 6

endash: –

emdash: —

ellipsis: …

inline equation: $A = \pi * r^2$

image:

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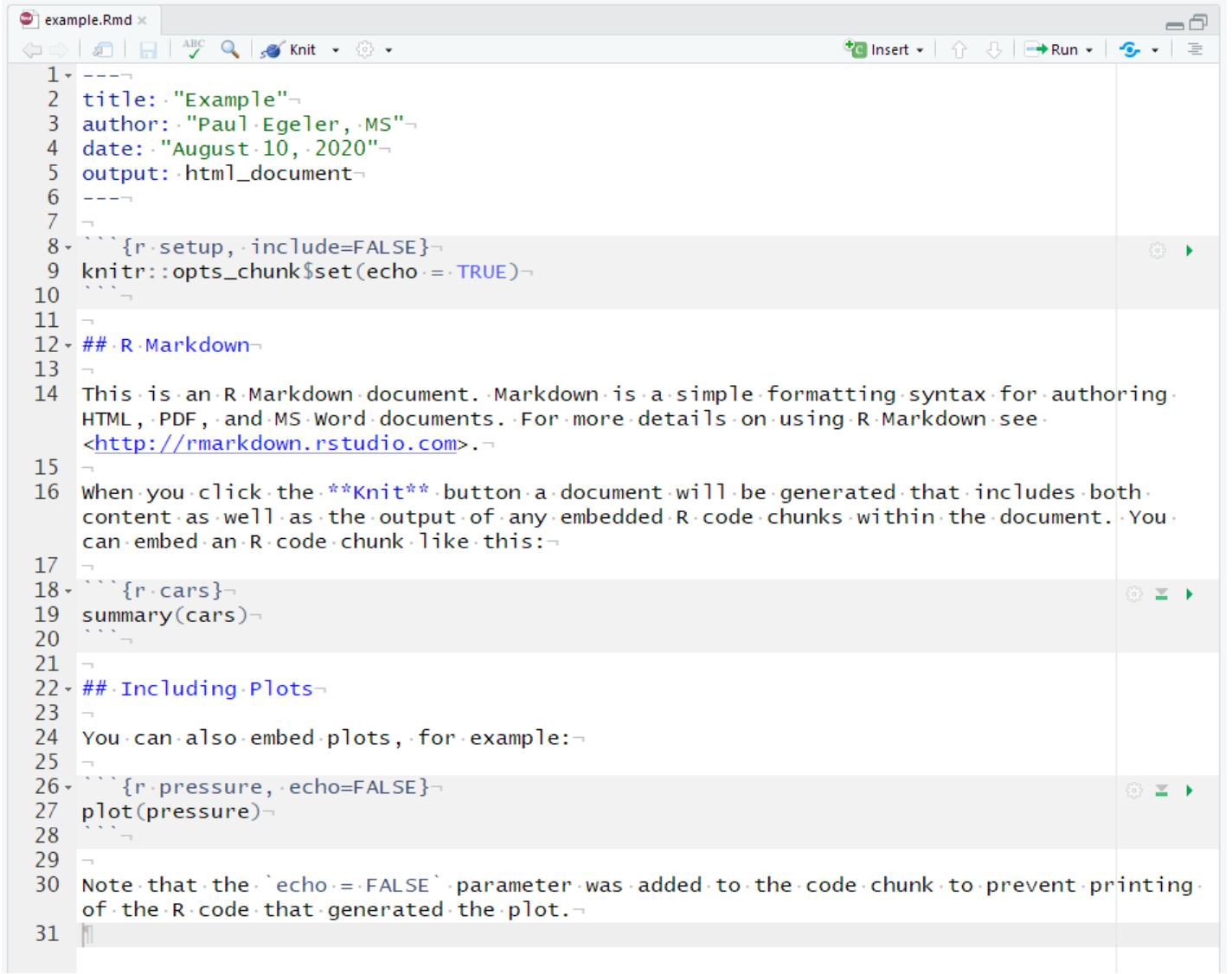
What is it?

File format that combines

- report text
- formatting instructions
- code chunks
- compilation options



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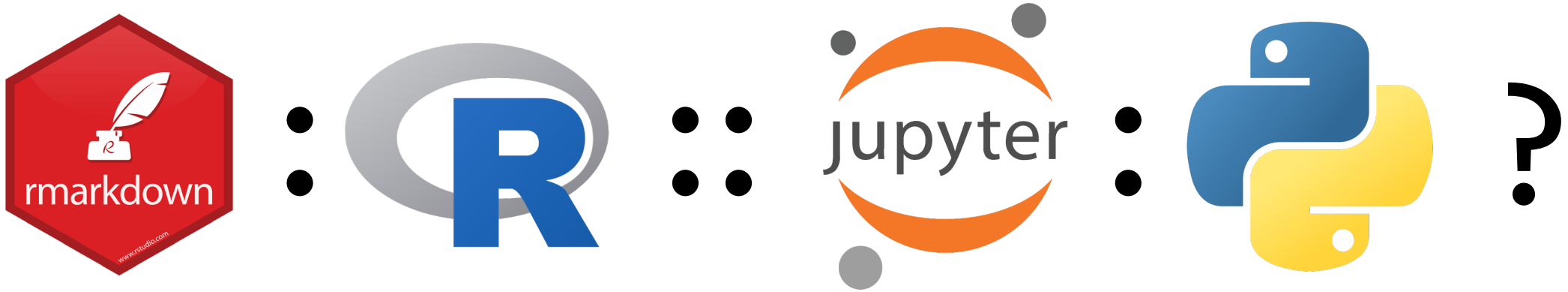
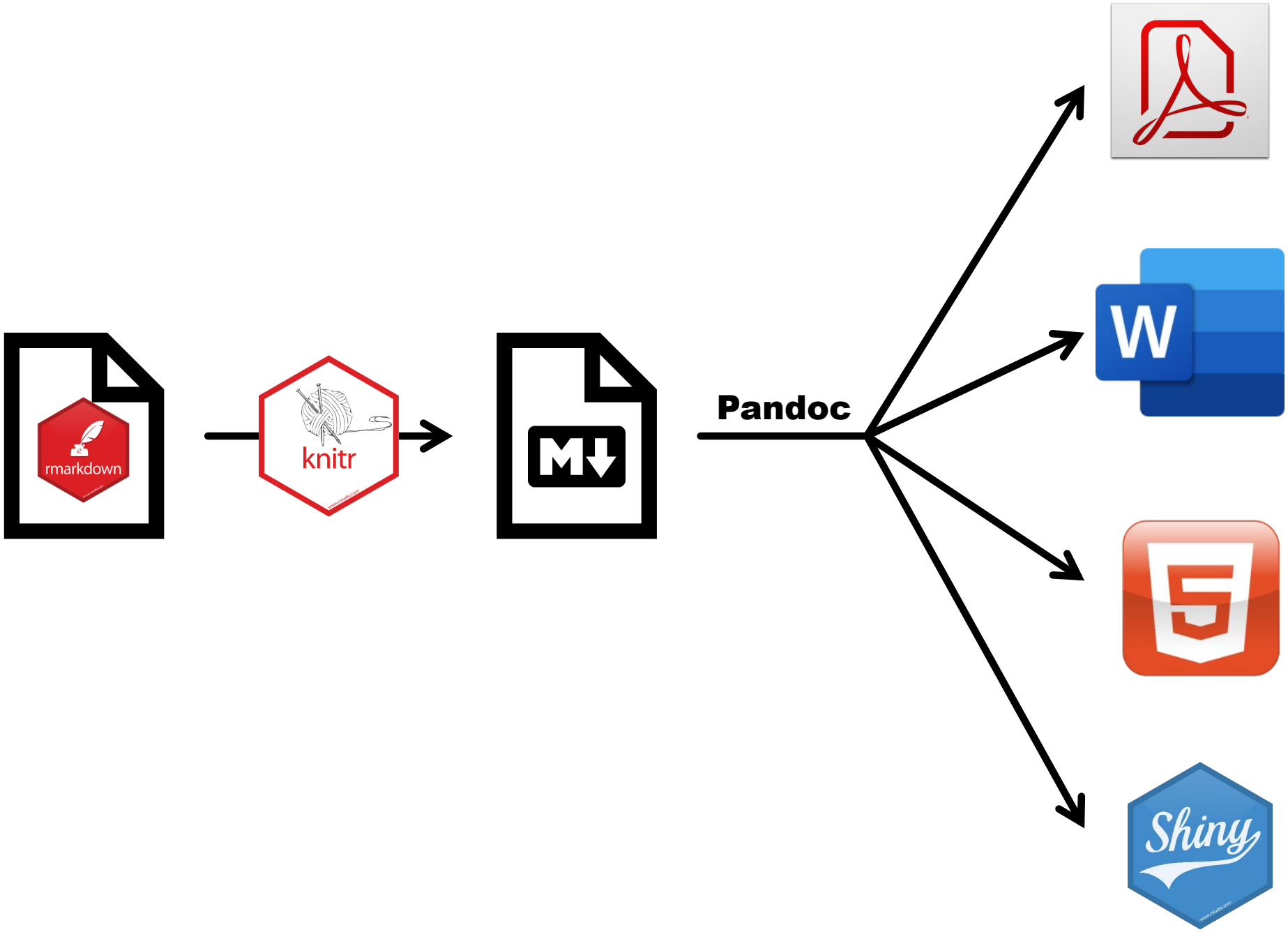
Like a Jupyter notebook, but for R?



Well, sort of… this blog post explains.



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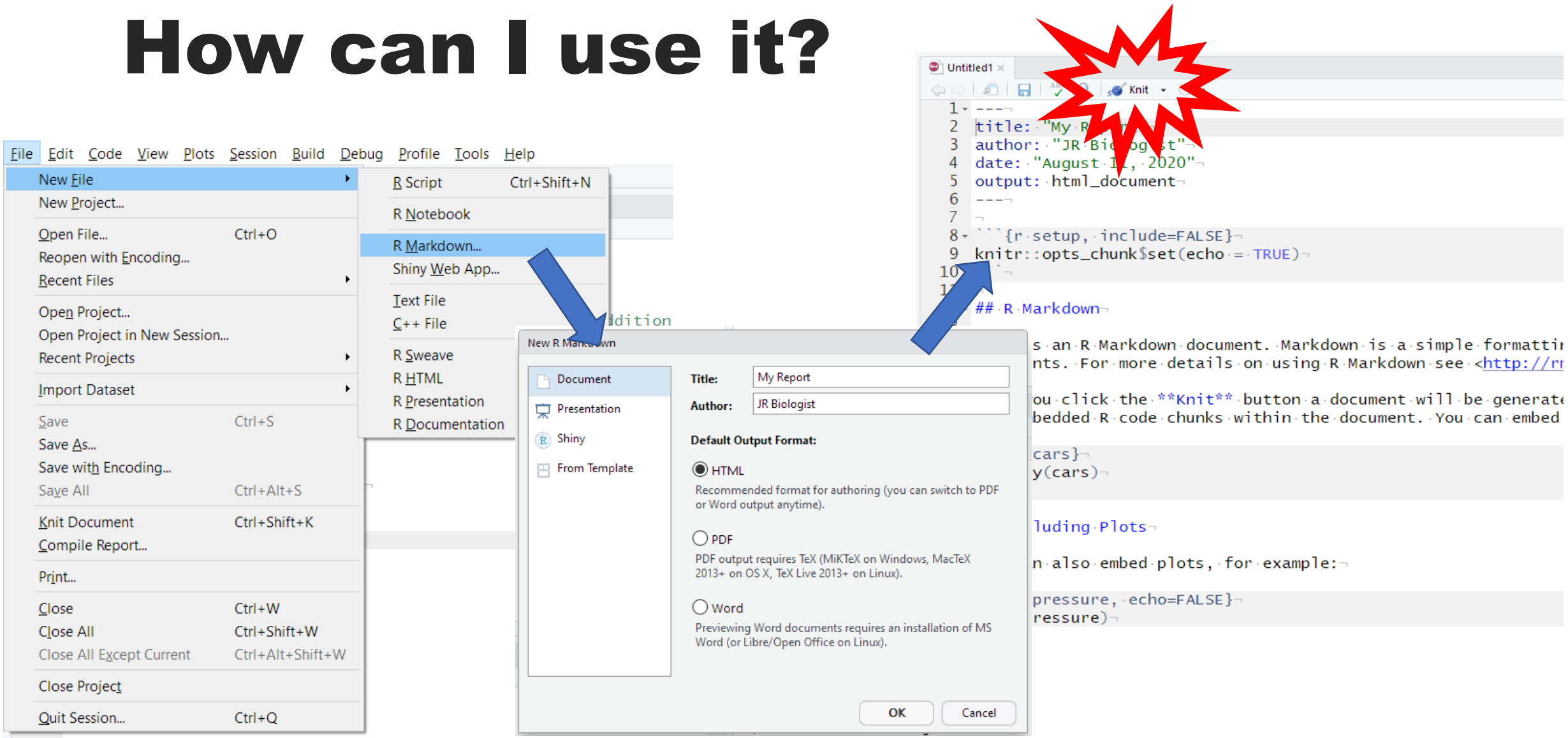
Why is it used?

- Report and code in one place
- Easily update when new data comes in
- Versatile output formats
- Plain text file format is "future-proof"
- WYSIWYM (contrast WYSIWYG)

How do these relate to our motivating concepts?

How can I use it?



You can also use Ctl+Shft+K in the RStudio IDE or `rmarkdown::render("myReport.Rmd")` from the R console!!!

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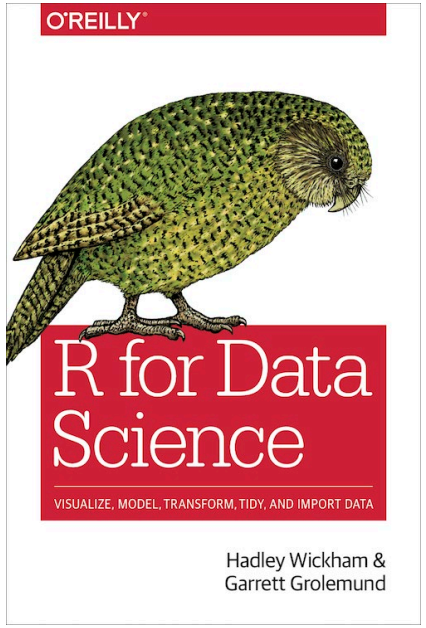
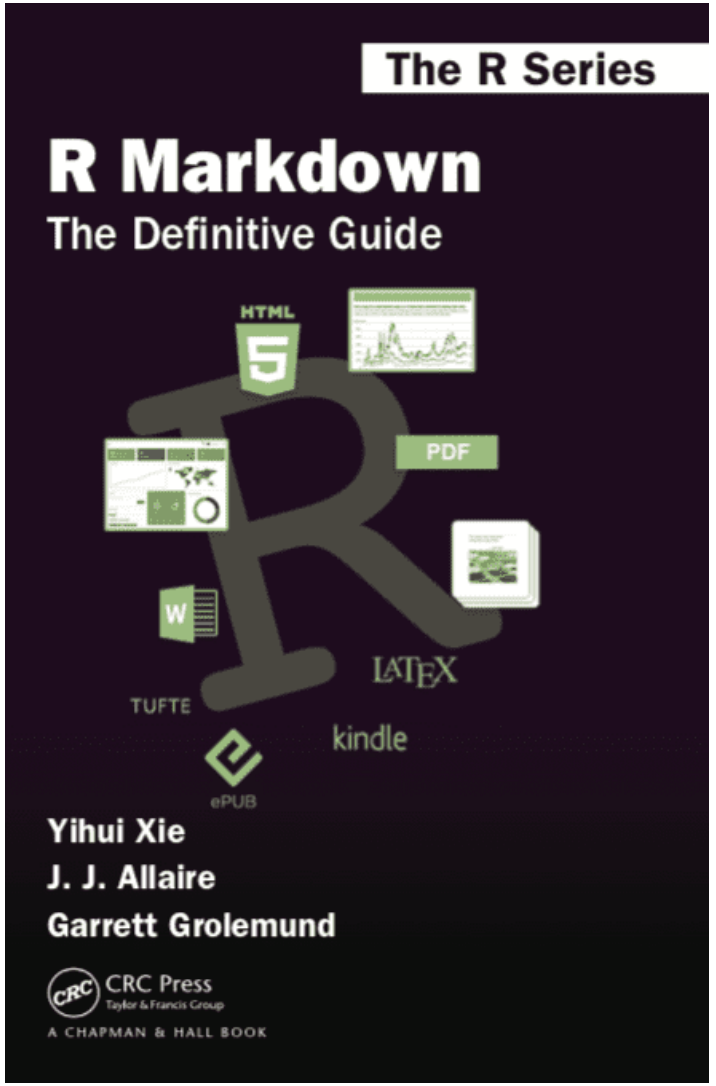
Further Reading

- R Markdown: The Definitive Guide
- R Markdown Reference Guide
- R Markdown Cheat Sheet
- R Markdown Quick Tour
- R Markdown Tutorial





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R Packages

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What is it?

- R code
  - Function definitions
  - Classes
- Low level compiled language code (C, FORTRAN, C++, Java)
- Documentation
- Vignettes (long-form documentation)
- Data
- Tests
- Additional external files

Why is it used?

Modular code—**reusable**

Bundled code—**shareable**

Standardized code—**reproducible**

How can I use it?

Install existing packages

- Online Repositories (repos)
  - CRAN
  - Omegahat
  - Bioconductor
- Code hosting platforms
  - GitHub
  - BitBucket
- Local locations

Build your own

- RStudio IDE
- R packages
  - devtools
  - usethis
  - roxygen2
  - testthat
  - Rcpp

RStudio Desktop

RStudio Server

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Installing packages

Development environment

Run this line to make sure you can compile source code

```
devtools::has_devel()
```

If returns `FALSE`, install development tools:

- Windows
  - RTools
- MacOS
  - XCode
- Linux
  - (depends on the distro)

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Installing from online repositories

```
# Install from CRAN
pkgs <- c("remotes", "usethis", "devtools", "rmarkdown", "shiny")
install.packages(pkgs)

# From Omegahat
install.packages("RDCOMClient", repos = "http://www.omegahat.net/R")

# Bioconductor (R >= 3.5.0)
if (!require("BiocManager")) install.packages("BiocManager")
BiocManager::install()

# Bioconductor (R < 3.5.0)
source("https://bioconductor.org/biocLite.R")
BiocInstaller::biocLite(c("GenomicFeatures", "AnnotationDbi"))
```

Installing from code hosting sites

```
# Need the 'remotes' package
if (!require("remotes")) install.packages("remotes")

# Package in root directory of git repo
remotes::install_github("SpectrumHealthResearch/samplesizeCMH")

# Package in a subfolder of git repo
remotes::install_github("SpectrumHealthResearch/REDCapRITS/R")

# Package in a subfolder and specified branch of git repo
remotes::install_github("pegeler/mlaibr@deprecation-warnings")

# DEVELOPMENT version of Bioconductor package
remotes::install_bioc("SummarizedExperiment")
```

Local and network locations

```
# Using base R
install.packages("/path/to/package_1.2.0.zip", repos = NULL)

# Using 'remotes' package
remotes::install_local("/path/to/package")

# Using 'devtools' package
devtools::install("/path/to/package")
```

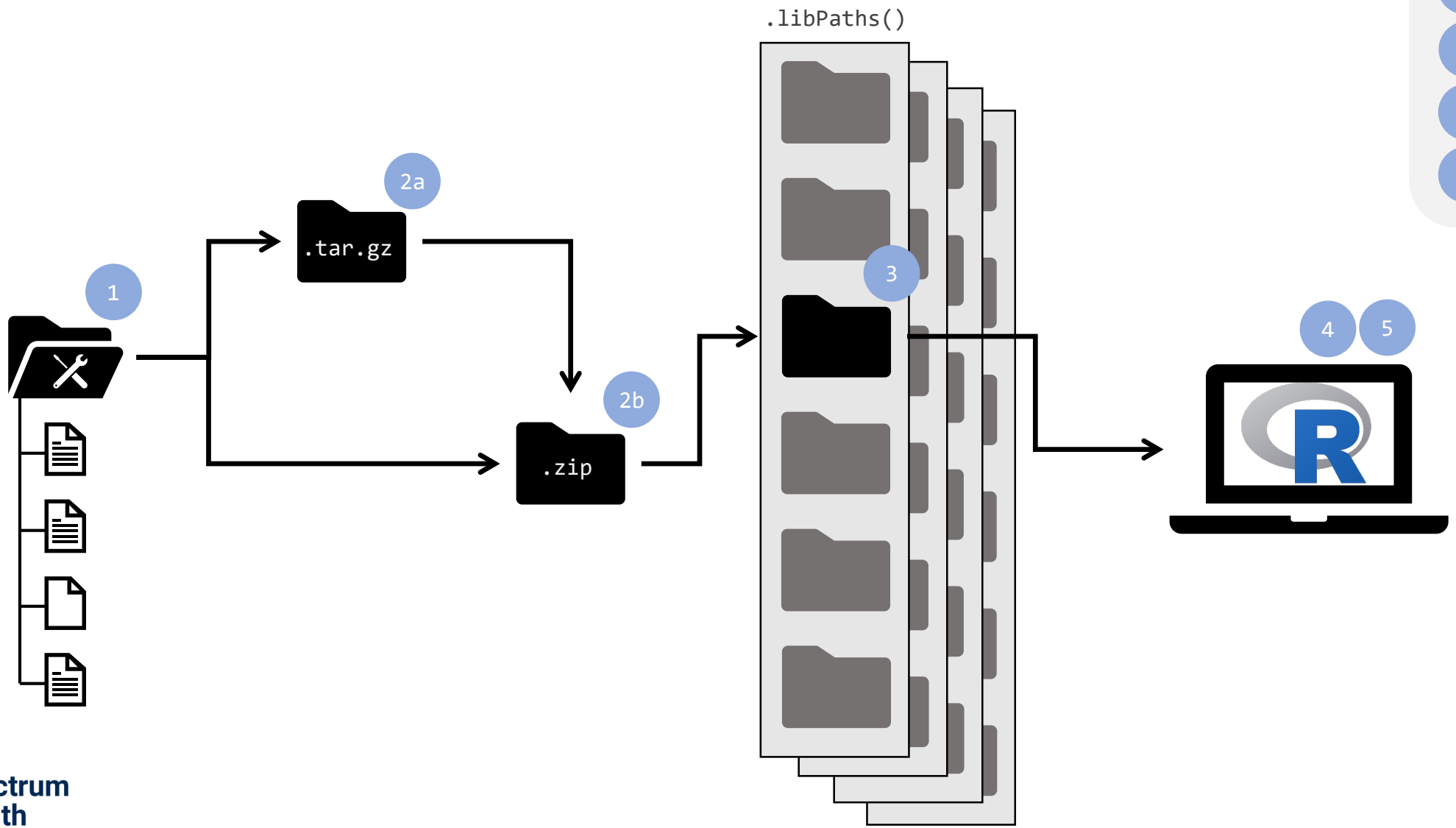
You can also do all your package installation and development from the bash terminal.

```
$ R CMD INSTALL /path/to/package
```

Build your own packages

Package lifecycle

1. Source
2a. Bundled
2b. Binary
3. Installed
4. Loaded
5. Attached



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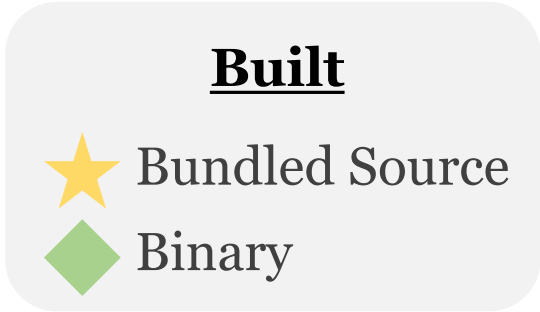
samplesizeCMH: Power and Sample Size Calculation for the Cochran-Mantel-Haenszel Test

Calculates the power and sample size for Cochran-Mantel-Haenszel tests. There are also several helper functions for working with probability, odds, relative risk, and odds ratio values.

Version:	0.0.0
Depends:	R (≥ 3.4.0)
Imports:	stats
Suggests:	knitr, rmarkdown, DescTools, datasets, testthat
Published:	2017-12-21
Author:	Paul Egeler [aut, cre], Spectrum Health, Grand Rapids, MI [cph]
Maintainer:	Paul Egeler <paul.egeler at spectrumhealth.org>
BugReports:	https://github.com/pegeler/samplesizeCMH/issues
License:	GPL-2 | GPL-3
Copyright:	Spectrum Health, Grand Rapids, MI
URL:	https://github.com/pegeler/samplesizeCMH
NeedsCompilation:	no
Materials:	README
CRAN checks:	samplesizeCMH results



Downloads:

Reference manual:	samplesizeCMH.pdf
Vignettes:	Introduction to the Cochran-Mantel-Haenszel Test Power Calculation for the Cochran-Mantel-Haenszel Test Sample Size Calculation for the Cochran-Mantel-Haenszel Test
Package source:	samplesizeCMH_0.0.0.tar.gz
Windows binaries:	r-devel: samplesizeCMH_0.0.0.zip, r-release: samplesizeCMH_0.0.0.zip, r-oldrel: samplesizeCMH_0.0.0.zip
macOS binaries:	r-release: samplesizeCMH_0.0.0.tgz, r-oldrel: samplesizeCMH_0.0.0.tgz

Linking:

Please use the canonical form https://CRAN.R-project.org/package=samplesizeCMH to link to this page.

Folder structure

- DESCRIPTION
- NAMESPACE
- README.md
- .Rbuildignore
- NEWS.md

- R/
- src/
- man/
- data/
- tests/
- inst/
- vignettes/

```
$ tree
.
├── data
│   └── rides.rda
├── data-raw
│   └── rides.r
├── DESCRIPTION
├── eddington.Rproj
├── inst
│   └── include
│       ├── eddington.h
│       └── eddington_RcppExports.h
├── man
│   ├── E_cum.Rd
│   ├── E_next.Rd
│   ├── E_num.Rd
│   ├── E_req.Rd
│   ├── E_sat.Rd
│   └── rides.Rd
├── NAMESPACE
├── NEWS.md
├── R
│   ├── eddington.r
│   ├── RcppExports.R
│   └── rides.r
├── README.md
├── README.Rmd
├── src
│   ├── eddington.cpp
│   └── RcppExports.cpp
├── tests
│   ├── testthat
│   │   ├── refdata.rds
│   │   ├── simdata.rds
│   │   └── test-package.r
│   └── testthat.R
└── vignettes
    └── eddington.Rmd

10 directories, 26 files
```

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The DESCRIPTION file

```
Package: samplesizeCMH
Title: Power and Sample Size Calculation for the Cochran-Mantel-Haenszel Test
Date: 2019-12-03
Version: 0.0.1
Authors@R: c(
    person("Paul", "Egeler", email = "paul.egeler@spectrumhealth.org", role = c("aut", "cre")),
    person("Spectrum Health, Grand Rapids, MI", role = "cph"))
Copyright: Spectrum Health, Grand Rapids, MI
Description:
    Calculates the power and sample size for Cochran-Mantel-Haenszel tests.
    There are also several helper functions for working with probability,
    odds, relative risk, and odds ratio values.
Depends: R (>= 3.4.0)
Imports: stats
License: GPL-2 | GPL-3
Encoding: UTF-8
LazyData: true
Suggests:
    knitr,
    rmarkdown,
    DescTools,
    datasets,
    testthat
VignetteBuilder: knitr
RoxygenNote: 6.0.1
URL: https://github.com/SpectrumHealthResearch/samplesizeCMH
BugReports: https://github.com/SpectrumHealthResearch/samplesizeCMH/issues
```

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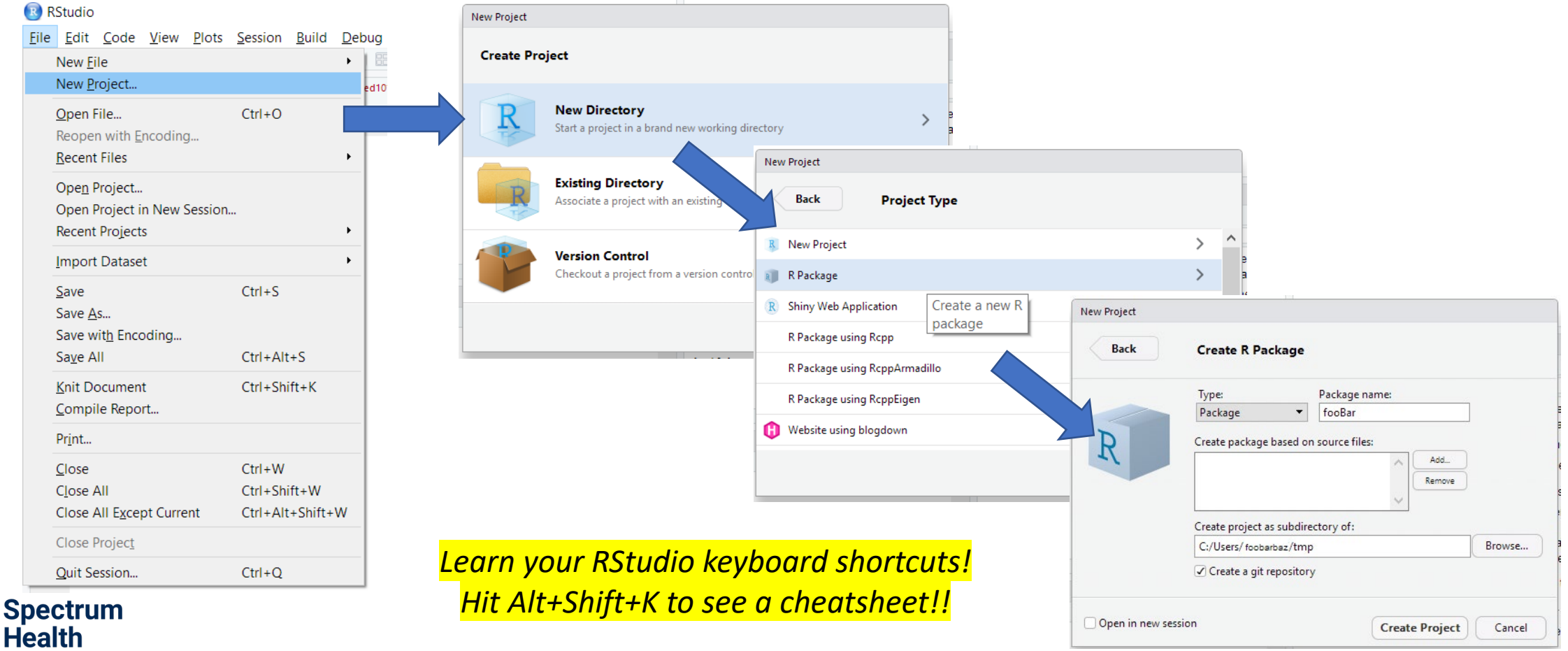
Create a package in RStudio

HIGHLY recommend developing in the RStudio IDE



Learn your RStudio keyboard shortcuts!
Hit Alt+Shift+K to see a cheatsheet!!

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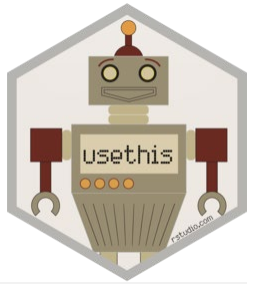
Adding components




```
# Create a package with 'usethis' package
usethis::create_package("/path/to/package")

# Create some useful files
usethis::use_r("myFunction.R")
usethis::use_data_raw("myData.R")
usethis::use_readme_rmd()
usethis::use_gpl3_license()
usethis::use_vignette("myVignette")

# Add package dependency
usethis::use_package("primes")

# Make a git repo
usethis::use_git()
```

Documenting with roxygen2

```
#' Add two numbers
#'
#' This function adds two numbers together.
#'
#' This paragraph goes into detail about the theory of addition.
#'
#' @param a,b Numbers to be added together.
#' @examples
#' add_numbers(1, 2)
#' ## [1]  3
#' @return An numeric vector.
#' @author Paul Egeler, MS
#' @export
add_numbers <- function(a, b) {
  a + b
}
```

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Documenting with roxy

```
#' Add two numbers
#'
#' This function adds two numbers together.
#'
#' This paragraph goes i                    of
#'
#' @param a,b Numbers to
#' @examples
#' add_numbers(1, 2)
#' ## [1]  3
#' @return An numeric vector.
#' @author Paul Egeler, MS
#' @export
add_numbers <- function(a, b) {
  a + b
}
```

devtools::document()
or
ctl+shft+D

Files | Plots | Packages | Help | Viewer

add_numbers.Rd | Find in Topic

add_numbers {foobar}

Add two numbers

Description

This function adds two numbers together.

Usage

```
add_numbers(a, b)
```

Arguments

a, b	Numbers to be added together.

Details

This paragraph goes into detail about the theory of addition.

Value

An numeric vector.

Author(s)

Paul Egeler, MS

Examples

```
add_numbers(1, 2)
## [1]  3
```

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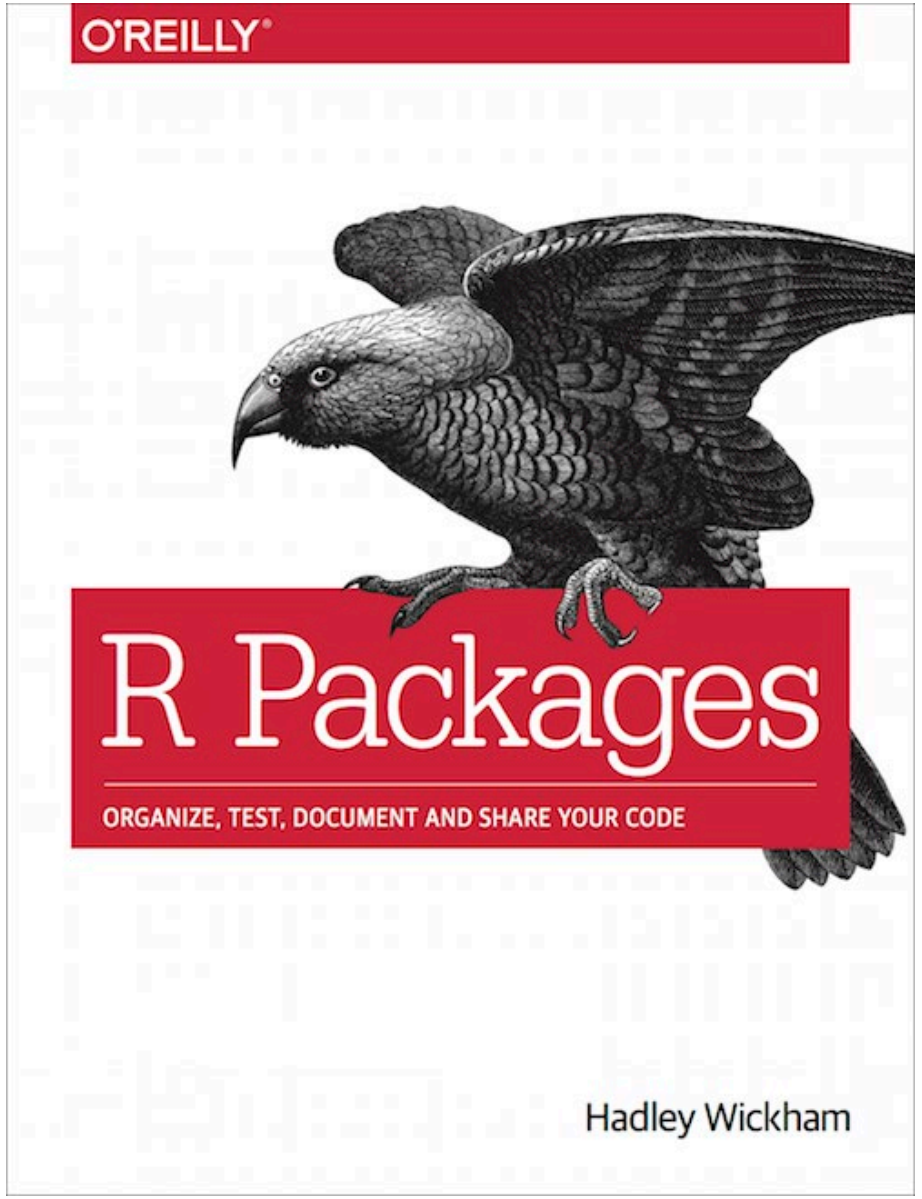
Further Reading

- R Packages by Hadley Wickham
- Writing R Extensions



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R Shiny

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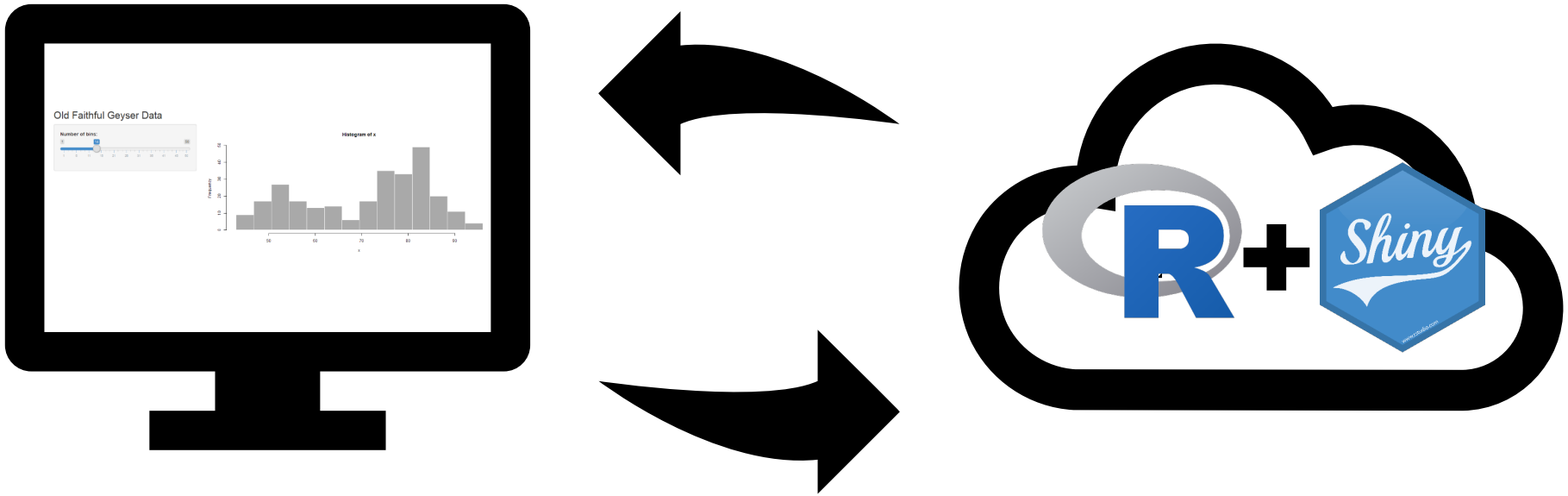
What is it?

A web server with an R backend



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What is it?

Two components:

- User interface (ui)
- Server function (server)

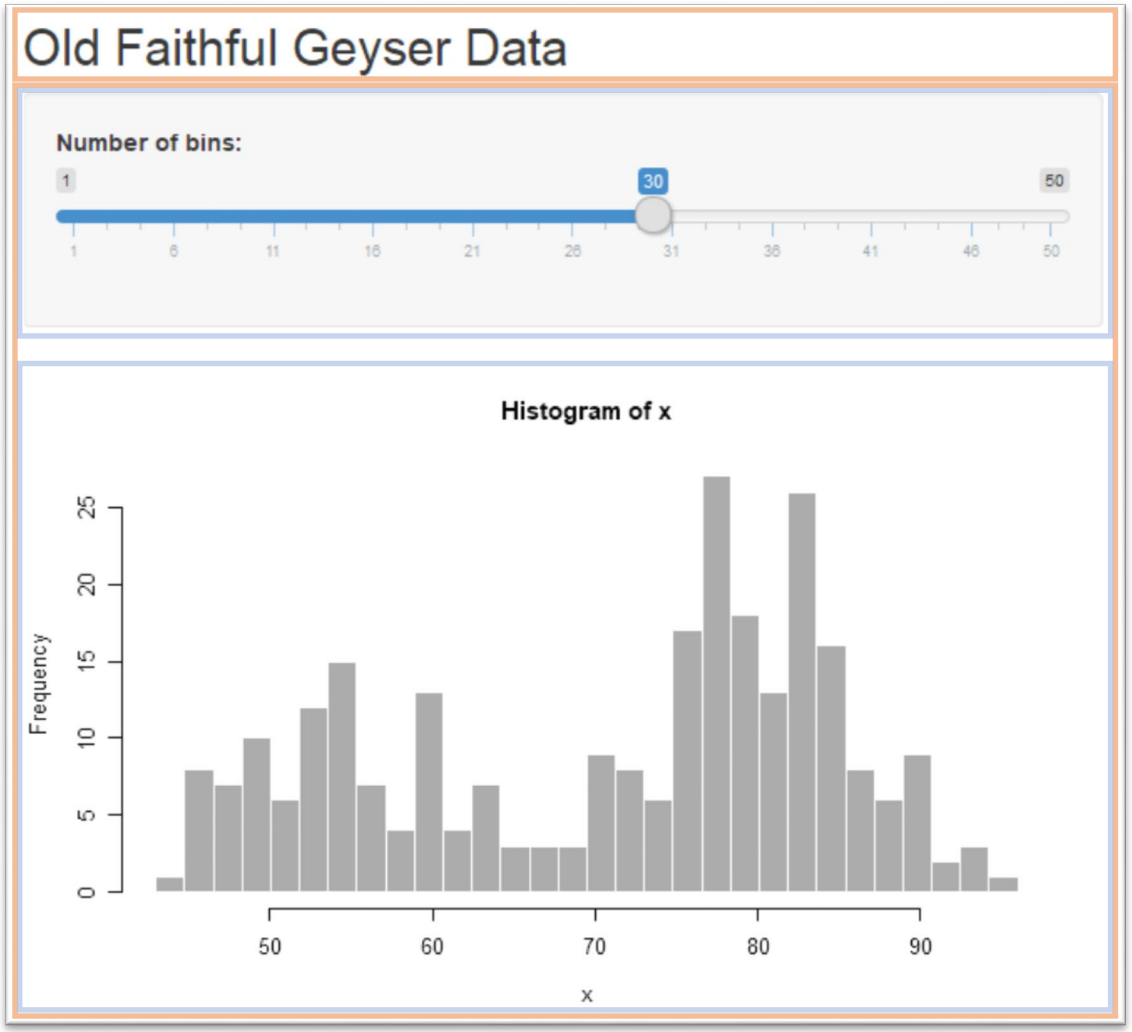
```
library(shiny)

ui <- fluidPage()

server <- function(input, output) {}

shinyApp(ui = ui, server = server)
```

What is it?




```
app.R
Reload App
1  #
2  # This is a Shiny web application. You can run the application by clicking
3  # the 'Run App' button above.
4  #
5  # Find out more about building applications with Shiny here:
6  #
7  #    http://shiny.rstudio.com/
8  #
9
10 library(shiny)
11
12 # Define UI for application that draws a histogram
13 ui <- fluidPage(
14
15    # Application title
16    titlePanel("Old Faithful Geyser Data"),
17
18    # Sidebar with a slider input for number of bins
19    sidebarLayout(
20       sidebarPanel(
21          sliderInput("bins",
22                      "Number of bins:",
23                      min = 1,
24                      max = 50,
25                      value = 30)
26       ),
27
28       # Show a plot of the generated distribution
29       mainPanel(
30          plotOutput("distPlot")
31       )
32    )
33 )
34
35 # Define server logic required to draw a histogram
36 server <- function(input, output) {
37
38    output$distPlot <- renderPlot({
39       # generate bins based on input$bins from ui.R
40       x    <- faithful[, 2]
41       bins <- seq(min(x), max(x), length.out = input$bins + 1)
42
43       # draw the histogram with the specified number of bins
44       hist(x, breaks = bins, col = 'darkgray', border = 'white')
45    })
46 }
47
48 # Run the application
49 shinyApp(ui = ui, server = server)
50
51
```

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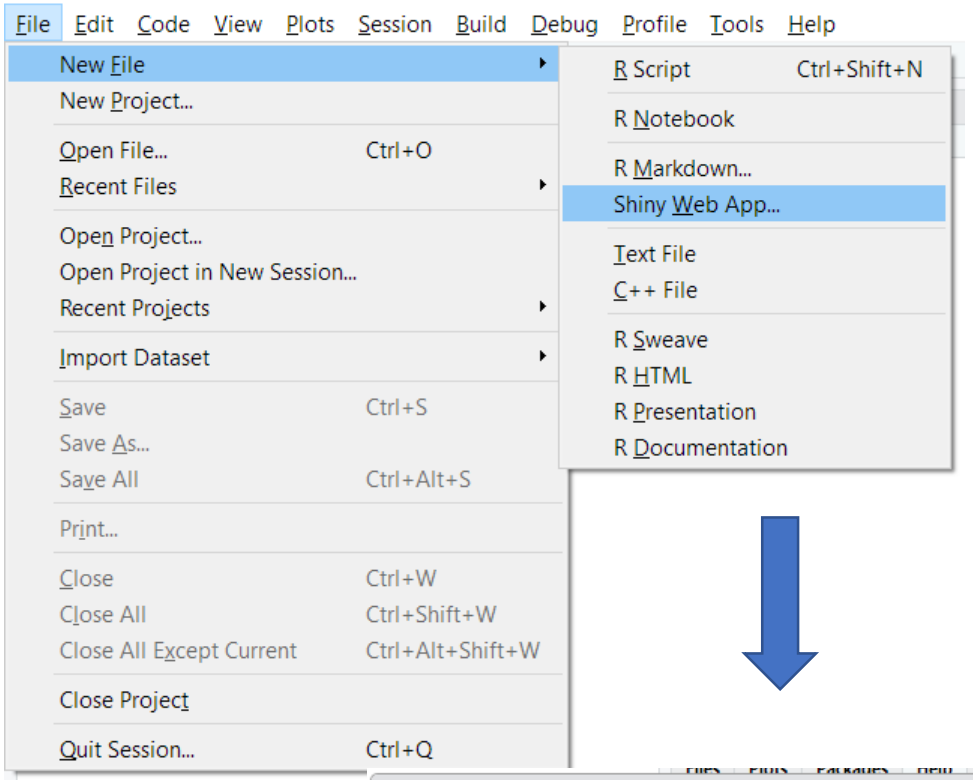
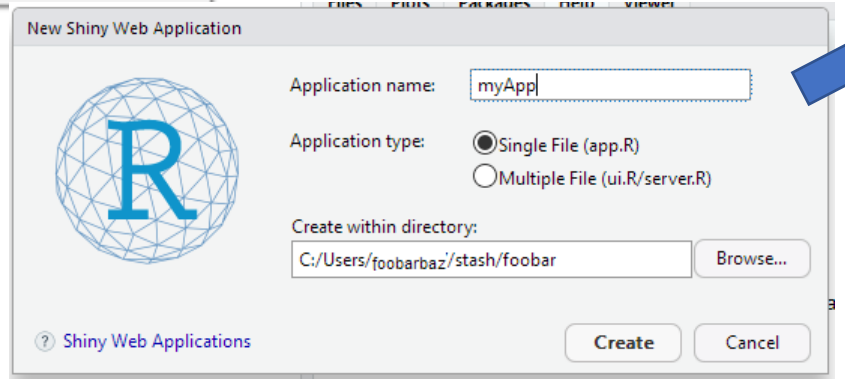
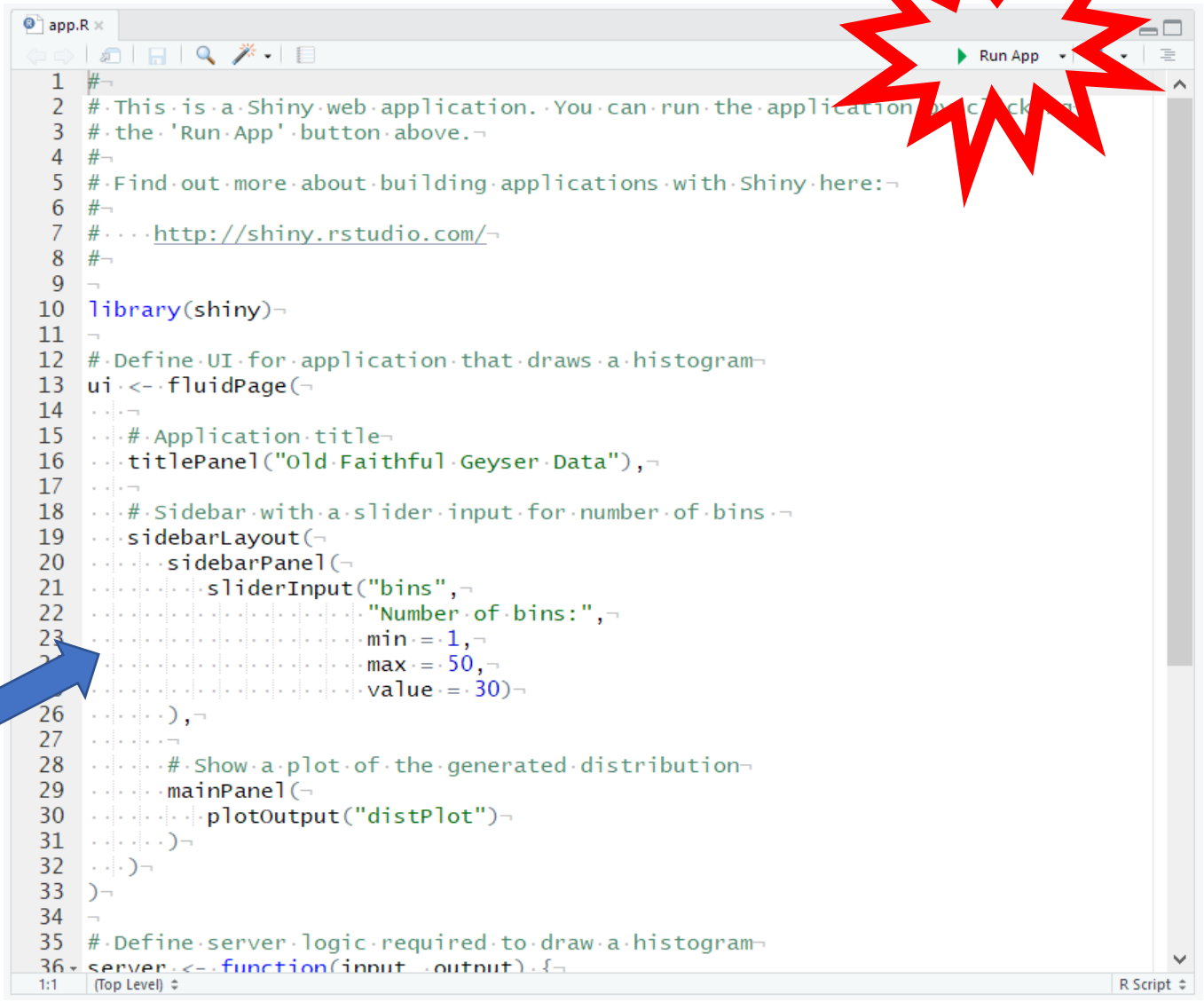
Why is it used?

- Interactive plots and maps
- Dashboards
- Explore tabular data
- Full websites

How can I use it?







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Sharing your work

- Shiny Server
- RStudio Connect
- Shinyapps.io

Further Reading

- Shiny Tutorial
- Mastering Shiny
- Shiny Cheat Sheet
- Shiny Training at rstudio::conf 2018

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Image credit:
Tambako The Jaguar - originally posted to Flickr as Happy snowkitty, CC BY-SA 2.0, https://commons.wikimedia.org/w/index.php?curid=11402681

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Questions?

Thank you.

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Afternoon session

Creating an R package LIVE!

We will cover…

- Writing functions
- Infix operators
- S3 classes and methods
- Integrate with git and GitHub
- Rmarkdown for README.md and vignettes
- roxygen2 for documentation
- Create a Shiny app?

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