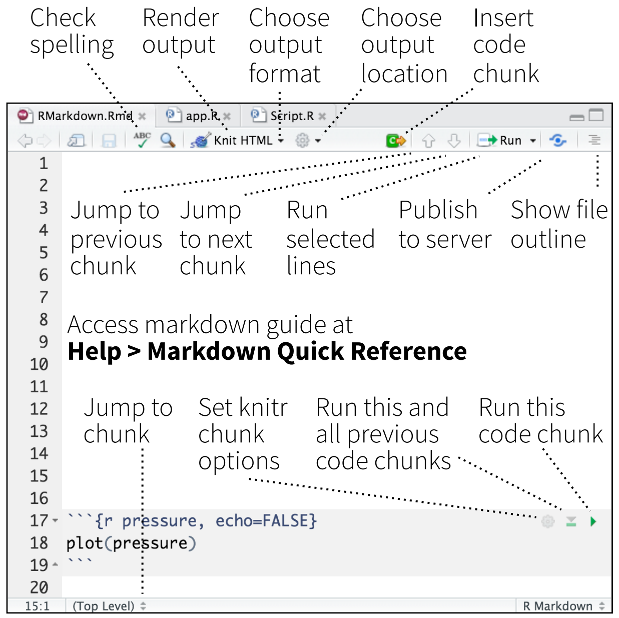
RStudio IDE : : CHEAT SHEET

Documents and Apps

Open Shiny, R Markdown, knitr, Sweave, LaTeX, .Rd files and more in Source Pane



Check spelling | Render output | Choose output format | Choose output location | Insert code chunk

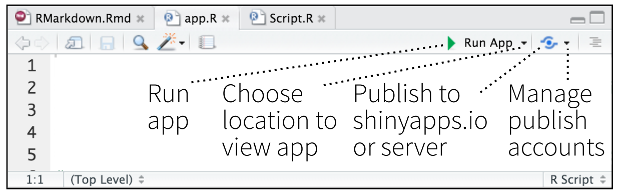
Jump to previous chunk | Jump to next chunk | Run selected lines | Publish to server | Show file outline

Access markdown guide at **Help > Markdown Quick Reference**

Jump to chunk | Set knitr chunk options | Run this and all previous code chunks | Run this code chunk

~~~
```{r pressure, echo=FALSE}
plot(pressure)
```
~~~

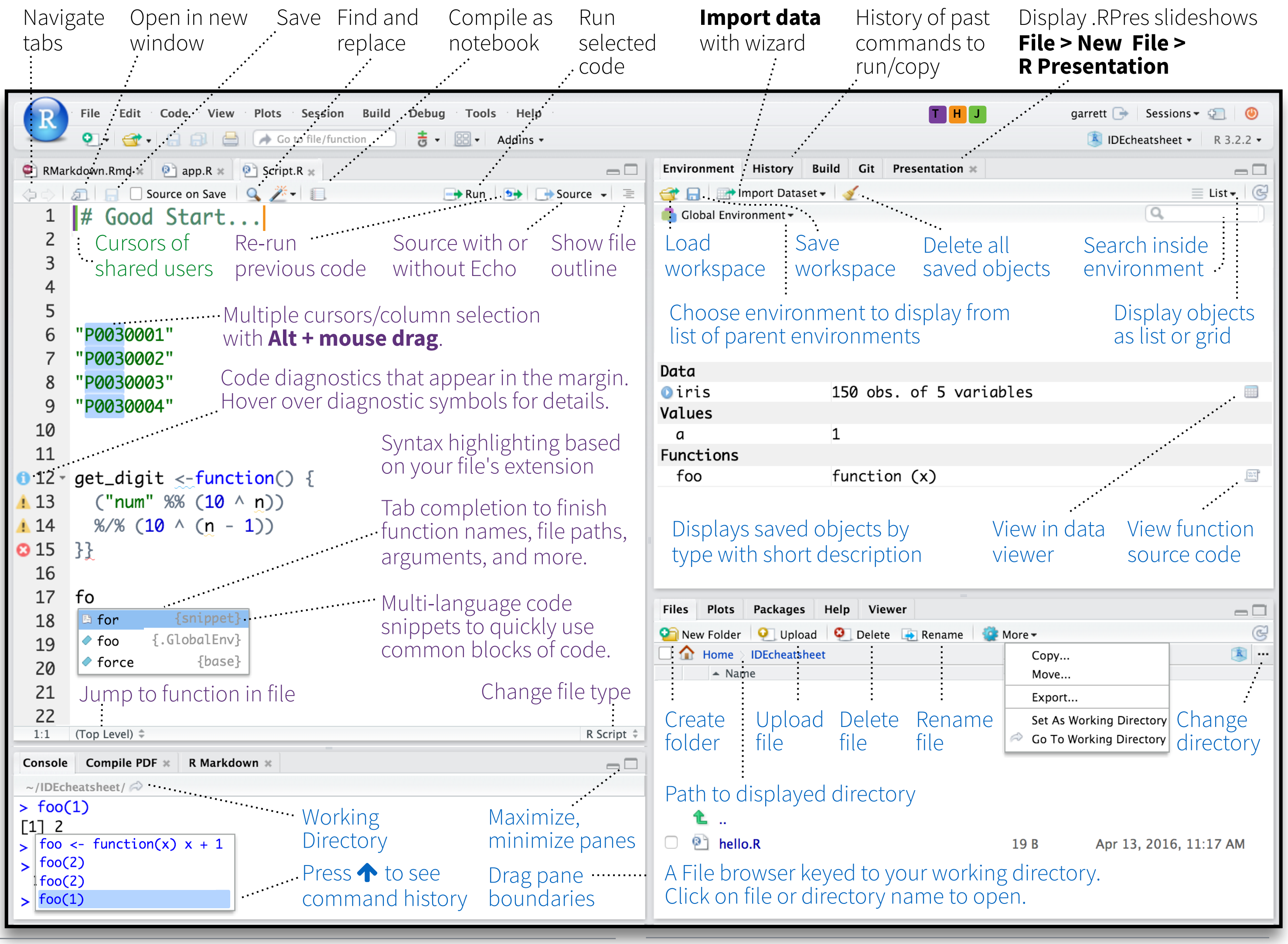
RStudio recognizes that files named **app.R**, **server.R**, **ui.R**, and **global.R** belong to a shiny app



Run app | Choose location to view app | Publish to shinyapps.io or server | Manage publish accounts

Write Code

R Support



Navigate tabs | Open in new window | Save | Find and replace | Compile as notebook | Run selected code

```
# Good Start...

"P0030001"
"P0030002"
"P0030003"
"P0030004"

get_digit <-function() {
  ("num" %% (10 ^ n))
  %/% (10 ^ (n - 1))
}}

fo
```

Cursors of shared users

Re-run previous code

Source with or without Echo

Show file outline

Multiple cursors/column selection with **Alt + mouse drag**.

Code diagnostics that appear in the margin. Hover over diagnostic symbols for details.

Syntax highlighting based on your file's extension

Tab completion to finish function names, file paths, arguments, and more.

Multi-language code snippets to quickly use common blocks of code.

Jump to function in file

Change file type

```
> foo(1)
[1] 2
> foo <- function(x) x + 1
> foo(2)
  foo(2)
> foo(1)
```

Working Directory

Maximize, minimize panes

Press ↑ to see command history

Drag pane boundaries

Import data with wizard

History of past commands to run/copy

Display .RPres slideshows **File > New File > R Presentation**

Load workspace | Save workspace | Delete all saved objects | Search inside environment

Choose environment to display from list of parent environments

Display objects as list or grid

```
Data
iris          150 obs. of 5 variables
Values
  a           1
Functions
  foo         function (x)
```

Displays saved objects by type with short description

View in data viewer

View function source code

Create folder | Upload file | Delete file | Rename file | Change directory

Path to displayed directory

A File browser keyed to your working directory. Click on file or directory name to open.

Pro Features

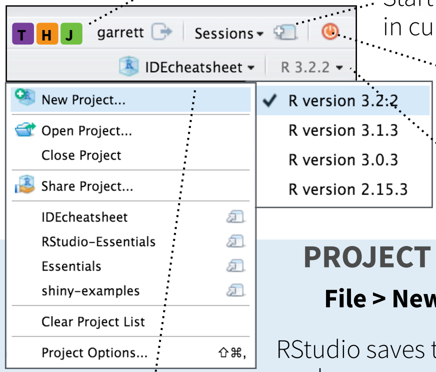
Share Project with Collaborators

Active shared collaborators

Start **new R Session** in current project

Close R Session in project

Select R Version



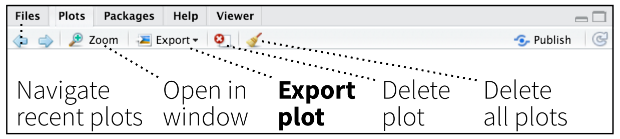
Name of current project

PROJECT SYSTEM

File > New Project

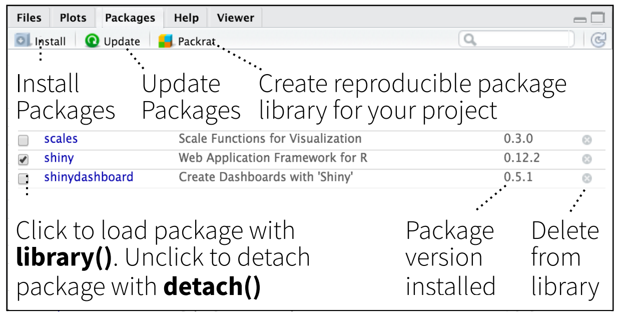
RStudio saves the call history, workspace, and working directory associated with a project. It reloads each when you re-open a project.

RStudio opens plots in a dedicated Plots pane



Navigate recent plots | Open in window | **Export plot** | Delete plot | Delete all plots

GUI Package manager lists every installed package



Install Packages | Update Packages | Create reproducible package library for your project

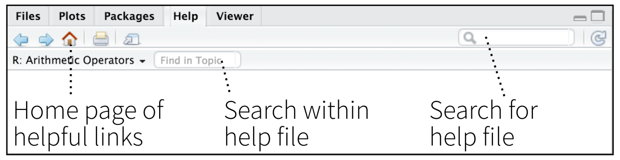
scales	Scale Functions for Visualization	0.3.0
shiny	Web Application Framework for R	0.12.2
shinydashboard	Create Dashboards with 'Shiny'	0.5.1

Click to load package with **library()**. Unclick to detach package with **detach()**

Package version installed

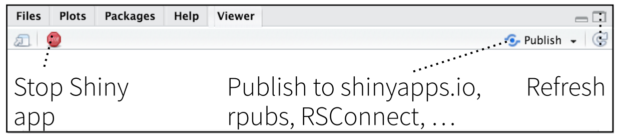
Delete from library

RStudio opens documentation in a dedicated Help pane



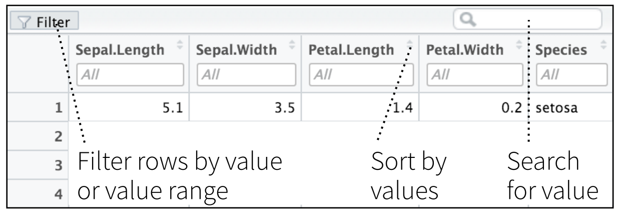
Home page of helpful links | Search within help file | Search for help file

Viewer Pane displays HTML content, such as Shiny apps, RMarkdown reports, and interactive visualizations



Stop Shiny app | Publish to shinyapps.io, rpubs, RSConnect, … | Refresh

View(<data>) opens spreadsheet like view of data set



	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2					
3					
4					

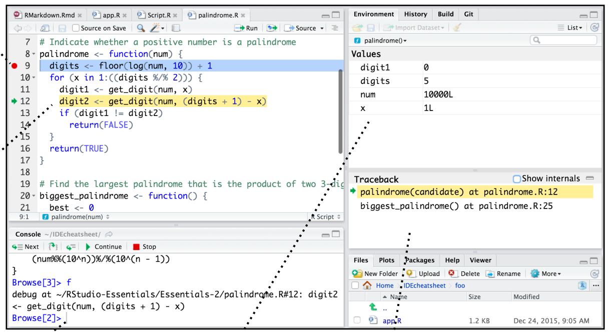
Filter rows by value or value range | Sort by values | Search for value

Debug Mode

Open with **debug(), browse(),** or a breakpoint. RStudio will open the debugger mode when it encounters a breakpoint while executing code.

Launch debugger mode from origin of error

Open traceback to examine the functions that R called before the error occurred



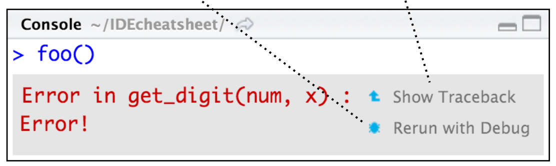
```
# Indicate whether a positive number is a palindrome
palindrome <- function(num) {
  digits <- floor(log(num, 10)) + 1
  for (x in 1:((digits %/% 2))) {
    digit1 <- get_digit(num, x)
    digit2 <- get_digit(num, (digits + 1) - x)
    if (digit1 != digit2)
      return(FALSE)
  }
  return(TRUE)
}

# Find the largest palindrome that is the product of two 3-dig
biggest_palindrome <- function() {
  best <- 0
```

```
Values
  digit1    0
  digits    5
  num       10000L
  x         1L

Traceback
palindrome(candidate) at palindrome.R:12
biggest_palindrome() at palindrome.R:25
```

```
    (num%%(10^n))%/%(10^(n - 1))
}
Browse[3]> f
debug at ~/RStudio-Essentials/Essentials-2/palindrome.R#12: digit2
<- get_digit(num, (digits + 1) - x)
Browse[2]>
```

Click next to line number to add/remove a breakpoint.

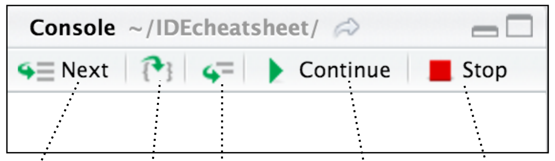
Highlighted line shows where execution has paused



```
> foo()
Error in get_digit(num, x) :
Error!
```

Show Traceback

Rerun with Debug



Run commands in environment where execution has paused

Examine variables in executing environment

Select function in traceback to debug

Step through code one line at a time

Step into and out of functions to run

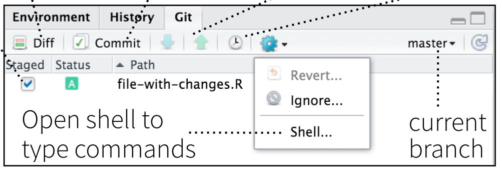
Resume execution

Quit debug mode

Version Control with Git or SVN

Turn on at **Tools > Project Options > Git/SVN**

Stage files: | Show file diff | Commit staged files | Push/Pull to remote | View History



- A Added
- D Deleted
- M Modified
- R Renamed
- ? Untracked

Open shell to type commands

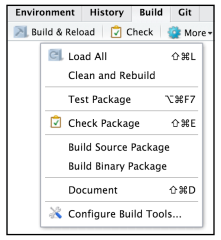
current branch

Package Writing

File > New Project > New Directory > R Package

Turn project into package, Enable roxygen documentation with **Tools > Project Options > Build Tools**

Roxygen guide at **Help > Roxygen Quick Reference**



RStudio® is a trademark of RStudio, Inc. • • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **www.rstudio.com** • RStudio IDE 0.99.832 • Updated: 2016-01

1 LAYOUT	Windows/Linux	Mac
Move focus to Source Editor	Ctrl+1	Ctrl+1
Move focus to Console	Ctrl+2	Ctrl+2
Move focus to Help	Ctrl+3	Ctrl+3
Show History	Ctrl+4	Ctrl+4
Show Files	Ctrl+5	Ctrl+5
Show Plots	Ctrl+6	Ctrl+6
Show Packages	Ctrl+7	Ctrl+7
Show Environment	Ctrl+8	Ctrl+8
Show Git/SVN	Ctrl+9	Ctrl+9
Show Build	Ctrl+0	Ctrl+0

2 RUN CODE	Windows/Linux	Mac
Search command history	**Ctrl+↑**	**Cmd+↑**
Navigate command history	↑/↓	↑/↓
Move cursor to start of line	Home	Cmd+←
Move cursor to end of line	End	Cmd+→
Change working directory	Ctrl+Shift+H	Ctrl+Shift+H
Interrupt current command	**Esc**	**Esc**
Clear console	**Ctrl+L**	**Ctrl+L**
Quit Session (desktop only)	Ctrl+Q	Cmd+Q
Restart R Session	**Ctrl+Shift+F10**	**Cmd+Shift+F10**
Run current line/selection	**Ctrl+Enter**	**Cmd+Enter**
Run current (retain cursor)	Alt+Enter	Option+Enter
Run from current to end	Ctrl+Alt+E	Cmd+Option+E
Run the current function	Ctrl+Alt+F	Cmd+Option+F
Source a file	Ctrl+Alt+G	Cmd+Option+G
Source the current file	**Ctrl+Shift+S**	**Cmd+Shift+S**
Source with echo	Ctrl+Shift+Enter	Cmd+Shift+Enter

3 NAVIGATE CODE	Windows /Linux	Mac
Goto File/Function	**Ctrl+.**	**Ctrl+.**
Fold Selected	Alt+L	Cmd+Option+L
Unfold Selected	Shift+Alt+L	Cmd+Shift+Option+L
Fold All	Alt+O	Cmd+Option+O
Unfold All	Shift+Alt+O	Cmd+Shift+Option+O
Go to line	Shift+Alt+G	Cmd+Shift+Option+G
Jump to	Shift+Alt+J	Cmd+Shift+Option+J
Switch to tab	Ctrl+Shift+.	Ctrl+Shift+.
Previous tab	Ctrl+F11	Ctrl+F11
Next tab	Ctrl+F12	Ctrl+F12
First tab	Ctrl+Shift+F11	Ctrl+Shift+F11
Last tab	Ctrl+Shift+F12	Ctrl+Shift+F12
Navigate back	Ctrl+F9	Cmd+F9
Navigate forward	Ctrl+F10	Cmd+F10
Jump to Brace	Ctrl+P	Ctrl+P
Select within Braces	Ctrl+Shift+Alt+E	Ctrl+Shift+Option+E
Use Selection for Find	Ctrl+F3	Cmd+E
Find in Files	Ctrl+Shift+F	Cmd+Shift+F
Find Next	Win: F3, Linux: Ctrl+G	Cmd+G
Find Previous	W: Shift+F3, L:	Cmd+Shift+G
Jump to Word	Ctrl+ ←/→	Option+ ←/→
Jump to Start/End	Ctrl+↑/↓	Cmd+↑/↓
Toggle Outline	Ctrl+Shift+O	Cmd+Shift+O

4 WRITE CODE	Windows /Linux	Mac
Attempt completion	**Tab or Ctrl+Space**	**Tab or Cmd+Space**
Navigate candidates	↑/↓	↑/↓
Accept candidate	Enter, Tab, or →	Enter, Tab, or →
Dismiss candidates	Esc	Esc
Undo	Ctrl+Z	Cmd+Z
Redo	Ctrl+Shift+Z	Cmd+Shift+Z
Cut	Ctrl+X	Cmd+X
Copy	Ctrl+C	Cmd+C
Paste	Ctrl+V	Cmd+V
Select All	Ctrl+A	Cmd+A
Delete Line	Ctrl+D	Cmd+D
Select	Shift+[Arrow]	Shift+[Arrow]
Select Word	Ctrl+Shift+ ←/→	Option+Shift+ ←/→
Select to Line Start	Alt+Shift+←	Cmd+Shift+←
Select to Line End	Alt+Shift+→	Cmd+Shift+→
Select Page Up/Down	Shift+PageUp/Down	Shift+PageUp/Down
Select to Start/End	Shift+Alt+↑/↓	Cmd+Shift+↑/↓
Delete Word Left	Ctrl+Backspace	Ctrl+Opt+Backspace
Delete Word Right		Option+Delete
Delete to Line End		Ctrl+K
Delete to Line Start		Option+Backspace
Indent	Tab (at start of line)	Tab (at start of line)
Outdent	Shift+Tab	Shift+Tab
Yank line up to cursor	Ctrl+U	Ctrl+U
Yank line after cursor	Ctrl+K	Ctrl+K
Insert yanked text	Ctrl+Y	Ctrl+Y
Insert <-	**Alt+-**	**Option+-**
Insert %>%	**Ctrl+Shift+M**	**Cmd+Shift+M**
Show help for function	F1	F1
Show source code	F2	F2
New document	Ctrl+Shift+N	Cmd+Shift+N
New document (Chrome)	Ctrl+Alt+Shift+N	Cmd+Shift+Opt+N
Open document	Ctrl+O	Cmd+O
Save document	Ctrl+S	Cmd+S
Close document	Ctrl+W	Cmd+W
Close document (Chrome)	Ctrl+Alt+W	Cmd+Option+W
Close all documents	Ctrl+Shift+W	Cmd+Shift+W
Extract function	Ctrl+Alt+X	Cmd+Option+X
Extract variable	Ctrl+Alt+V	Cmd+Option+V
Reindent lines	Ctrl+I	Cmd+I
(Un)Comment lines	**Ctrl+Shift+C**	**Cmd+Shift+C**
Reflow Comment	Ctrl+Shift+/	Cmd+Shift+/
Reformat Selection	Ctrl+Shift+A	Cmd+Shift+A
Select within braces	Ctrl+Shift+E	Ctrl+Shift+E
Show Diagnostics	Ctrl+Shift+Alt+P	Cmd+Shift+Opt+P
Transpose Letters		Ctrl+T
Move Lines Up/Down	Alt+↑/↓	Option+↑/↓
Copy Lines Up/Down	Shift+Alt+↑/↓	Cmd+Option+↑/↓
Add New Cursor Above	Ctrl+Alt+Up	Ctrl+Option+Up
Add New Cursor Below	Ctrl+Alt+Down	Ctrl+Option+Down
Move Active Cursor Up	Ctrl+Alt+Shift+Up	Ctrl+Option+Shift+Up
Move Active Cursor Down	Ctrl+Alt+Shift+Down	Ctrl+Opt+Shift+Down
Find and Replace	Ctrl+F	Cmd+F
Use Selection for Find	Ctrl+F3	Cmd+E
Replace and Find	Ctrl+Shift+J	Cmd+Shift+J

WHY RSTUDIO SERVER PRO?

RSP extends the the open source server with a commercial license, support, and more:

- open and run multiple R sessions at once
- tune your resources to improve performance
- edit the same project at the same time as others
- see what you and others are doing on your server
- switch easily from one version of R to a different version
- integrate with your authentication, authorization, and audit practices

Download a free 45 day evaluation at
www.rstudio.com/products/rstudio-server-pro/

5 DEBUG CODE	Windows/Linux	Mac
Toggle Breakpoint	Shift+F9	Shift+F9
Execute Next Line	F10	F10
Step Into Function	Shift+F4	Shift+F4
Finish Function/Loop	Shift+F6	Shift+F6
Continue	Shift+F5	Shift+F5
Stop Debugging	Shift+F8	Shift+F8

6 VERSION CONTROL	Windows/Linux	Mac
Show diff	Ctrl+Alt+D	Ctrl+Option+D
Commit changes	Ctrl+Alt+M	Ctrl+Option+M
Scroll diff view	Ctrl+↑/↓	Ctrl+↑/↓
Stage/Unstage (Git)	Spacebar	Spacebar
Stage/Unstage and move to next	Enter	Enter

7 MAKE PACKAGES	Windows/Linux	Mac
Build and Reload	Ctrl+Shift+B	Cmd+Shift+B
Load All (devtools)	**Ctrl+Shift+L**	**Cmd+Shift+L**
Test Package (Desktop)	**Ctrl+Shift+T**	**Cmd+Shift+T**
Test Package (Web)	Ctrl+Alt+F7	Cmd+Opt+F7
Check Package	Ctrl+Shift+E	Cmd+Shift+E
Document Package	**Ctrl+Shift+D**	**Cmd+Shift+D**

8 DOCUMENTS AND APPS	Windows/Linux	Mac
Preview HTML (Markdown, etc.)	Ctrl+Shift+K	Cmd+Shift+K
Knit Document (knitr)	**Ctrl+Shift+K**	**Cmd+Shift+K**
Compile Notebook	Ctrl+Shift+K	Cmd+Shift+K
Compile PDF (TeX and Sweave)	Ctrl+Shift+K	Cmd+Shift+K
Insert chunk (Sweave and Knitr)	Ctrl+Alt+I	Cmd+Option+I
Insert code section	Ctrl+Shift+R	Cmd+Shift+R
Re-run previous region	Ctrl+Shift+P	Cmd+Shift+P
Run current document	Ctrl+Alt+R	Cmd+Option+R
Run from start to current line	**Ctrl+Alt+B**	**Cmd+Option+B**
Run the current code section	**Ctrl+Alt+T**	**Cmd+Option+T**
Run previous Sweave/Rmd code	Ctrl+Alt+P	Cmd+Option+P
Run the current chunk	Ctrl+Alt+C	Cmd+Option+C
Run the next chunk	Ctrl+Alt+N	Cmd+Option+N
Sync Editor & PDF Preview	Ctrl+F8	Cmd+F8
Previous plot	Ctrl+Alt+F11	Cmd+Option+F11
Next plot	Ctrl+Alt+F12	Cmd+Option+F12
Show Keyboard Shortcuts	**Alt+Shift+K**	**Option+Shift+K**

RStudio

R Markdown : : **CHEAT SHEET**

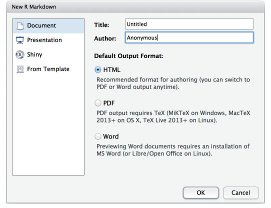
What is R Markdown?

.Rmd files • An R Markdown (.Rmd) file is a record of your research. It contains the code that a scientist needs to reproduce your work along with the narration that a reader needs to understand your work.

Reproducible Research • At the click of a button, or the type of a command, you can rerun the code in an R Markdown file to reproduce your work and export the results as a finished report.

Dynamic Documents • You can choose to export the finished report in a variety of formats, including html, pdf, MS Word, or RTF documents; html or pdf based slides, Notebooks, and more.

Workflow


New R Markdown

Document
Presentation
Shiny
From Template

Title: Untitled
Author: Anonymous

Default Output Format:

● HTML
Recommended format for authoring (you can switch to PDF or Word output anytime).

○ PDF
PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

○ Word
Previewing Word documents requires an installation of MS Word (or Libre/Open Office on Linux).

1 **Open a new .Rmd file** at File ▶ New File ▶ R Markdown. Use the wizard that opens to pre-populate the file with a template

2 **Write document** by editing template

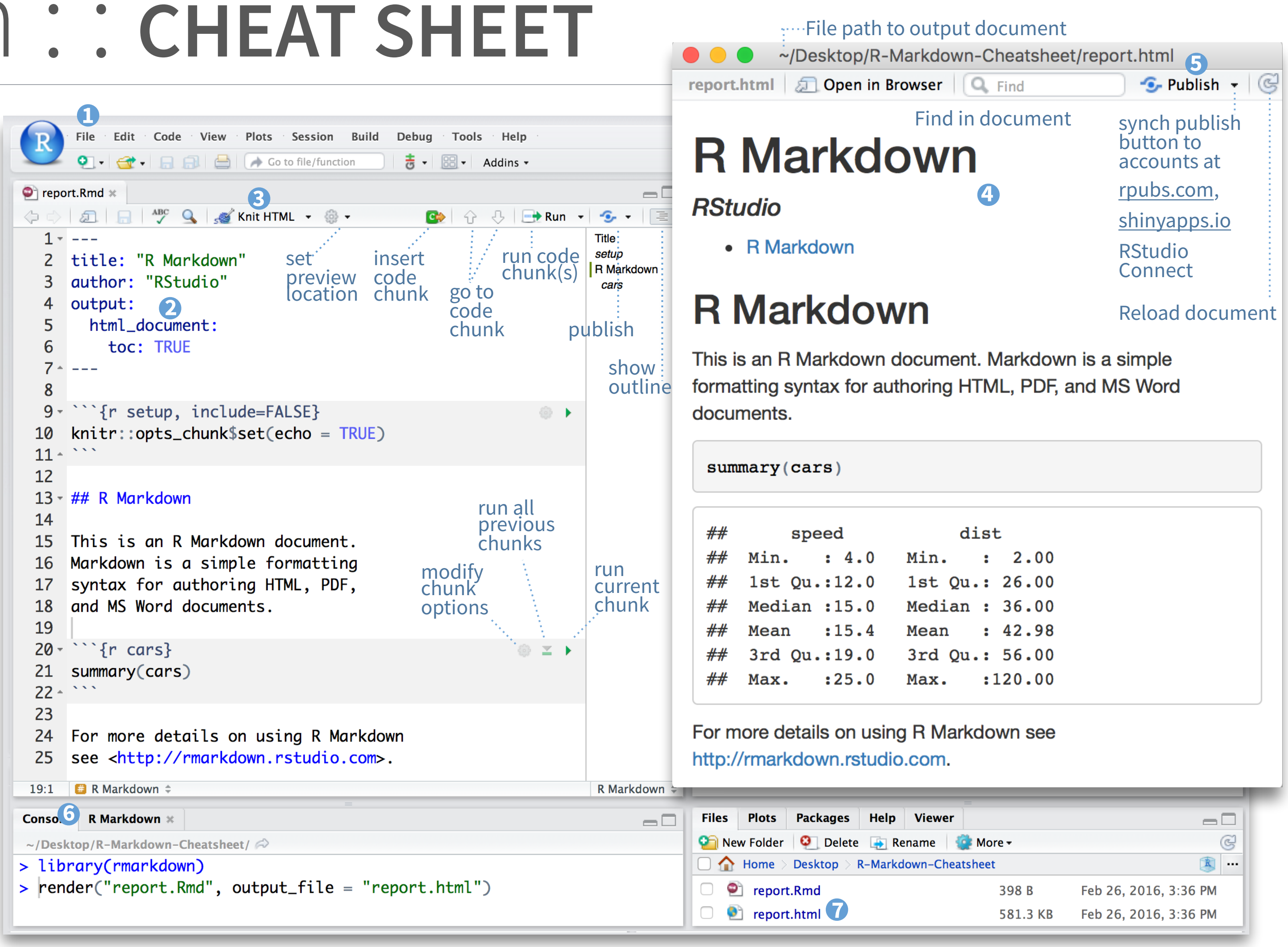
3 **Knit document to create report**; use knit button or **render()** to knit

4 **Preview Output** in IDE window

5 **Publish** (optional) to web server

6 **Examine build log** in R Markdown console

7 **Use output file** that is saved along side .Rmd



~~~
---
title: "R Markdown"
author: "RStudio"
output:
  html_document:
    toc: TRUE
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
~~~

R Markdown

This is an R Markdown document.
Markdown is a simple formatting
syntax for authoring HTML, PDF,
and MS Word documents.

```{r cars}
summary(cars)
```

For more details on using R Markdown
see <http://rmarkdown.rstudio.com>.
```

```
~/Desktop/R-Markdown-Cheatsheet/
> library(rmarkdown)
> render("report.Rmd", output_file = "report.html")
```

~/Desktop/R-Markdown-Cheatsheet/report.html

R Markdown

RStudio

- R Markdown

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents.

```
summary(cars)
```

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

For more details on using R Markdown see http://rmarkdown.rstudio.com.

| | | | |
|---|---|---|---|
| ☐ | report.Rmd | 398 B | Feb 26, 2016, 3:36 PM |
| ☐ | report.html | 581.3 KB | Feb 26, 2016, 3:36 PM |

## render

Use rmarkdown::**render()** to render/knit at cmd line. Important args:

**input** - file to render
**output_format**

**output_options** - List of render options (as in YAML)

**output_file**
**output_dir**

**params** - list of params to use

**envir** - environment to evaluate code chunks in

**encoding** - of input file

## Embed code with knitr syntax

### INLINE CODE

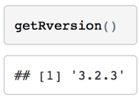
Insert with **`r <code>`**. Results appear as text without code.

Built with `r getRversion()` → Built with 3.2.3

### CODE CHUNKS

One or more lines surrounded with **```{r}** and **```**. Place chunk options within curly braces, after **r**. Insert with

```{r echo=TRUE}
getRversion()
```



```
getRversion()
```

```
## [1] '3.2.3'
```

GLOBAL OPTIONS

Set with knitr::**opts_chunk$set()**, e.g.

```{r include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```

IMPORTANT CHUNK OPTIONS

cache - cache results for future knits (default = FALSE)

cache.path - directory to save cached results in (default = "cache/")

child - file(s) to knit and then include (default = NULL)

collapse - collapse all output into single block (default = FALSE)

comment - prefix for each line of results (default = '##')

dependson - chunk dependencies for caching (default = NULL)

echo - Display code in output document (default = TRUE)

engine - code language used in chunk (default = 'R')

error - Display error messages in doc (TRUE) or stop render when errors occur (FALSE) (default = FALSE)

eval - Run code in chunk (default = TRUE)

fig.align - 'left', 'right', or 'center' (default = 'default')

fig.cap - figure caption as character string (default = NULL)

fig.height, fig.width - Dimensions of plots in inches

highlight - highlight source code (default = TRUE)

include - Include chunk in doc after running (default = TRUE)

message - display code messages in document (default = TRUE)

results (default = 'markup')
'asis' - passthrough results
'hide' - do not display results
'hold' - put all results below all code

tidy - tidy code for display (default = FALSE)

warning - display code warnings in document (default = TRUE)

Options not listed above: R.options, aniopts, autodep, background, cache.comments, cache.lazy, cache.rebuild, cache.vars, dev, dev.args, dpi, engine.opts, engine.path, fig.asp, fig.env, fig.ext, fig.keep, fig.lp, fig.path, fig.pos, fig.process, fig.retina, fig.scap, fig.show, fig.showtext, fig.subcap, interval, out.extra, out.height, out.width, prompt, purl, ref.label, render, size, split, tidy.opts

.rmd Structure

YAML Header
Optional section of render (e.g. pandoc) options written as key:value pairs (YAML).

At start of file

Between lines of - - -

Text
Narration formatted with markdown, mixed with:

Code Chunks
Chunks of embedded code. Each chunk:

Begins with ```**{r}**

ends with ```

R Markdown will run the code and append the results to the doc.

It will use the location of the .Rmd file as the **working directory**

Parameters

Parameterize your documents to reuse with different inputs (e.g., data, values, etc.)

1. **Add parameters** • Create and set parameters in the header as sub-values of params

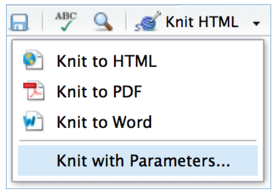
```
---
params:
  n: 100
  d: !r Sys.Date()
---
```

2. **Call parameters** • Call parameter values in code as params$<name>

```
Today's date
is `r params$d`
```

3. **Set parameters** • Set values wth Knit with parameters or the params argument of render():

render("doc.Rmd", params = list(n = 1, d = as.Date("2015-01-01"))

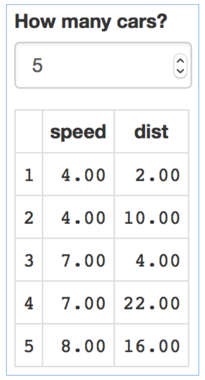


Interactive Documents

Turn your report into an interactive Shiny document in 4 steps

1. Add runtime: shiny to the YAML header.
2. Call Shiny input functions to embed input objects.
3. Call Shiny render functions to embed reactive output.
4. Render with rmarkdown::run or click Run Document in RStudio IDE

~~~
---
output: html_document
runtime: shiny
---

```{r, echo = FALSE}
numericInput("n",
  "How many cars?", 5)

renderTable({
  head(cars, input$n)
})
```
~~~



How many cars?

5

	speed	dist
1	4.00	2.00
2	4.00	10.00
3	7.00	4.00
4	7.00	22.00
5	8.00	16.00

Embed a complete app into your document with shiny::**shinyAppDir()**

NOTE: *Your report will rendered as a Shiny app, which means you must choose an html output format, like **html_document**, and serve it with an active R Session.*

RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **rmarkdown.rstudio.com** • rmarkdown 1.6 • Updated: 2016-02

Pandoc's Markdown

Write with syntax on the left to create effect on right (after render)

```
Plain text
End a line with two spaces
to start a new paragraph.
*italics* and **bold**
`verbatim code`
sub/superscript^2^~2~
~~strikethrough~~
escaped: \* \_ \\
endash: --, emdash: ---
equation: $A = \pi*r^{2}$
equation block:

$$E = mc^{2}$$

> block quote

# Header1 {#anchor}

## Header 2 {#css_id}

### Header 3 {.css_class}

#### Header 4

##### Header 5

###### Header 6

<!--Text comment-->

\textbf{Tex ignored in HTML}
<em>HTML ignored in pdfs</em>

<http://www.rstudio.com>
[link](www.rstudio.com)
Jump to [Header 1](#anchor)
image:

![Caption](smallorb.png)

* unordered list
  + sub-item 1
  + sub-item 2
    - sub-sub-item 1

* item 2

  Continued (indent 4 spaces)

1. ordered list
2. item 2
  i) sub-item 1
     A.  sub-sub-item 1

(@)  A list whose numbering

continues after

(@)  an interruption

Term 1

:   Definition 1

| Right | Left | Default | Center |
|------:|:-----|---------|:------:|
|   12  |  12  |    12   |    12  |
|  123  |  123 |   123   |   123  |
|    1  |    1 |     1   |     1  |

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

***

A footnote [^1]

[^1]: Here is the footnote.
```

Plain text
End a line with two spaces
to start a new paragraph.
italics and **bold**
`verbatim code`
sub/superscript$^2{}_2$
~~strikethrough~~
escaped: * _ \
endash: –, emdash: —
equation: $A = \pi * r^2$
equation block:

$$E = mc^2$$

> block quote

Header1

Header 2

Header 3

Header 4

Header 5

Header 6

HTML ignored in pdfs

http://www.rstudio.com
link
Jump to Header 1
image:

Caption

- unordered list
  - sub-item 1
  - sub-item 2
    - sub-sub-item 1
- item 2

  Continued (indent 4 spaces)

1. ordered list
2. item 2
   i. sub-item 1
      A. sub-sub-item 1

1. A list whose numbering

continues after

2. an interruption

Term 1

Definition 1

Right	Left	Default	Center
12	12	12	12
123	123	123	123
1	1	1	1

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

A footnote [1]

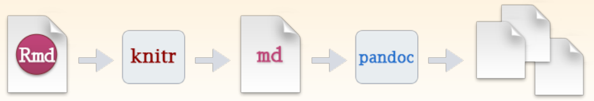
---

1. Here is the footnote.↩

Set render options with YAML

When you render, R Markdown

1. runs the R code, embeds results and text into .md file with knitr
2. then converts the .md file into the finished format with pandoc



Set a document's default output format in the YAML header:

```
---
output: html_document
---
# Body
```

output value	creates
html_document	html
pdf_document	pdf (requires Tex)
word_document	Microsoft Word (.docx)
odt_document	OpenDocument Text
rtf_document	Rich Text Format
md_document	Markdown
github_document	Github compatible markdown
ioslides_presentation	ioslides HTML slides
slidy_presentation	slidy HTML slides
beamer_presentation	Beamer pdf slides (requires Tex)

Customize output with sub-options (listed to the right):

Indent 2 spaces

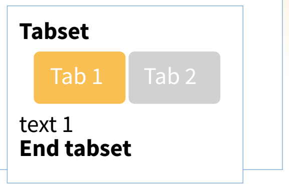
Indent 4 spaces

```
---
output: html_document:
  code_folding: hide
  toc_float: TRUE
---
# Body
```

html tabsets

Use tablet css class to place sub-headers into tabs

```
# Tabset {.tabset .tabset-fade .tabset-pills}
## Tab 1
text 1
## Tab 2
text 2
### End tabset
```



Tabset

text 1

End tabset

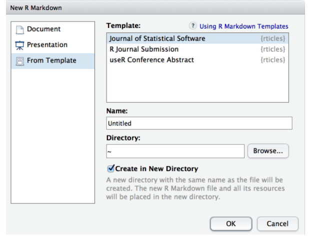
sub-option	description	html	pdf	word	odt	rtf	md	gituhb	ioslides	slidy	beamer
citation_package	The LaTeX package to process citations, natbib, biblatex or none		X				X				X
code_folding	Let readers to toggle the display of R code, "none", "hide", or "show"	X									
colortheme	Beamer color theme to use										X
css	CSS file to use to style document	X							X	X	
dev	Graphics device to use for figure output (e.g. "png")	X	X				X	X	X	X	X
duration	Add a countdown timer (in minutes) to footer of slides									X	
fig_caption	Should figures be rendered with captions?	X	X	X	X				X	X	X
fig_height, fig_width	Default figure height and width (in inches) for document	X	X	X	X	X	X	X	X	X	X
highlight	Syntax highlighting: "tango", "pygments", "kate","zenburn", "textmate"	X	X	X						X	X
includes	File of content to place in document (in_header, before_body, after_body)	X	X		X		X	X	X	X	X
incremental	Should bullets appear one at a time (on presenter mouse clicks)?								X	X	X
keep_md	Save a copy of .md file that contains knitr output	X		X	X	X			X	X	
keep_tex	Save a copy of .tex file that contains knitr output		X								X
latex_engine	Engine to render latex, "pdflatex", "xelatex", or "lualatex"		X								X
lib_dir	Directory of dependency files to use (Bootstrap, MathJax, etc.)	X							X	X	
mathjax	Set to local or a URL to use a local/URL version of MathJax to render equations	X							X	X	
md_extensions	Markdown extensions to add to default definition or R Markdown	X	X	X	X	X	X	X	X	X	X
number_sections	Add section numbering to headers	X	X								
pandoc_args	Additional arguments to pass to Pandoc	X	X	X	X	X	X	X	X	X	X
preserve_yaml	Preserve YAML front matter in final document?						X				
reference_docx	docx file whose styles should be copied when producing docx output			X							
self_contained	Embed dependencies into the doc	X							X	X	
slide_level	The lowest heading level that defines individual slides										X
smaller	Use the smaller font size in the presentation?								X		
smart	Convert straight quotes to curly, dashes to em-dashes, … to ellipses, etc.	X							X	X	
template	Pandoc template to use when rendering file quarterly_report.html).	X	X		X					X	X
theme	Bootswatch or Beamer theme to use for page	X									X
toc	Add a table of contents at start of document	X	X	X		X	X	X			X
toc_depth	The lowest level of headings to add to table of contents	X	X	X		X	X	X			
toc_float	Float the table of contents to the left of the main content	X									

Create a Reusable Template

1. **Create a new package** with a inst/rmarkdown/templates directory
2. In the directory, **Place a folder** that contains:
   template.yaml (see below)
   skeleton.Rmd (contents of the template)
   any supporting files
3. **Install the package**
4. **Access template** in wizard at File ▶ New File ▶ R Markdown

template.yaml

```
---
name: My Template
—
```



Journal of Statistical Software {rticles}
R Journal Submission {rticles}
useR Conference Abstract {rticles}

Name: Untitled

Directory: ~

☑ Create in New Directory

A new directory with the same name as the file will be created. The new R Markdown file and all its resources will be placed in the new directory.

Table Suggestions

Several functions format R data into tables

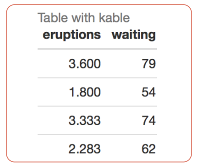
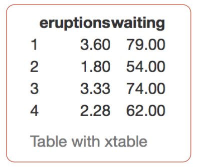


Table with kable

eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62



	eruptions	waiting
1	3.60	79.00
2	1.80	54.00
3	3.33	74.00
4	2.28	62.00

Table with xtable

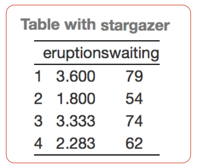


Table with stargazer

	eruptions	waiting
1	3.600	79
2	1.800	54
3	3.333	74
4	2.283	62

~~~
data <- faithful[1:4, ]

```{r results = 'asis'}
knitr::kable(data, caption = "Table with kable”)
~~~

```{r results = "asis"}
print(xtable::xtable(data, caption = "Table with xtable”),
      type = "html", html.table.attributes = "border=0"))
```

```{r results = "asis"}
stargazer::stargazer(data, type = "html", title = "Table
                    with stargazer")
```
```

Learn more in the **stargazer**, **xtable**, and **knitr** packages.

# Citations and Bibliographies

Create citations with .bib, .bibtex, .copac, .enl, .json, .medline, .mods, .ris, .wos, and .xml files

1. **Set bibliography file** and CSL 1.0 Style file (optional) in the YAML header
2. **Use citation keys in text**

```
---
bibliography: refs.bib
csl: style.csl
---
```

```
Smith cited [@smith04].
Smith cited without author [-@smith04].
@smith04 cited in line.
```

3. **Render.** Bibliography will be added to end of document

Smith cited (Joe Smith 2004).
Smith cited without author (2004).
Joe Smith (2004) cited in line.
```

Base R
Cheat Sheet

Getting Help

Accessing the help files

?mean

Get help of a particular function.

help.search(‘weighted mean’)

Search the help files for a word or phrase.

help(package = ‘dplyr’)

Find help for a package.

More about an object

str(iris)

Get a summary of an object’s structure.

class(iris)

Find the class an object belongs to.

Using Packages

install.packages(‘dplyr’)

Download and install a package from CRAN.

library(dplyr)

Load the package into the session, making all its functions available to use.

dplyr::select

Use a particular function from a package.

data(iris)

Load a built-in dataset into the environment.

Working Directory

getwd()

Find the current working directory (where inputs are found and outputs are sent).

setwd(‘C://file/path’)

Change the current working directory.

Use projects in RStudio to set the working directory to the folder you are working in.

Vectors

Creating Vectors

`c(2, 4, 6)`	`2 4 6`	Join elements into a vector
`2:6`	`2 3 4 5 6`	An integer sequence
`seq(2, 3, by=0.5)`	`2.0 2.5 3.0`	A complex sequence
`rep(1:2, times=3)`	`1 2 1 2 1 2`	Repeat a vector
`rep(1:2, each=3)`	`1 1 1 2 2 2`	Repeat elements of a vector

Vector Functions

sort(x)

Return x sorted.

table(x)

See counts of values.

rev(x)

Return x reversed.

unique(x)

See unique values.

Selecting Vector Elements

By Position

`x[4]`	The fourth element.
`x[-4]`	All but the fourth.
`x[2:4]`	Elements two to four.
`x[-(2:4)]`	All elements except two to four.
`x[c(1, 5)]`	Elements one and five.

By Value

`x[x == 10]`	Elements which are equal to 10.
`x[x < 0]`	All elements less than zero.
`x[x %in% c(1, 2, 5)]`	Elements in the set 1, 2, 5.

Named Vectors

`x[‘apple’]`	Element with name ‘apple’.

Programming

For Loop

```
for (variable in sequence){
   Do something
}
```

Example

```
for (i in 1:4){
   j <- i + 10
   print(j)
}
```

While Loop

```
while (condition){
   Do something
}
```

Example

```
while (i < 5){
   print(i)
   i <- i + 1
}
```

If Statements

```
if (condition){
   Do something
} else {
   Do something different
}
```

Example

```
if (i > 3){
   print(‘Yes’)
} else {
   print(‘No’)
}
```

Functions

```
function_name <- function(var){
   Do something
   return(new_variable)
}
```

Example

```
square <- function(x){
   squared <- x*x
   return(squared)
}
```

Reading and Writing Data

Also see the **readr** package.

Input	Ouput	Description
`df <- read.table(‘file.txt’)`	`write.table(df, ‘file.txt’)`	Read and write a delimited text file.
`df <- read.csv(‘file.csv’)`	`write.csv(df, ‘file.csv’)`	Read and write a comma separated value file. This is a special case of read.table/write.table.
`load(‘file.RData’)`	`save(df, file = ’file.Rdata’)`	Read and write an R data file, a file type special for R.

Conditions	`a == b`	Are equal	`a > b`	Greater than	`a >= b`	Greater than or equal to	`is.na(a)`	Is missing
	`a != b`	Not equal	`a < b`	Less than	`a <= b`	Less than or equal to	`is.null(a)`	Is null

RStudio® is a trademark of RStudio, Inc. • CC BY Mhairi McNeill • mhairihmcneill@gmail.com

Learn more at web page or vignette • package version • Updated: 3/15

Types

Converting between common data types in R. Can always go from a higher value in the table to a lower value.

`as.logical`	`TRUE, FALSE, TRUE`	Boolean values (TRUE or FALSE).
`as.numeric`	`1, 0, 1`	Integers or floating point numbers.
`as.character`	`'1', '0', '1'`	Character strings. Generally preferred to factors.

`as.factor`	`'1', '0', '1',`
	`levels: '1', '0'`
		Character strings with preset levels. Needed for some statistical models.

Maths Functions

`log(x)`	Natural log.	`sum(x)`	Sum.
`exp(x)`	Exponential.	`mean(x)`	Mean.
`max(x)`	Largest element.	`median(x)`	Median.
`min(x)`	Smallest element.	`quantile(x)`	Percentage quantiles.
`round(x, n)`	Round to n decimal places.	`rank(x)`	Rank of elements.
`signif(x, n)`	Round to n significant figures.	`var(x)`	The variance.
`cor(x, y)`	Correlation.	`sd(x)`	The standard deviation.

Variable Assignment

```
> a <- 'apple'
> a
[1] 'apple'
```

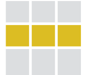
The Environment

`ls()`	List all variables in the environment.
`rm(x)`	Remove x from the environment.
`rm(list = ls())`	Remove all variables from the environment.

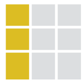
You can use the environment panel in RStudio to browse variables in your environment.

Matrices

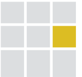
`m <- matrix(x, nrow = 3, ncol = 3)`
Create a matrix from x.



`m[2, ]` - Select a row



`m[ , 1]` - Select a column



`m[2, 3]` - Select an element

`t(m)`
Transpose

`m %*% n`
Matrix Multiplication

`solve(m, n)`
Find x in: m * x = n

Lists

`l <- list(x = 1:5, y = c('a', 'b'))`
A list is a collection of elements which can be of different types.

`l[[2]]`	`l[1]`	`l$x`	`l['y']`
Second element of l.	New list with only the first element.	Element named x.	New list with only element named y.

Also see the **dplyr** package.

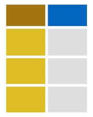
Data Frames

`df <- data.frame(x = 1:3, y = c('a', 'b', 'c'))`
A special case of a list where all elements are the same length.

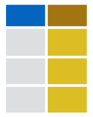
x	y
1	a
2	b
3	c

List subsetting

`df$x`



`df[[2]]`

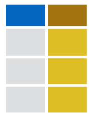


Understanding a data frame

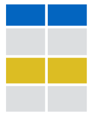
`View(df)`	See the full data frame.
`head(df)`	See the first 6 rows.

Matrix subsetting

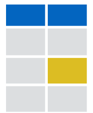
`df[ , 2]`



`df[2, ]`



`df[2, 2]`

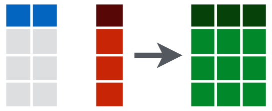


`nrow(df)`
Number of rows.

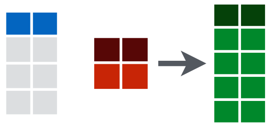
`ncol(df)`
Number of columns.

`dim(df)`
Number of columns and rows.

cbind - Bind columns.



rbind - Bind rows.



Strings

Also see the **stringr** package.

`paste(x, y, sep = ' ')`	Join multiple vectors together.
`paste(x, collapse = ' ')`	Join elements of a vector together.
`grep(pattern, x)`	Find regular expression matches in x.
`gsub(pattern, replace, x)`	Replace matches in x with a string.
`toupper(x)`	Convert to uppercase.
`tolower(x)`	Convert to lowercase.
`nchar(x)`	Number of characters in a string.

Factors

`factor(x)`
Turn a vector into a factor. Can set the levels of the factor and the order.

`cut(x, breaks = 4)`
Turn a numeric vector into a factor by 'cutting' into sections.

Statistics

`lm(y ~ x, data=df)`
Linear model.

`glm(y ~ x, data=df)`
Generalised linear model.

`summary`
Get more detailed information out a model.

`t.test(x, y)`
Perform a t-test for difference between means.

`pairwise.t.test`
Perform a t-test for paired data.

`prop.test`
Test for a difference between proportions.

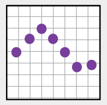
`aov`
Analysis of variance.

Distributions

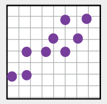
	Random Variates	Density Function	Cumulative Distribution	Quantile
Normal	`rnorm`	`dnorm`	`pnorm`	`qnorm`
Poisson	`rpois`	`dpois`	`ppois`	`qpois`
Binomial	`rbinom`	`dbinom`	`pbinom`	`qbinom`
Uniform	`runif`	`dunif`	`punif`	`qunif`

Plotting

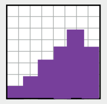
Also see the **ggplot2** package.



`plot(x)`
Values of x in order.



`plot(x, y)`
Values of x against y.



`hist(x)`
Histogram of x.

Dates

See the **lubridate** package.

RStudio® is a trademark of RStudio, Inc. • CC BY Mhairi McNeill • mhairihmcneill@gmail.com • 844-448-1212 • rstudio.com

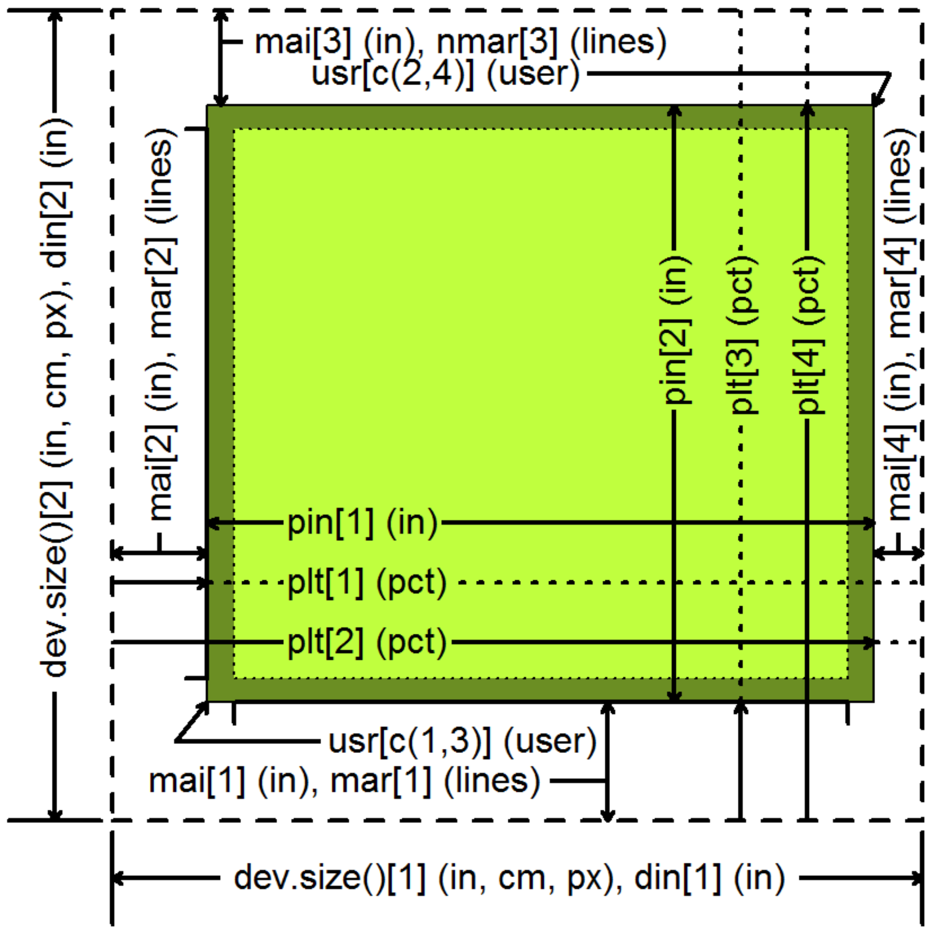
Learn more at web page or vignette • package version • Updated: 3/15

How Big is Your Graph?

An R Cheat Sheet

Introduction

All functions that open a device for graphics will have **height** and **width** arguments to control the size of the graph and a **pointsize** argument to control the relative font size. In **knitr**, you control the size of the graph with the chunk options, **fig.width** and **fig.height**. This sheet will help you with calculating the size of the graph and various parts of the graph within R.


mai[3] (in), nmar[3] (lines)
usr[c(2,4)] (user)
dev.size()[2] (in, cm, px), din[2] (in)
mai[2] (in), mar[2] (lines)
pin[2] (in)
plt[3] (pct)
plt[4] (pct)
mai[4] (in), mar[4] (lines)
pin[1] (in)
plt[1] (pct)
plt[2] (pct)
usr[c(1,3)] (user)
mai[1] (in), mar[1] (lines)
dev.size()[1] (in, cm, px), din[1] (in)

Your graphics device

dev.size() (width, height)
par("din") *(r.o.)* (width, height) in inches

Both the **dev.size** function and the **din** argument of **par** will tell you the size of the graphics device. The **dev.size** function will report the size in

1. inches (**units="in"**), the default
2. centimeters (**units="cm"**)
3. pixels (**units="px"**)

Like several other **par** arguments, **din** is read only *(r.o.)* meaning that you can ask its current value (**par("din")**) but you cannot change it (**par(din=c(5,7))** will fail).

Your plot margins

par("mai") (bottom, left, top, right) in inches
par("mar") (bottom, left, top, right) in lines

Margins provide you space for your axes, axis, labels, and titles.

A "line" is the amount of vertical space needed for a line of text.

If your graph has no axes or titles, you can remove the margins (and maximize the plotting region) with

```
par(mar=rep(0,4))
```

Your plotting region

par("pin") (width, height) in inches
par("plt") (left, right, bottom, top) in pct

The **pin** argument **par** gives you the size of the plotting region (the size of the device minus the size of the margins) in inches.

The **plt** argument gives you the percentage of the device from the left/bottom edge up to the left edge of the plotting region, the right edge, the bottom edge, and the top edge. The first and third values are equivalent to the percentage of space devoted to the left and bottom margins. Subtract the second and fourth values from 1 to get the percentage of space devoted to the right and top margins.

Your x-y coordinates

par("usr") (xmin, ymin, xmax, ymax)

Your x-y coordinates are the values you use when plotting your data. This normally is not the same as the values you specified with the xlim and ylim arguments in plot. By default, R adds an extra 4% to the plotting range (see the dark green region on the figure) so that points right up on the edges of your plot do not get partially clipped. You can override this by setting xaxs="i" and/or the yaxs="i" in par.

Run par("usr") to find the minimum X value, the maximum X value, the minimum Y value, and the maximum Y value. If you assign new values to usr, you will update the x-y coordinates to the new values.

Getting a square graph

par("pty")

You can produce a square graph manually by setting the width and height to the same value and setting the margins so that the sum of the top and bottom margins equal the sum of the left and right margins. But a much easier way is to specify **pty="s"**, which adjusts the margins so that the size of the plotting region is always square, even if you resize the graphics window.

Converting units

For many applications, you need to be able to translate user coordinates to pixels or inches. There are some cryptic shortcuts, but the simplest way is to get the range in user coordinates and measure the proportion of the graphics device devoted to the plotting region.

```
user.range <- par("usr")[c(2,4)] -
  par("usr")[c(1,3)]

region.pct <- par("plt")[c(2,4)] -
  par("plt")[c(1,3)]

region.px <-
  dev.size(units="px") * region.pct

px.per.xy <- region.px / user.range
```

To convert a horizontal or distance from the x-coordinate value to pixels, multiply by **px.per.xy[1]**. To convert a vertical distance, multiply by **region.px.per.xy[2]**. To convert a diagonal distance, you need to invoke Pyhthagoras.

```
a.px <- x.dist*px.per.xy[1]
b.px <- y.dist*px.per.xy[2]
c.px <- sqrt(a.px^2+b.px^2)
```

To rotate a string to match the slope of a line segment, you need to convert the distances to pixels, calculate the arctangent, and convert from radians to degrees.

```
segments(x0, y0, x1, y1)
delta.x <- (x1 – x0) * px.per.xy[1]
delta.y <- (y1 – y0) * px.per.xy[y]
angle.radians <- atan2(delta.y, delta.x)
angle.degrees <- angle.radians * 180 / pi
text(x1, y1, "TEXT", srt=angle.degrees)
```

CC BY Steve Simon, P.Mean Consulting • mail@pmean.com • https://www.rstudio.com/resources/cheatsheets/

Learn more at blog.pmean.com/cheatsheets • Updated: August 2017

Panels

par("fig") (width, height) in pct
par("fin") (width, height) in inches

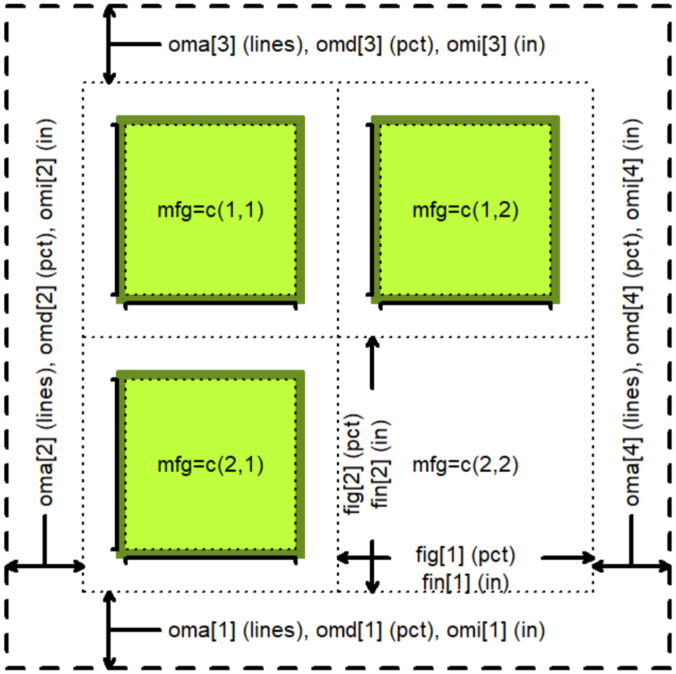
If you display multiple plots within a single graphics window (e.g., with the **mfrow** or **mfcol** arguments of **par** or with the **layout** function), then the **fig** and **fin** arguments will tell you the size of the current subplot window in percent or inches, respectively.

par("oma") (bottom, left, top, right) in lines
par("omd") (bottom, left, top, right) in pct
par("omi") (bottom, left, top, right) in inches

Each subplot will have margins specified by **mai** or **mar**, but no outer margin around the entire set of plots, unless you specify them using **oma**, **omd**, or **omi**. You can place text in the outer margins using the **mtext** function with the argument **outer=TRUE**.

par("mfg") (r, c) or (r, c, maxr, maxc)

The **mfg** argument of **par** will allow you to jump to a subplot in a particular row and column. If you query with **par("mfg")**, you will get the current row and column followed by the maximum row and column.



oma[3] (lines), omd[3] (pct), omi[3] (in)
mfg=c(1,1)
mfg=c(1,2)
mfg=c(2,1)
mfg=c(2,2)
oma[2] (lines), omd[2] (pct), omi[2] (in)
oma[4] (lines), omd[4] (pct), omi[4] (in)
fig[2] (pct)
fin[2] (in)
fig[1] (pct)
fin[1] (in)
oma[1] (lines), omd[1] (pct), omi[1] (in)

Character and string sizes

strheight()

The **strheight** functions will tell you the height of a specified string in inches (**units="inches"**), x-y user coordinates (**units="user"**) or as a percentage of the graphics device (**units="figure"**).

For a single line of text, **strheight** will give you the height of the letter "M". If you have a string with one of more linebreaks ("\n"), the **strheight** function will measure the height of the letter "M" plus the height of one or more additional lines. The height of a line is dependent on the line spacing, set by the **lheight** argument of **par**. The default line height (**lheight=1**), corresponding to single spaced lines, produces a line height roughly 1.5 times the height of "M".

strwidth()

The **strwidth** function will produce different widths to individual characters, representing the proportional spacing used by most fonts (a "W" using much more space than an "i"). For the width of a string, the **strwidth** function will sum up the lengths of the individual characters in the string.

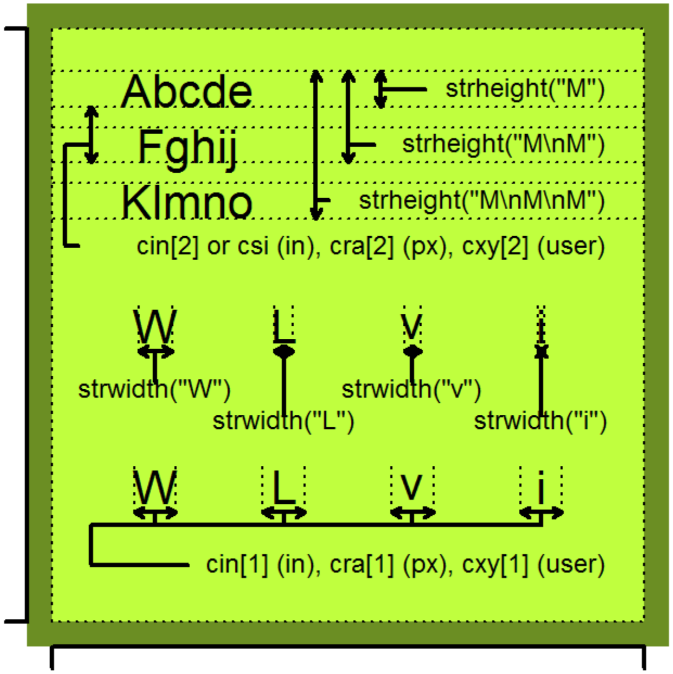
par("cin") *(r.o.)* (width, height) in inches
par("csi") *(r.o.)* height in inches
par("cra") *(r.o.)* (width, height) in pixels
par("cxy") *(r.o.)* (width, height) in xy coordinates

The single value returned by the **csi** argument of **par** gives you the height of a line of text in inches. The second of the two values returned by **cin**, **cra**, and **cxy** gives you the height of a line, in inches, pixels, or xy (user) coordinates.

The first of the two values returned by the **cin**, **cra**, and **cxy** arguments to **par** gives you the approximate width of a single character, in inches, pixels, or xy (user) coordinates. The width, very slightly smaller than the actual width of the letter "W", is a rough estimate at best and ignores the variable with of individual letters.

These values are useful, however, in providing fast ratios of the relative sizes of the differing units of measure

px.per.in <- par("cra") / par("cin")
px.per.xy <- par("cra") / par("cxy")
xy.per.in <- par("cxy") / par("cin")



If your fonts are too big or too small

Fixing this takes a bit of trial and error.

1. Specify a larger/smaller value for the **pointsize** argument when you open your graphics device.

2. Trying opening your graphics device with different values for **height** and **width**. Fonts that look too big might be better proportioned in a larger graphics window.

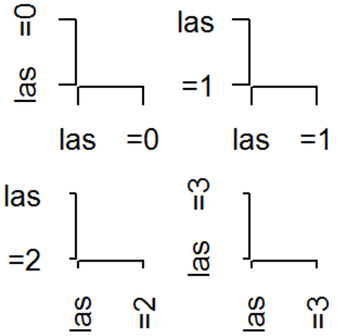
3. Use the **cex** argument to increase or decrease the relative size of your fonts.

If your axes don't fit

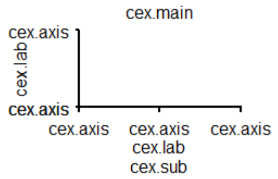
There are several possible solutions.

1. You can assign wider margins using the **mar** or **mai** argument in **par**.

2. You can change the orientation of the axis labels with **las**. Choose among
   a. **las=0** both axis labels parallel
   b. **las=1** both axis labels horizontal
   c. **las=2** both axis labels perpendicular
   d. **las=3** both axis labels vertical.



3. change the relative size of the font
   a. **cex.axis** for the tick mark labels.
   b. **cex.lab** for **xlab** and **ylab**.
   c. **cex.main** for the main title
   d. **cex.sub** for the subtitle.



Data Import : : CHEAT SHEET

R's **tidyverse** is built around **tidy data** stored in **tibbles**, which are enhanced data frames.

The front side of this sheet shows how to read text files into R with **readr**.

The reverse side shows how to create tibbles with **tibble** and to layout tidy data with **tidyr**.

OTHER TYPES OF DATA

Try one of the following packages to import other types of files

- **haven** - SPSS, Stata, and SAS files
- **readxl** - excel files (.xls and .xlsx)
- **DBI** - databases
- **jsonlite** - json
- **xml2** - XML
- **httr** - Web APIs
- **rvest** - HTML (Web Scraping)

Save Data

Save **x**, an R object, to **path**, a file path, as:

Comma delimited file
write_csv(x, path, na = "NA", append = FALSE, col_names = !append**)**

File with arbitrary delimiter
write_delim(x, path, delim = " ", na = "NA", append = FALSE, col_names = !append**)**

CSV for excel
write_excel_csv(x, path, na = "NA", append = FALSE, col_names = !append**)**

String to file
write_file(x, path, append = FALSE**)**

String vector to file, one element per line
write_lines(x,path, na = "NA", append = FALSE**)**

Object to RDS file
write_rds(x, path, compress = c("none", "gz", "bz2", "xz"), ...**)**

Tab delimited files
write_tsv(x, path, na = "NA", append = FALSE, col_names = !append**)**

Read Tabular Data - These functions share the common arguments:

read_*(file, col_names = TRUE, col_types = NULL, locale = default_locale(), na = c("", "NA"), quoted_na = TRUE, comment = "", trim_ws = TRUE, skip = 0, n_max = Inf, guess_max = min(1000, n_max), progress = interactive()**)**

```
a,b,c
1,2,3
4,5,NA
```

→

A	B	C
1	2	3
4	5	NA

Comma Delimited Files
read_csv("file.csv"**)**
To make file.csv run:
write_file(x = "a,b,c\n1,2,3\n4,5,NA", path = "file.csv")

```
a;b;c
1;2;3
4;5;NA
```

→

A	B	C
1	2	3
4	5	NA

Semi-colon Delimited Files
read_csv2("file2.csv"**)**
write_file(x = "a;b;c\n1;2;3\n4;5;NA", path = "file2.csv")

```
a|b|c
1|2|3
4|5|NA
```

→

A	B	C
1	2	3
4	5	NA

Files with Any Delimiter
read_delim("file.txt", delim = "|"**)**
write_file(x = "a|b|c\n1|2|3\n4|5|NA", path = "file.txt")

```
a b c
1 2 3
4 5 NA
```

→

A	B	C
1	2	3
4	5	NA

Fixed Width Files
read_fwf("file.fwf", col_positions = c(1, 3, 5)**)**
write_file(x = "a b c\n1 2 3\n4 5 NA", path = "file.fwf")

Tab Delimited Files
read_tsv("file.tsv"**)** Also **read_table().**
write_file(x = "a\tb\tc\n1\t2\t3\n4\t5\tNA", path = "file.tsv")

USEFUL ARGUMENTS

```
a,b,c
1,2,3
4,5,NA
```

Example file
write_file("a,b,c\n1,2,3\n4,5,NA","file.csv")
f <- "file.csv"

A	B	C
1	2	3
4	5	NA

No header
read_csv(f, **col_names = FALSE**)

x	y	z
A	B	C
1	2	3
4	5	NA

Provide header
read_csv(f, **col_names = c("x", "y", "z")**)

1	2	3
4	5	NA

Skip lines
read_csv(f, **skip = 1**)

A	B	C
1	2	3

Read in a subset
read_csv(f, **n_max = 1**)

A	B	C
NA	2	3
4	5	NA

Missing Values
read_csv(f, **na = c("1", ".")**)

Read Non-Tabular Data

Read a file into a single string
read_file(file, locale = default_locale()**)**

Read each line into its own string
read_lines(file, skip = 0, n_max = -1L, na = character(), locale = default_locale(), progress = interactive()**)**

Read Apache style log files
read_log(file, col_names = FALSE, col_types = NULL, skip = 0, n_max = -1, progress = interactive()**)**

Read a file into a raw vector
read_file_raw(file**)**

Read each line into a raw vector
read_lines_raw(file, skip = 0, n_max = -1L, progress = interactive()**)**

Data types

readr functions guess the types of each column and convert types when appropriate (but will NOT convert strings to factors automatically).

A message shows the type of each column in the result.

```
## Parsed with column specification:
## cols(
##   age = col_integer(),
##   sex = col_character(),
##   earn = col_double()
## )
```

age is an integer

sex is a character

earn is a double (numeric)

1. Use **problems()** to diagnose problems
x <- read_csv("file.csv"); problems(x)

2. Use a col_ function to guide parsing
- **col_guess()** - the default
- **col_character()**
- **col_double(), col_euro_double()**
- **col_datetime(**format = ""**)** Also **col_date(**format = ""**), col_time(**format = ""**)**
- **col_factor(**levels, ordered = FALSE**)**
- **col_integer()**
- **col_logical()**
- **col_number(), col_numeric()**
- **col_skip()**

x <- read_csv("file.csv", col_types = cols(
A = col_double(),
B = col_logical(),
C = col_factor()))

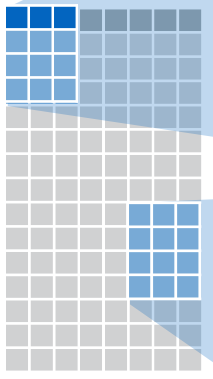
3. Else, read in as character vectors then parse with a parse_ function.
- **parse_guess()**
- **parse_character()**
- **parse_datetime()** Also **parse_date()** and **parse_time()**
- **parse_double()**
- **parse_factor()**
- **parse_integer()**
- **parse_logical()**
- **parse_number()**

x$A <- parse_number(x$A)

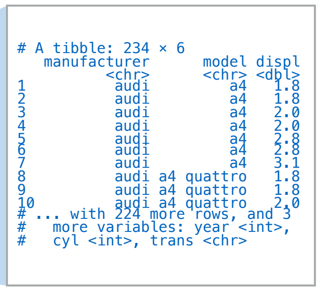
Tibbles - an enhanced data frame

The **tibble** package provides a new S3 class for storing tabular data, the tibble. Tibbles inherit the data frame class, but improve three behaviors:

- **Subsetting** - [always returns a new tibble, [[and $ always return a vector.
- **No partial matching** - You must use full column names when subsetting
- **Display** - When you print a tibble, R provides a concise view of the data that fits on one screen

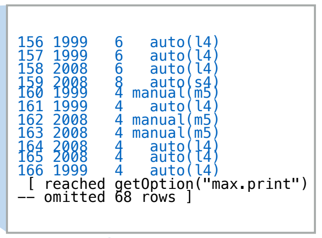


A large table to display



```
# A tibble: 234 × 6
   manufacturer      model displ
          <chr>      <chr> <dbl>
1          audi         a4   1.8
2          audi         a4   1.8
3          audi         a4   2.0
4          audi         a4   2.0
5          audi         a4   2.8
6          audi         a4   2.8
7          audi         a4   3.1
8          audi a4 quattro   1.8
9          audi a4 quattro   1.8
10         audi a4 quattro   2.0
# ... with 224 more rows, and 3
#   more variables: year <int>,
#   cyl <int>, trans <chr>
```

tibble display



```
156 1999   6   auto(l4)
157 1999   6   auto(l4)
158 2008   6   auto(l4)
159 2008   8   auto(s4)
160 1999   4 manual(m5)
161 1999   4   auto(l4)
162 2008   4 manual(m5)
163 2008   4 manual(m5)
164 2008   4   auto(l4)
165 2008   4   auto(l4)
166 1999   4   auto(l4)
 [ reached getOption("max.print")
-- omitted 68 rows ]
```

data frame display

- Control the default appearance with options:

  options(tibble.print_max = n, tibble.print_min = m, tibble.width = Inf**)**

- View full data set with **View()** or **glimpse()**
- Revert to data frame with **as.data.frame()**

CONSTRUCT A TIBBLE IN TWO WAYS

tibble(…)
Construct by columns.
tibble(x = 1:3, y = c("a", "b", "c"))

Both make this tibble

tribble(…)
Construct by rows.
tribble(~x, ~y,
1, "a",
2, "b",
3, "c")

```
A tibble: 3 × 2
      x     y
  <int> <dbl>
1     1     a
2     2     b
3     3     c
```

as_tibble(x, …) Convert data frame to tibble.

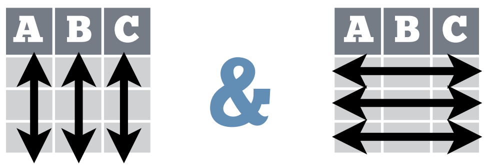
enframe(x, name = "name", value = "value")
Convert named vector to a tibble

is_tibble(x) Test whether x is a tibble.

Tidy Data with Tidyr

Tidy data is a way to organize tabular data. It provides a consistent data structure across packages.

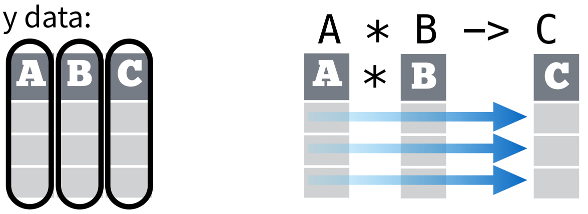
A table is tidy if:



Each **variable** is in its own **column**

Each **observation**, or **case**, is in its own **row**

Tidy data:



Makes variables easy to access as vectors

Preserves cases during vectorized operations

Reshape Data - change the layout of values in a table

Use **gather()** and **spread()** to reorganize the values of a table into a new layout.

gather(data, key, value, ..., na.rm = FALSE, convert = FALSE, factor_key = FALSE**)**

Gather moves column names into a **key** column, gathering the column values into a single **value** column.

table4a

country	1999	2000
A	0.7K	2K
B	37K	80K
C	212K	213K

→

country	year	cases
A	1999	0.7K
B	1999	37K
C	1999	212K
A	2000	2K
B	2000	80K
C	2000	213K

key value

gather(table4a, `1999`, `2000`, key = "year", value = "cases")

spread(data, key, value, fill = NA, convert = FALSE, drop = TRUE, sep = NULL**)**

Spread moves the unique values of a **key** column into the column names, spreading the values of a **value** column across the new columns.

table2

country	year	type	count
A	1999	cases	0.7K
A	1999	pop	19M
A	2000	cases	2K
A	2000	pop	20M
B	1999	cases	37K
B	1999	pop	172M
B	2000	cases	80K
B	2000	pop	174M
C	1999	cases	212K
C	1999	pop	1T
C	2000	cases	213K
C	2000	pop	1T

key value

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172M
B	2000	80K	174M
C	1999	212K	1T
C	2000	213K	1T

spread(table2, type, count)

Handle Missing Values

drop_na(data, ...**)**

Drop rows containing NA's in … columns.

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
D	3

drop_na(x, x2)

fill(data, ..., .direction = c("down", "up")**)**

Fill in NA's in … columns with most recent non-NA values.

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
B	1
C	1
D	3
E	3

fill(x, x2)

replace_na(data, replace = list(), ...**)**

Replace NA's by column.

x

x1	x2
A	1
B	NA
C	NA
D	3
E	NA

→

x1	x2
A	1
B	2
C	2
D	3
E	2

replace_na(x, list(x2 = 2))

Expand Tables - quickly create tables with combinations of values

complete(data, ..., fill = list()**)**

Adds to the data missing combinations of the values of the variables listed in …
complete(mtcars, cyl, gear, carb)

expand(data, ...**)**

Create new tibble with all possible combinations of the values of the variables listed in …
expand(mtcars, cyl, gear, carb)

Split Cells

Use these functions to split or combine cells into individual, isolated values.

separate(data, col, into, sep = "[^[:alnum:]]+", remove = TRUE, convert = FALSE, extra = "warn", fill = "warn", ...**)**

Separate each cell in a column to make several columns.

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M
C	1999	212K/1T
C	2000	213K/1T

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172
B	2000	80K	174
C	1999	212K	1T
C	2000	213K	1T

separate(table3, rate, into = c("cases", "pop"))

separate_rows(data, ..., sep = "[^[:alnum:].]+", convert = FALSE**)**

Separate each cell in a column to make several rows. Also **separate_rows_()**.

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M
C	1999	212K/1T
C	2000	213K/1T

→

country	year	rate
A	1999	0.7K
A	1999	19M
A	2000	2K
A	2000	20M
B	1999	37K
B	1999	172M
B	2000	80K
B	2000	174M
C	1999	212K
C	1999	1T
C	2000	213K
C	2000	1T

separate_rows(table3, rate)

unite(data, col, ..., sep = "_", remove = TRUE**)**

Collapse cells across several columns to make a single column.

table5

country	century	year
Afghan	19	99
Afghan	20	0
Brazil	19	99
Brazil	20	0
China	19	99
China	20	0

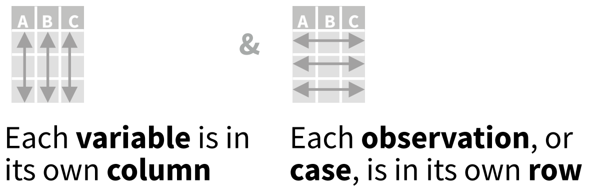
→

country	year
Afghan	1999
Afghan	2000
Brazil	1999
Brazil	2000
China	1999
China	2000

unite(table5, century, year, col = "year", sep = "")

Data Transformation with dplyr : : **CHEAT SHEET**

dplyr functions work with pipes and expect **tidy data**. In tidy data:



Each **variable** is in its own **column** & Each **observation**, or **case**, is in its own **row**

pipes

x %>% f(y) becomes **f(x, y)**

Summarise Cases

These apply **summary functions** to columns to create a new table. Summary functions take vectors as input and return one value (see back).

summary function

summarise(.data, …)
Compute table of summaries. Also **summarise_**().
summarise(mtcars, avg = mean(mpg))

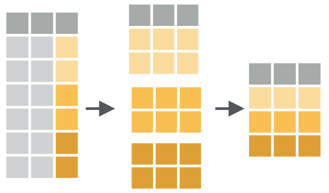
count(x, ..., wt = NULL, sort = FALSE)
Count number of rows in each group defined by the variables in … Also **tally**().
count(iris, Species)

VARIATIONS

summarise_all() - Apply funs to every column.
summarise_at() - Apply funs to specific columns.
summarise_if() - Apply funs to all cols of one type.

Group Cases

Use **group_by()** to created a "grouped" copy of a table. dplyr functions will manipulate each "group" separately and then combine the results.



```
mtcars %>%
group_by(cyl) %>%
summarise(avg = mean(mpg))
```

group_by(.data, ..., add = FALSE**)**
Returns copy of table grouped by …
g_iris <- group_by(iris, Species)

ungroup(x, …**)**
Returns ungrouped copy of table.
ungroup(g_iris)

Manipulate Cases

EXTRACT CASES

Row functions return a subset of rows as a new table. Use a variant that ends in _ for non-standard evaluation friendly code.

filter(.data, …**)** Extract rows that meet logical criteria. Also **filter_()**. *filter(iris, Sepal.Length > 7)*

distinct(.data, ..., .keep_all = FALSE**)** Remove rows with duplicate values. Also **distinct_()**.
distinct(iris, Species)

sample_frac(tbl, size = 1, replace = FALSE, weight = NULL, .env = parent.frame()**)** Randomly select fraction of rows.
sample_frac(iris, 0.5, replace = TRUE)

sample_n(tbl, size, replace = FALSE, weight = NULL, .env = parent.frame()**)** Randomly select size rows. *sample_n(iris, 10, replace = TRUE)*

slice(.data, …**)** Select rows by position. Also **slice_()**. *slice(iris, 10:15)*

top_n(x, n, wt**)** Select and order top n entries (by group if grouped data). *top_n(iris, 5, Sepal.Width)*

Logical and boolean operators to use with filter()

<	<=	is.na()	%in%	|	xor()
>	>=	!is.na()	!	&	

See **?base::logic** and **?Comparison** for help.

ARRANGE CASES

arrange(.data, …**)**
Order rows by values of a column (low to high), use with **desc()** to order from high to low.
arrange(mtcars, mpg)
arrange(mtcars, desc(mpg))

ADD CASES

add_row(.data, ..., .before = NULL, .after = NULL**)**
Add one or more rows to a table.
add_row(faithful, eruptions = 1, waiting = 1)

Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new table. Use a variant that ends in _ for non-standard evaluation friendly code.

select(.data, …**)**
Extract columns by name. Also **select_if()**
select(iris, Sepal.Length, Species)

Use these helpers with select (),
e.g. select(iris, starts_with("Sepal"))

contains(match**)**	**num_range(**prefix, range**)**	**:**, e.g. mpg:cyl
ends_with(match**)**	**one_of(**…**)**	**-**, e.g, -Species
matches(match**)**	**starts_with(**match**)**	

MAKE NEW VARIABLES

These apply **vectorized functions** to columns. Vectorized funs take vectors as input and return vectors of the same length as output (see back).

vectorized function

mutate(.data, …**)**
Compute new column(s).
mutate(mtcars, gpm = 1/mpg)

transmute(.data, …**)**
Compute new column(s), drop others.
transmute(mtcars, gpm = 1/mpg)

mutate_all(.tbl, .funs, …**)** Apply funs to every column. Use with **funs()**.
mutate_all(faithful, funs(log(.), log2(.)))

mutate_at(.tbl, .cols, .funs, …**)** Apply funs to specific columns. Use with **funs()**, **vars()** and the helper functions for select().
mutate_at(iris, vars(-Species), funs(log(.)))

mutate_if(.tbl, .predicate, .funs, …**)**
Apply funs to all columns of one type. Use with **funs()**.
mutate_if(iris, is.numeric, funs(log(.)))

add_column(.data, ..., .before = NULL, .after = NULL**)** Add new column(s).
add_column(mtcars, new = 1:32)

rename(.data, …**)** Rename columns.
rename(iris, Length = Sepal.Length)

RStudio

Vectorized Functions

TO USE WITH MUTATE ()

mutate() and **transmute()** apply vectorized functions to columns to create new columns. Vectorized functions take vectors as input and return vectors of the same length as output.

vectorized function

OFFSETS

dplyr::**lag()** - Offset elements by 1
dplyr::**lead()** - Offset elements by -1

CUMULATIVE AGGREGATES

dplyr::**cumall()** - Cumulative all()
dplyr::**cumany()** - Cumulative any()
cummax() - Cumulative max()
dplyr::**cummean()** - Cumulative mean()
cummin() - Cumulative min()
cumprod() - Cumulative prod()
cumsum() - Cumulative sum()

RANKINGS

dplyr::**cume_dist()** - Proportion of all values <=
dplyr::**dense_rank()** - rank with ties = min, no gaps
dplyr::**min_rank()** - rank with ties = min
dplyr::**ntile()** - bins into n bins
dplyr::**percent_rank()** - min_rank scaled to [0,1]
dplyr::**row_number()** - rank with ties = "first"

MATH

+, - , *, /, ^, %/%, %% - arithmetic ops
log(), log2(), log10() - logs
<, <=, >, >=, !=, == - logical comparisons

MISC

dplyr::**between()** - x >= left & x <= right
dplyr::**case_when()** - multi-case if_else()
dplyr::**coalesce()** - first non-NA values by element across a set of vectors
dplyr::**if_else()** - element-wise if() + else()
dplyr::**na_if()** - replace specific values with NA
pmax() - element-wise max()
pmin() - element-wise min()
dplyr::**recode()** - Vectorized switch()
dplyr::**recode_factor()** - Vectorized switch() for factors

Summary Functions

TO USE WITH SUMMARISE ()

summarise() applies summary functions to columns to create a new table. Summary functions take vectors as input and return single values as output.

summary function

COUNTS

dplyr::**n()** - number of values/rows
dplyr::**n_distinct()** - # of uniques
sum(!is.na()) - # of non-NA's

LOCATION

mean() - mean, also **mean(!is.na())**
median() - median

LOGICALS

mean() - Proportion of TRUE's
sum() - # of TRUE's

POSITION/ORDER

dplyr::**first()** - first value
dplyr::last() - last value
dplyr::nth() - value in nth location of vector

RANK

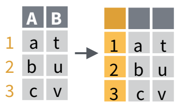
quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

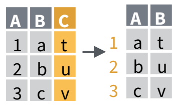
IQR() - Inter-Quartile Range
mad() - mean absolute deviation
sd() - standard deviation
var() - variance

Row Names

Tidy data does not use rownames, which store a variable outside of the columns. To work with the rownames, first move them into a column.



rownames_to_column()
Move row names into col.
a <- rownames_to_column(iris, var = "C")

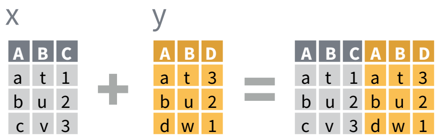


column_to_rownames()
Move col in row names.
column_to_rownames(a, var = "C")

Also has **rownames()**, **remove_rownames()**

Combine Tables

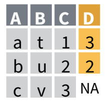
COMBINE VARIABLES



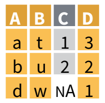
Use **bind_cols()** to paste tables beside each other as they are.

bind_cols(...) Returns tables placed side by side as a single table.
BE SURE THAT ROWS ALIGN.

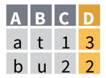
Use a "**Mutating Join**" to join one table to columns from another, matching values with the rows that they correspond to. Each join retains a different combination of values from the tables.



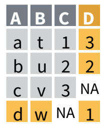
left_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),...)
Join matching values from y to x.



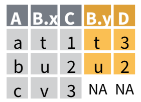
right_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),...)
Join matching values from x to y.



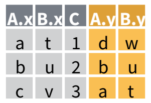
inner_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),...)
Join data. Retain only rows with matches.



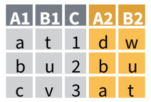
full_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),...)
Join data. Retain all values, all rows.



Use **by = c("col1", "col2")** to specify the column(s) to match on.
left_join(x, y, by = "A")

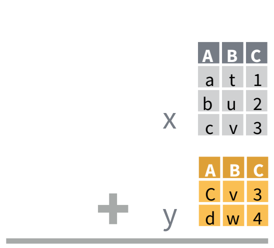


Use a named vector, **by = c("col1" = "col2")**, to match on columns with different names in each data set.
left_join(x, y, by = c("C" = "D"))

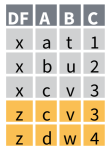


Use **suffix** to specify suffix to give to duplicate column names.
left_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

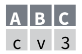
COMBINE CASES



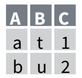
Use **bind_rows()** to paste tables below each other as they are.



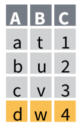
bind_rows(..., .id = NULL**)**
Returns tables one on top of the other as a single table. Set .id to a column name to add a column of the original table names (as pictured)



intersect(x, y, ...)
Rows that appear in both x and z.



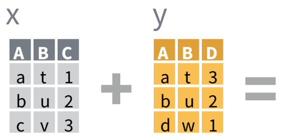
setdiff(x, y, ...)
Rows that appear in x but not z.



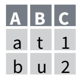
union(x, y, ...)
Rows that appear in x or z. (Duplicates removed). union_all() retains duplicates.

Use **setequal()** to test whether two data sets contain the exact same rows (in any order).

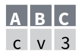
EXTRACT ROWS



Use a "**Filtering Join**" to filter one table against the rows of another.



semi_join(x, y, by = NULL, ...)
Return rows of x that have a match in y. USEFUL TO SEE WHAT WILL BE JOINED.



anti_join(x, y, by = NULL, ...)
Return rows of x that do not have a match in y. USEFUL TO SEE WHAT WILL NOT BE JOINED.

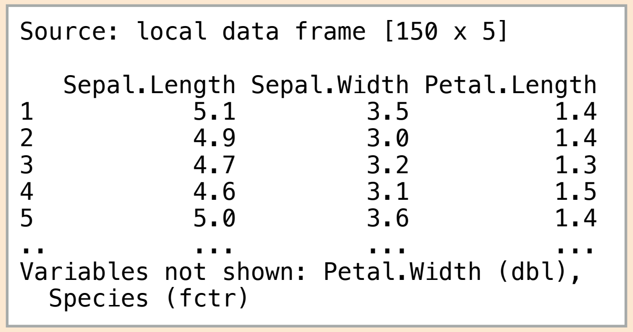
Data Wrangling
with dplyr and tidyr
Cheat Sheet

RStudio®

Syntax - Helpful conventions for wrangling

dplyr::**tbl_df(iris)**

Converts data to tbl class. tbl's are easier to examine than data frames. R displays only the data that fits onscreen:



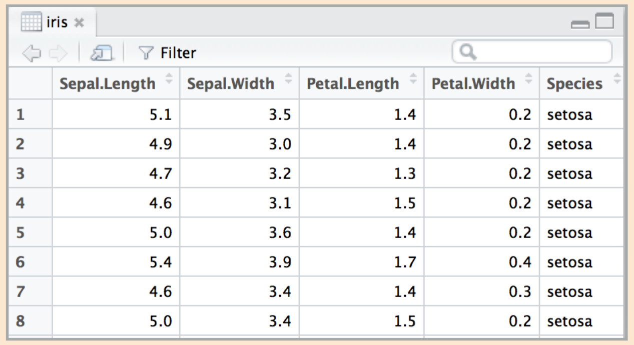
```
Source: local data frame [150 x 5]

  Sepal.Length Sepal.Width Petal.Length
1          5.1         3.5          1.4
2          4.9         3.0          1.4
3          4.7         3.2          1.3
4          4.6         3.1          1.5
5          5.0         3.6          1.4
..         ...         ...          ...
Variables not shown: Petal.Width (dbl),
  Species (fctr)
```

dplyr::**glimpse(iris)**

Information dense summary of tbl data.

utils::**View(iris)**

View data set in spreadsheet-like display (note capital V).



	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa

dplyr::**%>%**

Passes object on left hand side as first argument (or . argument) of function on righthand side.

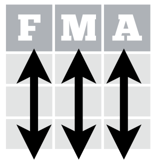
```
        x %>% f(y)   is the same as   f(x, y)
   y %>% f(x, ., z)   is the same as   f(x, y, z )
```

"Piping" with %>% makes code more readable, e.g.

```
iris %>%
  group_by(Species) %>%
  summarise(avg = mean(Sepal.Width)) %>%
  arrange(avg)
```

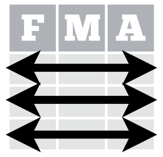
Tidy Data - A foundation for wrangling in R

In a tidy data set:



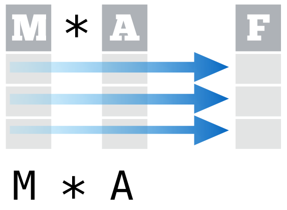
Each **variable** is saved in its own **column**

&

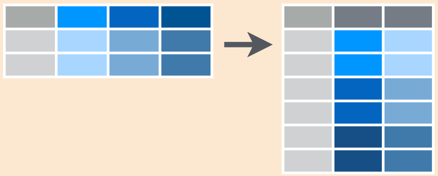


Each **observation** is saved in its own **row**

Tidy data complements R's **vectorized operations**. R will automatically preserve observations as you manipulate variables. No other format works as intuitively with R.

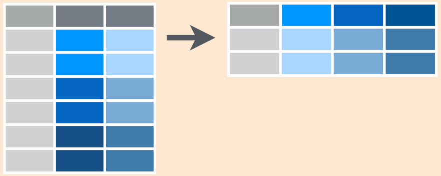


Reshaping Data - Change the layout of a data set



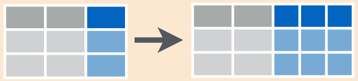
tidyr::**gather(cases, "year", "n", 2:4)**

Gather columns into rows.



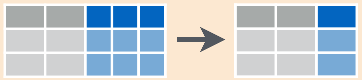
tidyr::**spread(pollution, size, amount)**

Spread rows into columns.



tidyr::**separate(storms, date, c("y", "m", "d"))**

Separate one column into several.



tidyr::**unite(data, col, ..., sep)**

Unite several columns into one.

dplyr::**data_frame(a = 1:3, b = 4:6)**

Combine vectors into data frame (optimized).

dplyr::**arrange(mtcars, mpg)**

Order rows by values of a column (low to high).

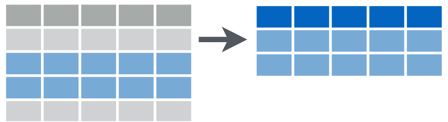
dplyr::**arrange(mtcars, desc(mpg))**

Order rows by values of a column (high to low).

dplyr::**rename(tb, y = year)**

Rename the columns of a data frame.

Subset Observations (Rows)



dplyr::**filter(iris, Sepal.Length > 7)**

Extract rows that meet logical criteria.

dplyr::**distinct(iris)**

Remove duplicate rows.

dplyr::**sample_frac(iris, 0.5, replace = TRUE)**

Randomly select fraction of rows.

dplyr::**sample_n(iris, 10, replace = TRUE)**

Randomly select n rows.

dplyr::**slice(iris, 10:15)**

Select rows by position.

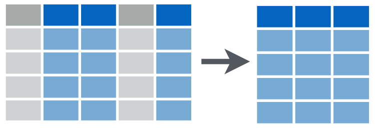
dplyr::**top_n(storms, 2, date)**

Select and order top n entries (by group if grouped data).

Logic in R - ?Comparison, ?base::Logic

<	Less than	!=	Not equal to
>	Greater than	%in%	Group membership
==	Equal to	is.na	Is NA
<=	Less than or equal to	!is.na	Is not NA
>=	Greater than or equal to	&,|,!,xor,any,all	Boolean operators

Subset Variables (Columns)



dplyr::**select(iris, Sepal.Width, Petal.Length, Species)**

Select columns by name or helper function.

Helper functions for select - ?select

select(iris, **contains(".")**)

Select columns whose name contains a character string.

select(iris, **ends_with("Length")**)

Select columns whose name ends with a character string.

select(iris, **everything()**)

Select every column.

select(iris, **matches(".t.")**)

Select columns whose name matches a regular expression.

select(iris, **num_range("x", 1:5)**)

Select columns named x1, x2, x3, x4, x5.

select(iris, **one_of(c("Species", "Genus")**))

Select columns whose names are in a group of names.

select(iris, **starts_with("Sepal")**)

Select columns whose name starts with a character string.

select(iris, **Sepal.Length:Petal.Width**)

Select all columns between Sepal.Length and Petal.Width (inclusive).

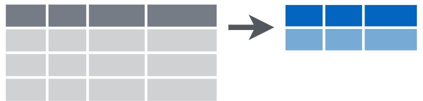
select(iris, **-Species**)

Select all columns except Species.

devtools::install_github("rstudio/EDAWR") for data sets

Learn more with **browseVignettes(package = c("dplyr", "tidyr"))** • dplyr 0.4.0• tidyr 0.2.0 • Updated: 1/15

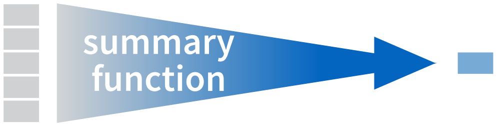
Summarise Data



dplyr::summarise(iris, avg = mean(Sepal.Length))
Summarise data into single row of values.

dplyr::summarise_each(iris, funs(mean))
Apply summary function to each column.

dplyr::count(iris, Species, wt = Sepal.Length)
Count number of rows with each unique value of variable (with or without weights).



Summarise uses **summary functions**, functions that take a vector of values and return a single value, such as:

dplyr::first
First value of a vector.

dplyr::last
Last value of a vector.

dplyr::nth
Nth value of a vector.

dplyr::n
# of values in a vector.

dplyr::n_distinct
# of distinct values in a vector.

IQR
IQR of a vector.

min
Minimum value in a vector.

max
Maximum value in a vector.

mean
Mean value of a vector.

median
Median value of a vector.

var
Variance of a vector.

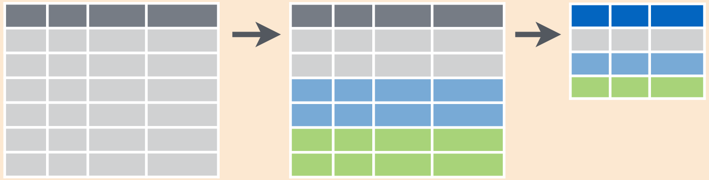
sd
Standard deviation of a vector.

Group Data

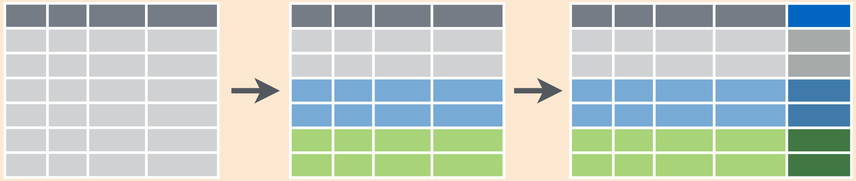
dplyr::group_by(iris, Species)
Group data into rows with the same value of Species.

dplyr::ungroup(iris)
Remove grouping information from data frame.

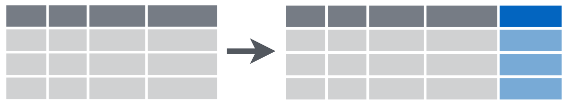
iris %>% group_by(Species) %>% summarise(…)
Compute separate summary row for each group.



iris %>% group_by(Species) %>% mutate(…)
Compute new variables by group.



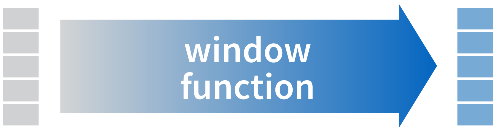
Make New Variables



dplyr::mutate(iris, sepal = Sepal.Length + Sepal. Width)
Compute and append one or more new columns.

dplyr::mutate_each(iris, funs(min_rank))
Apply window function to each column.

dplyr::transmute(iris, sepal = Sepal.Length + Sepal. Width)
Compute one or more new columns. Drop original columns.



Mutate uses **window functions**, functions that take a vector of values and return another vector of values, such as:

dplyr::lead
Copy with values shifted by 1.

dplyr::lag
Copy with values lagged by 1.

dplyr::dense_rank
Ranks with no gaps.

dplyr::min_rank
Ranks. Ties get min rank.

dplyr::percent_rank
Ranks rescaled to [0, 1].

dplyr::row_number
Ranks. Ties got to first value.

dplyr::ntile
Bin vector into n buckets.

dplyr::between
Are values between a and b?

dplyr::cume_dist
Cumulative distribution.

dplyr::cumall
Cumulative `all`

dplyr::cumany
Cumulative `any`

dplyr::cummean
Cumulative `mean`

cumsum
Cumulative `sum`

cummax
Cumulative `max`

cummin
Cumulative `min`

cumprod
Cumulative `prod`

pmax
Element-wise `max`

pmin
Element-wise `min`

Combine Data Sets

a

x1	x2
A	1
B	2
C	3

+

b

x1	x3
A	T
B	F
D	T

=

Mutating Joins

x1	x2	x3
A	1	T
B	2	F
C	3	NA

dplyr::left_join(a, b, by = "x1")
Join matching rows from b to a.

x1	x3	x2
A	T	1
B	F	2
D	T	NA

dplyr::right_join(a, b, by = "x1")
Join matching rows from a to b.

x1	x2	x3
A	1	T
B	2	F

dplyr::inner_join(a, b, by = "x1")
Join data. Retain only rows in both sets.

x1	x2	x3
A	1	T
B	2	F
C	3	NA
D	NA	T

dplyr::full_join(a, b, by = "x1")
Join data. Retain all values, all rows.

Filtering Joins

x1	x2
A	1
B	2

dplyr::semi_join(a, b, by = "x1")
All rows in a that have a match in b.

x1	x2
C	3

dplyr::anti_join(a, b, by = "x1")
All rows in a that do not have a match in b.

y

x1	x2
A	1
B	2
C	3

+

z

x1	x2
B	2
C	3
D	4

=

Set Operations

x1	x2
B	2
C	3

dplyr::intersect(y, z)
Rows that appear in both y and z.

x1	x2
A	1
B	2
C	3
D	4

dplyr::union(y, z)
Rows that appear in either or both y and z.

x1	x2
A	1

dplyr::setdiff(y, z)
Rows that appear in y but not z.

Binding

x1	x2
A	1
B	2
C	3
B	2
C	3
D	4

dplyr::bind_rows(y, z)
Append z to y as new rows.

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

dplyr::bind_cols(y, z)
Append z to y as new columns.
Caution: matches rows by position.

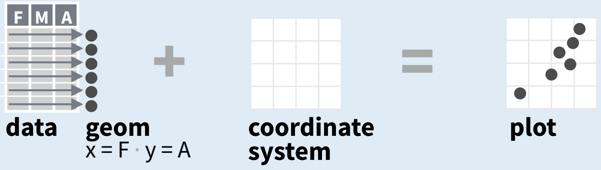
devtools::install_github("rstudio/EDAWR") for data sets

Learn more with **browseVignettes(package = c("dplyr", "tidyr"))** • dplyr 0.4.0• tidyr 0.2.0 • Updated: 1/15

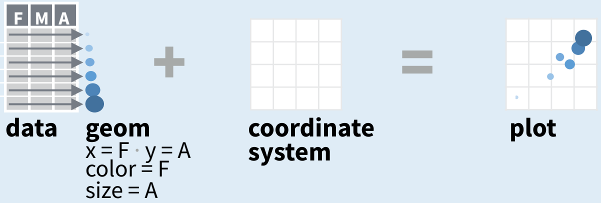
Data Visualization with ggplot2 : : CHEAT SHEET

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and geoms—visual marks that represent data points.



To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

ggplot (data = <DATA>) +
<GEOM_FUNCTION>(mapping = aes(<MAPPINGS>),
stat = **<STAT>** , position = **<POSITION>**) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>

required

Not required, sensible defaults supplied

ggplot(data = mpg, **aes(**x = cty, y = hwy**))** Begins a plot that you finish by adding layers to. Add one geom function per layer.

aesthetic mappings data geom

qplot(x = cty, y = hwy, data = mpg, geom = “point"**)** Creates a complete plot with given data, geom, and mappings. Supplies many useful defaults.

last_plot() Returns the last plot

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5’ x 5’ file named "plot.png" in working directory. Matches file type to file extension.

Geoms

Use a geom function to represent data points, use the geom’s aesthetic properties to represent variables. Each function returns a layer.

GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank()
(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1,
xend=long+1,curvature=z)**)** - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend="butt", linejoin="round", linemitre=1**)**
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group)**)**
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)**)** - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900)**)** - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept=0, slope=1)**)**
b + geom_hline(aes(yintercept = lat)**)**
b + geom_vline(aes(xintercept = long)**)**

b + geom_segment(aes(yend=lat+1, xend=long+1)**)**
b + geom_spoke(aes(angle = 1:1155, radius = 1)**)**

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian"**)**
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly() x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5**)** x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy)**)** x, y, alpha, color, fill, linetype, size, weight

discrete

d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

continuous x , continuous y

e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)** x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_jitter(height = 2, width = 2**)**
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile(), x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"**)**, x, y, alpha, color, linetype, size

e + geom_smooth(method = lm**)**, x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)**, x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

discrete x , continuous y

f <- ggplot(mpg, aes(class, hwy))

f + geom_col(), x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot(), x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"**)**, x, y, alpha, color, fill, group

f + geom_violin(scale = "area"**)**, x, y, alpha, color, fill, group, linetype, size, weight

discrete x , discrete y

g <- ggplot(diamonds, aes(cut, color))

g + geom_count(), x, y, alpha, color, fill, shape, size, stroke

continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500)**)**
x, y, alpha, color, fill, linetype, size, weight

h + geom_density2d()
x, y, alpha, colour, group, linetype, size

h + geom_hex()
x, y, alpha, colour, fill, size

continuous function

i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

j + geom_crossbar(fatten = 2**)**
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

data <- data.frame(murder = USArrests$Murder,
state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map**)**
+ expand_limits(x = map$long, y = map$lat**)**,
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2))l <- ggplot(seals, aes(long, lat))

l + geom_contour(aes(z = z))
x, y, z, alpha, colour, group, linetype, size, weight

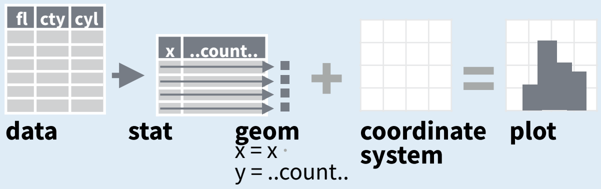
l + geom_raster(aes(fill = z)**)**, hjust=0.5, vjust=0.5, interpolate=FALSE)
x, y, alpha, fill

l + geom_tile(aes(fill = z)**)**, x, y, alpha, color, fill, linetype, size, width

RStudio

Stats An alternative way to build a layer

A stat builds new variables to plot (e.g., count, prop).



Visualize a stat by changing the default stat of a geom function, **geom_bar(stat="count")** or by using a stat function, **stat_count(geom="bar")**, which calls a default geom to make a layer (equivalent to a geom function). Use **..name..** syntax to map stat variables to aesthetics.

geom to use — stat function — geommappings

i + stat_density2d(aes(fill = ..level..),
geom = "polygon")

variable created by stat

c + stat_bin(binwidth = 1, origin = 10)
x, y | ..count.., ..ncount.., ..density.., ..ndensity..

c + stat_count(width = 1) **x, y,** | ..count.., ..prop..

c + stat_density(adjust = 1, kernel = "gaussian")
x, y, | ..count.., ..density.., ..scaled..

e + stat_bin_2d(bins = 30, drop = T)
x, y, fill | ..count.., ..density..

e + stat_bin_hex(bins=30) **x, y, fill** | ..count.., ..density..

e + stat_density_2d(contour = TRUE, n = 100)
x, y, color, size | ..level..

e + stat_ellipse(level = 0.95, segments = 51, type = "t")

l + stat_contour(aes(z = z)) **x, y, z, order** | ..level..

l + stat_summary_hex(aes(z = z), bins = 30, fun = max)
x, y, z, fill | ..value..

l + stat_summary_2d(aes(z = z), bins = 30, fun = mean)
x, y, z, fill | ..value..

f + stat_boxplot(coef = 1.5) **x, y** | ..lower.., ..middle.., ..upper.., ..width.. , ..ymin.., ..ymax..

f + stat_ydensity(kernel = "gaussian", scale = "area") **x, y** | ..density.., ..scaled.., ..count.., ..n.., ..violinwidth.., ..width..

e + stat_ecdf(n = 40) **x, y** | ..x.., ..y..

e + stat_quantile(quantiles = c(0.1, 0.9), formula = y ~ log(x), method = "rq") **x, y** | ..quantile..

e + stat_smooth(method = "lm", formula = y ~ x, se=T, level=0.95) **x, y** | ..se.., ..x.., ..y.., ..ymin.., ..ymax..

ggplot() + stat_function(aes(x = -3:3), n = 99, fun = dnorm, args = list(sd=0.5)) **x** | ..x.., ..y..

e + stat_identity(na.rm = TRUE)

ggplot() + stat_qq(aes(sample=1:100), dist = qt, dparam=list(df=5)) **sample, x, y** | ..sample.., ..theoretical..

e + stat_sum() x, y, size | ..n.., ..prop..

e + stat_summary(fun.data = "mean_cl_boot")

h + stat_summary_bin(fun.y = "mean", geom = "bar")

e + stat_unique()

Scales

Scales map data values to the visual values of an aesthetic. To change a mapping, add a new scale.

(n <- d + geom_bar(aes(fill = fl)))

scale_ — aesthetic to adjust — prepackaged scale to use — scale-specific arguments

n + scale_fill_manual(
values = c("skyblue", "royalblue", "blue", "navy"),
limits = c("d", "e", "p", "r"), breaks =c("d", "e", "p", "r"),
name = "fuel", labels = c("D", "E", "P", "R"))

range of values to include in mapping — title to use in legend/axis — labels to use in legend/axis — breaks to use in legend/axis

GENERAL PURPOSE SCALES

Use with most aesthetics

scale_*_continuous() - map cont' values to visual ones

scale_*_discrete() - map discrete values to visual ones

scale_*_identity() - use data values **as** visual ones

scale_*_manual(values = c()) - map discrete values to manually chosen visual ones

scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - treat data values as dates.

scale_*_datetime() - treat data x values as date times. Use same arguments as scale_x_date(). See ?strptime for label formats.

X & Y LOCATION SCALES

Use with x or y aesthetics (x shown here)

scale_x_log10() - Plot x on log10 scale
scale_x_reverse() - Reverse direction of x axis
scale_x_sqrt() - Plot x on square root scale

COLOR AND FILL SCALES (DISCRETE)

n <- d + geom_bar(aes(fill = fl))

n + scale_fill_brewer(palette = "Blues")
For palette choices:
RColorBrewer::display.brewer.all()

n + scale_fill_grey(start = 0.2, end = 0.8, na.value = "red")

COLOR AND FILL SCALES (CONTINUOUS)

o <- c + geom_dotplot(aes(fill = ..x..))

o + scale_fill_distiller(palette = "Blues")

o + scale_fill_gradient(low="red", high="yellow")

o + scale_fill_gradient2(low="red", high="blue", mid = "white", midpoint = 25)

o + scale_fill_gradientn(colours=topo.colors(6))
Also: rainbow(), heat.colors(), terrain.colors(), cm.colors(), RColorBrewer::brewer.pal()

SHAPE AND SIZE SCALES

p <- e + geom_point(aes(shape = fl, size = cyl))
p + scale_shape() + scale_size()
p + scale_shape_manual(values = c(3:7))

0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
□	○	△	+	×	◇	▽	⊠	✳	⊕	⊕	✡	⊞	⊗	⊠	□	○	△	◇	○	∘	●	■	◆	▲	▼

p + scale_radius(range = c(1,6))
p + scale_size_area(max_size = 6)

Coordinate Systems

r <- d + geom_bar()

r + coord_cartesian(xlim = c(0, 5))
xlim, ylim
The default cartesian coordinate system

r + coord_fixed(ratio = 1/2)
ratio, xlim, ylim
Cartesian coordinates with fixed aspect ratio between x and y units

r + coord_flip()
xlim, ylim
Flipped Cartesian coordinates

r + coord_polar(theta = "x", direction=1 **)**
theta, start, direction
Polar coordinates

r + coord_trans(ytrans = "sqrt")
xtrans, ytrans, limx, limy
Transformed cartesian coordinates. Set xtrans and ytrans to the name of a window function.

π + coord_quickmap()
π + coord_map(projection = "ortho", orientation=c(41, -74, 0))projection, orienztation, xlim, ylim
Map projections from the mapproj package (mercator (default), azequalarea, lagrange, etc.)

Position Adjustments

Position adjustments determine how to arrange geoms that would otherwise occupy the same space.

s <- ggplot(mpg, aes(fl, fill = drv))

s + geom_bar(position = "dodge")
Arrange elements side by side

s + geom_bar(position = "fill")
Stack elements on top of one another, normalize height

e + geom_point(position = "jitter")
Add random noise to X and Y position of each element to avoid overplotting

e + geom_label(position = "nudge")
Nudge labels away from points

s + geom_bar(position = "stack")
Stack elements on top of one another

Each position adjustment can be recast as a function with manual **width** and **height** arguments
s + geom_bar(position = position_dodge(width = 1))

Themes

r + theme_bw()
White background with grid lines

r + theme_gray()
Grey background (default theme)

r + theme_dark()
dark for contrast

r + theme_classic()

r + theme_light()

r + theme_linedraw()

r + theme_minimal()
Minimal themes

r + theme_void()
Empty theme

Faceting

Facets divide a plot into subplots based on the values of one or more discrete variables.

t <- ggplot(mpg, aes(cty, hwy)) + geom_point()

t + facet_grid(. ~ fl)
facet into columns based on fl

t + facet_grid(year ~ .)
facet into rows based on year

t + facet_grid(year ~ fl)
facet into both rows and columns

t + facet_wrap(~ fl)
wrap facets into a rectangular layout

Set **scales** to let axis limits vary across facets

t + facet_grid(drv ~ fl, scales = "free")
x and y axis limits adjust to individual facets
"free_x" - x axis limits adjust
"free_y" - y axis limits adjust

Set **labeller** to adjust facet labels

t + facet_grid(. ~ fl, labeller = label_both)

fl: c	**fl: d**	**fl: e**	**fl: p**	**fl: r**

t + facet_grid(fl ~ ., labeller = label_bquote(alpha ^ .(fl)**))**

α^c	α^d	α^e	α^p	α^r

t + facet_grid(. ~ fl, labeller = label_parsed)

c	**d**	**e**	**p**	**r**

Labels

t + labs(**x** = "New x axis label", **y** = "New y axis label",
title ="Add a title above the plot",
subtitle = "Add a subtitle below title",
caption = "Add a caption below plot",
<AES> = "New <AES> legend title")

Use scale functions to update legend labels

t + annotate(geom = "text", x = 8, y = 9, label = "A")

geom to place — manual values for geom's aesthetics

Legends

n + theme(legend.position = "bottom")
Place legend at "bottom", "top", "left", or "right"

n + guides(fill = "none")
Set legend type for each aesthetic: colorbar, legend, or none (no legend)

n + scale_fill_discrete(name = "Title", labels = c("A", "B", "C", "D", "E"))
Set legend title and labels with a scale function.

Zooming

Without clipping (preferred)

t + coord_cartesian(
xlim = c(0, 100), ylim = c(10, 20))

With clipping (removes unseen data points)

t + xlim(0, 100) **+ ylim(**10, 20)

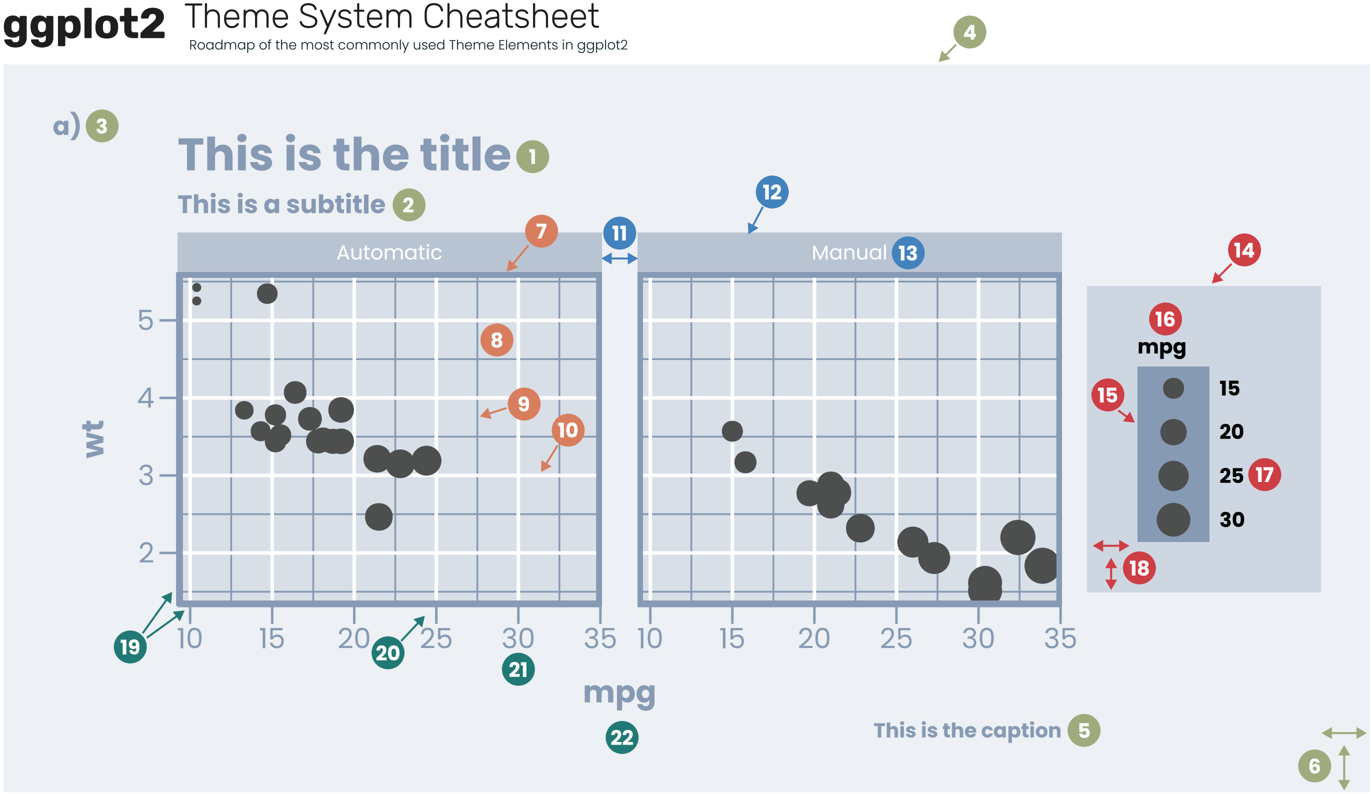
t + scale_x_continuous(limits = c(0, 100)) **+**
scale_y_continuous(limits = c(0, 100))

RStudio

ggplot2 Theme System Cheatsheet

Roadmap of the most commonly used Theme Elements in ggplot2

ggplot2 version 3.3.5
@TheDataInkLab



Element functions

element_text()

(font) family
(font) face
(font) colour
(font) size (in points)
hjust [0..1] (0=left, 1=right)
vjust [0..1] (0=bottom, 1=top)
angle (in degrees)
lineheight (as ratio of fontcase)
margin
  margin (t, r, b, l)
  #remember trouble

element_line()

(line) colour
size (width of line)
linetype
  An integer (0:8)
  A name ("blank", "solid", "dashed", "dotted", "dotdash", "longdash", "twodash")
lineend
  "round", "butt", "square"
arrow
  An arrow specification: arrow()

element_rect()

fill
colour
size (width of border)
linetype (of border) (see element_line)

element_blank()

Eliminates element
Doesn't take parameters

Plot elements

1 **plot.title**
element_text()

2 **plot.subtitle**
element_text()

3 **plot.tag**
element_text()

plot.tag.position
"topleft", "top", "topright", "left", "right", "bottomleft", "bottom", "bottomright"
or a coordinate

4 **plot.background**
element_rect()

5 **plot.caption**
element_text()

6 **plot.margin**
margin()

Panel elements

7 **panel.border**
element_rect()

8 **panel.background**
element_rect()

9 **panel.grid.minor**
element_line()

10 **panel.grid.major**
element_line()

● **aspect.ratio**
numeric

Facet elements

11 **panel.spacing**
unit()

12 **strip.background**
element_rect()

13 **strip.text**
element_text()

Legend elements

14 **legend.background**
element_rect()

15 **legend.key**
element_rect()

16 **legend.title**
element_text()

legend.title.align
Numeric between 0 to 1,
where: 0=left, 1=right

17 **legend.text**
element_text()

legend.text.align
Numeric between 0 to 1,
where: 0=left, 1=right

18 **legend.margin**
margin()

● **legend.position**
"none", "left", "right", "bottom", "top",
or two-element numeric vector

Axis elements

19 **axis.line**
element_line()

20 **axis.ticks**
element_line()

axis.ticks.length
unit()

21 **axis.text**
element_text()

22 **axis.title**
element_text()

Global

These affect all elements of same type in the plot. Useful to define defaults.

text
element_text()

line
element_text()

rect
element_rect()

title
element_text()

Note.

Of those elements that have two components, the way to access is by appending .x or .y at the end. e.g. axis.line.y will change only the "y" axis line. Idem with "x". If nothing is specified (e.g axis.line), both elements (x and y) will be changed.

This material is part of the course: Learn ggplot2 in R for Data Visualization
https://www.udemy.com/course/learn-ggplot2-in-r-for-data-viz/?referralCode=E98592E4E943F800ECBB

See the full list of Theme Elements here: https://ggplot2.tidyverse.org/reference/theme.html

Animate ggplots with gganimate : : CHEAT SHEET

Core Concepts

gganimate builds on ggplot2's grammar of graphics to provide functions for animation. You add them to plots created with `ggplot()` the same way you add a geom.

Main Function Groups

- **`transition_*()`**: What variable controls change and how?
- **`view_*()`**: Should the axes change with the data?
- **`enter/exit_*()`**: How does new data get added the plot? How does old data leave?
- **`shadow_*()`**: Should previous data be "remembered" and shown with current data?
- **`ease_aes()`**: How do you want to handle the pace of change between transition values?

Note: you only need a `transition_*()` or `view_*()` to make an animation. The other function groups enable you to add features or alter gganimate's default settings .

Starting Plots

```
library(tidyverse)
library(gganimate)

a <- ggplot(diamonds,
            aes(carat, price)) +
  geom_point()

b <- ggplot(txhousing,
            aes(month, sales)) +
  geom_col()

c <- ggplot(economics,
            aes(date, psavert)) +
  geom_line()
```

transition_*()

We're cycling between values of **color**, ...

transition_states()

```
a + transition_states(color, transition_length = 3, state_length = 1)
```

… and spending **3** times as long going to the next cut as we do pausing there.

We're cycling through each **year** of the data...

transition_time()

```
b + transition_time(year, range = c(2002L,2006L))
```

...from **2002** to **2006** (range is optional; default is the whole time frame). Unlike `transition_states()`, `transition_time()` treats the data as continuous and so the transition length is based on the actual values. Using **2002L** instead of **2002** because the underlying data is an integer.

transition_reveal()

```
c + transition_reveal(date)
```

We're adding each **date** of the data on top of 'old' data

`transition_length` and `filter_length` work the same as `transition/state_length()` in `transition_states()`...

transition_filters()

```
a + transition_filter(transition_length = 3,
                      filter_length = 1,
                      cut == "Ideal",
                      Deep = depth >= 60)
```

… but now we're cycling between these two filtering conditions. **Names** are optional, but can be useful (see "Label variables" on next page).

Other transitions

- **`transition_manual()`**: Similar to transition_states(), but without intermediate states.
- **`transition_layers()`**: Add layers (geoms) one at time.
- **`transition_components()`**: Transition elements independently from each other.
- **`transition_events()`**: Each element's duration can be controlled individually.

Baseline Animation

```
anim_a <- a + transition_states(color, transition_length = 3, state_length = 1)
```

view_*()

view_follow()

```
anim_a +
  view_follow(fixed_x = TRUE,
              fixed_y = c(2500, NA))
```

x-axis shows **full range**, y shows **[2500, as much is needed for that frame]**. Default is for both axis to vary as needed.

We're spending **twice** as long moving between views as staying at them...

view_step()

```
anim_a  +
  view_step(pause_length = 2,
            step_length = 1,
            nstep = 7)
```

… and we're cycling between **seven** views. Seven is the number of steps in the transition, so the view is changing when the points are static, and visa versa. Views are determined by what data is in the current frame.

view_zoom()

`view_zoom()` works similarly to `view_step()`, except it changes the view by zooming and panning.

Note: both `view_step()` and `view_zoom()` have `view_*_manual()` versions for setting views directly instead of inferring it from frame data.

RStudio® is a trademark of RStudio, Inc. • CC by Karl Hailperin • khailper@gmail.com • Learn more at www.gganimate.com • package version 1.0.3 • Updated: 2019-05

Animate ggplots with gganimate : : CHEAT SHEET

enter/exit_*()

Every `enter_*()` function has a corresponding `exit_*()` function, and visa versa.

enter/exit_fade()

```
anim_a + enter_fade()
```

When new points need to be added, they will start transparent and become opaque.

enter_grow()/exit_shrink()

```
anim_a + exit_shrink()
```

When extra points need to be removed, they will shrink in size before disappearing.

enter/exit_fly()

```
anim_a + enter_fly(x_loc = 0,
                   y_loc = 0)
```

When new points need to be added, they will fly in from **(0, 0)**.

enter/exit_drift()

```
anim_a + exit_drift(x_mod = 3, y_mod = -2)
```

When extra points need to be removed, They drift **3** units to the right and down 2 units before disappearing.

enter/exit_recolour() (or enter/exit_recolor())

```
anim_a + enter_recolour(color = "red")
```

When new points need to be added, they start as **red** before transitioning to their correct color.

Note: `enter/exit_*()` functions can be combined so that you can have old data fade away and shrink to nothing by adding `exit_fade()` and `exit_shrink()` to the plot.

shadow_*()

shadow_wake()

```
anim_a + shadow_wake(wake_length = 0.05)
```

Points have a wake of points with the data from the last **5%** of frames.

shadow_trail()

```
anim_a + shadow_trail(distance = 0.05)
```

Animation will keep the points from **5%** of the frames, spaced as evenly as possible.

shadow_mark()

```
anim_a + shadow_mark(color = "red")
```

Animation will keep past states plotted in **red** (but not the intermediate frames).

ease_aes()

`ease_aes()` allows you to set an easing function to control the rate of change between transition states. See ?ease_aes for the full list.

Compare:

```
anim_a
anim_a + ease_aes(“cubic-in") # Change easing of all aesthetics
anim_a + ease_aes(x = “elastic-in") # Only change `x` (others remain “linear”)
```

Saving animations

```
animation_to_save <- anim_a  + exit_shrink()
anim_save("first_saved_animation.gif", animation = animation_to_save)
```

Since the `animation` argument uses your last rendered animation by default, this also works:

```
anim_a  + exit_shrink()
anim_save("second_saved_animation.gif")
```

`anim_save()` uses gifski to render the animation as a .gif file by default. You can use the `renderer` argument for other output types including video files (`av_renderer()` or `ffmeg_renderer()`) or spritesheets (`sprite_renderer()`):

```
# requires you to have the av package installed
anim_save("third_saved_animation.mp4",
          renderer =  av_renderer())
```

Label variables

gganimate’s `transition_*()` functions create label variables you can pass to (sub)titles and other labels with the glue package. For example, `transition_states()` has `next_state`, which is the name of the state the animation is transitioning towards. Label variables are different between transitions, and details are included in the documentation of each.

```
anim_a + labs(subtitle = “Moving to {next_state}”)
```

We’re using the **next_state** label variable to tell the viewer where we’re going.

Label variable	Description	Transitions
`transitioning`	TRUE if the current frame is an transition frame, FALSE otherwise	states, layers, filter
`previous_state/layer`	Last shown state/layer	states, layers
`next_state/layer`	State/layer that will been shown next	states, layers
`closest_state/layer`	State/layer that current frame is closest to (if between states/layers, either next or closest).	states, layers
`previous/closest/ next_filter/ expression`	Similar to their state/layer analogs. `*_filter` variables return the name of the filter, `*_expression` variables return the condition.	filter
`frame_time`	Time of current frame	time, components, events
`frame_along`	Current frame’s value for the dimension we’re transitioning over	reveal
`nlayers`	Number of layers (total, not just currently shown)	layer

RStudio® is a trademark of RStudio, Inc. • CC by Karl Hailperin • khailper@gmail.com • Learn more at www.gganimate.com • package version 1.0.3 • Updated: 2019-05

ggmap quickstart

For more functionality, see ggmap documentation and https://dl.dropboxusercontent.com/u/24648660/ggmap%20useR%202012.pdf

There are 2 basic steps to making a map using ggmap:

Part 1: Download map raster → Part 2: Plot raster and overlay data

Part 1: Downloading the map raster

Start by loading the package: library(ggmap)

1. Define location: 3 ways

- location/address
  myLocation <- "University of Washington”
- lat/long
  myLocation <- c(lon = -95.3632715, lat = 29.7632836)
- bounding box lowerleftlon, lowerleftlat, upperrightlon, upperrightlat (a little glitchy for google maps)
  myLocation <- c(-130, 30, -105, 50)

Convert location/address its lat/long coordinates:
geocode(“University of Washington”)

2. Define map source, type, and color

The get_map function provides a general approach for quickly obtaining maps from multiple sources. I like this option for exploring different styles of maps.

There are 4 map “sources” to obtain a map raster, and each of these sources has multiple “map types” (displayed on right).

- stamen: maptype = c(“terrain”, “toner”, “watercolor”)
- google: maptype = c(“roadmap”, “terrain”, “satellite”, “hybrid”)
- osm: open street map
- cloudmade: 1000s of maps, but an api key must be obtained from http://cloudmade.com

myMap <- get_map(location=myLocation, source="stamen", maptype=“watercolor", crop=FALSE)
ggmap(myMap)

This will produce a map that looks something like this

NOTE: crop = FALSE because otherwise, with stamen plots, the map is slightly shifted when I overlay data.

3. Fine tune the scale of the map using zoom

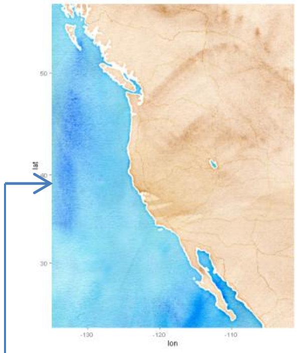
The get_map function takes a guess at the zoom level, but you can alter it:

zoom = integer from 3-21
3 = continent, 10=city, 21=building
(openstreetmap limit of 18)

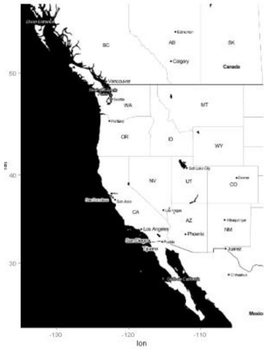
The following maps show different map source/type options (except cloudmade)

The appearance of these maps may be very different depending on zoom/scale

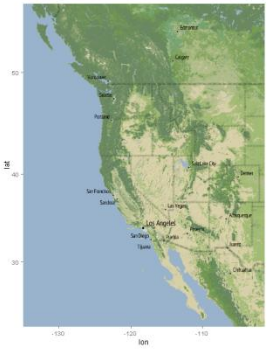
stamen: watercolor



stamen: toner

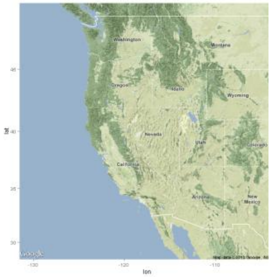


stamen: terrain

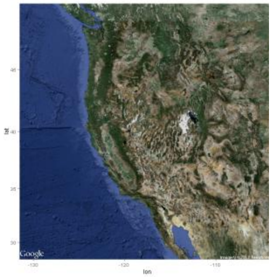


If you can’t get the map you want by adjusting the location/zoom variables, the functions designed for the different map sources provide more options:
get_googlemap,
get_openstreetmap,
get_stamenmap,
get_cloudmademap

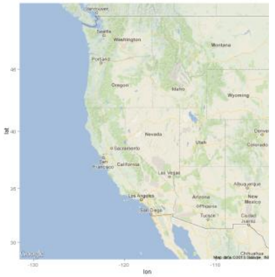
google: terrain



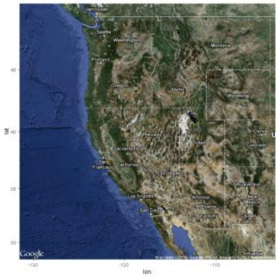
google: satellite



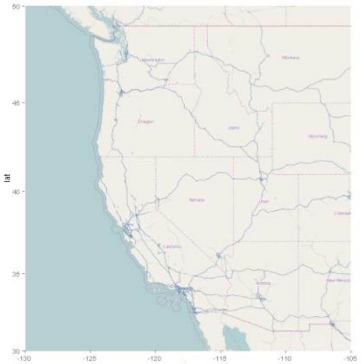
google: roadmap



google: hybrid

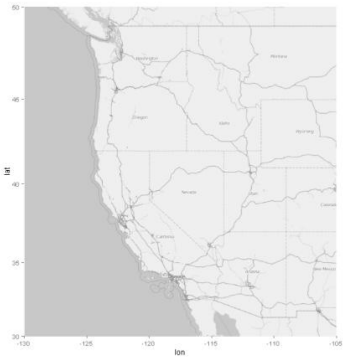


osm*



*Open street maps may return a '503 Service Unavailable‘ error. This means their server is unavailable, and you must wait for it to become available again.

All maps can be displayed in black and white
color = “bw”



myMap <- get_map(location=myLocation, source=“osm”, color=“bw”))

- If you use Rstudio: Sometimes a plot will not display. Increasing the size of the plot window may help. dev.off() prior to plotting may also help.
- The urlonly = TRUE will return a url that will display your map in a web browser. Which is pretty cool and may be handy!
- legend=“topleft” will inset the legend on the top left of the map is data is overlayed (page 2).

ggmap quickstart

Part 2: Plotting the maps and data

1. Plot the raster:

```
ggmap(myMap)
```

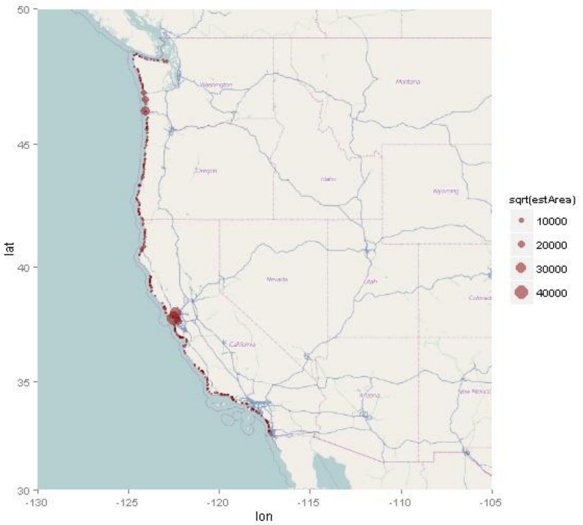
2. Add points with latitude/longitude coordinates:

```
ggmap(myMap)+
geom_point(aes(x = Longitude, y = Latitude), data = data,
        alpha = .5, color="darkred", size = 3)
```

alpha = transparency
color = color
size = size of points

The size, color, alpha, and shape of the points can be scaled relative to another variable (in this case estArea) within the aes function:

```
ggmap(myMap)+
geom_point(aes(x = Longitude, y = Latitude, size=sqrt(estArea)),
data = data, alpha = .5, color="darkred")
```



Additional functions can be added to control scaling, e.g.:

```
ggmap(myMap)+
  geom_point(aes(x = Longitude, y = Latitude, size=sqrt(estArea)),
  data = data, alpha = .5, color="darkred")+
  scale_size(range=c(3,20))
```

3. Add polygons from shp file

The shp file is imported into R using the rgdal package, and must be transformed to geographic coordinates (latitude/longitude) on the World Geodetic System of 1984 (WGS84) datum using the rgdal package:

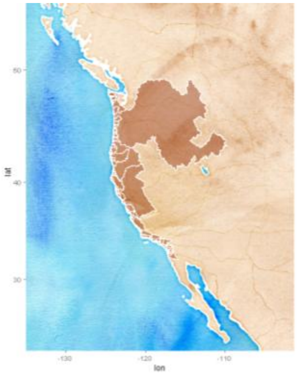
```
library(rgdal)
shpData <- readOGR(dsn="C:\\Documents and Settings\\Watershed", layer="WS")
proj4string(shpData)    # describes data's current coordinate reference system
# to change to correct projection:
shpData <- spTransform(shpData,
CRS("+proj=longlat +datum=WGS84"))
```

To plot the data:

```
geom_polygon(aes(x = long, y = lat, group=id),
data = shpData, color ="white", fill ="orangered4",
alpha = .4, size = .2)
```

color= outline color
fill = polygon color

alpha = transparency
size = outline size



4. Annotate figure

```
baylor <- get_map('baylor university', zoom = 15, maptype = 'satellite')
ggmap(baylor) +
 annotate('rect', xmin=-97.11, ymin=31.54, xmax=-97.12, ymax=31.55, col="red“, fill=“white”)+
 annotate('text', x=-97.12, y=31.54, label = 'Statistical Sciences', colour = I(‘red'), size = 8)+
 annotate('segment', x=-97.12, xend=-97.12, y=31.55, yend=31.55,
        colour=I('red'), arrow = arrow(length=unit(0.3,"cm")), size = 1.5) +
 labs(x = 'Longitude', y = 'Latitude') + ggtitle('Baylor University')
```

Controlling size and color

size

```
scale_size(range = c(3, 20))
```

But, the following is better for display because it is based on area (rather than radius)

```
scale_area(range=c(3,20))
```

color

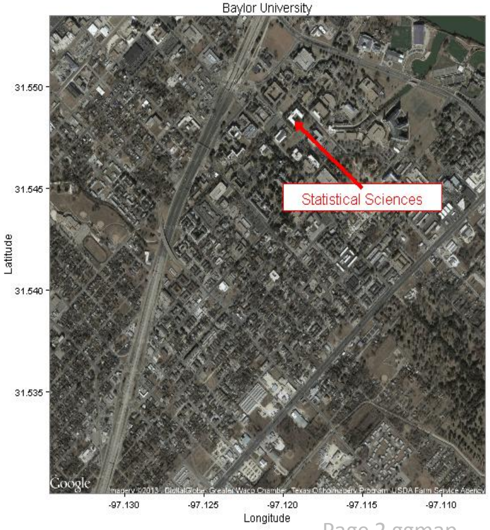
Continuous variables: color gradient between n colors, e.g.:

```
scale_colour_gradientn(colours =
rainbow_hcl(7))
```

Discrete variables, e.g.:

```
scale_colour_manual(values=rainbow_hcl(7))
scale_colour_manual(values=c("8" = "red",
"4" = "blue","6" = "green“)
```

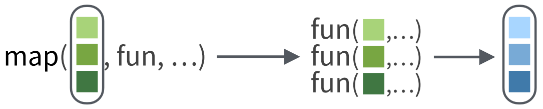
*Use colorspace and RColorBrewer to choose color combinations



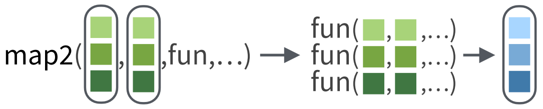
Apply functions with purrr : : CHEAT SHEET

Apply Functions

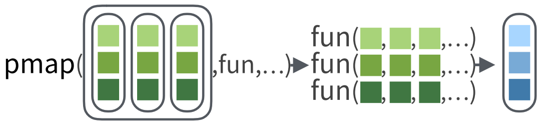
Map functions apply a function iteratively to each element of a list or vector.



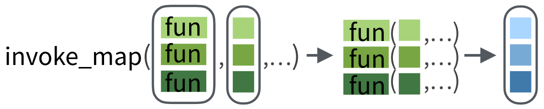
map(.x, .f, …) Apply a function to each element of a list or vector. *map(x, is.logical)*



map2(.x, ,y, .f, …) Apply a function to pairs of elements from two lists, vectors. *map2(x, y, sum)*



pmap(.l, .f, …) Apply a function to groups of elements from list of lists, vectors. *pmap(list(x, y, z), sum, na.rm = TRUE)*



invoke_map(.f, .x = list(NULL), …, .env=NULL) Run each function in a list. Also **invoke**. *l <- list(var, sd); invoke_map(l, x = 1:9)*

lmap(.x, .f, ...) Apply function to each list-element of a list or vector.
imap(.x, .f, ...) Apply .f to each element of a list or vector and its index.

OUTPUT

map(), map2(), pmap(), imap and **invoke_map** each return a list. Use a suffixed version to return the results as a specific type of flat vector, e.g. **map2_chr**, **pmap_lgl**, etc.

Use **walk**, **walk2**, and **pwalk** to trigger side effects. Each return its input invisibly.

function	returns
map	list
map_chr	character vector
map_dbl	double (numeric) vector
map_dfc	data frame (column bind)
map_dfr	data frame (row bind)
map_int	integer vector
map_lgl	logical vector
walk	triggers side effects, returns the input invisibly

SHORTCUTS - within a purrr function:

"name" becomes **function(x) x$name.** e.g. *map(l, "a")* extracts *$a* from each element of *l*

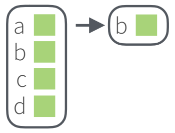
~ . becomes **function(x) x.** e.g. *map(l, ~ 2 +.)* becomes *map(l, function(x) 2 + x)*

~ .x .y becomes **function(.x, .y) .x .y.** e.g. *map2(l, p, ~ .x +.y)* becomes *map2(l, p, function(l, p) l + p)*

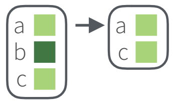
~ ..1 ..2 etc becomes **function(..1, ..2,** etc) **..1 ..2** etc e.g. *pmap(list(a, b, c), ~ ..3 + ..1 - ..2)* becomes *pmap(list(a, b, c), function(a, b, c) c + a - b)*

Work with Lists

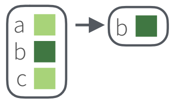
FILTER LISTS



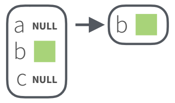
pluck(.x, ..., .default=NULL) Select an element by name or index, *pluck(x,"b")* ,or its attribute with **attr_getter**. *pluck(x,"b",attr_getter("n"))*



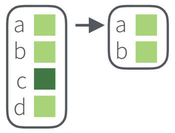
keep(.x, .p, …) Select elements that pass a logical test. *keep(x, is.na)*



discard(.x, .p, …) Select elements that do not pass a logical test. *discard(x, is.na)*

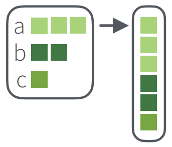


compact(.x, .p = identity) Drop empty elements. *compact(x)*

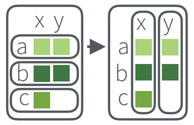


head_while(.x, .p, …) Return head elements until one does not pass. Also **tail_while**. *head_while(x, is.character)*

RESHAPE LISTS

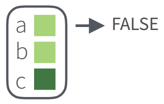


flatten(.x) Remove a level of indexes from a list. Also **flatten_chr**, **flatten_dbl**, **flatten_dfc**, **flatten_dfr**, **flatten_int**, **flatten_lgl**. *flatten(x)*

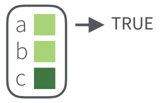


transpose(.l, .names = NULL) Transposes the index order in a multi-level list. *transpose(x)*

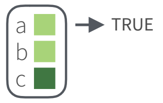
SUMMARISE LISTS



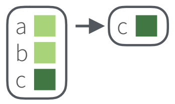
every(.x, .p, …) Do all element pass a test? *every(x, is.character)*



some(.x, .p, …) Do some elements pass a test? *some(x, is.character)*

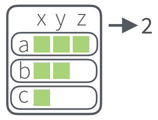


has_element(.x, .y) Does a list contain an element? *has_element(x, "foo")*



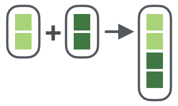
detect(.x, .f, ..., .right=FALSE, .p) Find first element to pass. *detect(x, is.character)*

detect_index(.x, .f, ..., .right = FALSE, .p) Find index of first element to pass. *detect_index(x, is.character)*

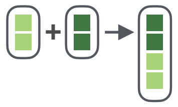


vec_depth(x) Return depth (number of levels of indexes). *vec_depth(x)*

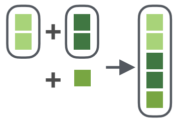
JOIN (TO) LISTS



append(x, values, after = length(x)) Add to end of list. *append(x, list(d = 1))*

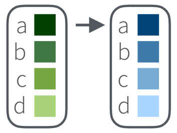


prepend(x, values, before = 1) Add to start of list. *prepend(x, list(d = 1))*

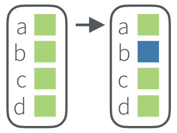


splice(…) Combine objects into a list, storing S3 objects as sub-lists. *splice(x, y, "foo")*

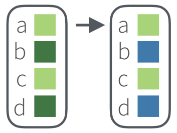
TRANSFORM LISTS



modify(.x, .f, ...) Apply function to each element. Also **map**, **map_chr**, **map_dbl**, **map_dfc**, **map_dfr**, **map_int**, **map_lgl**. *modify(x, ~.+ 2)*



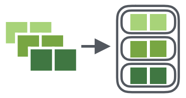
modify_at(.x, .at, .f, ...) Apply function to elements by name or index. Also **map_at**. *modify_at(x, "b", ~.+ 2)*



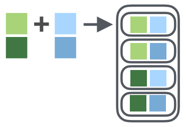
modify_if(.x, .p, .f, ...) Apply function to elements that pass a test. Also **map_if**. *modify_if(x, is.numeric,~.+2)*

modify_depth(.x,.depth,.f,...) Apply function to each element at a given level of a list. *modify_depth(x, 1, ~.+ 2)*

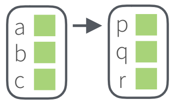
WORK WITH LISTS



array_tree(array, margin = NULL) Turn array into list. Also **array_branch**. *array_tree(x, margin = 3)*

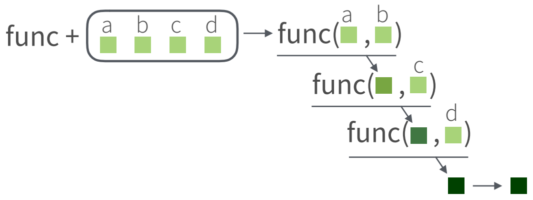


cross2(.x, .y, .filter = NULL) All combinations of .x and .y. Also **cross**, **cross3**, **cross_df**. *cross2(1:3, 4:6)*

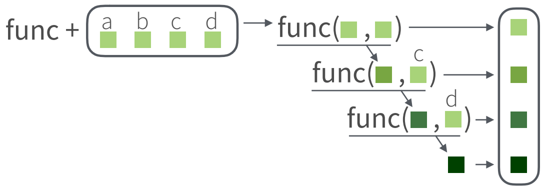


set_names(x, nm = x) Set the names of a vector/list directly or with a function. *set_names(x, c("p", "q", "r"))* *set_names(x, tolower)*

Reduce Lists



reduce(.x, .f, ..., .init) Apply function recursively to each element of a list or vector. Also **reduce_right**, **reduce2**, **reduce2_right**. *reduce(x, sum)*



accumulate(.x, .f, ..., .init) Reduce, but also return intermediate results. Also **accumulate_right**. *accumulate(x, sum)*

Modify function behavior

compose() Compose multiple functions.

lift() Change the type of input a function takes. Also **lift_dl**, **lift_dv**, **lift_ld**, **lift_lv**, **lift_vd**, **lift_vl**.

rerun() Rerun expression n times.

negate() Negate a predicate function (a pipe friendly !)

partial() Partially apply a function, filling in some args.

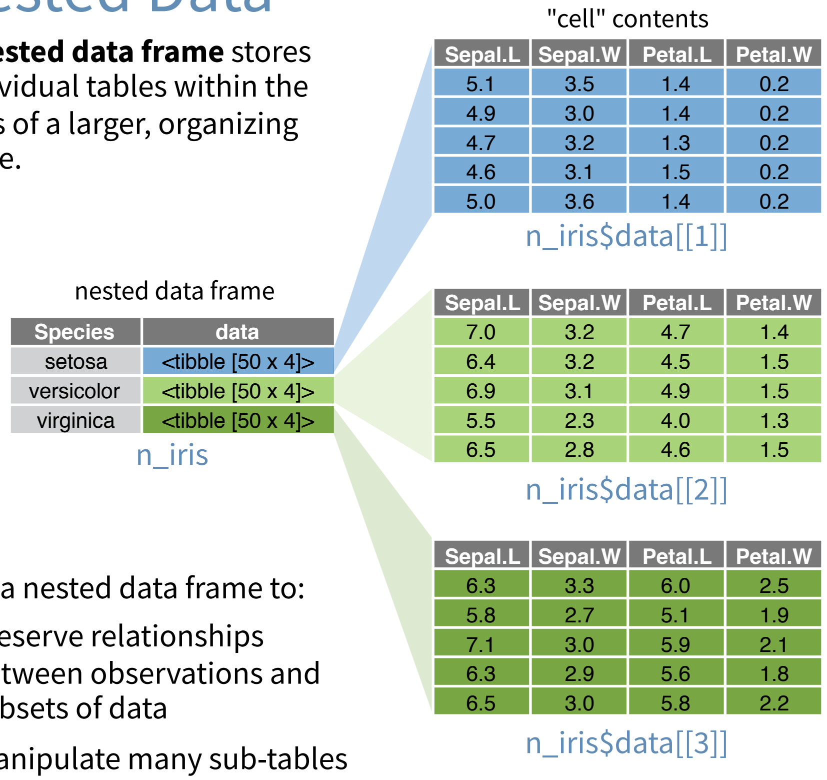
safely() Modify func to return list of results and errors.

quietly() Modify function to return list of results, output, messages, warnings.

possibly() Modify function to return default value whenever an error occurs (instead of error).

RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **purrr.tidyverse.org** • purrr 0.2.3 • Updated: 2017-09

Nested Data



A **nested data frame** stores individual tables within the cells of a larger, organizing table.

"cell" contents

Sepal.L	Sepal.W	Petal.L	Petal.W
5.1	3.5	1.4	0.2
4.9	3.0	1.4	0.2
4.7	3.2	1.3	0.2
4.6	3.1	1.5	0.2
5.0	3.6	1.4	0.2

n_iris$data[[1]]

nested data frame

Species	data
setosa	<tibble [50 x 4]>
versicolor	<tibble [50 x 4]>
virginica	<tibble [50 x 4]>

n_iris

Sepal.L	Sepal.W	Petal.L	Petal.W
7.0	3.2	4.7	1.4
6.4	3.2	4.5	1.5
6.9	3.1	4.9	1.5
5.5	2.3	4.0	1.3
6.5	2.8	4.6	1.5

n_iris$data[[2]]

Sepal.L	Sepal.W	Petal.L	Petal.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8
6.5	3.0	5.8	2.2

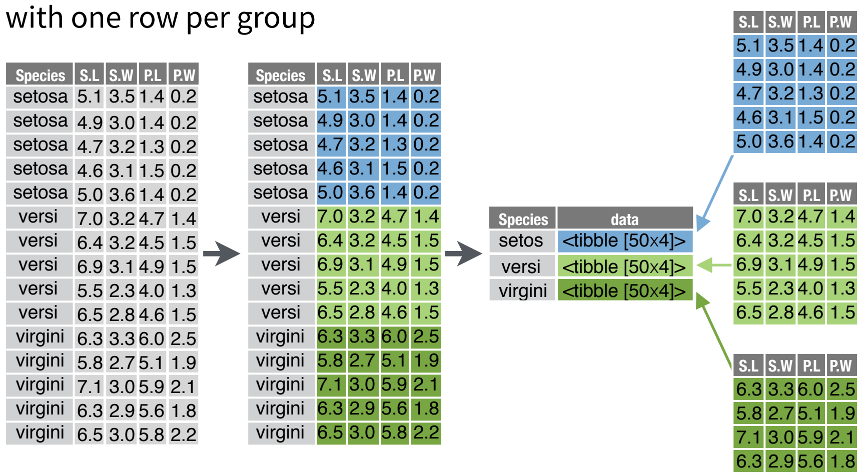
n_iris$data[[3]]

Use a nested data frame to:

- preserve relationships between observations and subsets of data
- manipulate many sub-tables at once with the **purrr** functions **map()**, **map2()**, or **pmap()**.

Use a two step process to create a nested data frame:

1. Group the data frame into groups with **dplyr::group_by()**
2. Use **nest()** to create a nested data frame with one row per group



Species	S.L	S.W	P.L	P.W
setosa	5.1	3.5	1.4	0.2
setosa	4.9	3.0	1.4	0.2
setosa	4.7	3.2	1.3	0.2
setosa	4.6	3.1	1.5	0.2
setosa	5.0	3.6	1.4	0.2
versi	7.0	3.2	4.7	1.4
versi	6.4	3.2	4.5	1.5
versi	6.9	3.1	4.9	1.5
versi	5.5	2.3	4.0	1.3
versi	6.5	2.8	4.6	1.5
virgini	6.3	3.3	6.0	2.5
virgini	5.8	2.7	5.1	1.9
virgini	7.1	3.0	5.9	2.1
virgini	6.3	2.9	5.6	1.8
virgini	6.5	3.0	5.8	2.2

Species	S.L	S.W	P.L	P.W
setosa	5.1	3.5	1.4	0.2
setosa	4.9	3.0	1.4	0.2
setosa	4.7	3.2	1.3	0.2
setosa	4.6	3.1	1.5	0.2
setosa	5.0	3.6	1.4	0.2
versi	7.0	3.2	4.7	1.4
versi	6.4	3.2	4.5	1.5
versi	6.9	3.1	4.9	1.5
versi	5.5	2.3	4.0	1.3
versi	6.5	2.8	4.6	1.5
virgini	6.3	3.3	6.0	2.5
virgini	5.8	2.7	5.1	1.9
virgini	7.1	3.0	5.9	2.1
virgini	6.3	2.9	5.6	1.8
virgini	6.5	3.0	5.8	2.2

Species	data
setos	<tibble [50x4]>
versi	<tibble [50x4]>
virgini	<tibble [50x4]>

S.L	S.W	P.L	P.W
5.1	3.5	1.4	0.2
4.9	3.0	1.4	0.2
4.7	3.2	1.3	0.2
4.6	3.1	1.5	0.2
5.0	3.6	1.4	0.2

S.L	S.W	P.L	P.W
7.0	3.2	4.7	1.4
6.4	3.2	4.5	1.5
6.9	3.1	4.9	1.5
5.5	2.3	4.0	1.3
6.5	2.8	4.6	1.5

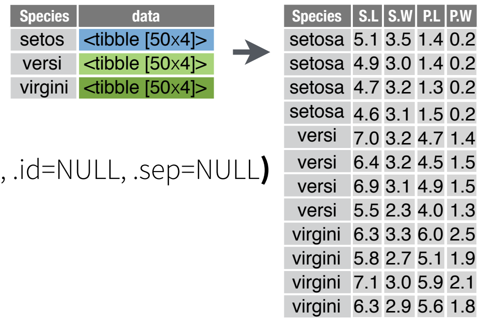
S.L	S.W	P.L	P.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8
6.5	3.0	5.8	2.2

```
n_iris <- iris %>% group_by(Species) %>% nest()
```

tidyr::**nest(**data, ..., .key = data**)**
For grouped data, moves groups into cells as data frames.

Unnest a nested data frame with **unnest()**:

```
n_iris %>% unnest()
```



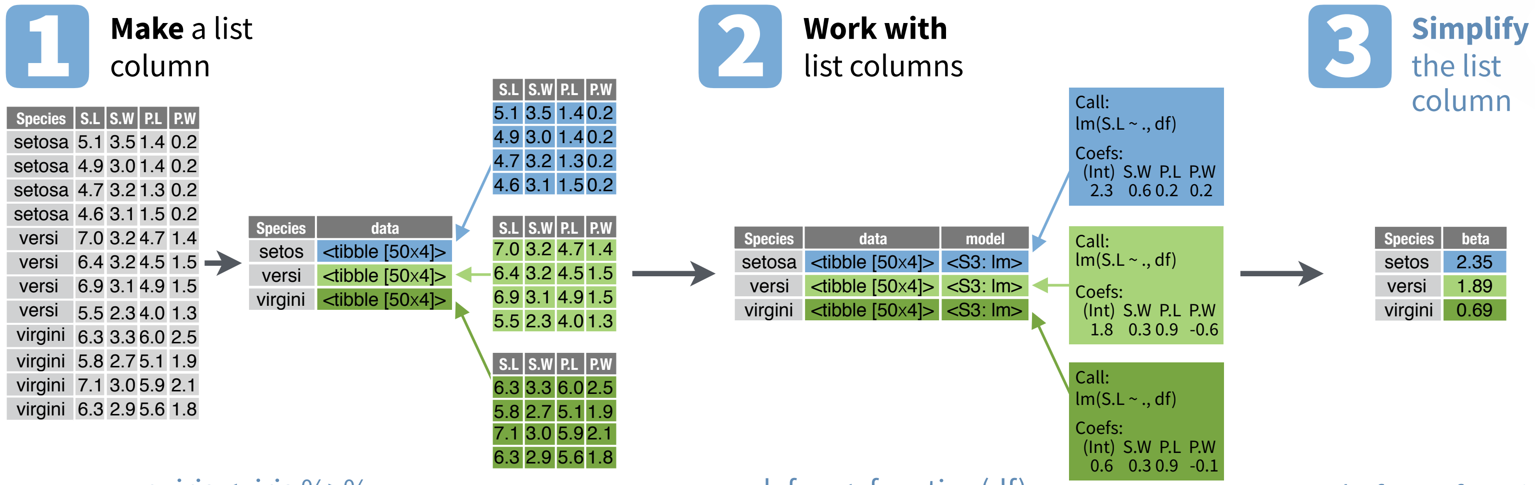
Species	data
setos	<tibble [50x4]>
versi	<tibble [50x4]>
virgini	<tibble [50x4]>

Species	S.L	S.W	P.L	P.W
setosa	5.1	3.5	1.4	0.2
setosa	4.9	3.0	1.4	0.2
setosa	4.7	3.2	1.3	0.2
setosa	4.6	3.1	1.5	0.2
versi	7.0	3.2	4.7	1.4
versi	6.4	3.2	4.5	1.5
versi	6.9	3.1	4.9	1.5
versi	5.5	2.3	4.0	1.3
virgini	6.3	3.3	6.0	2.5
virgini	5.8	2.7	5.1	1.9
virgini	7.1	3.0	5.9	2.1
virgini	6.3	2.9	5.6	1.8

tidyr::**unnest(**data, ..., .drop = NA, .id=NULL, .sep=NULL**)**
Unnests a nested data frame.

List Column Workflow

Nested data frames use a **list column**, a list that is stored as a column vector of a data frame. A typical **workflow** for list columns:



1 **Make** a list column

Species	S.L	S.W	P.L	P.W
setosa	5.1	3.5	1.4	0.2
setosa	4.9	3.0	1.4	0.2
setosa	4.7	3.2	1.3	0.2
setosa	4.6	3.1	1.5	0.2
versi	7.0	3.2	4.7	1.4
versi	6.4	3.2	4.5	1.5
versi	6.9	3.1	4.9	1.5
versi	5.5	2.3	4.0	1.3
virgini	6.3	3.3	6.0	2.5
virgini	5.8	2.7	5.1	1.9
virgini	7.1	3.0	5.9	2.1
virgini	6.3	2.9	5.6	1.8

Species	data
setos	<tibble [50x4]>
versi	<tibble [50x4]>
virgini	<tibble [50x4]>

S.L	S.W	P.L	P.W
5.1	3.5	1.4	0.2
4.9	3.0	1.4	0.2
4.7	3.2	1.3	0.2
4.6	3.1	1.5	0.2

S.L	S.W	P.L	P.W
7.0	3.2	4.7	1.4
6.4	3.2	4.5	1.5
6.9	3.1	4.9	1.5
5.5	2.3	4.0	1.3

S.L	S.W	P.L	P.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8

```
n_iris <- iris %>%
  group_by(Species) %>%
  nest()
```

2 **Work with** list columns

Species	data	model
setosa	<tibble [50x4]>	<S3: lm>
versi	<tibble [50x4]>	<S3: lm>
virgini	<tibble [50x4]>	<S3: lm>

```
Call:
lm(S.L ~ ., df)

Coefs:
 (Int)  S.W  P.L  P.W
  2.3   0.6 0.2  0.2
```

```
Call:
lm(S.L ~ ., df)

Coefs:
 (Int)  S.W  P.L  P.W
  1.8   0.3 0.9  -0.6
```

```
Call:
lm(S.L ~ ., df)

Coefs:
 (Int)  S.W  P.L  P.W
  0.6   0.3 0.9  -0.1
```

```
mod_fun <- function(df)
  lm(Sepal.Length ~ ., data = df)

m_iris <- n_iris %>%
  mutate(model = map(data, mod_fun))
```

3 **Simplify** the list column

Species	beta
setos	2.35
versi	1.89
virgini	0.69

```
b_fun <- function(mod)
  coefficients(mod)[[1]]

m_iris %>% transmute(Species,
  beta = map_dbl(model, b_fun))
```

1. MAKE A LIST COLUMN - You can create list columns with functions in the **tibble** and **dplyr** packages, as well as **tidyr**'s nest()

tibble::**tribble(**…**)**
Makes list column when needed

```
tribble( ~max, ~seq,
            3,   1:3,
            4,   1:4,
            5,   1:5)
```

max	seq
3	<int [3]>
4	<int [4]>
5	<int [5]>

tibble::**tibble(**…**)**
Saves list input as list columns

```
tibble(max = c(3, 4, 5), seq = list(1:3, 1:4, 1:5))
```

tibble::**enframe(**x, name="name", value="value"**)**
Converts multi-level list to tibble with list cols

```
enframe(list('3'=1:3, '4'=1:4, '5'=1:5), 'max', 'seq')
```

dplyr::**mutate(**.data, …**)** Also **transmute()**
Returns list col when result returns list.

```
mtcars %>% mutate(seq = map(cyl, seq))
```

dplyr::**summarise(**.data, …**)**
Returns list col when result is wrapped with **list()**

```
mtcars %>% group_by(cyl) %>%
  summarise(q = list(quantile(mpg)))
```

2. WORK WITH LIST COLUMNS - Use the purrr functions **map()**, **map2()**, and **pmap()** to apply a function that returns a result element-wise to the cells of a list column. **walk()**, **walk2()**, and **pwalk()** work the same way, but return a side effect.

purrr::**map(**.x, .f, ...**)**
Apply .f element-wise to .x as .f(.x)

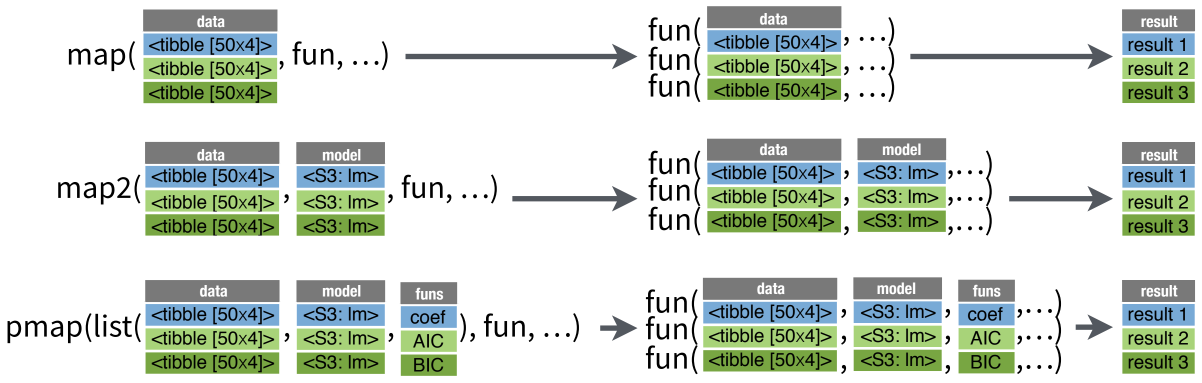
```
n_iris %>% mutate(n = map(data, dim))
```

purrr::**map2(**.x, .y, .f, ...**)**
Apply .f element-wise to .x and .y as .f(.x, .y)

```
m_iris %>% mutate(n = map2(data, model, list))
```

purrr::**pmap(**.l, .f, ...**)**
Apply .f element-wise to vectors saved in .l

```
m_iris %>%
  mutate(n = pmap(list(data, model, data), list))
```



```
map( data                , fun, …)  →  fun( data              , …)  →  result
     <tibble [50x4]>                        <tibble [50x4]>                result 1
     <tibble [50x4]>                   fun( <tibble [50x4]>   , …)         result 2
     <tibble [50x4]>                   fun( <tibble [50x4]>   , …)         result 3

map2( data            , model      , fun, …)  →  fun( data            , model      ,…)  →  result
      <tibble [50x4]>   <S3: lm>                      <tibble [50x4]> , <S3: lm>   ,…)     result 1
      <tibble [50x4]> , <S3: lm>                 fun( <tibble [50x4]> , <S3: lm>   ,…)     result 2
      <tibble [50x4]>   <S3: lm>                 fun( <tibble [50x4]> , <S3: lm>   ,…)     result 3

pmap(list( data            , model      , funs ), fun, …)  →  fun( data            , model     , funs ,…)  →  result
           <tibble [50x4]>   <S3: lm>     coef                     <tibble [50x4]> , <S3: lm>  , coef ,…)     result 1
           <tibble [50x4]> , <S3: lm>   , AIC                 fun( <tibble [50x4]> , <S3: lm>  , AIC  ,…)     result 2
           <tibble [50x4]>   <S3: lm>     BIC                 fun( <tibble [50x4]> , <S3: lm>  , BIC  ,…)     result 3
```

3. SIMPLIFY THE LIST COLUMN (into a regular column)

Use the purrr functions **map_lgl()**, **map_int()**, **map_dbl()**, **map_chr()**, as well as tidyr's **unnest()** to reduce a list column into a regular column.

purrr::**map_lgl(**.x, .f, ...**)**
Apply .f element-wise to .x, return a logical vector

```
n_iris %>% transmute(n = map_lgl(data, is.matrix))
```

purrr::**map_int(**.x, .f, ...**)**
Apply .f element-wise to .x, return an integer vector

```
n_iris %>% transmute(n = map_int(data, nrow))
```

purrr::**map_dbl(**.x, .f, ...**)**
Apply .f element-wise to .x, return a double vector

```
n_iris %>% transmute(n = map_dbl(data, nrow))
```

purrr::**map_chr(**.x, .f, ...**)**
Apply .f element-wise to .x, return a character vector

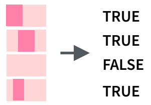
```
n_iris %>% transmute(n = map_chr(data, nrow))
```

RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **purrr.tidyverse.org** • purrr 0.2.3 • Updated: 2017-09

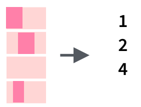
Work with strings with stringr : : CHEAT SHEET

The **stringr** package provides a set of internally consistent tools for working with character strings, i.e. sequences of characters surrounded by quotation marks.

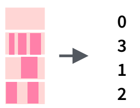
Detect Matches



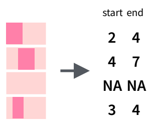
str_detect(string, **pattern**) Detect the presence of a pattern match in a string. *str_detect(fruit, "a")*



str_which(string, **pattern**) Find the indexes of strings that contain a pattern match. *str_which(fruit, "a")*

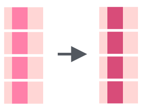


str_count(string, **pattern**) Count the number of matches in a string. *str_count(fruit, "a")*

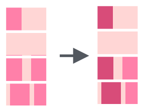


str_locate(string, **pattern**) Locate the positions of pattern matches in a string. Also **str_locate_all**. *str_locate(fruit, "a")*

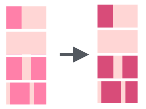
Mutate Strings



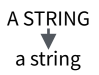
str_sub() **<-** value. Replace substrings by identifying the substrings with str_sub() and assigning into the results. *str_sub(fruit, 1, 3) <- "str"*



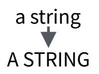
str_replace(string, **pattern**, replacement) Replace the first matched pattern in each string. *str_replace(fruit, "a", "-")*



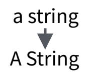
str_replace_all(string, **pattern**, replacement) Replace all matched patterns in each string. *str_replace_all(fruit, "a", "-")*



str_to_lower(string, locale = "en")[1] Convert strings to lower case. *str_to_lower(sentences)*

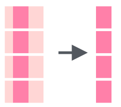


str_to_upper(string, locale = "en")[1] Convert strings to upper case. *str_to_upper(sentences)*

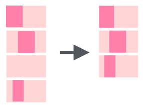


str_to_title(string, locale = "en")[1] Convert strings to title case. *str_to_title(sentences)*

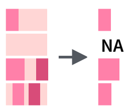
Subset Strings



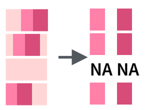
str_sub(string, start = 1L, end = -1L) Extract substrings from a character vector. *str_sub(fruit, 1, 3); str_sub(fruit, -2)*



str_subset(string, **pattern**) Return only the strings that contain a pattern match. *str_subset(fruit, "b")*

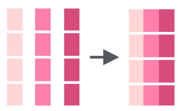


str_extract(string, **pattern**) Return the first pattern match found in each string, as a vector. Also **str_extract_all** to return every pattern match. *str_extract(fruit, "[aeiou]")*

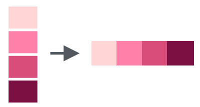


str_match(string, **pattern**) Return the first pattern match found in each string, as a matrix with a column for each ( ) group in pattern. Also **str_match_all**. *str_match(sentences, "(a|the) ([^]+)")*

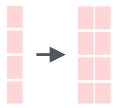
Join and Split



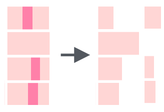
str_c(..., sep = "", collapse = NULL) Join multiple strings into a single string. *str_c(letters, LETTERS)*



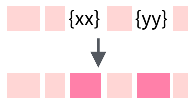
str_c(..., sep = "", **collapse = NULL**) Collapse a vector of strings into a single string. *str_c(letters, collapse = "")*



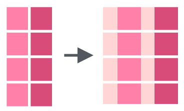
str_dup(string, times) Repeat strings times times. *str_dup(fruit, times = 2)*



str_split_fixed(string, **pattern**, n) Split a vector of strings into a matrix of substrings (splitting at occurrences of a pattern match). Also **str_split** to return a list of substrings. *str_split_fixed(fruit, " ", n=2)*

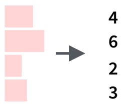


glue::glue(..., .sep = "", .envir = parent.frame(), .open = "{", .close = "}") Create a string from strings and {expressions} to evaluate. *glue::glue("Pi is {pi}")*

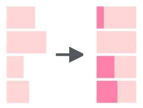


glue::glue_data(.x, ..., .sep = "", .envir = parent.frame(), .open = "{", .close = "}") Use a data frame, list, or environment to create a string from strings and {expressions} to evaluate. *glue::glue_data(mtcars, "{rownames(mtcars)} has {hp} hp")*

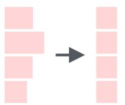
Manage Lengths



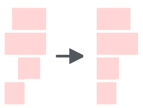
str_length(string) The width of strings (i.e. number of code points, which generally equals the number of characters). *str_length(fruit)*



str_pad(string, width, side = c("left", "right", "both"), pad = " ") Pad strings to constant width. *str_pad(fruit, 17)*

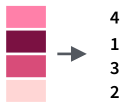


str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "...") Truncate the width of strings, replacing content with ellipsis. *str_trunc(fruit, 3)*

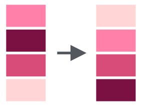


str_trim(string, side = c("both", "left", "right")) Trim whitespace from the start and/or end of a string. *str_trim(fruit)*

Order Strings



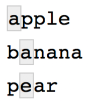
str_order(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...)[1] Return the vector of indexes that sorts a character vector. *x[str_order(x)]*



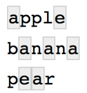
str_sort(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...)[1] Sort a character vector. *str_sort(x)*

Helpers

str_conv(string, encoding) Override the encoding of a string. *str_conv(fruit,"ISO-8859-1")*



str_view(string, **pattern**, match = NA) View HTML rendering of first regex match in each string. *str_view(fruit, "[aeiou]")*



str_view_all(string, **pattern**, match = NA) View HTML rendering of all regex matches. *str_view_all(fruit, "[aeiou]")*

str_wrap(string, width = 80, indent = 0, exdent = 0) Wrap strings into nicely formatted paragraphs. *str_wrap(sentences, 20)*

[1] See **bit.ly/ISO639-1** for a complete list of locales.

RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **stringr.tidyverse.org** • Diagrams from **@LVaudor** • stringr 1.2.0 • Updated: 2017-10

Need to Know

Pattern arguments in stringr are interpreted as regular expressions *after any special characters have been parsed.*

In R, you write regular expressions as *strings*, sequences of characters surrounded by quotes (**""**) or single quotes(**''**).

Some characters cannot be represented directly in an R string . These must be represented as **special characters**, sequences of characters that have a specific meaning., e.g.

Special Character	Represents
\\	\
\"	"
\n	new line

Run **?"'"** to see a complete list

Because of this, whenever a \ appears in a regular expression, you must write it as \\ in the string that represents the regular expression.

Use **writeLines**() to see how R views your string after all special characters have been parsed.

```
writeLines("\\.")
# \.

writeLines("\\ is a backslash")
# \ is a backslash
```

INTERPRETATION

Patterns in stringr are interpreted as regexs To change this default, wrap the pattern in one of:

regex(pattern, ignore_case = FALSE, multiline = FALSE, comments = FALSE, dotall = FALSE, ...) Modifies a regex to ignore cases, match end of lines as well of end of strings, allow R comments within regex's , and/or to have . match everything including \n.
str_detect("I", regex("i", TRUE))

fixed() Matches raw bytes but will miss some characters that can be represented in multiple ways (fast). *str_detect("\u0130", fixed("i"))*

coll() Matches raw bytes and will use locale specific collation rules to recognize characters that can be represented in multiple ways (slow).
str_detect("\u0130", coll("i", TRUE, locale = "tr"))

boundary() Matches boundaries between characters, line_breaks, sentences, or words.
str_split(sentences, boundary("word"))

Regular Expressions -

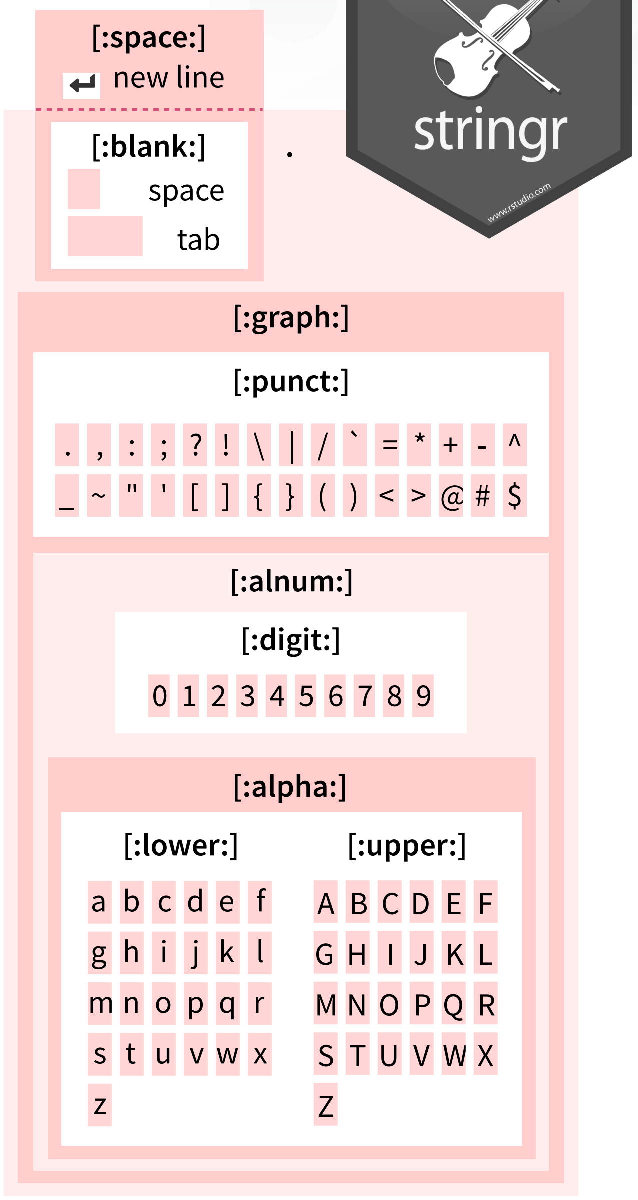
Regular expressions, or *regexps*, are a concise language for describing patterns in strings.

MATCH CHARACTERS

see <- function(rx) str_view_all("abc ABC 123\t.!?\\(){}\n", rx)

string (type this)	**regexp** (to mean this)	**matches** (which matches this)	**example**	
	a (etc.)	a (etc.)	see("a")	abc ABC 123 .!?\(){}
\\.	\.	.	see("\\.")	abc ABC 123 .!?\(){}
\\!	\!	!	see("\\!")	abc ABC 123 .!?\(){}
\\?	\?	?	see("\\?")	abc ABC 123 .!?\(){}
\\\\	\\	\	see("\\\\")	abc ABC 123 .!?\(){}
\\(	\(	(	see("\\(")	abc ABC 123 .!?\(){}
\\)	\)	)	see("\\)")	abc ABC 123 .!?\(){}
\\{	\{	{	see("\\{")	abc ABC 123 .!?\(){}
\\}	\}	}	see("\\}")	abc ABC 123 .!?\(){}
\\n	\n	new line (return)	see("\\n")	abc ABC 123 .!?\(){}
\\t	\t	tab	see("\\t")	abc ABC 123 .!?\(){}
\\s	\s	any whitespace (**\S** *for non-whitespaces)*	see("\\s")	abc ABC 123 .!?\(){}
\\d	\d	any digit (**\D** *for non-digits)*	see("\\d")	abc ABC 123 .!?\(){}
\\w	\w	any word character (**\W** *for non-word chars)*	see("\\w")	abc ABC 123 .!?\(){}
\\b	\b	word boundaries	see("\\b")	abc ABC 123 .!?\(){}
	[:digit:] [1]	digits	see("[:digit:]")	abc ABC 123 .!?\(){}
	[:alpha:] [1]	letters	see("[:alpha:]")	abc ABC 123 .!?\(){}
	[:lower:] [1]	lowercase letters	see("[:lower:]")	abc ABC 123 .!?\(){}
	[:upper:] [1]	uppercase letters	see("[:upper:]")	abc ABC 123 .!?\(){}
	[:alnum:] [1]	letters and numbers	see("[:alnum:]")	abc ABC 123 .!?\(){}
	[:punct:] [1]	punctuation	see("[:punct:]")	abc ABC 123 .!?\(){}
	[:graph:] [1]	letters, numbers, and punctuation	see("[:graph:]")	abc ABC 123 .!?\(){}
	[:space:] [1]	space characters (i.e. \s)	see("[:space:]")	abc ABC 123 .!?\(){}
	[:blank:] [1]	space and tab (but not new line)	see("[:blank:]")	abc ABC 123 .!?\(){}
	.	every character except a new line	see(".")	abc ABC 123 .!?\(){}

[1] Many base R functions require classes to be wrapped in a second set of **[ ]**, e.g. **[[:digit:]]**



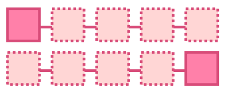
ALTERNATES

alt <- function(rx) str_view_all("abcde", rx)

regexp	**matches**	**example**	
ab|d	or	alt("ab|d")	abcde
[abe]	one of	alt("[abe]")	abcde
[^abe]	anything but	alt("[^abe]")	abcde
[a-c]	range	alt("[a-c]")	abcde

ANCHORS

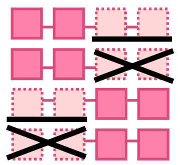
anchor <- function(rx) str_view_all("aaa", rx)



regexp	**matches**	**example**	
^a	start of string	anchor("^a")	aaa
a$	end of string	anchor("a$")	aaa

LOOK AROUNDS

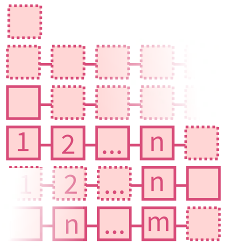
look <- function(rx) str_view_all("bacad", rx)



regexp	**matches**	**example**	
a(?=c)	followed by	look("a(?=c)")	bacad
a(?!c)	not followed by	look("a(?!c)")	bacad
(?<=b)a	preceded by	look("(?<=b)a")	bacad
(?<!b)a	not preceded by	look("(?<!b)a")	bacad

QUANTIFIERS

quant <- function(rx) str_view_all(".a.aa.aaa", rx)



regexp	**matches**	**example**	
a?	zero or one	quant("a?")	.a.aa.aaa
a*	zero or more	quant("a*")	.a.aa.aaa
a+	one or more	quant("a+")	.a.aa.aaa
a{n}	exactly **n**	quant("a{2}")	.a.aa.aaa
a{n, }	**n** or more	quant("a{2,}")	.a.aa.aaa
a{n, m}	between **n** and **m**	quant("a{2,4}")	.a.aa.aaa

GROUPS

ref <- function(rx) str_view_all("abbaab", rx)

Use parentheses to set precedent (order of evaluation) and create groups

regexp	**matches**	**example**	
(ab|d)e	sets precedence	alt("(ab|d)e")	abcde

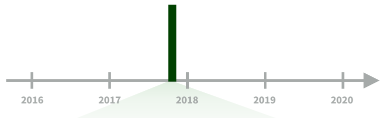
Use an escaped number to refer to and duplicate parentheses groups that occur earlier in a pattern. Refer to each group by its order of appearance

string (type this)	**regexp** (to mean this)	**matches** (which matches this)	**example** (the result is the same as ref("abba"))	
\\1	\1 (etc.)	first () group, etc.	ref("(a)(b)\\2\\1")	abbaab

RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **stringr.tidyverse.org** • Diagrams from **@LVaudor** • stringr 1.2.0 • Updated: 2017-10

Dates and times with lubridate : : CHEAT SHEET

Date-times



2017-11-28 12:00:00

2017-11-28 12:00:00

A **date-time** is a point on the timeline, stored as the number of seconds since 1970-01-01 00:00:00 UTC

*dt <- **as_datetime**(1511870400)*
## "2017-11-28 12:00:00 UTC"

2017-11-28

A **date** is a day stored as the number of days since 1970-01-01

*d <- **as_date**(17498)*
## "2017-11-28"

12:00:00

An hms is a **time** stored as the number of seconds since 00:00:00

*t <- hms::**as.hms**(85)*
## 00:01:25

PARSE DATE-TIMES (Convert strings or numbers to date-times)

1. Identify the order of the year (**y**), month (**m**), day (**d**), hour (**h**), minute (**m**) and second (**s**) elements in your data
2. Use the function below whose name replicates the order. Each accepts a wide variety of input formats.

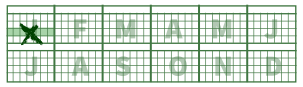
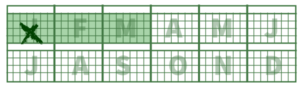
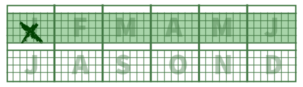
2017-11-28T14:02:00	**ymd_hms**(), **ymd_hm**(), **ymd_h**(). *ymd_hms("2017-11-28T14:02:00")*
2017-22-12 10:00:00	**ydm_hms**(), **ydm_hm**(), **ydm_h**(). *ydm_hms("2017-22-12 10:00:00")*
11/28/2017 1:02:03	**mdy_hms**(), **mdy_hm**(), **mdy_h**(). *mdy_hms("11/28/2017 1:02:03")*
1 Jan 2017 23:59:59	**dmy_hms**(), **dmy_hm**(), **dmy_h**(). *dmy_hms("1 Jan 2017 23:59:59")*
20170131	**ymd**(), **ydm**(). *ymd(20170131)*
July 4th, 2000	**mdy**(), **myd**(). *mdy("July 4th, 2000")*
4th of July '99	**dmy**(), **dym**(). *dmy("4th of July '99")*
2001: Q3	**yq**() Q for quarter. *yq("2001: Q3")*
2:01	hms::**hms**() Also lubridate::**hms**(), **hm**() and **ms**(), which return periods.* *hms::hms(sec = 0, min= 1, hours = 2)*
2017.5	**date_decimal**(decimal, tz = "UTC") Q for quarter. *date_decimal(2017.5)*
	now(tzone = "") Current time in tz (defaults to system tz). *now()*
	today(tzone = "") Current date in a tz (defaults to system tz). *today()*
	fast_strptime() Faster strptime. *fast_strptime('9/1/01', '%y/%m/%d')*
	parse_date_time() Easier strptime. *parse_date_time("9/1/01", "ymd")*

GET AND SET COMPONENTS

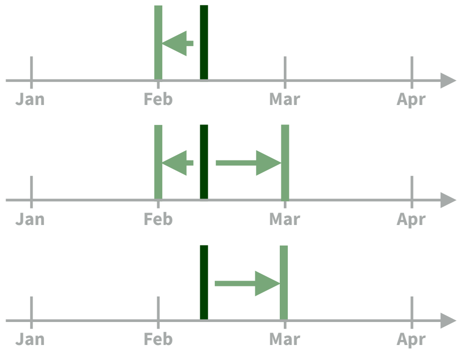
Use an accessor function to get a component.

Assign into an accessor function to change a component in place.

d ## "2017-11-28"
day(d) ## 28
day(d) <- 1
d ## "2017-11-01"

2018-01-31 11:59:59	**date**(x) Date component. *date(dt)*
2018-01-31 11:59:59	**year**(x) Year. *year(dt)* **isoyear**(x) The ISO 8601 year. **epiyear**(x) Epidemiological year.
2018-**01**-31 11:59:59	**month**(x, label, abbr) Month. *month(dt)*
2018-01-**31** 11:59:59	**day**(x) Day of month. *day(dt)* **wday**(x,label,abbr) Day of week. **qday**(x) Day of quarter.
2018-01-31 **11**:59:59	**hour**(x) Hour. *hour(dt)*
2018-01-31 11:**59**:59	**minute**(x) Minutes. *minute(dt)*
2018-01-31 11:59:**59**	**second**(x) Seconds. *second(dt)*
	**week**(x) Week of the year. *week(dt)* **isoweek**() ISO 8601 week. **epiweek**() Epidemiological week.
	**quarter**(x, with_year = FALSE) Quarter. *quarter(dt)*
	**semester**(x, with_year = FALSE) Semester. *semester(dt)*
☼ | ◐	**am**(x) Is it in the am? *am(dt)* **pm**(x) Is it in the pm? *pm(dt)*
	dst(x) Is it daylight savings? *dst(d)*
	leap_year(x) Is it a leap year? *leap_year(d)*
	update(object, ..., simple = FALSE) *update(dt, mday = 2, hour = 1)*

Round Date-times



floor_date(x, unit = "second")
Round down to nearest unit.
floor_date(dt, unit = "month")

round_date(x, unit = "second")
Round to nearest unit.
round_date(dt, unit = "month")

ceiling_date(x, unit = "second", change_on_boundary = NULL)
Round up to nearest unit.
ceiling_date(dt, unit = "month")

rollback(dates, roll_to_first = FALSE, preserve_hms = TRUE)
Roll back to last day of previous month. *rollback(dt)*

Stamp Date-times

stamp() Derive a template from an example string and return a new function that will apply the template to date-times. Also **stamp_date**() and **stamp_time**().

1. Derive a template, create a function
   sf <- stamp("Created Sunday, Jan 17, 1999 3:34")
2. Apply the template to dates
   sf(ymd("2010-04-05"))
   ## [1] "Created Monday, Apr 05, 2010 00:00"

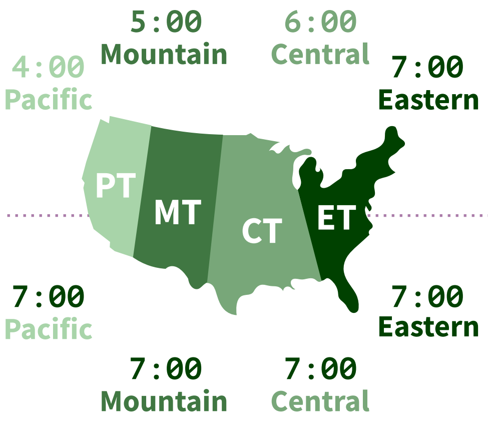
Tip: use a date with day > 12

Time Zones

R recognizes ~600 time zones. Each encodes the time zone, Daylight Savings Time, and historical calendar variations for an area. R assigns *one* time zone per vector.

Use the **UTC** time zone to avoid Daylight Savings.

OlsonNames() Returns a list of valid time zone names. *OlsonNames()*



with_tz(time, tzone = "") Get the **same instant** in a new time zone (a new clock time).
with_tz(dt, "US/Pacific")

force_tz(time, tzone = "") Get the **same clock time** in a new time zone (a new instant).
force_tz(dt, "US/Pacific")

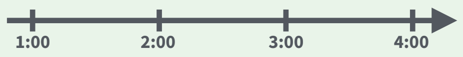
RStudio® is a trademark of RStudio, Inc. • CC BY RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **lubridate.tidyverse.org** • lubridate 1.6.0 • Updated: 2017-12

Math with Date-times — Lubridate provides three classes of timespans to facilitate math with dates and date-times

Math with date-times relies on the **timeline**, which behaves inconsistently. Consider how the timeline behaves during:

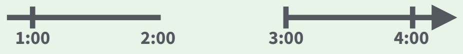
A normal day

nor <- ymd_hms("2018-01-01 01:30:00",tz="US/Eastern")



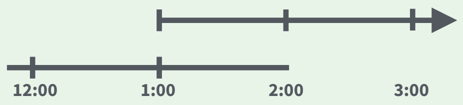
The start of daylight savings (spring forward)

gap <- ymd_hms("2018-03-11 01:30:00",tz="US/Eastern")



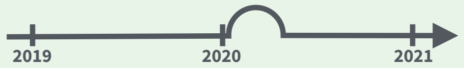
The end of daylight savings (fall back)

lap <- ymd_hms("2018-11-04 00:30:00",tz="US/Eastern")



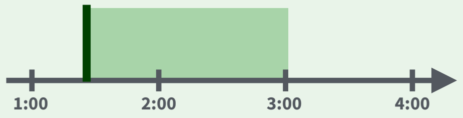
Leap years and leap seconds

leap <- ymd("2019-03-01")

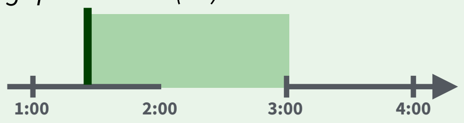


Periods track changes in clock times, which ignore time line irregularities.

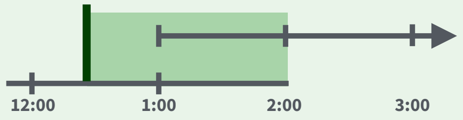
normal + minutes(90)



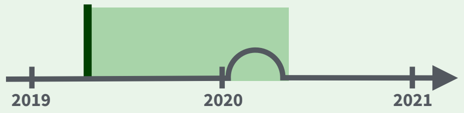
gap + minutes(90)



lap + minutes(90)

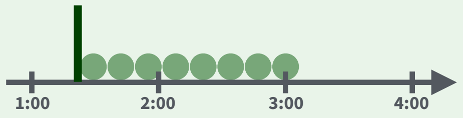


leap + years(1)

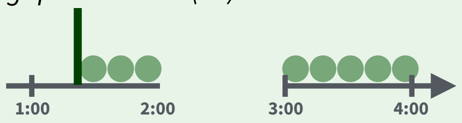


Durations track the passage of physical time, which deviates from clock time when irregularities occur.

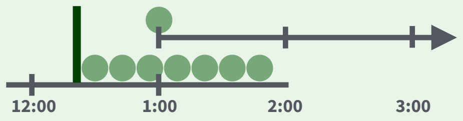
normal + dminutes(90)



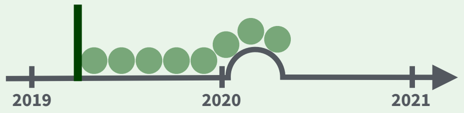
gap + dminutes(90)



lap + dminutes(90)

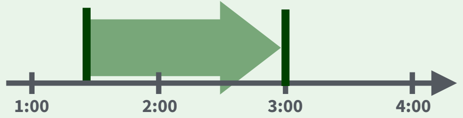


leap + dyears(1)

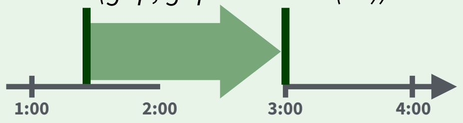


Intervals represent specific intervals of the timeline, bounded by start and end date-times.

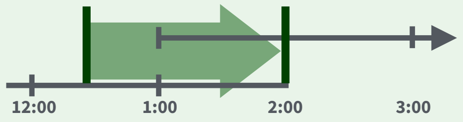
interval(normal, normal + minutes(90))



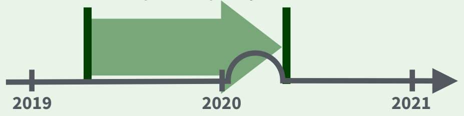
interval(gap, gap + minutes(90))



interval(lap, lap + minutes(90))



interval(leap, leap + years(1))



Not all years are 365 days due to **leap days**.

Not all minutes are 60 seconds due to **leap seconds**.

It is possible to create an imaginary date by adding **months**, e.g. February 31st

```
jan31 <- ymd(20180131)
jan31 + months(1)
## NA
```

%m+% and **%m-%** will roll imaginary dates to the last day of the previous month.

```
jan31 %m+% months(1)
## "2018-02-28"
```

add_with_rollback(e1, e2, roll_to_first = TRUE) will roll imaginary dates to the first day of the new month.

```
add_with_rollback(jan31, months(1),
roll_to_first = TRUE)
## "2018-03-01"
```

PERIODS

Add or subtract periods to model events that happen at specific clock times, like the NYSE opening bell.

Make a period with the name of a time unit ***pluralized***, e.g.

```
p <- months(3) + days(12)
p
"3m 12d 0H 0M 0S"
```

Number of months | Number of days | etc.

years(x = 1) x years.
months(x) x months.
weeks(x = 1) x weeks.
days(x = 1) x days.
hours(x = 1) x hours.
minutes(x = 1) x minutes.
seconds(x = 1) x seconds.
milliseconds(x = 1) x milliseconds.
microseconds(x = 1) x microseconds
nanoseconds(x = 1) x milliseconds.
picoseconds(x = 1) x picoseconds.

period(num = NULL, units = "second", ...) An automation friendly period constructor. *period(5, unit = "years")*

as.period(x, unit) Coerce a timespan to a period, optionally in the specified units. Also **is.period**(). *as.period(i)*

period_to_seconds(x) Convert a period to the "standard" number of seconds implied by the period. Also **seconds_to_period**(). *period_to_seconds(p)*

DURATIONS

Add or subtract durations to model physical processes, like battery life. Durations are stored as seconds, the only time unit with a consistent length. **Difftimes** are a class of durations found in base R.

Make a duration with the name of a period prefixed with a ***d***, e.g.

```
dd <- ddays(14)
dd
"1209600s (~2 weeks)"
```

Exact length in seconds | Equivalent in common units

dyears(x = 1) 31536000x seconds.
dweeks(x = 1) 604800x seconds.
ddays(x = 1) 86400x seconds.
dhours(x = 1) 3600x seconds.
dminutes(x = 1) 60x seconds.
dseconds(x = 1) x seconds.
dmilliseconds(x = 1) x × 10^{-3} seconds.
dmicroseconds(x = 1) x × 10^{-6} seconds.
dnanoseconds(x = 1) x × 10^{-9} seconds.
dpicoseconds(x = 1) x × 10^{-12} seconds.

duration(num = NULL, units = "second", ...) An automation friendly duration constructor. *duration(5, unit = "years")*

as.duration(x, …) Coerce a timespan to a duration. Also **is.duration**(), **is.difftime**(). *as.duration(i)*

make_difftime(x) Make difftime with the specified number of units. *make_difftime(99999)*

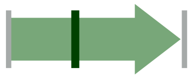
INTERVALS

Divide an interval by a duration to determine its physical length, divide and interval by a period to determine its implied length in clock time.

Make an interval with **interval**() or **%--%**, e.g.

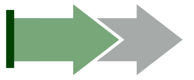
Start Date | End Date

```
i <- interval(ymd("2017-01-01"), d)     ## 2017-01-01 UTC--2017-11-28 UTC
j <- d %--% ymd("2017-12-31")           ## 2017-11-28 UTC--2017-12-31 UTC
```

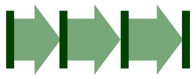


a **%within%** b Does interval or date-time *a* fall within interval *b*? *now() %within% i*

int_start(int) Access/set the start date-time of an interval. Also **int_end**(). *int_start(i) <- now(); int_start(i)*

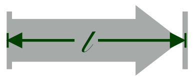


int_aligns(int1, int2) Do two intervals share a boundary? Also **int_overlaps**(). *int_aligns(i, j)*

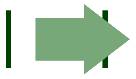


int_diff(times) Make the intervals that occur between the date-times in a vector. *v <-c(dt, dt + 100, dt + 1000)); int_diff(v)*

int_flip(int) Reverse the direction of an interval. Also **int_standardize**(). *int_flip(i)*



int_length(int) Length in seconds. *int_length(i)*



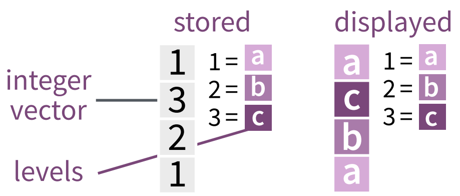
int_shift(int, by) Shifts an interval up or down the timeline by a timespan. *int_shift(i, days(-1))*

as.interval(x, start, …) Coerce a timespans to an interval with the start date-time. Also **is.interval**(). *as.interval(days(1), start = now())*

Factors with forcats : : CHEAT SHEET

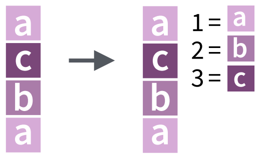
The **forcats** package provides tools for working with factors, which are R's data structure for categorical data.

Factors



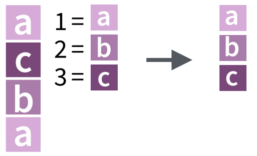
R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the levels associated with them.

Create a factor with factor()



factor(x = character(), levels, labels = levels, exclude = NA, ordered = is.ordered(x), nmax = NA**)** Convert a vector to a factor. Also **as_factor()**.
f <- factor(c("a", "c", "b", "a"), levels = c("a", "b", "c"))

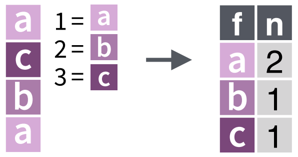
Return its levels with levels()



levels(x**)** Return/set the levels of a factor. levels(f); levels(f) <- c("x","y","z")

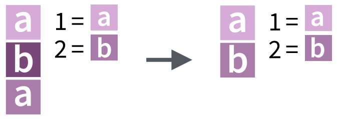
Use unclass() to see its structure

Inspect Factors



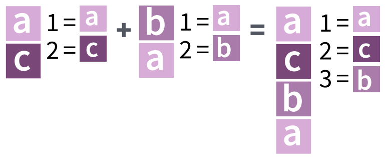
fct_count(f, sort = FALSE, prop = FALSE**)** Count the number of values with each level. fct_count(f)

fct_match(f, lvls**)** Check for lvls in f. fct_match(f, "a")

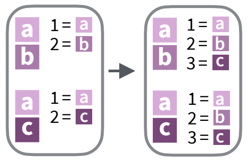


fct_unique(f**)** Return the unique values, removing duplicates. fct_unique(f)

Combine Factors

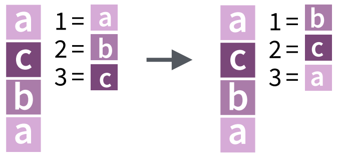


fct_c(…**)** Combine factors with different levels. Also **fct_cross()**.
f1 <- factor(c("a", "c"))
f2 <- factor(c("b", "a"))
fct_c(f1, f2)

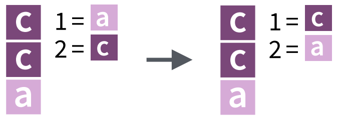


fct_unify(fs, levels = lvls_union(fs)**)** Standardize levels across a list of factors. fct_unify(list(f2, f1))

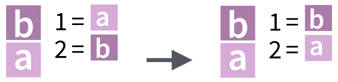
Change the order of levels



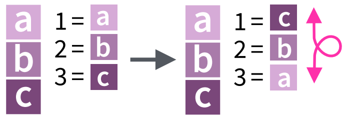
fct_relevel(.f, ..., after = 0L**)** Manually reorder factor levels.
fct_relevel(f, c("b", "c", "a"))



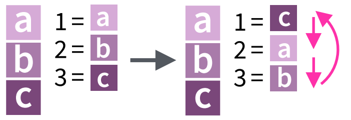
fct_infreq(f, ordered = NA**)** Reorder levels by the frequency in which they appear in the data (highest frequency first). Also **fct_inseq()**.
f3 <- factor(c("c", "c", "a"))
fct_infreq(f3)



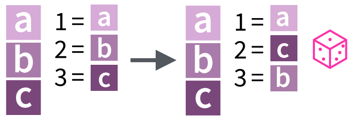
fct_inorder(f, ordered = NA**)** Reorder levels by order in which they appear in the data.
fct_inorder(f2)



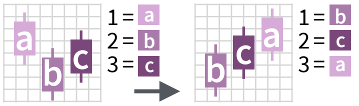
fct_rev(f**)** Reverse level order.
f4 <- factor(c("a","b","c"))
fct_rev(f4)



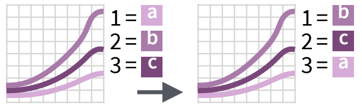
fct_shift(f**)** Shift levels to left or right, wrapping around end.
fct_shift(f4)



fct_shuffle(f, n = 1L**)** Randomly permute order of factor levels.
fct_shuffle(f4)

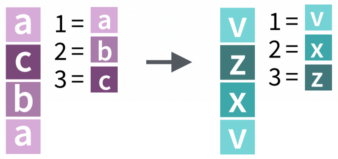


fct_reorder(.f, .x, .fun = median, ..., .desc = FALSE**)** Reorder levels by their relationship with another variable.
boxplot(data = PlantGrowth, weight ~ reorder(group, weight))

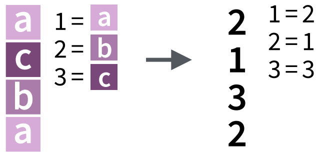


fct_reorder2(.f, .x, .y, .fun = last2, ..., .desc = TRUE**)** Reorder levels by their final values when plotted with two other variables.
ggplot(diamonds,aes(carat, price, color = fct_reorder2(color, carat, price))) + geom_smooth()

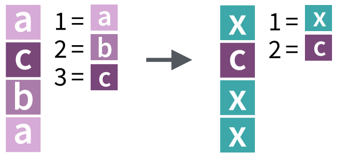
Change the value of levels



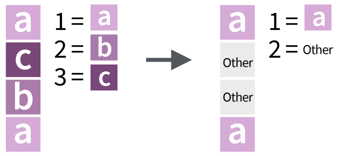
fct_recode(.f, ...**)** Manually change levels. Also **fct_relabel()** which obeys purrr::map syntax to apply a function or expression to each level.
fct_recode(f, v = "a", x = "b", z = "c")
fct_relabel(f, ~ paste0("x", .x))



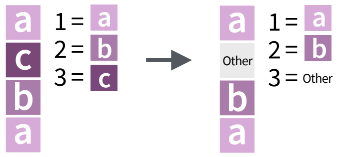
fct_anon(f, prefix = ""**)** Anonymize levels with random integers.
fct_anon(f)



fct_collapse(.f, …, other_level = NULL**)** Collapse levels into manually defined groups.
fct_collapse(f, x = c("a", "b"))

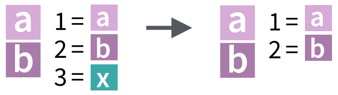


fct_lump_min(f, min, w = NULL, other_level = "Other"**)** Lumps together factors that appear fewer than min times. Also **fct_lump_n()**, **fct_lump_prop()**, and **fct_lump_lowfreq()**.
fct_lump_min(f, min = 2)

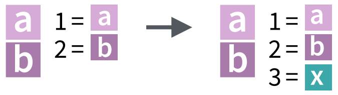


fct_other(f, keep, drop, other_level = "Other"**)** Replace levels with "other."
fct_other(f, keep = c("a", "b"))

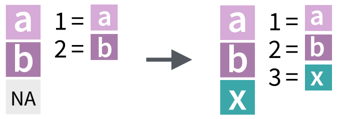
Add or drop levels



fct_drop(f, only**)** Drop unused levels.
f5 <- factor(c("a","b"),c("a","b","x"))
f6 <- fct_drop(f5)



fct_expand(f, …**)** Add levels to a factor.
fct_expand(f6, "x")



fct_explicit_na(f, na_level="(Missing)"**)** Assigns a level to NAs to ensure they appear in plots, etc.
fct_explicit_na(factor(c("a", "b", NA)))

RStudio® is a trademark of RStudio, PBC • CC BY SA RStudio • info@rstudio.com • 844-448-1212 • rstudio.com • Learn more at **forcats.tidyverse.org** • Diagrams inspired by **@LVaudor** on Twitter • forcats 0.5.1 • Updated: 2021-07

Package Development: : CHEAT SHEET

devtools

Package Structure

A package is a convention for organizing files into directories.

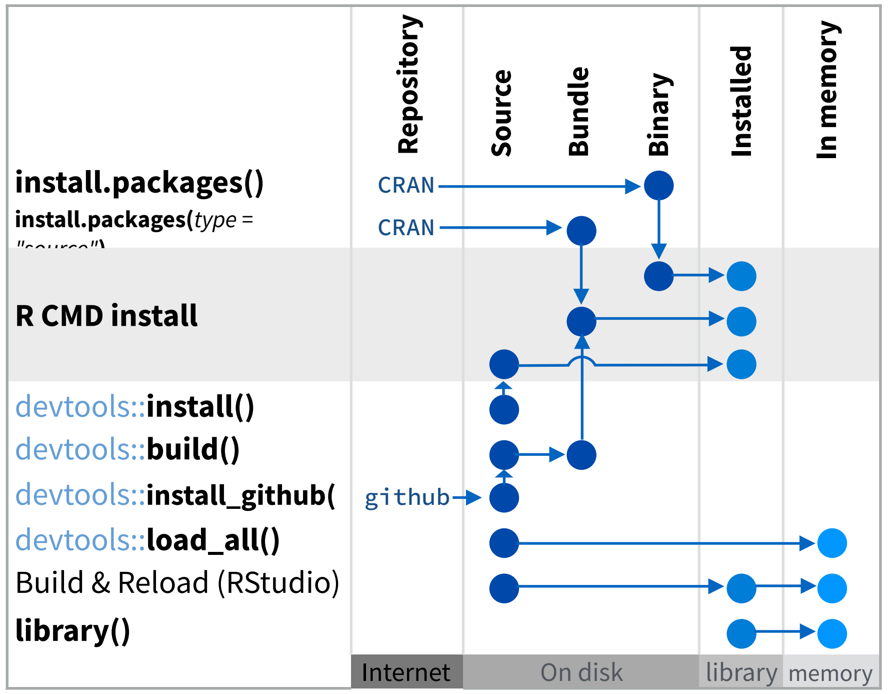
This sheet shows how to work with the 7 most common parts of an R package:

Package	
DESCRIPTION	SETUP
R/	WRITE CODE
tests/	TEST
man/	DOCUMENT
vignettes/	TEACH
data/	ADD DATA
NAMESPACE	ORGANIZE

The contents of a package can be stored on disk as a:

- **source** - a directory with sub-directories (as above)
- **bundle** - a single compressed file (*.tar.gz*)
- **binary** - a single compressed file optimized for a specific OS

Or installed into an R library (loaded into memory during an R session) or archived online in a repository. Use the functions below to move between these states.



devtools::**add_build_ignore(**"*file*"**)**

Adds file to .Rbuildignore, a list of files that will not be included when package is built.

Setup (DESCRIPTION)

The DESCRIPTION file describes your work, sets up how your package will work with other packages, and applies a copyright.

☑ You must have a DESCRIPTION file

☑ Add the packages that yours relies on with

devtools::**use_package()**

Adds a package to the Imports or Suggests field

CC0	**MIT**	**GPL-2**
No strings attached.	MIT license applies to your code if re-shared.	GPL-2 license applies to your code, *and all code anyone bundles with it*, if re-shared.

```
Package: mypackage
Title: Title of Package
Version: 0.1.0
Authors@R: person("Hadley", "Wickham", email =
    "hadley@me.com", role = c("aut", "cre"))
Description: What the package does (one paragraph)
Depends: R (>= 3.1.0)
License: GPL-2
LazyData: true
Imports:
    dplyr (>= 0.4.0),
    ggvis (>= 0.2)
Suggests:
    knitr (>= 0.1.0)
```

Import packages that your package *must have* to work. R will install them when it installs your package.

Suggest packages that are not very essential to yours. Users can install them manually, or not, as they like.

Write Code (R/)

All of the R code in your package goes in R/. A package with just an R/ directory is still a very useful package.

☑ Create a new package project with

devtools::**create(**"path/to/name"**)**

Create a template to develop into a package.

☑ Save your code in R/ as scripts (extension .R)

WORKFLOW

1. Edit your code.
2. Load your code with one of

   devtools::**load_all()**

   Re-loads all *saved* files in R/ into memory.

   Ctrl/Cmd + Shift + L (keyboard shortcut)

   Saves all open files then calls load_all().

3. Experiment in the console.
4. Repeat.

- Use consistent style with **r-pkgs.had.co.nz/r.html#style**
- Click on a function and press **F2** to open its definition
- Search for a function with **Ctrl + .**

Visit **r-pkgs.had.co.nz** to learn much more about writing and publishing packages for R

Test (tests/)

Use tests/ to store tests that will alert you if your code breaks.

☑ Add a **tests/** directory

☑ Import **testthat** with devtools::**use_testthat()**, which sets up package to use automated tests with testthat

☑ Write tests with **context()**, **test()**, and expect statements

☑ Save your tests as .R files in **tests/testthat/**

WORKFLOW

1. Modify your code or tests.
2. Test your code with one of

   devtools::**test()**

   Runs all tests in tests/

   Ctrl/Cmd + Shift + T

   (keyboard shortcut)

3. Repeat until all tests pass

Example Test

```
context("Arithmetic")

test_that("Math works", {
  expect_equal(1 + 1, 2)
  expect_equal(1 + 2, 3)
  expect_equal(1 + 3, 4)
})
```

Expect statement	Tests
expect_equal()	is equal within small numerical tolerance?
expect_identical()	is exactly equal?
expect_match()	matches specified string or regular
expect_output()	prints specified output?
expect_message()	displays specified message?
expect_warning()	displays specified warning?
expect_error()	throws specified error?
expect_is()	output inherits from certain class?
expect_false()	returns FALSE?
expect_true()	returns TRUE?

R Studio

Document (🗀 man/)

🗀 man/ contains the documentation for your functions, the help pages in your package.

☑ Use roxygen comments to document each function beside its definition

☑ Document the name of each exported data set

☑ Include helpful examples for each function

WORKFLOW

1. Add roxygen comments in your .R files
2. Convert roxygen comments into documentation with one of:

   devtools::**document()**

   Converts roxygen comments to .Rd files and places them in 🗀 man/. Builds NAMESPACE.

   Ctrl/Cmd + Shift + D (Keyboard Shortcut)

3. Open help pages with **?** to preview documentation
4. Repeat

.Rd FORMATTING TAGS

```
\emph{italic text}
\strong{bold text}
\code{function(args)}
\pkg{package}

\dontrun{code}
\dontshow{code}
\donttest{code}

\deqn{a + b (block)}
\eqn{a + b (inline)}
```

```
\email{name@@foo.com}
\href{url}{display}
\url{url}

\link[=dest]{display}
\linkS4class{class}
\code{\link{function}}
\code{\link[package]{function}}

\tabular{lcr}{
  left \tab centered \tab right \cr
  cell \tab cell     \tab cell  \cr
}
```

ROXYGEN2

The **roxygen2** package lets you write documentation inline in your .R files with a shorthand syntax. devtools implements roxygen2 to make documentation.

- Add roxygen documentation as comment lines that begin with **#'**.
- Place comment lines directly above the code that defines the object documented.
- Place a roxygen **@** tag (right) after **#'** to supply a specific section of documentation.
- Untagged lines will be used to generate a title, description, and details section (in that order)

```
#' 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)
#' @export
add <- function(x, y) {
  x + y
}
```

COMMON ROXYGEN TAGS

@aliases	@inheritParams	**@seealso**	
@concepts	@keywords	@format	
@describeIn	**@param**	@source	data
@examples	@rdname	@include	
@export	**@return**	@slot	S4
@family	@section	@field	RC

Teach (🗀 vignettes/)

🗀 vignettes/ holds documents that teach your users how to solve real problems with your tools.

☑ Create a 🗀 vignettes/ directory and a template vignette with

devtools::**use_vignette()**

Adds template vignette as vignettes/my-vignette.Rmd.

☑ Append YAML headers to your vignettes (like right)

☑ Write the body of your vignettes in R Markdown (rmarkdown.rstudio.com)

```
---
title: "Vignette Title"
author: "Vignette Author"
date: "`r Sys.Date()`"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  \usepackage[utf8]{inputenc}
---
```

Add Data (🗀 data/)

The 🗀 data/ directory allows you to include data with your package.

☑ Save data as .Rdata files (suggested)

☑ Store data in one of **data/**, **R/Sysdata.rda**, **inst/extdata**

☑ Always use **LazyData: true** in your DESCRIPTION file.

devtools::**use_data()**

Adds a data object to data/ (R/Sysdata.rda if **internal = TRUE**)

devtools::**use_data_raw()**

Adds an R Script used to clean a data set to data-raw/. Includes data-raw/ on .Rbuildignore.

Store data in

- **data/** to make data available to package users
- **R/sysdata.rda** to keep data internal for use by your functions.
- **inst/extdata** to make raw data available for loading and parsing examples. Access this data with **system.file()**

Organize (🗎 NAMESPACE)

The 🗎 NAMESPACE file helps you make your package self-contained: it won't interfere with other packages, and other packages won't interfere with it.

☑ Export functions for users by placing **@export** in their roxygen comments

☑ Import objects from other packages with **package::object** (recommended) or **@import**, **@importFrom**, **@importClassesFrom**, **@importMethodsFrom** (not always recommended)

WORKFLOW

1. Modify your code or tests.
2. Document your package (devtools::**document()**)
3. Check NAMESPACE
4. Repeat until NAMESPACE is correct

SUBMIT YOUR PACKAGE

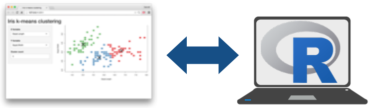
r-pkgs.had.co.nz/release.html

RStudio

Shiny : : CHEAT SHEET

Basics

A Shiny app is a web page (UI) connected to a computer running a live R session (Server)



Users can manipulate the UI, which will cause the server to update the UI's displays (by running R code).

APP TEMPLATE

Begin writing a new app with this template. Preview the app by running the code at the R command line.

```
library(shiny)
ui <- fluidPage()
server <- function(input, output){}
shinyApp(ui = ui, server = server)
```

- ui - nested R functions that assemble an HTML user interface for your app
- server - a function with instructions on how to build and rebuild the R objects displayed in the UI
- shinyApp - combines ui and server into an app. Wrap with runApp() if calling from a sourced script or inside a function.

SHARE YOUR APP - in three ways:

1. Host it on shinyapps.io, a cloud based service from RStudio. To do so:
   - Create a free or professional account at http://shinyapps.io
   - Click the Publish icon in RStudio IDE, or run: rsconnect::deployApp("<path to directory>")
2. Purchase RStudio Connect, a publishing platform for R and Python. www.rstudio.com/products/connect/
3. Build your own Shiny Server https://rstudio.com/products/shiny/shiny-server/

Building an App

Complete the template by adding arguments to fluidPage() and a body to the server function.

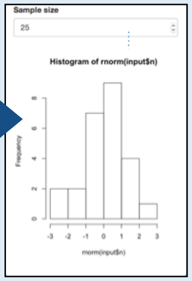
Add inputs to the UI with *Input() functions

Add outputs with *Output() functions

Tell server how to render outputs with R in the server function. To do this:

1. Refer to outputs with output$<id>
2. Refer to inputs with input$<id>
3. Wrap code in a render*() function before saving to output

```
library(shiny)

ui <- fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)

server <- function(input, output) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}

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



Save your template as app.R. Alternatively, split your template into two files named ui.R and server.R.

```
library(shiny)
ui <- fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)
server <- function(input, output) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}
shinyApp(ui = ui, server = server)
```

```
# ui.R
fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)
```

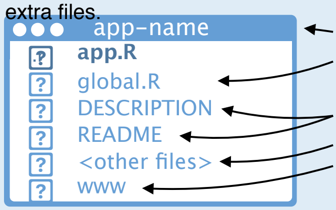
ui.R contains everything you would save to ui.

```
# server.R
function(input, output) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}
```

server.R ends with the function you would save to server.

No need to call shinyApp().

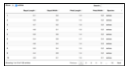
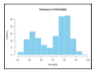
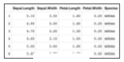
Save each app as a directory that holds an app.R file (or a server.R file and a ui.R file) plus optional extra files.



- app-name — The directory name is the name of the app
- app.R
- global.R — (optional) defines objects available to both ui.R and server.R
- DESCRIPTION — (optional) used in showcase mode
- README — (optional) used in showcase mode
- <other files> — (optional) data, scripts, etc.
- www — (optional) directory of files to share with web browsers (images, CSS, .js, etc.) Must be named "www"

Launch apps with runApp(<path to directory>)

Outputs - render*() and *Output() functions work together to add R output to the UI

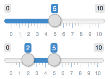
		works with	
	DT::renderDataTable(expr, options, callback, escape, env, quoted)		dataTableOutput(outputId, icon, …)
	renderImage(expr, env, quoted, deleteFile)		imageOutput(outputId, width, height, click, dblclick, hover, hoverDelay, inline, hoverDelayType, brush, clickId, hoverId)
	renderPlot(expr, width, height, res, …, env, quoted, func)		plotOutput(outputId, width, height, click, dblclick, hover, hoverDelay, inline, hoverDelayType, brush, clickId, hoverId)
	renderPrint(expr, env, quoted, func, width)		verbatimTextOutput(outputId)
	renderTable(expr,…, env, quoted, func)		tableOutput(outputId)
foo	renderText(expr, env, quoted, func)		textOutput(outputId, container, inline)

	renderUI(expr, env, quoted, func)	&	uiOutput(outputId, inline, container, …)
			htmlOutput(outputId, inline, container, …)

Inputs

collect values from the user

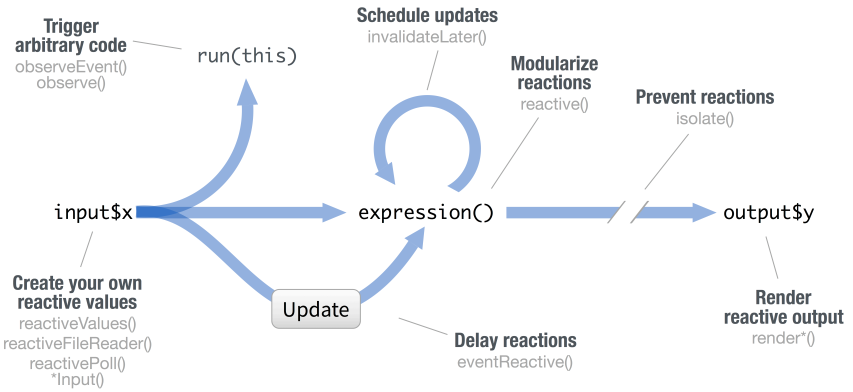
Access the current value of an input object with input$<inputId>. Input values are reactive.

Action	actionButton(inputId, label, icon, …)
Link	actionLink(inputId, label, icon, …)
☑ Choice 1 ☑ Choice 2 □ Choice 3	checkboxGroupInput(inputId, label, choices, selected, inline)
☑ Check me	checkboxInput(inputId, label, value)
	dateInput(inputId, label, value, min, max, format, startview, weekstart, language)
	dateRangeInput(inputId, label, start, end, min, max, format, startview, weekstart, language, separator)
Choose File	fileInput(inputId, label, multiple, accept)
1	numericInput(inputId, label, value, min, max, step)
••••••••	passwordInput(inputId, label, value)
● Choice A ○ Choice B ○ Choice C	radioButtons(inputId, label, choices, selected, inline)
Choice 1 Choice 1 Choice 2	selectInput(inputId, label, choices, selected, multiple, selectize, width, size) (also selectizeInput())
	sliderInput(inputId, label, min, max, value, step, round, format, locale, ticks, animate, width, sep, pre, post)
Apply Changes	submitButton(text, icon) (Prevents reactions across entire app)
Enter text	textInput(inputId, label, value)

RStudio

Reactivity

Reactive values work together with reactive functions. Call a reactive value from within the arguments of one of these functions to avoid the error Operation not allowed without an active reactive context.



Trigger arbitrary code
observeEvent()
observe()

run(this)

Schedule updates
invalidateLater()

Modularize reactions
reactive()

Prevent reactions
isolate()

input$x

expression()

output$y

Create your own reactive values
reactiveValues()
reactiveFileReader()
reactivePoll()
*Input()

Update

Delay reactions
eventReactive()

Render reactive output
render*()

CREATE YOUR OWN REACTIVE VALUES

```
# example snippets

ui <- fluidPage(
 textInput("a","","A")
)

server <- function(input,output){
 rv <- reactiveValues()
 rv$number <- 5
}
```

*Input() functions
(see front page)

reactiveValues(...)

Each input function creates a reactive value stored as input$<inputId>

reactiveValues() creates a list of reactive values whose values you can set.

RENDER REACTIVE OUTPUT

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 textOutput("b")
)

server <- function(input,output)
{
 output$b <-
  renderText({
   input$a
  })
}

shinyApp(ui, server)
```

render*() functions
(see front page)

Builds an object to display. Will rerun code in body to rebuild the object whenever a reactive value in the code changes.

Save the results to output$<outputId>

PREVENT REACTIONS

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 textOutput("b")
)

server <- function(input,output)
{
 output$b <-
  renderText({
   isolate({input$a})
  })
}

shinyApp(ui, server)
```

isolate(expr)

Runs a code block. Returns a non-reactive copy of the results.

TRIGGER ARBITRARY CODE

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 actionButton("go","Go")
)

server <- function(input,output){
 observeEvent(input$go,{
  print(input$a)
 })
}

shinyApp(ui, server)
```

observeEvent(eventExpr, handlerExpr, event.env, event.quoted, handler.env, handler.quoted, labe, suspended, priority, domain, autoDestroy, ignoreNULL)

Runs code in 2nd argument when reactive values in 1st argument change. See observe() for alternative.

MODULARIZE REACTIONS

```
ui <- fluidPage(
 textInput("a","","A"),
 textInput("z","","Z"),
 textOutput("b"))

server <- function(input,output){
 re <- reactive({
  paste(input$a,input$z)})
 output$b <- renderText({
  re()
 })
}
shinyApp(ui, server)
```

reactive(x, env, quoted, label, domain)

Creates a reactive expression that

- caches its value to reduce computation
- can be called by other code
- notifies its dependencies when it ha been invalidated

Call the expression with function syntax, e.g. re()

DELAY REACTIONS

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 actionButton("go","Go"),
 textOutput("b")
)

server <- function(input,output){
 re <- eventReactive(
  input$go,{input$a})
 output$b <- renderText({
  re()
 })
}
```

eventReactive(eventExpr, valueExpr, event.env, event.quoted, value.env, value.quoted, label, domain, ignoreNULL)

Creates reactive expression with code in 2nd argument that only invalidates when reactive values in 1st argument change.

UI - An app's UI is an HTML document.

Use Shiny's functions to assemble this HTML with R.

```
fluidPage(
 textInput("a","")
)
## <div class="container-fluid">
##  <div class="form-group shiny-input-container">
##    <label for="a"></label>
##    <input id="a" type="text"
##       class="form-control" value=""/>
##   </div>
## </div>
```

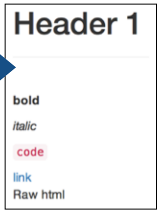
Returns HTML

Add static HTML elements with tags, a list of functions that parallel common HTML tags, e.g. tags$a(). Unnamed arguments will be passed into the tag; named arguments will become tag attributes.

tags$a
tags$abbr
tags$address
tags$area
tags$article
tags$aside
tags$audio
tags$b
tags$base
tags$bdi
tags$bdo
tags$blockquote
tags$body
tags$br
tags$button
tags$canvas
tags$caption
tags$cite
tags$code
tags$col
tags$colgroup
tags$data
tags$datalist
tags$dd
tags$del
tags$details
tags$dfn
tags$div
tags$dl
tags$dt
tags$em
tags$embed
tags$eventsource
tags$fieldset
tags$figcaption
tags$figure
tags$footer
tags$form
tags$h1
tags$h2
tags$h3
tags$h4
tags$h6
tags$head
tags$header
tags$hgroup
tags$hr
tags$HTML
tags$i
tags$iframe
tags$img
tags$input
tags$ins
tags$kbd
tags$keygen
tags$label
tags$legend
tags$li
tags$link
tags$mark
tags$map
tags$menu
tags$meta
tags$meter
tags$nav
tags$noscript
tags$object
tags$ol
tags$optgroup
tags$option
tags$output
tags$p
tags$param
tags$pre
tags$progress
tags$q
tags$ruby
tags$rp
tags$rt
tags$s
tags$samp
tags$script
tags$section
tags$select
tags$small
tags$source
tags$span
tags$strong
tags$style
tags$sub
tags$summary
tags$sup
tags$table
tags$tbody
tags$td
tags$textarea
tags$tfoot
tags$th
tags$thead
tags$time
tags$title
tags$tr
tags$track
tags$u
tags$ul
tags$var
tags$video
tags$wbr

The most common tags have wrapper functions. You do not need to prefix their names with tags$

```
ui <- fluidPage(
 h1("Header 1"),
 hr(),
 br(),
 p(strong("bold")),
 p(em("italic")),
 p(code("code")),
 a(href="", "link"),
 HTML("<p>Raw html</p>")
)
```



Header 1

bold

italic

code

link

Raw html

To include a CSS file, use includeCSS(), or
1. Place the file in the www subdirectory
2. Link to it with

```
tags$head(tags$link(rel = "stylesheet",
 type = "text/css", href = "<file name>"))
```

To include JavaScript, use includeScript() or
1. Place the file in the www subdirectory
2. Link to it with

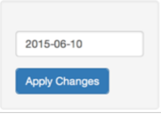
```
tags$head(tags$script(src = "<file name>"))
```

To include an image
1. Place the file in the www subdirectory
2. Link to it with `img(src="<file name>")`

Layouts

Combine multiple elements into a "single element" that has its own properties with a panel function, e.g.

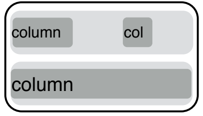
```
wellPanel(dateInput("a", ""),
     submitButton()
)
```



absolutePanel()
conditionalPanel()
fixedPanel()
headerPanel()
inputPanel()
mainPanel()
navlistPanel()
sidebarPanel()
tabPanel()
tabsetPanel()
titlePanel()
wellPanel()

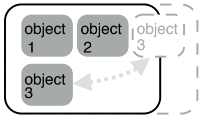
Organize panels and elements into a layout with a layout function. Add elements as arguments of the layout functions.

fluidRow()



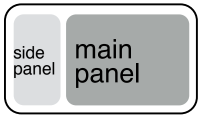
```
ui <- fluidPage(
 fluidRow(column(width = 4),
     column(width = 2,  offset =
3)),
 fluidRow(column(width = 12))
)
```

flowLayout()



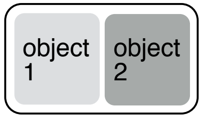
```
ui <- fluidPage(
 flowLayout( # object 1,
           # object 2,
           # object 3
  )
)
```

sidebarLayout()



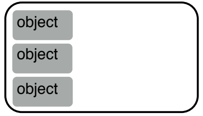
```
ui <- fluidPage(
  sidebarLayout(
   sidebarPanel(),
   mainPanel()
  )
)
```

splitLayout()



```
ui <- fluidPage(
 splitLayout( # object 1,
           # object 2
  )
)
```

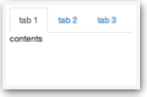
verticalLayout()



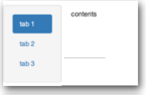
```
ui <- fluidPage(
 verticalLayout( # object 1,
               # object
2,
               # object
3
  )
)
```

Layer tabPanels on top of each other, and navigate between them, with:

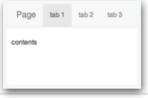
```
ui <- fluidPage( tabsetPanel(
    tabPanel("tab 1", "contents"),
    tabPanel("tab 2", "contents"),
    tabPanel("tab 3",
"contents")))
```



```
ui <- fluidPage( navlistPanel(
    tabPanel("tab 1",
"contents"),
    tabPanel("tab 2",
"contents"),
    tabPanel("tab 3",
"contents")))
```



```
ui <- navbarPage(title =
"Page",
    tabPanel("tab 1",
"contents"),
    tabPanel("tab 2",
"contents"),
    tabPanel("tab 3",
"contents"))
```



Using Git and GitHub with RStudio: : CHEATSHEET

Version control control, also known as **source control**, is the practice of tracking and managing changes to software code.

Version control systems are software tools that help software teams manage changes to source code over time.

Git is an **open-source** software for version control, originally developed in 2005 by Linus Torvalds, the creator of the Linux operating system kernel.

Git it is a version control tool to track the changes in the source code of a project.

Github is the most popular hosting service for collaborating on code using Git.

Requirements

1. R and RStudio installed
2. Git installed
3. Register a free Github account

Check that Git is installed

In the Terminal of RStudio, enter which git to request the path to your Git executable:

```
which git
## /usr/bin/git
```

and git --version to see its version:

```
git --version
## git version 2.34.1
```

Introduce yourself to Git

Open a shell from RStudio *Tools* > *Shell* and type each line separately by substituting your name and the email associated with your GitHub account:

```
git config --global user.name 'Jane Doe'
git config --global user.email 'jane@example.com'
```

Github Glossary

This glossary introduces common Git and GitHub terminology.

Basics

git init <directory>	Create empty Git repository in specified directory.
git clone <repository>	Clone a repository located at <repository> on your local machine.
git config user.name <username>	Define author name to be used for all commits in current repository.
git add <directory>	Stage all changes in <directory> for the next commit.
get commit -m <"message">	Commit the staged snapshot, but instead of launching a text editor, use <"message"> as the commit message.
get status	List which files are staged, unstaged, and untracked.
git log	Display the entire commit history using the default format.
git diff	Show unstaged changes between your index and working directory.

Remote Repositories

git remote add <name> <url>	Create a new connection to a remote repository. After adding a remote, you can use <name> as a shortcut for <url> in other commands.
git fetch <remote> <branch>	Fetches a specific <branch>, from the repository. Leave off <branch> to fetch all remote refs.
git pull <remote>	Fetch the specified remote's copy of current branch and **immediately** merge it into the local copy.
git push <remote> <branch>	Push the branch to <remote>, along with necessary commits and objects. Creates named branch in the remote repository if it doesn't exist.

Undoing Changes

git revert <commit>	Create new commit that undoes all of the changes made in <commit>, then apply it to the current branch.
git reset <file>	Remove <file> from the staging area but leave the working directory unchanged. This unstages a file without overwriting any changes.
git clean -n	Shows which files would be removed from working directory. Use the –f flag in place of the –n flag to execute the clean.

Rewriting Git History

git commit --amend	Replace the last commit with the staged changes and last commit combined. Use with nothing staged to edit the last commit's message.
git rebase <base>	Rebase the current branch onto <base>. <base> can be a commit ID, branch name, a tag, or a relative reference to HEAD.
git reflog	Show a log of changes to the local repository's HEAD. Add --relative-date flag to show date info or --all to show all refs.

Git Branches

git branch	List all of the branches in your repo. Add a <branch> argument to create a new branch with the name <branch>.
git checkout –b <branch>	Create and check out a new named <branch>. Drop the –b flag to checkout an existing branch.
git merge <branch>	Merge <branch> into the current branch.

RStudio® is a trademark of RStudio, Inc. • CC BY SA Mouna Belaid • belaid.mounaa@gmail.com • mounabelaid.netlify.app • Learn more at Happy Git and Github for the useR • Updated: 2022-01

RStudio Community - rstudio.link/community

Developer Blog - rstudio.link/developer_blog

Tensorflow Blog - rstudio.link/tensorflow_blog

R Views Blog - rstudio.link/rviews_blog

Twitter - rstudio.link/twitter

GitHub - rstudio.link/github

LinkedIn - rstudio.link/linkedin

YouTube - rstudio.link/youtube

Facebook - rstudio.link/facebook