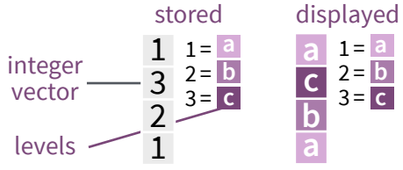
Factors with forcats : : **CHEAT SHEET**

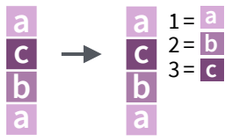
The **forcats** package provides tools for working with factors, which are R's data structure for categorical data.

Factors



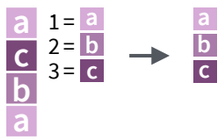
R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the levels associated with them.

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"))

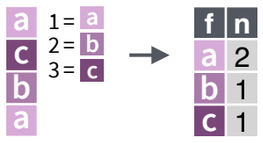
Return its levels with levels()



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

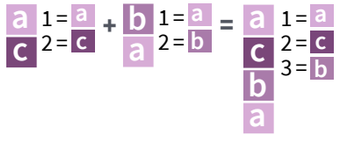


fct_count(f, sort = FALSE, prop = FALSE**)** Count the number of values with each level. fct_count(f)

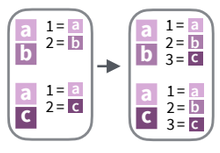
fct_match(f, lvls**)** Check for lvls in f. fct_match(f, "a")

fct_unique(f**)** Return the unique values, removing duplicates. fct_unique(f)

Combine Factors

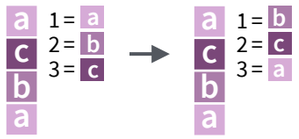


fct_c(…**)** Combine factors with different levels. Also **fct_cross()**.
f1 <- factor(c("a", "c"))
f2 <- factor(c("b", "a"))
fct_c(f1, f2)

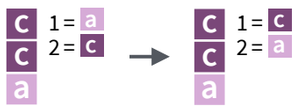


fct_unify(fs, levels = lvls_union(fs)**)** Standardize levels across a list of factors.
fct_unify(list(f2, f1))

Change the order of levels

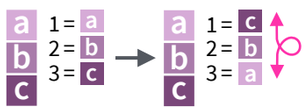


fct_relevel(.f, ..., after = 0L**)**
Manually reorder factor levels.
fct_relevel(f, c("b", "c", "a"))

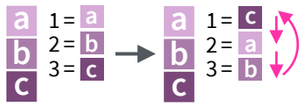


fct_infreq(f, ordered = NA**)**
Reorder levels by the frequency in which they appear in the data (highest frequency first). Also **fct_inseq()**.
f3 <- factor(c("c", "c", "a"))
fct_infreq(f3)

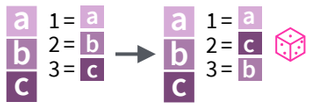
fct_inorder(f, ordered = NA**)**
Reorder levels by order in which they appear in the data.
fct_inorder(f2)



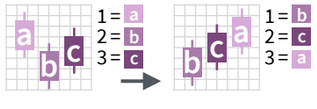
fct_rev(f**)** Reverse level order.
f4 <- factor(c("a","b","c"))
fct_rev(f4)



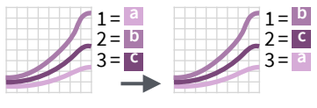
fct_shift(f**)** Shift levels to left or right, wrapping around end.
fct_shift(f4)



fct_shuffle(f, n = 1L**)** Randomly permute order of factor levels.
fct_shuffle(f4)

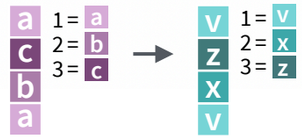


fct_reorder(.f, .x, .fun = median, ..., .desc = FALSE**)** Reorder levels by their relationship with another variable.
boxplot(data = PlantGrowth, weight ~ reorder(group, weight))

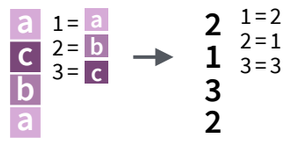


fct_reorder2(.f, .x, .y, .fun = last2, ..., .desc = TRUE**)** Reorder levels by their final values when plotted with two other variables.
ggplot(diamonds,aes(carat, price, color = fct_reorder2(color, carat, price))) + geom_smooth()

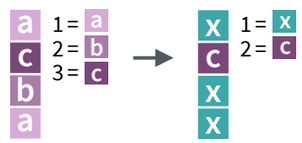
Change the value of levels



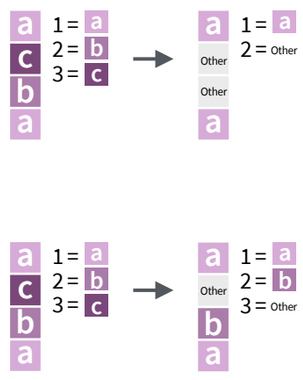
fct_recode(.f, ...**)** Manually change levels. Also **fct_relabel()** which obeys purrr::map syntax to apply a function or expression to each level.
fct_recode(f, v = "a", x = "b", z = "c")
fct_relabel(f, ~ paste0("x", .x))



fct_anon(f, prefix = ""**)**
Anonymize levels with random integers.
fct_anon(f)



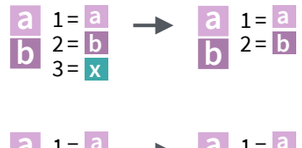
fct_collapse(.f, …, other_level = NULL**)** Collapse levels into manually defined groups.
fct_collapse(f, x = c("a", "b"))



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)

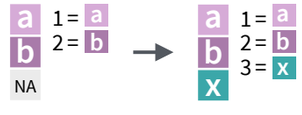
fct_other(f, keep, drop, other_level = "Other"**)** Replace levels with "other."
fct_other(f, keep = c("a", "b"))

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)))

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>) +                                  ] required
<GEOM_FUNCTION>(mapping = aes(<MAPPINGS>),
 stat =<STAT>, position =<POSITION>) +                    ] Not required, sensible defaults supplied
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>
```

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

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.

Aes

Common aesthetic values.

color and **fill** - string ("red", "#RRGGBB")

linetype - integer or string (0 = "blank", 1 = "solid", 2 = "dashed", 3 = "dotted", 4 = "dotdash", 5 = "longdash", 6 = "twodash")

lineend - string ("round", "butt", or "square")

linejoin - string ("round", "mitre", or "bevel")

size - integer (line width in mm)

shape - integer/shape name or a single character ("a")

RStudio

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))

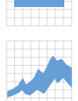
a + geom_blank() and **a + expand_limits()**
Ensure limits include values across all plots.

b + geom_curve(aes(yend = lat + 1, xend = long + 1), curvature = 1**)** - 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(alpha = 50)**)** - x, y, alpha, color, fill, group, subgroup, 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 both continuous

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

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

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**)** - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

one discrete, one continuous

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

both discrete

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

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

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

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_density_2d()
x, y, alpha, color, group, linetype, size

h + geom_hex()
x, y, alpha, color, 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, color, group, linetype, size, weight

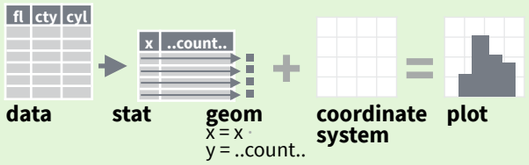
l + geom_contour_filled(aes(fill = z)**)**
x, y, alpha, color, fill, group, linetype, size, subgroup

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

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_density_2d(aes(fill = ..level..), geom = "polygon"**)**

variable created by stat

c + stat_bin(binwidth = 1, boundary = 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() + xlim(-5, 5**) + stat_function(**fun = dnorm,
n = 20, geom = "point"**) x** | ..x.., ..y..

ggplot() + stat_qq(aes(sample = 1:100)**)**
x, y, sample | ..sample.., ..theoretical..

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

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

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

e + stat_identity()

e + stat_unique()

Scales Override defaults with **scales** package.

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_*_binned() - Map continuous values to discrete bins.
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 values as date times. Same as scale_*_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 the direction of the x axis.
scale_x_sqrt() - Plot x on square root scale.

COLOR AND FILL SCALES (DISCRETE)

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(colors = 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.

ggplot(mpg, aes(y = fl)**) + geom_bar()**
Flip cartesian coordinates by switching x and y aesthetic mappings.

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

r + coord_trans(y = "sqrt"**)** - x, y, xlim, ylim
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, 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 theme.

r + theme_void()
Empty theme.

r + theme() Customize aspects of the theme such as axis, legend, panel, and facet properties.
r + ggtitle("Title") + theme(plot.title.postion = "plot")
r + theme(panel.background = element_rect(fill = "blue"))

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(cols = vars(fl))
Facet into columns based on fl.

t + facet_grid(rows = vars(year))
Facet into rows based on year.

t + facet_grid(rows = vars(year), cols = vars(fl))
Facet into both rows and columns.

t + facet_wrap(vars(fl))
Wrap facets into a rectangular layout.

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

t + facet_grid(rows = vars(drv), cols = vars(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 label:

t + facet_grid(cols = vars(fl), labeller = label_both)

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

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

α^c α^d α^e α^p α^r

Labels and Legends

Use **labs()** to label the elements of your plot.

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",
alt = "Add alt text to the plot",
<AES> = "New <AES> legend title"**)**

t + annotate(geom = "text", x = 8, y = 9, label = "A"**)**
Places a geom with manually selected aesthetics.

p + guides(x = guide_axis(n.dodge = 2)**)** Avoid crowded or overlapping labels with guide_axis(n.dodge or angle).

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

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

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

Zooming

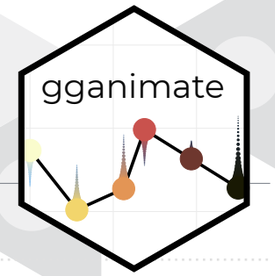
Without clipping (preferred):
t + coord_cartesian(xlim = c(0, 100), ylim = c(10, 20)**)**

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

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)
```

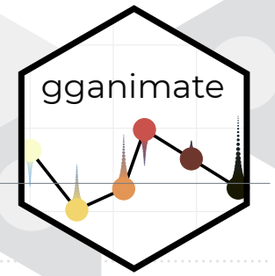
... and we're cycling between **seven** views. Seven is the number of steps in the transition, so the view is changing when the points are static, and visa versa. Views are determined by what data is in the current frame.

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.

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

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

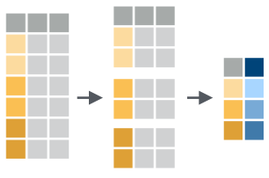
Apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

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

count(.data, …, wt = NULL, sort = FALSE, name = NULL**)** Count number of rows in each group defined by the variables in … Also **tally()**.
count(mtcars, cyl)

Group Cases

Use **group_by(**.data, …, .add = FALSE, .drop = TRUE**)** to create a "grouped" copy of a table grouped by columns in ... dplyr functions will manipulate each "group" separately and combine the results.



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

Use **rowwise(**.data, …**)** to group data into individual rows. dplyr functions will compute results for each row. Also apply functions to list-columns. See tidyr cheat sheet for list-column workflow.

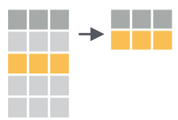
```
starwars %>%
  rowwise() %>%
  mutate(film_count = length(films))
```

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

Manipulate Cases

EXTRACT CASES

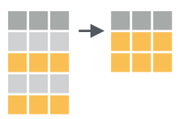
Row functions return a subset of rows as a new table.



filter(.data, …, .preserve = FALSE**)** Extract rows that meet logical criteria.
filter(mtcars, mpg > 20)

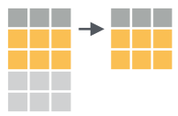
distinct(.data, …, .keep_all = FALSE**)** Remove rows with duplicate values.
distinct(mtcars, gear)

slice(.data, …, .preserve = FALSE**)** Select rows by position.
slice(mtcars, 10:15)



slice_sample(.data, …, n, prop, weight_by = NULL, replace = FALSE**)** Randomly select rows. Use n to select a number of rows and prop to select a fraction of rows.
slice_sample(mtcars, n = 5, replace = TRUE)

slice_min(.data, order_by, …, n, prop, with_ties = TRUE**)** and **slice_max()** Select rows with the lowest and highest values.
slice_min(mtcars, mpg, prop = 0.25)



slice_head(.data, …, n, prop**)** and **slice_tail()** Select the first or last rows.
slice_head(mtcars, n = 5)

Logical and boolean operators to use with filter()

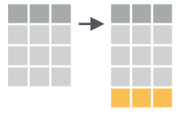
==	<	<=	is.na()	%in%	|	xor()
!=	>	>=	!is.na()	!	&	

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

ARRANGE CASES

arrange(.data, …, .by_group = FALSE**)** Order rows by values of a column or columns (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(cars, speed = 1, dist = 1)

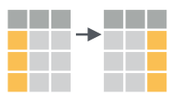
Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.

pull(.data, var = -1, name = NULL, …**)** Extract column values as a vector, by name or index.
pull(mtcars, wt)

select(.data, …**)** Extract columns as a table.
select(mtcars, mpg, wt)



relocate(.data, …, .before = NULL, .after = NULL**)** Move columns to new position.
relocate(mtcars, mpg, cyl, .after = last_col())

Use these helpers with select() and across()
e.g. select(mtcars, mpg:cyl)

contains(match**)**	**num_range(**prefix, range**)**	**:**, e.g. mpg:cyl
ends_with(match**)**	**all_of(**x**)/any_of(**x, …, vars**)**	**-**, e.g, -gear
starts_with(match**)**	**matches(**match**)**	**everything()**

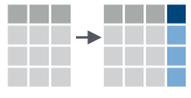
MANIPULATE MULTIPLE VARIABLES AT ONCE

across(.cols, .funs, …, .names = NULL**)** Summarise or mutate multiple columns in the same way.
summarise(mtcars, across(everything(), mean))

c_across(.cols**)** Compute across columns in row-wise data.
transmute(rowwise(UKgas), total = sum(c_across(1:2)))

MAKE NEW VARIABLES

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



mutate(.data, …, .keep = "all", .before = NULL, .after = NULL**)** Compute new column(s). Also **add_column(), add_count(),** and **add_tally().**
mutate(mtcars, gpm = 1 / mpg)

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

rename(.data, …**)** Rename columns. Use **rename_with()** to rename with a function.
rename(cars, distance = dist)

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

OFFSET

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

CUMULATIVE AGGREGATE

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

RANKING

dplyr::**cume_dist()** - proportion of all values <=
dplyr::**dense_rank()** - rank w 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
dplyr::**between()** - x >= left & x <= right
dplyr::**near()** - safe == for floating point numbers

MISCELLANEOUS

dplyr::**case_when()** - multi-case if_else()

```
starwars %>%
  mutate(type = case_when(
    height > 200 | mass > 200 ~ "large",
      species == "Droid"      ~ "robot",
      TRUE                    ~ "other")
    )
```

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()

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

COUNT

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

POSITION

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

LOGICAL

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

ORDER

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

RANK

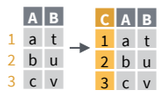
quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

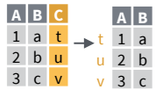
IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

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.



tibble::**rownames_to_column()**
Move row names into col.
a <- rownames_to_column(mtcars, var = "C")

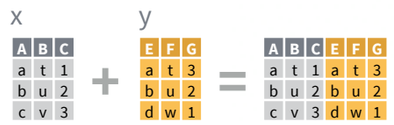


tibble::**column_to_rownames()**
Move col into row names.
column_to_rownames(a, var = "C")

Also tibble::**has_rownames()** and tibble::**remove_rownames()**.

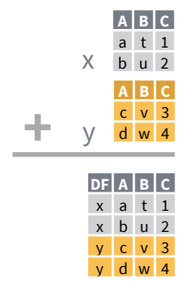
Combine Tables

COMBINE VARIABLES



bind_cols(…, .name_repair**)** Returns tables placed side by side as a single table. Column lengths must be equal. Columns will NOT be matched by id (to do that look at Relational Data below), so be sure to check that both tables are ordered the way you want before binding.

COMBINE CASES



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).

RELATIONAL DATA

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"), …, keep = FALSE, na_matched = "na"**)** Join matching values from y to x.

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

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

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

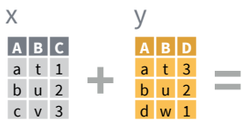
COLUMN MATCHING FOR JOINS

Use **by = c("col1", "col2", ...)** to specify one or more common columns to match on.
left_join(x, y, by = "A")

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

Use **suffix** to specify the suffix to give to unmatched columns that have the same name in both tables.
left_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

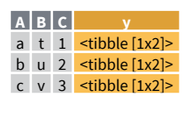
Use a "**Filtering Join**" to filter one table against the rows of another.



semi_join(x, y, by = NULL, copy = FALSE, …, na_matches = "na"**)** Return rows of x that have a match in y. Use to see what will be included in a join.

anti_join(x, y, by = NULL, copy = FALSE, …, na_matches = "na"**)** Return rows of x that do not have a match in y. Use to see what will not be included in a join.

Use a "**Nest Join**" to inner join one table to another into a nested data frame.



nest_join(x, y, by = NULL, copy = FALSE, keep = FALSE, name = NULL, …**)** Join data, nesting matches from y in a single new data frame column.

SET OPERATIONS

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

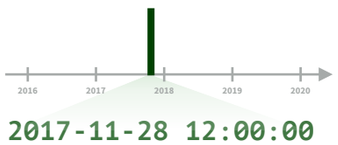
setdiff(x, y, ...)
Rows that appear in x but not y.

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

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

Dates and times with lubridate : : **CHEAT SHEET**

Date-times



`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 tz argument to set the time zone, e.g. ymd(x, tz = "UTC").

`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")

`07-2020` **my(), ym().** my("07-2020")

`2:01` hms::**hms()** Also lubridate::**hms()**, **hm()** and **ms()**, which return periods.* hms::hms(sec = 0, min= 1, hours = 2, roll = FALSE)

`2017.5` **date_decimal(**decimal, tz = "UTC"**)** 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.

```
d ## "2017-11-28"
day(d) ## 28
```

Assign into an accessor function to change a component in place.

```
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)

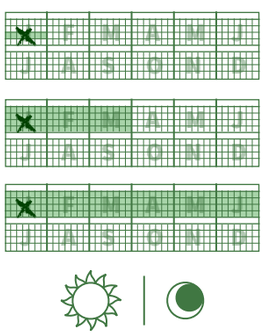
`2018-01-31 11:59:59` **day(**x**)** Day of month. day(dt)
wday(x, label, abbr**)** Day of week.
qday(x**)** Day of quarter.

`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)

`2018-01-31 11:59:59 UTC` **tz(**x**)** Time zone. tz(dt)



week(x**)** Week of the year. week(dt)
isoweek() ISO 8601 week.
epiweek() Epidemiological week.

quarter(x**)** Quarter. quarter(dt)

semester(x, with_year = FALSE**)** Semester. semester(dt)

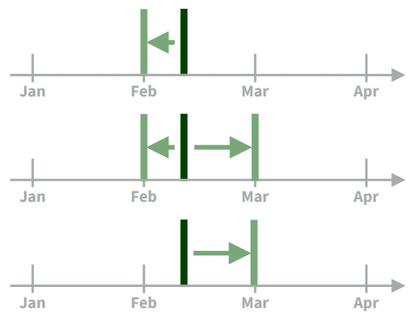
am(x**)** Is it in the am? am(dt)
pm(x**)** Is it in the pm? pm(dt)

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")

Valid units are second, minute, hour, day, week, month, bimonth, quarter, season, halfyear and year.

rollback(dates, roll_to_first = FALSE, preserve_hms = TRUE**)** Roll back to last day of previous month. Also **rollforward()**. 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

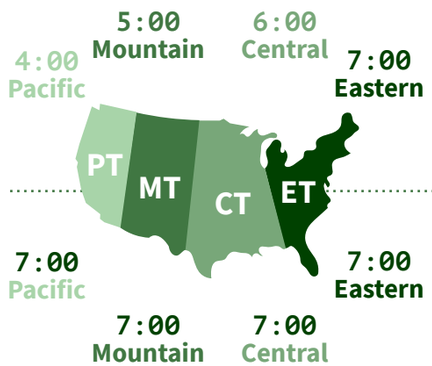
Time Zones

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()

Sys.timezone() Gets current time zone.



with_tz(time, tzone = ""**)** Get the **same date-time** in a new time zone (a new clock time). Also **local_time(**dt, tz, units**)**. with_tz(dt, "US/Pacific")

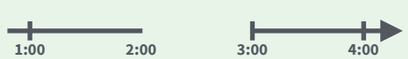
force_tz(time, tzone = ""**)** Get the **same clock time** in a new time zone (a new date-time). Also **force_tzs()**. force_tz(dt, "US/Pacific")

Math with Date-times – Lubridate provides three classes of timespans to facilitate math with dates and date-times.

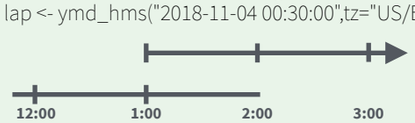
Math with date-times relies on the **timeline**, which behaves inconsistently. Consider how the timeline behaves during:

A normal day
nor <- ymd_hms("2018-01-01 01:30:00",tz="US/Eastern")

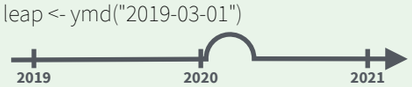
The start of daylight savings (spring forward)
gap <- ymd_hms("2018-03-11 01:30:00",tz="US/Eastern")



The end of daylight savings (fall back)
lap <- ymd_hms("2018-11-04 00:30:00",tz="US/Eastern")

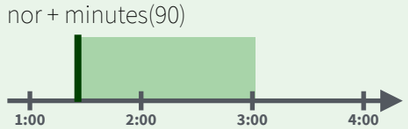


Leap years and leap seconds
leap <- ymd("2019-03-01")

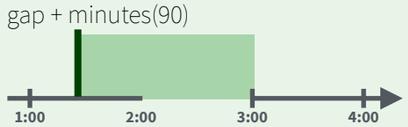


Periods track changes in clock times, which ignore time line irregularities.

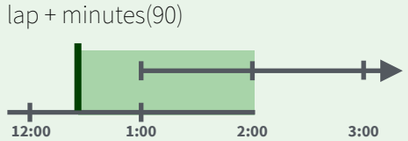
nor + minutes(90)



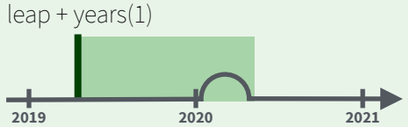
gap + minutes(90)



lap + minutes(90)

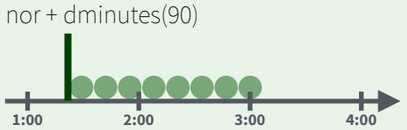


leap + years(1)

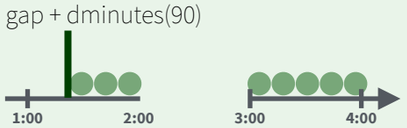


Durations track the passage of physical time, which deviates from clock time when irregularities occur.

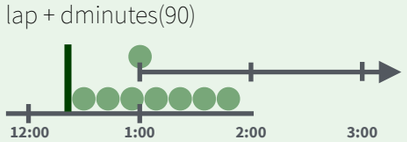
nor + dminutes(90)



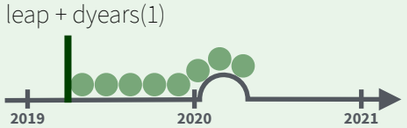
gap + dminutes(90)



lap + dminutes(90)

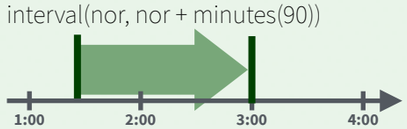


leap + dyears(1)

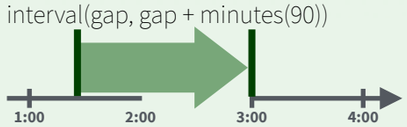


Intervals represent specific intervals of the timeline, bounded by start and end date-times.

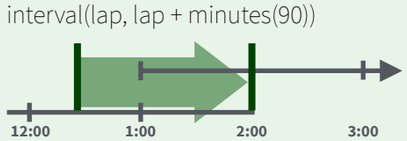
interval(nor, nor + minutes(90))



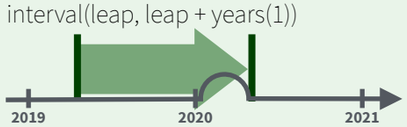
interval(gap, gap + minutes(90))



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 nanoseconds.
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.
dmonths(x = 1**)** 2629800x 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 $\times 10^{-3}$ seconds.
dmicroseconds(x = 1**)** x $\times 10^{-6}$ seconds.
dnanoseconds(x = 1**)** x $\times 10^{-9}$ seconds.
dpicoseconds(x = 1**)** x $\times 10^{-12}$ 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)

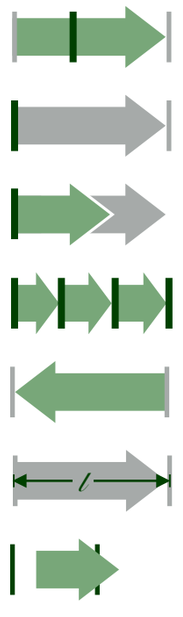
INTERVALS

Divide an interval by a duration to determine its physical length, divide an 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)
j <- d %--% ymd("2017-12-31")
## 2017-01-01 UTC--2017-11-28 UTC
## 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 timespan to an interval with the start date-time. Also **is.interval()**. as.interval(days(1), start = now())

Data import with the tidyverse : : **CHEAT SHEET**

Read Tabular Data with readr

read_*(file, col_names = TRUE, col_types = NULL, col_select = NULL, id = NULL, locale, n_max = Inf, skip = 0, na = c("", "NA"), guess_max = min(1000, n_max), show_col_types = TRUE) See **?read_delim**

A|B|C
1|2|3
4|5|NA

A	B	C
1	2	3
4	5	NA

read_delim("file.txt", delim = "|"**)** Read files with any delimiter. If no delimiter is specified, it will automatically guess.
To make file.txt, run: write_file("A|B|C\n1|2|3\n4|5|NA", file = "file.txt")

A,B,C
1,2,3
4,5,NA

A	B	C
1	2	3
4	5	NA

read_csv("file.csv"**)** Read a comma delimited file with period decimal marks.
write_file("A,B,C\n1,2,3\n4,5,NA", file = "file.csv")

A;B;C
1,5;2;3
4,5;5;NA

A	B	C
1.5	2	3
4.5	5	NA

read_csv2("file2.csv"**)** Read semicolon delimited files with comma decimal marks.
write_file("A;B;C\n1,5;2;3\n4,5;5;NA", file = "file2.csv")

A B C
1 2 3
4 5 NA

A	B	C
1	2	3
4	5	NA

read_tsv("file.tsv"**)** Read a tab delimited file. Also **read_table()**.
read_fwf("file.tsv", fwf_widths(c(2, 2, NA))**)** Read a fixed width file.
write_file("A\tB\tC\n1\t2\t3\n4\t5\tNA\n", file = "file.tsv")

USEFUL READ ARGUMENTS

A	B	C
1	2	3
4	5	NA

No header
read_csv("file.csv", col_names = FALSE)

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

Provide header
read_csv("file.csv",
col_names = c("x", "y", "z"))

Read multiple files into a single table
read_csv(c("f1.csv", "f2.csv", "f3.csv"),
id = "origin_file")

1	2	3
4	5	NA

Skip lines
read_csv("file.csv", skip = 1)

A	B	C
1	2	3

Read a subset of lines
read_csv("file.csv", n_max = 1)

A	B	C
NA	2	3
4	5	NA

Read values as missing
read_csv("file.csv", na = c("1"))

A;B;C
1,5;2;3,0

Specify decimal marks
read_delim("file2.csv", locale =
locale(decimal_mark = ","))

Save Data with readr

write_*(x, file, na = "NA", append, col_names, quote, escape, eol, num_threads, progress)

A	B	C
1	2	3
4	5	NA

A,B,C
1,2,3
4,5,NA

write_delim(x, file, delim = " "**)** Write files with any delimiter.

write_csv(x, file**)** Write a comma delimited file.

write_csv2(x, file**)** Write a semicolon delimited file.

write_tsv(x, file**)** Write a tab delimited file.

RStudio

One of the first steps of a project is to import outside data into R. Data is often stored in tabular formats, like csv files or spreadsheets.

The front page of this sheet shows how to import and save text files into R using **readr**.

The back page shows how to import spreadsheet data from Excel files using **readxl** or Google Sheets using **googlesheets4**.

OTHER TYPES OF DATA

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

- **haven** - SPSS, Stata, and SAS files
- **DBI** - databases
- **jsonlite** - json
- **xml2** - XML
- **httr** - Web APIs
- **rvest** - HTML (Web Scraping)
- **readr::read_lines()** - text data

Column Specification with readr

Column specifications define what data type each column of a file will be imported as. By default readr will generate a column spec when a file is read and output a summary.

spec(x**)** Extract the full column specification for the given imported data frame.

```
spec(x)
# cols(
#   age = col_integer(),
#   sex = col_character(),
#   earn = col_double()
# )
```

age is an integer
sex is a character
earn is a double (numeric)

COLUMN TYPES

Each column type has a function and corresponding string abbreviation.

- **col_logical()** - "l"
- **col_integer()** - "i"
- **col_double()** - "d"
- **col_number()** - "n"
- **col_character()** - "c"
- **col_factor(**levels, ordered = FALSE**)** - "f"
- **col_datetime(**format = ""**)** - "T"
- **col_date(**format = ""**)** - "D"
- **col_time(**format = ""**)** - "t"
- **col_skip()** - "-", "_"
- **col_guess()** - "?"

USEFUL COLUMN ARGUMENTS

Hide col spec message
read_*(file, show_col_types = FALSE)

Select columns to import
Use names, position, or selection helpers.
read_*(file, col_select = c(age, earn))

Guess column types
To guess a column type, read_ *() looks at the first 1000 rows of data. Increase with **guess_max**.
read_*(file, guess_max = Inf)

DEFINE COLUMN SPECIFICATION

Set a default type
```
read_csv(
  file,
  col_type = list(.default = col_double())
)
```

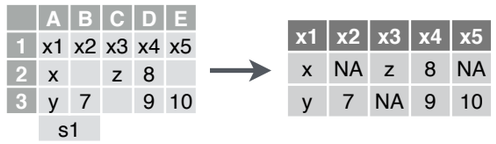
Use column type or string abbreviation
```
read_csv(
  file,
  col_type = list(x = col_double(), y = "l", z = "_")
)
```

Use a single string of abbreviations
```
# col types: skip, guess, integer, logical, character
read_csv(
  file,
  col_type = "_?ilc"
)
```

Import Spreadsheets

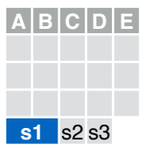
with readxl

READ EXCEL FILES



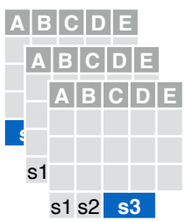
read_excel(path, sheet = NULL, range = NULL**)**
Read a .xls or .xlsx file based on the file extension. See front page for more read arguments. Also **read_xls()** and **read_xlsx()**.
read_excel("excel_file.xlsx")

READ SHEETS



read_excel(path, **sheet = NULL)** Specify which sheet to read by position or name.
read_excel(path, sheet = 1)
read_excel(path, sheet = "s1")

excel_sheets(path**)** Get a vector of sheet names.
excel_sheets("excel_file.xlsx")



To **read multiple sheets:**

1. Get a vector of sheet names from the file path.
2. Set the vector names to be the sheet names.
3. Use purrr::map_dfr() to read multiple files into one data frame.

```
path <- "your_file_path.xlsx"
path %>% excel_sheets() %>%
  set_names() %>%
  map_dfr(read_excel, path = path)
```

READXL COLUMN SPECIFICATION

Column specifications define what data type each column of a file will be imported as.

Use the **col_types** argument of **read_excel()** to set the column specification.

Guess column types
To guess a column type, read_ excel() looks at the first 1000 rows of data. Increase with the **guess_max** argument.
read_excel(path, guess_max = Inf)

Set all columns to same type, e.g. character
read_excel(path, col_types = "text")

Set each column individually
```
read_excel(
  path,
  col_types = c("text", "guess", "guess","numeric")
)
```

COLUMN TYPES

logical	numeric	text	date	list
TRUE	2	hello	1947-01-08	hello
FALSE	3.45	world	1956-10-21	1

- skip
- guess
- logical
- numeric
- text
- date
- list

Use **list** for columns that include multiple data types. See **tidyr** and **purrr** for list-column data.

with googlesheets4

READ SHEETS

read_sheet(ss, sheet = NULL, range = NULL**)**
Read a sheet from a URL, a Sheet ID, or a dribble from the googledrive package. See front page for more read arguments. Same as **range_read()**.

SHEETS METADATA

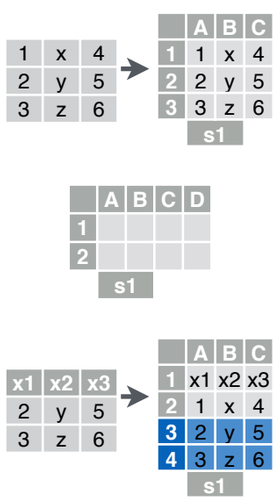
URLs are in the form:
https://docs.google.com/spreadsheets/d/
SPREADSHEET_ID/edit#gid=**SHEET_ID**

gs4_get(ss**)** Get spreadsheet meta data.

gs4_find(...) Get data on all spreadsheet files.

sheet_properties(ss**)** Get a tibble of properties for each worksheet. Also **sheet_names()**.

WRITE SHEETS



write_sheet(data, ss = NULL, sheet = NULL**)**
Write a data frame into a new or existing Sheet.

gs4_create(name, ..., sheets = NULL**)** Create a new Sheet with a vector of names, a data frame, or a (named) list of data frames.

sheet_append(ss, data, sheet = 1**)** Add rows to the end of a worksheet.

GOOGLESHEETS4 COLUMN SPECIFICATION

Column specifications define what data type each column of a file will be imported as.

Use the **col_types** argument of **read_sheet()/ range_read()** to set the column specification.

Guess column types
To guess a column type read_sheet()/ range_read() looks at the first 1000 rows of data. Increase with **guess_max**.
read_sheet(path, guess_max = Inf)

Set all columns to same type, e.g. character
read_sheet(path, col_types = "c")

Set each column individually
```
# col types: skip, guess, integer, logical, character
read_sheets(ss, col_types = "_?ilc")
```

COLUMN TYPES

l	n	c	D	L
TRUE	2	hello	1947-01-08	hello
FALSE	3.45	world	1956-10-21	1

- skip - "_" or "-"
- guess - "?"
- logical - "l"
- integer - "i"
- double - "d"
- numeric - "n"
- date - "D"
- datetime - "T"
- character - "c"
- list-column - "L"
- cell - "C" Returns list of raw cell data.

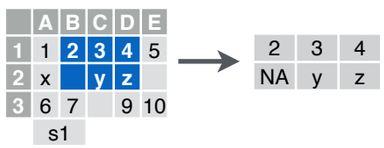
Use list for columns that include multiple data types. See **tidyr** and **purrr** for list-column data.

OTHER USEFUL EXCEL PACKAGES

For functions to write data to Excel files, see:
- **openxlsx**
- **writexl**

For working with non-tabular Excel data, see:
- **tidyxl**

CELL SPECIFICATION FOR READXL AND GOOGLESHEETS4



Use the **range** argument of **readxl::read_excel()** or **googlesheets4::read_sheet()** to read a subset of cells from a sheet.
read_excel(path, range = "Sheet1!B1:D2")
read_sheet(ss, range = "B1:D2")

Also use the range argument with cell specification functions **cell_limits()**, **cell_rows()**, **cell_cols()**, and **anchored().**

FILE LEVEL OPERATIONS

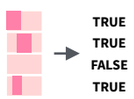
googlesheets4 also offers ways to modify other aspects of Sheets (e.g. freeze rows, set column width, manage (work)sheets). Go to **googlesheets4.tidyverse.org** to read more.

For whole-file operations (e.g. renaming, sharing, placing within a folder), see the tidyverse package **googledrive** at **googledrive.tidyverse.org**.

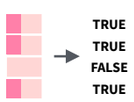
String manipulation with stringr : : **CHEAT SHEET**

The **stringr** package provides a set of internally consistent tools for working with character strings, i.e. sequences of characters surrounded by quotation marks.

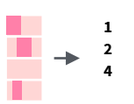
Detect Matches



str_detect(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match in a string. Also **str_like()**. str_detect(fruit, "a")

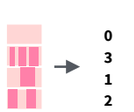


str_starts(string, **pattern**, negate = FALSE**)** Detect the presence of a pattern match at the beginning of a string. Also **str_ends()**. str_starts(fruit, "a")



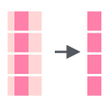
str_which(string, **pattern**, negate = FALSE**)** Find the indexes of strings that contain a pattern match. str_which(fruit, "a")

str_locate(string, **pattern**) Locate the positions of pattern matches in a string. Also **str_locate_all()**. str_locate(fruit, "a")

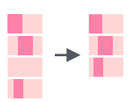


str_count(string, **pattern**) Count the number of matches in a string. str_count(fruit, "a")

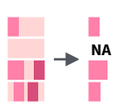
Subset Strings



str_sub(string, start = 1L, end = -1L**)** Extract substrings from a character vector. str_sub(fruit, 1, 3); str_sub(fruit, -2)



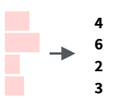
str_subset(string, **pattern**, negate = FALSE**)** Return only the strings that contain a pattern match. str_subset(fruit, "p")



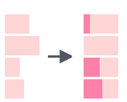
str_extract(string, **pattern**) Return the first pattern match found in each string, as a vector. Also **str_extract_all()** to return every pattern match. str_extract(fruit, "[aeiou]")

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) ([^ +])")

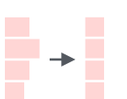
Manage Lengths



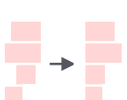
str_length(string**)** The width of strings (i.e. number of code points, which generally equals the number of characters). str_length(fruit)



str_pad(string, width, side = c("left", "right", "both"), pad = " "**)** Pad strings to constant width. str_pad(fruit, 17)



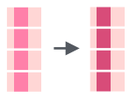
str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "..."**)** Truncate the width of strings, replacing content with ellipsis. str_trunc(sentences, 6)



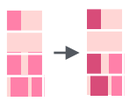
str_trim(string, side = c("both", "left", "right")**)** Trim whitespace from the start and/or end of a string. str_trim(str_pad(fruit, 17))

str_squish(string**)** Trim whitespace from each end and collapse multiple spaces into single spaces. str_squish(str_pad(fruit, 17, "both"))

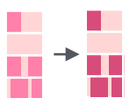
Mutate Strings



str_sub() <- value. Replace substrings by identifying the substrings with str_sub() and assigning into the results. str_sub(fruit, 1, 3) <- "str"



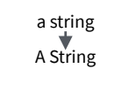
str_replace(string, **pattern**, replacement**)** Replace the first matched pattern in each string. Also **str_remove()**. str_replace(fruit, "p", "-")



str_replace_all(string, **pattern**, replacement**)** Replace all matched patterns in each string. Also **str_remove_all()**. str_replace_all(fruit, "p", "-")

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)

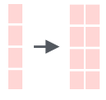


str_to_title(string, locale = "en"**)**[1] Convert strings to title case. Also **str_to_sentence()**. str_to_title(sentences)

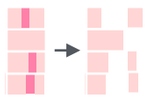
Join and Split

str_c(..., sep = "", collapse = NULL**)** Join multiple strings into a single string. str_c(letters, LETTERS)

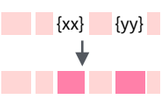
str_flatten(string, collapse = ""**)** Combines into a single string, separated by collapse. str_flatten(fruit, ", ")



str_dup(string, times**)** Repeat strings times times. Also **str_unique()** to remove duplicates. str_dup(fruit, times = 2)



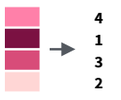
str_split_fixed(string, **pattern**, n**)** Split a vector of strings into a matrix of substrings (splitting at occurrences of a pattern match). Also **str_split()** to return a list of substrings and **str_split_n()** to return the nth substring. str_split_fixed(sentences, " ", n=3)



str_glue(..., .sep = "", .envir = parent.frame()**)** Create a string from strings and {expressions} to evaluate. str_glue("Pi is {pi}")

str_glue_data(.x, ..., .sep = "", .envir = parent.frame(), .na = "NA"**)** Use a data frame, list, or environment to create a string from strings and {expressions} to evaluate. str_glue_data(mtcars, "{rownames(mtcars)} has {hp} hp")

Order Strings

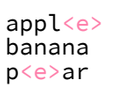


str_order(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...**)**[1] Return the vector of indexes that sorts a character vector. fruit[str_order(fruit)]

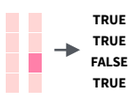
str_sort(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...**)**[1] Sort a character vector. str_sort(fruit)

Helpers

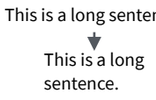
str_conv(string, encoding**)** Override the encoding of a string. str_conv(fruit,"ISO-8859-1")



str_view_all(string, **pattern**, match = NA**)** View HTML rendering of all regex matches. Also **str_view()** to see only the first match. str_view_all(sentences, "[aeiou]")



str_equal(x, y, locale = "en", ignore_case = FALSE, ...**)**[1] Determine if two strings are equivalent. str_equal(c("a", "b"), c("a", "c"))



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.

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:]]**

[:space:]
↵ new line

[:blank:]
space
tab

.

[:graph:]

[:punct:]
. , : ; ? ! / * @ #
- _ " ' [ ] { } ( )

[:symbol:]
| ` = + ^
~ < > $

[:alnum:]

[:digit:]
0 1 2 3 4 5 6 7 8 9

[:alpha:]

[:lower:]
a b c d e f
g h i j k l
m n o p q r
s t u v w x
y z

[:upper:]
A B C D E F
G H I J K L
M N O P Q R
S T U V W X
Y Z

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

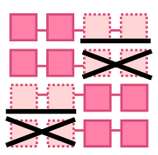
ANCHORS

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

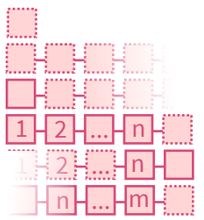
look <- function(rx) str_view_all("bacad", rx)



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

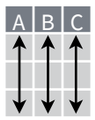
regexp	matches	example	
(ab|d)e	sets precedence	alt("(ab|d)e")	abcde

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

Data tidying with tidyr : : **CHEAT SHEET**

Tidy data is a way to organize tabular data in a consistent data structure across packages.
A table is tidy if:

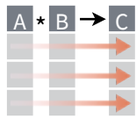


Each **variable** is in its own **column**

&

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

Access **variables** as **vectors**



Preserve **cases** in vectorized operations

Tibbles

AN ENHANCED DATA FRAME

Tibbles are a table format provided by the **tibble** package. They inherit the data frame class, but have improved behaviors:

- **Subset** a new tibble with], a vector with [[and $.
- **No partial matching** when subsetting columns.
- **Display** concise views of the data on one screen.

options(tibble.print_max = n, tibble.print_min = m, tibble.width = Inf**)** Control default display settings.

View() or **glimpse()** View the entire data set.

CONSTRUCT A TIBBLE

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

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

Both make this tibble

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

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

enframe(x, name = "name", value = "value"**)** Convert a named vector to a tibble. Also **deframe()**.

is_tibble(x**)** Test whether x is a tibble.

Reshape Data - Pivot data to reorganize values into a new layout.

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

pivot_longer(data, cols, names_to = "name", values_to = "value", values_drop_na = FALSE**)**

"Lengthen" data by collapsing several columns into two. Column names move to a new names_to column and values to a new values_to column.

pivot_longer(table4a, cols = 2:3, names_to ="year", values_to = "cases")

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

→

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

pivot_wider(data, names_from = "name", values_from = "value"**)**

The inverse of pivot_longer(). "Widen" data by expanding two columns into several. One column provides the new column names, the other the values.

pivot_wider(table2, names_from = type, values_from = count)

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

table5

country	century	year
A	19	99
A	20	00
B	19	99
B	20	00

→

country	year
A	1999
A	2000
B	1999
B	2000

unite(data, col, …, sep = "_", remove = TRUE, na.rm = FALSE**)** Collapse cells across several columns into a single column.

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

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M

→

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K	20M
B	1999	37K	172
B	2000	80K	174

separate(data, col, into, sep = "[^[:alnum:]]+", remove = TRUE, convert = FALSE, extra = "warn", fill = "warn", …**)** Separate each cell in a column into several columns. Also **extract()**.

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

table3

country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M

→

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

separate_rows(data, …, sep = "[^[:alnum:].]+", convert = FALSE**)** Separate each cell in a column into several rows.

separate_rows(table3, rate, sep = "/")

Expand Tables

Create new combinations of variables or identify implicit missing values (combinations of variables not present in the data).

x

x1	x2	x3
A	1	3
B	1	4
B	2	3

→

x1	x2
A	1
A	2
B	1
B	2

expand(data, …**)** Create a new tibble with all possible combinations of the values of the variables listed in … Drop other variables.
expand(mtcars, cyl, gear, carb)

x

x1	x2	x3
A	1	3
B	1	4
B	2	3

→

x1	x2	x3
A	1	3
A	2	NA
B	1	4
B	2	3

complete(data, …, fill = list()**)** Add missing possible combinations of values of variables listed in … Fill remaining variables with NA.
complete(mtcars, cyl, gear, carb)

Handle Missing Values

Drop or replace explicit missing values (NA).

x

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

→

x1	x2
A	1
D	3

drop_na(data, …**)** Drop rows containing NA's in … columns.
drop_na(x, x2)

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(data, …, .direction = "down"**)** Fill in NA's in … columns using the next or previous value.
fill(x, x2)

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(data, replace**)** Specify a value to replace NA in selected columns.
replace_na(x, list(x2 = 2))

Nested Data

A **nested data frame** stores individual tables as a list-column of data frames within a larger organizing data frame. List-columns can also be lists of vectors or lists of varying data types. Use a nested data frame to:

- Preserve relationships between observations and subsets of data. Preserve the type of the variables being nested (factors and datetimes aren't coerced to character).
- Manipulate many sub-tables at once with **purrr** funcitons like map(), map2(), or pmap() or with **dplyr** rowwise() grouping.

CREATE NESTED DATA

nest(data, …**)** Moves groups of cells into a list-column of a data frame. Use alone or with dplyr::**group_by()**:

1. Group the data frame with **group_by()** and use **nest()** to move the groups into a list-column.

```
n_storms <- storms %>%
  group_by(name) %>%
  nest()
```

2. Use **nest(new_col = c(x, y))** to specify the columns to group using dplyr::**select()** syntax.

```
n_storms <- storms %>%
  nest(data = c(year:long))
```

name	yr	lat	long
Amy	1975	27.5	-79.0
Amy	1975	28.5	-79.0
Amy	1975	29.5	-79.0
Bob	1979	22.0	-96.0
Bob	1979	22.5	-95.3
Bob	1979	23.0	-94.6
Zeta	2005	23.9	-35.6
Zeta	2005	24.2	-36.1
Zeta	2005	24.7	-36.6

name	yr	lat	long
Amy	1975	27.5	-79.0
Amy	1975	28.5	-79.0
Amy	1975	29.5	-79.0
Bob	1979	22.0	-96.0
Bob	1979	22.5	-95.3
Bob	1979	23.0	-94.6
Zeta	2005	23.9	-35.6
Zeta	2005	24.2	-36.1
Zeta	2005	24.7	-36.6

nested data frame

name	data
Amy	<tibble [50x3]>
Bob	<tibble [50x3]>
Zeta	<tibble [50x3]>

"cell" contents

yr	lat	long
1975	27.5	-79.0
1975	28.5	-79.0
1975	29.5	-79.0

yr	lat	long
1979	22.0	-96.0
1979	22.5	-95.3
1979	23.0	-94.6

yr	lat	long
2005	23.9	-35.6
2005	24.2	-36.1
2005	24.7	-36.6

Index list-columns with [[]]. n_storms$data[[1]]

CREATE TIBBLES WITH LIST-COLUMNS

tibble::**tribble(**…**)** Makes list-columns 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 a tibble with list-cols.

```
enframe(list('3'=1:3, '4'=1:4, '5'=1:5), 'max', 'seq')
```

OUTPUT LIST-COLUMNS FROM OTHER FUNCTIONS

dplyr::**mutate()**, **transmute()**, and **summarise()** will output list-columns if they return a list.

```
mtcars %>%
  group_by(cyl) %>%
  summarise(q = list(quantile(mpg)))
```

RESHAPE NESTED DATA

unnest(data, cols, ..., keep_empty = FALSE**)** Flatten nested columns back to regular columns. The inverse of nest().

```
n_storms %>% unnest(data)
```

unnest_longer(data, col, values_to = NULL, indices_to = NULL**)** Turn each element of a list-column into a row.

```
starwars %>%
  select(name, films) %>%
  unnest_longer(films)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

→

name	films
Luke	The Empire Strik…
Luke	Revenge of the S…
Luke	Return of the Jed…
C-3PO	The Empire Strik…
C-3PO	Attack of the Cl…
C-3PO	The Phantom M…
R2-D2	The Empire Strik…
R2-D2	Attack of the Cl…
R2-D2	The Phantom M…

unnest_wider(data, col**)** Turn each element of a list-column into a regular column.

```
starwars %>%
  select(name, films) %>%
  unnest_wider(films)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

→

name	..1	..2	..3
Luke	The Empire...	Revenge of...	Return of...
C-3PO	The Empire...	Attack of...	The Phantom...
R2-D2	The Empire...	Attack of...	The Phantom...

hoist(.data, .col, ..., .remove = TRUE) Selectively pull list components out into their own top-level columns. Uses purrr::pluck() syntax for selecting from lists.

```
starwars %>%
  select(name, films) %>%
  hoist(films, first_film = 1, second_film = 2)
```

name	films
Luke	<chr [5]>
C-3PO	<chr [6]>
R2-D2	<chr[7]>

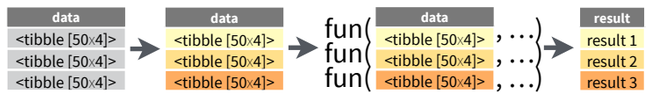
→

name	first_film	second_film	films
Luke	The Empire…	Revenge of…	<chr [3]>
C-3PO	The Empire…	Attack of…	<chr [4]>
R2-D2	The Empire…	Attack of…	<chr [5]>

TRANSFORM NESTED DATA

A vectorized function takes a vector, transforms each element in parallel, and returns a vector of the same length. By themselves vectorized functions cannot work with lists, such as list-columns.

dplyr::**rowwise(**.data, …**)** Group data so that each row is one group, and within the groups, elements of list-columns appear directly (accessed with [[ ), not as lists of length one. **When you use rowwise(), dplyr functions will seem to apply functions to list-columns in a vectorized fashion.**



Apply a function to a list-column and **create a new list-column.**

```
n_storms %>%
  rowwise() %>%
  mutate(n = list(dim(data)))
```

dim() returns two values per row

wrap with list to tell mutate to create a list-column

Apply a function to a list-column and **create a regular column.**

```
n_storms %>%
  rowwise() %>%
  mutate(n = nrow(data))
```

nrow() returns one integer per row

Collapse **multiple list-columns** into a single list-column**.**

```
starwars %>%
  rowwise() %>%
  mutate(transport = list(append(vehicles, starships)))
```

append() returns a list for each row, so col type must be list

Apply a function to **multiple list-columns.**

```
starwars %>%
  rowwise() %>%
  mutate(n_transports = length(c(vehicles, starships)))
```

length() returns one integer per row

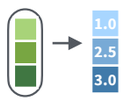
See **purrr** package for more list functions.

Apply functions with purrr : : **CHEAT SHEET**

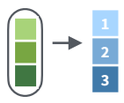
Map Functions

ONE LIST

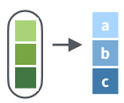
map(.x, .f, …**)** Apply a function to each element of a list or vector, return a list.
x <- list(1:10, 11:20, 21:30)
l1 <- list(x = c("a", "b"), y = c("c", "d"))
map(l1, sort, decreasing = TRUE)



map_dbl(.x, .f, …**)**
Return a double vector.
map_dbl(x, mean)



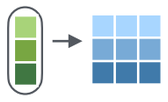
map_int(.x, .f, ...**)**
Return an integer vector.
map_int(x, length)



map_chr(.x, .f, …**)**
Return a character vector.
map_chr(l1, paste, collapse = "")

map_lgl(.x, .f, …**)**
Return a logical vector.
map_lgl(x, is.integer)

map_dfc(.x, .f, ...**)**
Return a data frame created by column-binding.
map_dfc(l1, rep, 3)



map_dfr(.x, .f, ..., .id = NULL**)**
Return a data frame created by row-binding.
map_dfr(x, summary)

walk(.x, .f, ...**)** Trigger side effects, return invisibly.
walk(x, print)

TWO LISTS

map2(.x, .y, .f, …**)** Apply a function to pairs of elements from two lists or vectors, return a list.
y <- list(1, 2, 3); z <- list(4, 5, 6); l2 <- list(x = "a", y = "z")
map2(x, y, ~ .x * .y)

map2_dbl(.x, .y, .f, …**)**
Return a double vector.
map2_dbl(y, z, ~ .x / .y)

map2_int(.x, .y, .f, …**)**
Return an integer vector.
map2_int(y, z, `+`)

map2_chr(.x, .y, .f, …**)**
Return a character vector.
map2_chr(l1, l2, paste, collapse = ",", sep = ":")

map2_lgl(.x, .y, .f, …**)**
Return a logical vector.
map2_lgl(l2, l1, `%in%`)

map2_dfc(.x, .y, .f, ...**)**
Return a data frame created by column-binding.
map2_dfc(l1, l2,
~ as.data.frame(c(.x, .y)))

map2_dfr(.x, .y, .f, ..., .id = NULL**)** Return a data frame created by row-binding.
map2_dfr(l1, l2,
~ as.data.frame(c(.x, .y)))

walk2(.x, .y, .f, ...**)** Trigger side effects, return invisibly.
walk2(objs, paths, save)

MANY LISTS

pmap(.l, .f, …**)** Apply a function to groups of elements from a list of lists or vectors, return a list.
pmap(list(x, y, z), ~ ..1 * (..2 + ..3))

pmap_dbl(.l, .f, …**)**
Return a double vector.
pmap_dbl(list(y, z), ~ .x / .y)

pmap_int(.l, .f, …**)**
Return an integer vector.
pmap_int(list(y, z), `+`)

pmap_chr(.l, .f, …**)**
Return a character vector.
pmap_chr(list(l1, l2), paste, collapse = ",", sep = ":")

pmap_lgl(.l, .f, …**)**
Return a logical vector.
pmap_lgl(list(l2, l1), `%in%`)

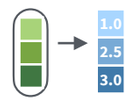
pmap_dfc(.l, .f, ...**)** Return a data frame created by column-binding.
pmap_dfc(list(l1, l2),
~ as.data.frame(c(.x, .y)))

pmap_dfr(.l, .f, ..., .id = NULL**)** Return a data frame created by row-binding.
pmap_dfr(list(l1, l2),
~ as.data.frame(c(.x, .y)))

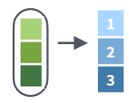
pwalk(.l, .f, ...**)** Trigger side effects, return invisibly.
pwalk(list(objs, paths), save)

LISTS AND INDEXES

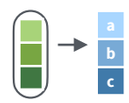
imap(.x, .f, ...**)** Apply .f to each element and its index, return a list.
imap(y, ~ paste0(.y, ": ", .x))



imap_dbl(.x, .f, …**)**
Return a double vector.
imap_dbl(y, ~ .y)

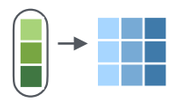


imap_int(.x, .f, ...**)**
Return an integer vector.
imap_int(y, ~ .y)



imap_chr(.x, .f, …**)**
Return a character vector.
imap_chr(y, ~ paste0(.y, ": ", .x))

imap_lgl(.x, .f, …**)**
Return a logical vector.
imap_lgl(l1, ~ is.character(.y))



imap_dfc(.x, .f, ...**)**
Return a data frame created by column-binding.
imap_dfc(l2,
~ as.data.frame(c(.x, .y)))

imap_dfr(.x, .f, ..., .id = NULL**)**
Return a data frame created by row-binding.
imap_dfr(l2,
~ as.data.frame(c(.x, .y)))

iwalk(.x, .f, ...**)** Trigger side effects, return invisibly.
iwalk(z, ~ print(paste0(.y, ": ", .x)))

Function Shortcuts

Use **~ .** with functions like **map()** that have single arguments.

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

Use **~ .x .y** with functions like **map2()** that have two arguments.

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

Use **~ ..1 ..2 ..3** etc with functions like **pmap()** that have many arguments.

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

Use **~ .x .y** with functions like **imap()**. .x will get the list value and .y will get the index.

imap(list(a, b, c), ~ paste0(.y, ": ", .x)
outputs **"index: value"** for each item

Use a **string** or an **integer** with any map function to index list elements by name or position. **map(l, "name")** becomes **map(l, function(x) x[["name"]])**

R Studio

Work with Lists

Filter

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

detect(.x, .f, ..., dir = c("forward", "backward"), .right = NULL, .default = NULL**)**
Find first element to pass.
detect(x, is.character)

detect_index(.x, .f, ..., dir = c("forward", "backward"), .right = NULL**)** Find index of first element to pass.
detect_index(x, is.character)

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

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

none(.x, .p, …**)**
Do no elements pass a test?
none(x, is.character)

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

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

Index

pluck(.x, ..., .default=NULL**)**
Select an element by name or index. Also **attr_getter()** and **chuck()**.
pluck(x, "b")
x %>% pluck("b")

assign_in(x, where, value**)**
Assign a value to a location using pluck selection.
assign_in(x, "b", 5)
x %>% assign_in("b", 5)

modify_in(.x, .where, .f**)**
Apply a function to a value at a selected location.
modify_in(x, "b", abs)
x %>% modify_in("b", abs)

Reshape

flatten(.x**)** Remove a level of indexes from a list.
Also **flatten_chr()** etc.
flatten(x)

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()**, and **cross_df()**.
cross2(1:3, 4:6)

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

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)

Modify

modify(.x, .f, ...**)** Apply a function to each element. Also **modify2()**, and **imodify()**.
modify(x, ~.+ 2)

modify_at(.x, .at, .f, ...**)** Apply a function to selected elements.
Also **map_at()**.
modify_at(x, "b", ~.+ 2)

modify_if(.x, .p, .f, ...**)** Apply a 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. Also **map_depth()**.
modify_depth(x, 2, ~.+ 2)

Combine

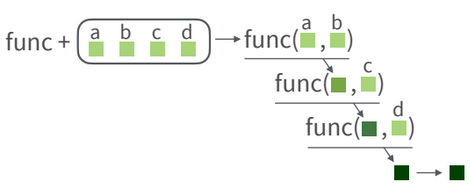
append(x, values, after = length(x)**)** Add values to end of list.
append(x, list(d = 1))

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

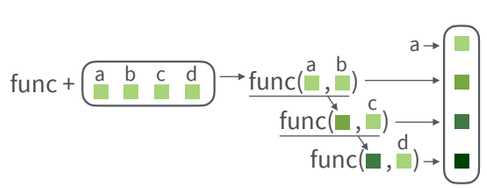
splice(…**)** Combine objects into a list, storing S3 objects as sub-lists.
splice(x, y, "foo")

Reduce

reduce(.x, .f, ..., .init, .dir = c("forward", "backward")**)** Apply function recursively to each element of a list or vector. Also **reduce2()**.
reduce(x, sum)



accumulate(.x, .f, ..., .init**)** Reduce a list, but also return intermediate results. Also **accumulate2()**.
accumulate(x, sum)



List-Columns

max	seq
3	<int [3]>
4	<int [4]>
5	<int [5]>

List-columns are columns of a data frame where each element is a list or vector instead of an atomic value. Columns can also be lists of data frames. See **tidyr** for more about nested data and list columns.

WORK WITH LIST-COLUMNS

Manipulate list-columns like any other kind of column, using **dplyr** functions like **mutate()** and **transmute()**. Because each element is a list, use **map functions** within a column function to manipulate each element.

map(), **map2()**, or **pmap()** return lists and will **create new list-columns**.

```
starwars %>%
  transmute(ships = map2(vehicles,
                         starships,
                         append)
```

list function, return list
list-columns
column function

Suffixed map functions like **map_int()** return an atomic data type and will **simplify list-columns into regular columns**.

```
starwars %>%
  mutate(n_films = map_int(films, length))
```

list function, return int
column function
list-column

Use Python with R with reticulate : : CHEAT SHEET

The **reticulate** package lets you use Python and R together seamlessly in R code, in R Markdown documents, and in the RStudio IDE.

Python in R Markdown

(Optional) Build Python env to use.

Add **knitr::knit_engines$set(python = reticulate::eng_python)** to the setup chunk to set up the reticulate Python engine (not required for knitr >= 1.18).

Suggest the Python environment to use, in your setup chunk.

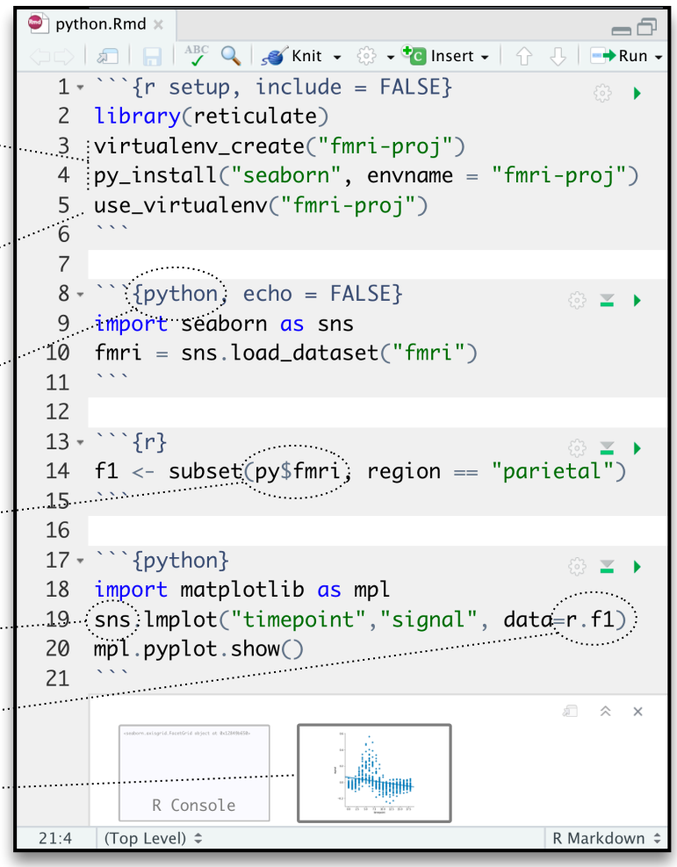
Begin Python chunks with **```{python}**. Chunk options like **echo**, **include**, etc. all work as expected.

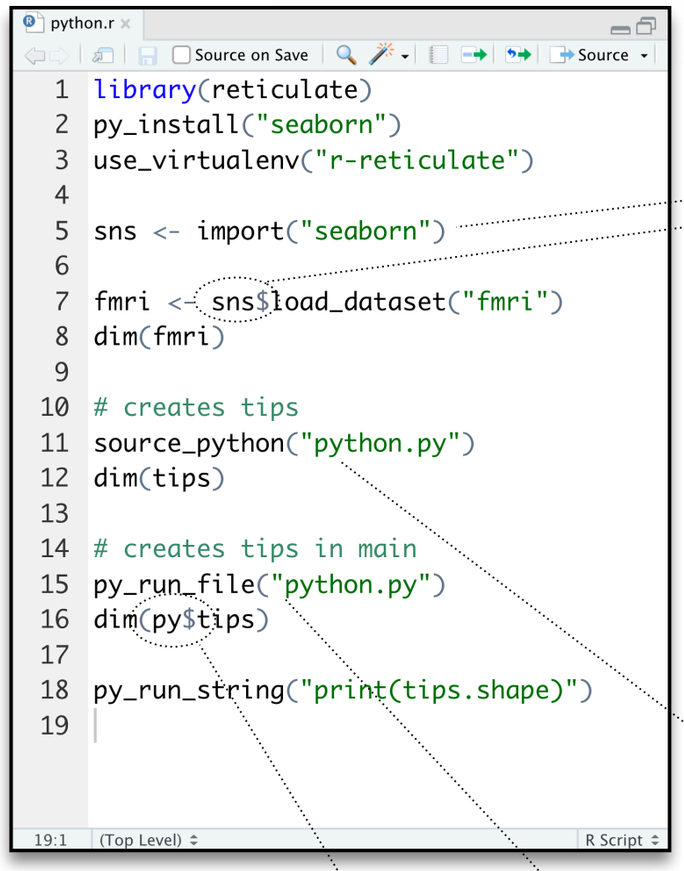
Use the **py** object to access objects created in Python chunks from R chunks.

Python chunks all execute within a **single** Python session so you have access to all objects created in previous chunks.

Use the **r** object to access objects created in R chunks from Python chunks.

Output displays below chunk, including matplotlib plots.





Python in R

Call Python from R code in three ways:

IMPORT PYTHON MODULES

Use **import()** to import any Python module. Access the attributes of a module with **$**.

- **import(**module, as = NULL, convert = TRUE, delay_load = FALSE**)** Import a Python module. If convert = TRUE, Python objects are converted to their equivalent R types. Also **import_from_path()**. import("pandas")
- **import_main(**convert = TRUE**)** Import the main module, where Python executes code by default. import_main()
- **import_builtins(**convert = TRUE**)** Import Python's built-in functions. import_builtins()

SOURCE PYTHON FILES

Use **source_python()** to source a Python script and make the Python functions and objects it creates available in the calling R environment.

- **source_python(**file, envir = parent.frame(), convert = TRUE**)** Run a Python script, assigning objects to a specified R environment. source_python("file.py")

RUN PYTHON CODE

Execute Python code into the **main** Python module with **py_run_file()** or **py_run_string()**.

- **py_run_string(**code, local = FALSE, convert = TRUE**)** Run Python code (passed as a string) in the main module. py_run_string("x = 10"); py$x
- **py_run_file(**file, local = FALSE, convert = TRUE**)** Run Python file in the main module. py_run_file("script.py")
- **py_eval(**code, convert = TRUE**)** Run a Python expression, return the result. Also **py_call()**. py_eval("1 + 1")

Access the results, and anything else in Python's **main** module, with **py**.

- **py** An R object that contains the Python main module and the results stored there. py$x

Object Conversion

Tip: To index Python objects begin at 0, use integers, e.g. 0L

Reticulate provides **automatic** built-in conversion between Python and R for many Python types.

R ⟷	Python
Single-element vector	Scalar
Multi-element vector	List
List of multiple types	Tuple
Named list	Dict
Matrix/Array	NumPy ndarray
Data Frame	Pandas DataFrame
Function	Python function
NULL, TRUE, FALSE	None, True, False

Or, if you like, you can convert manually with

py_to_r(x**)** Convert a Python object to an R object. Also **r_to_py()**. py_to_r(x)

tuple(..., convert = FALSE**)** Create a Python tuple. tuple("a", "b", "c")

dict(..., convert = FALSE**)** Create a Python dictionary object. Also **py_dict()** to make a dictionary that uses Python objects as keys. dict(foo = "bar", index = 42L)

np_array(data, dtype = NULL, order = "C"**)** Create NumPy arrays. np_array(c(1:8), dtype = "float16")

array_reshape(x, dim, order = c("C", "F")**)** Reshape a Python array. x <- 1:4; array_reshape(x, c(2, 2))

py_func(f**)** Wrap an R function in a Python function with the same signature. py_func(xor)

py_main_thread_func(f**)** Create a function that will always be called on the main thread.

iterate(it, f = base::identity, simplify = TRUE**)** Apply an R function to each value of a Python iterator or return the values as an R vector, draining the iterator as you go. Also **iter_next()** and **as_iterator()**. iterate(iter, print)

py_iterator(fn, completed = NULL**)** Create a Python iterator from an R function. seq_gen <- function(x){ n <- x; function() {n <<- n + 1; n}}; py_iterator(seq_gen(9))

Helpers

py_capture_output(expr, type = c("stdout", "stderr")**)** Capture and return Python output. Also **py_suppress_warnings()**. py_capture_output("x")

py_get_attr(x, name, silent = FALSE**)** Get an attribute of a Python object. Also **py_set_attr()**, **py_has_attr()**, and **py_list_attributes()**. py_get_attr(x)

py_help(object**)** Open the documentation page for a Python object. py_help(sns)

py_last_error() Get the last Python error encountered. Also **py_clear_last_error()** to clear the last error. py_last_error()

py_save_object(object, filename, pickle = "pickle", ...**)** Save and load Python objects with pickle. Also **py_load_object()**. py_save_object(x, "x.pickle")

with(data, expr, as = NULL, ...**)** Evaluate an expression within a Python context manager.

```
py <- import_builtins();
with(py$open("output.txt", "w") %as% file,
  { file$write("Hello, there!")})
```

RStudio

Python in the IDE

Requires reticulate plus RStudio v1.2+. Some features require v1.4+.

Syntax highlighting for Python scripts and chunks.

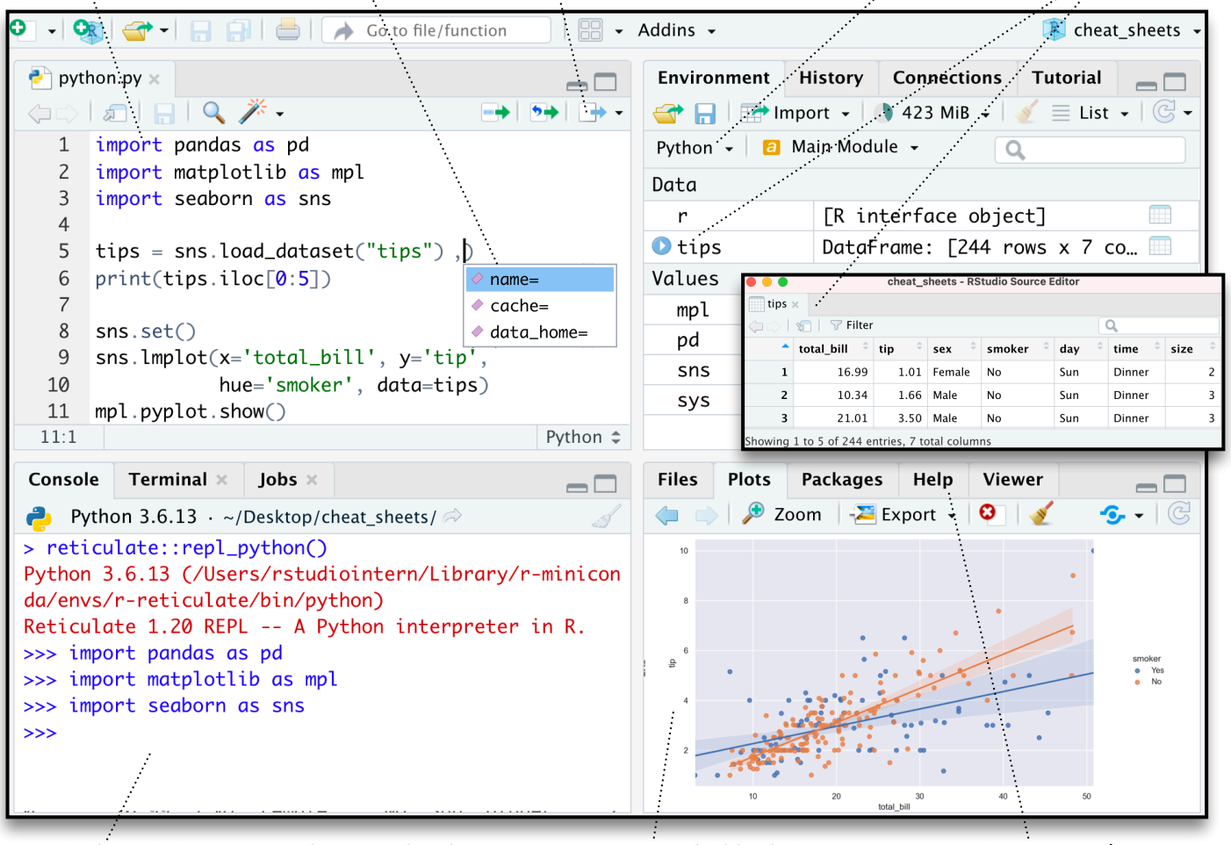
Tab completion for Python functions and objects (and Python modules imported in R scripts).

Source Python scripts.

Execute Python code line by line with **Cmd + Enter** (**Ctrl + Enter**).

View Python objects in the Environment Pane.

View Python objects in the Data Viewer.



A Python REPL opens in the console when you run Python code with a keyboard shortcut. Type **exit** to close.

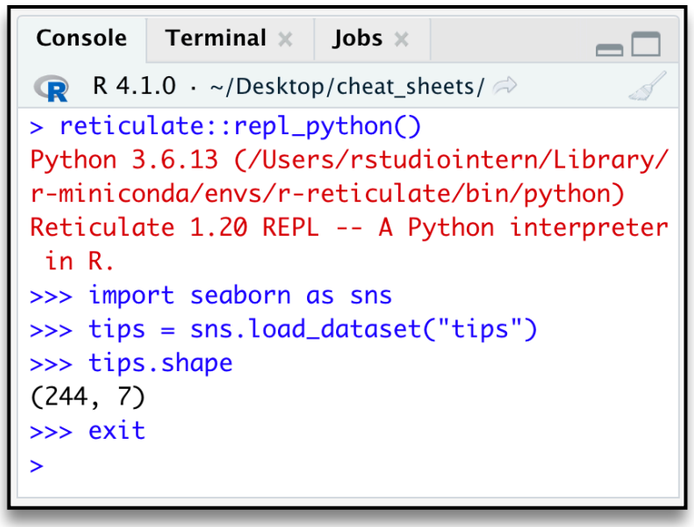
matplotlib plots display in plots pane.

Press **F1** over a Python symbol to display the help topic for that symbol.

Python REPL

A REPL (Read, Eval, Print Loop) is a command line where you can run Python code and view the results.

1. Open in the console with **repl_python()**, or by running code in a Python script with **Cmd + Enter** (**Ctrl + Enter**).
   - **repl_python(**module = NULL, quiet = getOption("reticulate.repl.quiet", default = FALSE), input = NULL**)** Launch a Python REPL. Run **exit** to close. repl_python()
2. Type commands at **>>>** prompt.
3. Press **Enter** to run code.
4. Type **exit** to close and return to R console.



Configure Python

Reticulate binds to a local instance of Python when you first call **import()** directly or implicitly from an R session. To control the process, find or build your desired Python instance. Then suggest your instance to reticulate. **Restart R to unbind.**

Find Python

- **install_python(**version, list = FALSE, force = FALSE**)** Download and install Python. install_python("3.6.13")
- **py_available(**initialize = FALSE**)** Check if Python is available on your system. Also **py_module_available()** and **py_numpy_module().** py_available()
- **py_discover_config()** Return all detected versions of Python. Use **py_config()** to check which version has been loaded. py_config()
- **virtualenv_list()** List all available virtualenvs. Also **virtualenv_root()**. virtualenv_list()
- **conda_list(**conda = "auto"**)** List all available conda envs. Also **conda_binary()** and **conda_version()**. conda_list()

Create a Python env

- **virtualenv_create(**envname = NULL, ...**)** Create a new virtual environment. virtualenv_create("r-pandas")
- **conda_create(**envname = NULL, ...**)** Create a new conda environment. conda_create("r-pandas", packages = "pandas")

Install Packages

Install Python packages with R (below) or the shell:

pip install SciPy
conda install SciPy

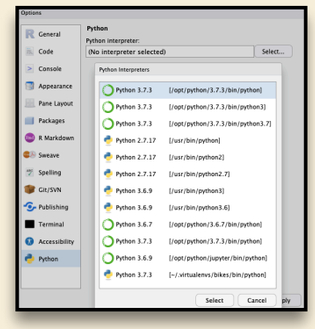
- **py_install(**packages, envname, ...**)** Installs Python packages into a Python env. py_install("pandas")
- **virtualenv_install(**envname, packages, ...**)** Install a package within a virtualenv. Also **virtualenv_remove()**. virtualenv_install("r-pandas", packages = "pandas")
- **conda_install(**envname, packages, ...**)** Install a package within a conda env. Also **conda_remove()**. conda_install("r-pandas", packages = "plotly")

Suggest an env to use

Set a default Python interpreter in the RStudio IDE Global or Project Options.

Go to **Tools > Global Options... > Python** for Global Options.

Within a project, go to **Tools > Project Options... >Python**.



Otherwise, to choose an instance of Python to bind to, reticulate scans the instances on your computer in the following order, **stopping at the first instance that contains the module called by import()**.

1. The instance referenced by the environment variable **RETICULATE_PYTHON** (if specified). **Tip: set in .Renviron file.**
   - **Sys.setenv(**RETICULATE_PYTHON = PATH**)** Set default Python binary. Persists across sessions! Undo with **Sys.unsetenv()**. Sys.setenv(RETICULATE_PYTHON = "/usr/local/bin/python")
2. The instances referenced by **use_** functions if called before import(). Will fail silently if called after import unless **required = TRUE**.
   - **use_python**(python, required = FALSE) Suggest a Python binary to use by path. use_python("/usr/local/bin/python")
   - **use_virtualenv**(virtualenv = NULL, required = FALSE) Suggest a Python virtualenv. use_virtualenv("~/myenv")
   - **use_condaenv**(condaenv = NULL, conda = "auto", required = FALSE) Suggest a conda env to use. use_condaenv(condaenv = "r-nlp", conda = "/opt/anaconda3/bin/conda")
3. Within virtualenvs and conda envs that carry the same name as the imported module. e.g. ~/anaconda/envs/nltk for import("nltk")
4. At the location of the Python binary discovered on the system PATH (i.e. Sys.which("python"))
5. At customary locations for Python, e.g. /usr/local/bin/python, /opt/local/bin/python...

rmarkdown : : CHEAT SHEET

What is rmarkdown?

.Rmd files • Develop your code and ideas side-by-side in a single document. Run code as individual chunks or as an entire document.

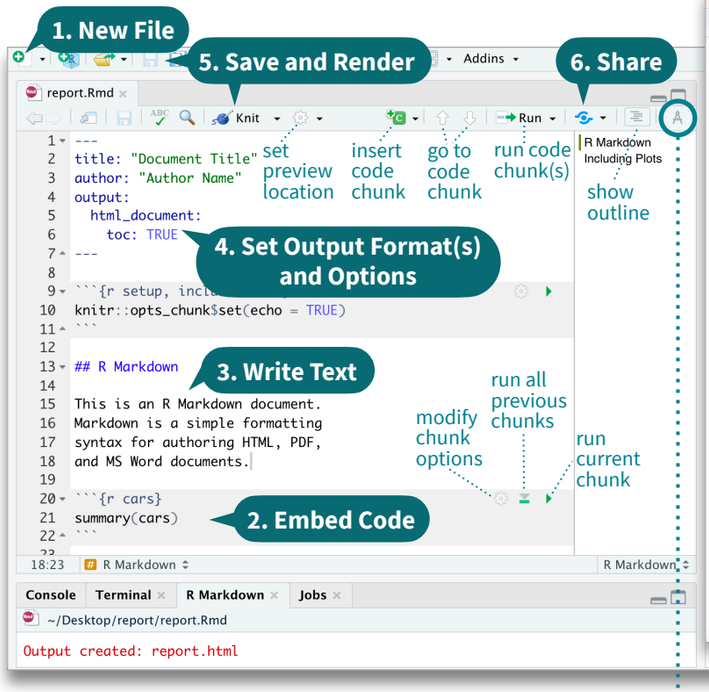
Dynamic Documents • Knit together plots, tables, and results with narrative text. Render to a variety of formats like HTML, PDF, MS Word, or MS Powerpoint.

Reproducible Research • Upload, link to, or attach your report to share. Anyone can read or run your code to reproduce your work.

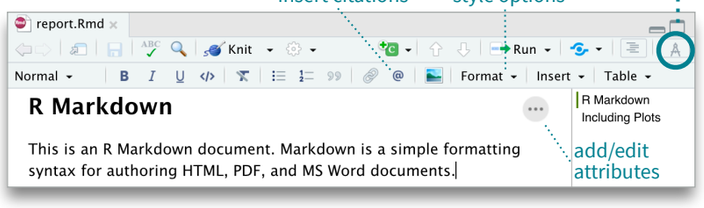
Workflow

1. Open a **new .Rmd file** in the RStudio IDE by going to *File > New File > R Markdown*.
2. **Embed code** in chunks. Run code by line, by chunk, or all at once.
3. **Write text** and add tables, figures, images, and citations. Format with Markdown syntax or the RStudio Visual Markdown Editor.
4. **Set output format(s) and options** in the YAML header. Customize themes or add parameters to execute or add interactivity with Shiny.
5. **Save and render** the whole document. Knit periodically to preview your work as you write.
6. **Share your work!**

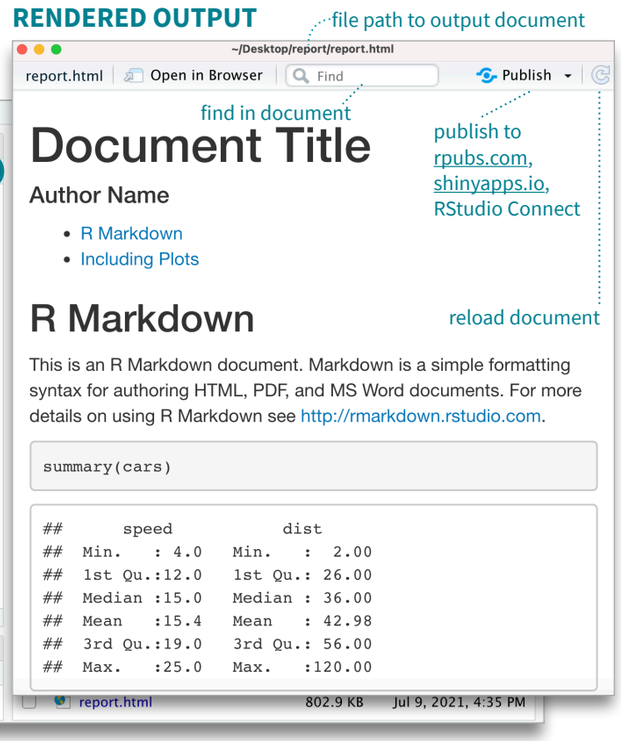
SOURCE EDITOR



VISUAL EDITOR



RENDERED OUTPUT



Insert Citations

Create citations from a bibliography file, a Zotero library, or from DOI references.

BUILD YOUR BIBLIOGRAPHY

- Add BibTeX or CSL bibliographies to the YAML header.

```
---
title: "My Document"
bibliography: references.bib
link-citations: TRUE
---
```

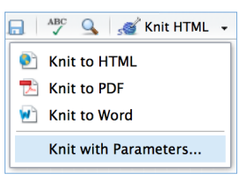
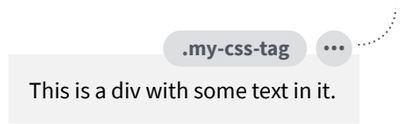
- If Zotero is installed locally, your main library will automatically be available.
- Add citations by DOI by searching "from DOI" in the **Insert Citation** dialog.

INSERT CITATIONS

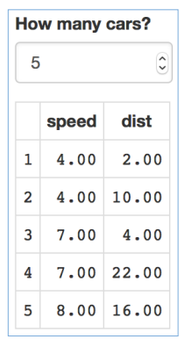
- Access the **Insert Citations** dialog in the Visual Editor by clicking the **@** symbol in the toolbar or by clicking **Insert > Citation**.
- Add citations with markdown syntax by typing **[@cite]** or **@cite**.

Insert Tables

Output data frames as tables using **kable(**data, caption**)**.

```
```{r}
data <- faithful[1:4, ]
knitr::kable(data,
             caption = "Table with kable")
```
```

Table with kable

eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62

Other table packages include **flextable**, **gt**, and **kableExtra**.

Write with Markdown

The syntax on the left renders as the output on the right.

Plain text. End a line with two spaces to start a new paragraph. Also end with a backslash\ to make a new line.	Plain text. End a line with two spaces to start a new paragraph. Also end with a backslash to make a new line.
italics and **bold** superscript^2^/subscript~2~ ~~strikethrough~~ escaped: * _ \\ endash: --, emdash: ---	*italics* and **bold** superscript^2/subscript$_2$ ~~strikethrough~~ escaped: * _ \ endash: –, emdash: —
# Header 1 ## Header 2 ... ###### Header 6	**Header 1** **Header 2** ... **Header 6**
- unordered list - item 2 - item 2a (indent 1 tab) - item 2b 1. ordered list 2. item 2 - item 2a (indent 1 tab) - item 2b	• unordered list • item 2 • item 2a (indent 1 tab) • item 2b 1. ordered list 2. item 2 • item 2a (indent 1 tab) • item 2b
<link url> [This is a link.](link url) [This is another link][id]. At the end of the document: [id]: link url ![Caption](image.png) or ![Caption][id2] At the end of the document: [id2]: image.png	http://www.rstudio.com/ This is a link. This is another link.  Caption.
`verbatim code` ``` multiple lines of verbatim code ```	`verbatim code` multiple lines of verbatim code
> block quotes	block quotes
equation: $e^{i \pi} + 1 = 0$ equation block: $$E = mc^{2}$$	equation: $e^{i\pi} + 1 = 0$ equation block: $$E = mc^2$$
horizontal rule: ---	horizontal rule:
| Right | Left | Default | Center | |-------:|:------|----------|:--------:| | 12 | 12 | 12 | 12 | | 123 | 123 | 123 | 123 | | 1 | 1 | 1 | 1 |	Right / Left / Default / Center 12 / 12 / 12 / 12 123 / 123 / 123 / 123 1 / 1 / 1 / 1
HTML Tabsets # Results {.tabset} ## Plots text text ## Tables more text	**Results** Plots | Tables text

Embed Code with knitr

CODE CHUNKS

Surround code chunks with ```` ```{r} ```` and ```` ``` ```` or use the Insert Code Chunk button. Add a chunk label and/or chunk options inside the curly braces after **r**.

```
```{r chunk-label, include=FALSE}
summary(mtcars)
```
```

SET GLOBAL OPTIONS

Set options for the entire document in the first chunk.

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

INLINE CODE

Insert **`r <code>`** into text sections. Code is evaluated at render and results appear as text.

"Built with `` `r getRversion()` `` " --> "Built with 4.1.0"

OPTION	DEFAULT	EFFECTS
echo	TRUE	display code in output document
error	FALSE	TRUE (display error messages in doc) FALSE (stop render when error occurs)
eval	TRUE	run code in chunk
include	TRUE	include chunk in doc after running
message	TRUE	display code messages in document
warning	TRUE	display code warnings in document
results	"markup"	"asis" (passthrough results) "hide" (don't display results) "hold" (put all results below all code)
fig.align	"default"	"left", "right", or "center"
fig.alt	NULL	alt text for a figure
fig.cap	NULL	figure caption as a character string
fig.path	"figure/"	prefix for generating figure file paths
fig.width & fig.height	7	plot dimensions in inches
out.width		rescales output width, e.g. "75%", "300px"
collapse	FALSE	collapse all sources & output into a single block
comment	"##"	prefix for each line of results
child	NULL	files(s) to knit and then include
purl	TRUE	include or exclude a code chunk when extracting source code with knitr::purl()

See more options and defaults by running **str(knitr::opts_chunk$get())**

RStudio

Set Output Formats and their Options in YAML

Use the document's YAML header to set an **output format** and customize it with **output options**.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    toc: TRUE
---
```

Indent format 2 characters, indent options 4 characters

OUTPUT FORMAT	CREATES
html_document	.html
pdf_document*	.pdf
word_document	Microsoft Word (.docx)
powerpoint_presentation	Microsoft Powerpoint (.pptx)
odt_document	OpenDocument Text
rtf_document	Rich Text Format
md_document	Markdown
github_document	Markdown for Github
ioslides_presentation	ioslides HTML slides
slidy_presentation	Slidy HTML slides
beamer_presentation*	Beamer slides

* Requires LaTeX, use **tinytex::install_tinytex()**

Also see **flexdashboard**, **bookdown**, **distill**, and **blogdown**.

IMPORTANT OPTIONS	DESCRIPTION	HTML	PDF	MS Word	MS PPT
anchor_sections	Show section anchors on mouse hover (TRUE or FALSE)	X			
citation_package	The LaTeX package to process citations ("default", "natbib", "biblatex")		X		
code_download	Give readers an option to download the .Rmd source code (TRUE or FALSE)	X			
code_folding	Let readers to toggle the display of R code ("none", "hide", or "show")	X			
css	CSS or SCSS file to use to style document (e.g. "style.css")	X			
dev	Graphics device to use for figure output (e.g. "png", "pdf")	X	X		
df_print	Method for printing data frames ("default", "kable", "tibble", "paged")	X	X	X	X
fig_caption	Should figures be rendered with captions (TRUE or FALSE)	X	X	X	X
highlight	Syntax highlighting ("tango", "pygments", "kate", "zenburn", "textmate")	X	X	X	
includes	File of content to place in doc ("in_header", "before_body", "after_body")	X	X		
keep_md	Keep the Markdown .md file generated by knitting (TRUE or FALSE)	X	X	X	X
keep_tex	Keep the intermediate TEX file used to convert to PDF (TRUE or FALSE)		X		
latex_engine	LaTeX engine for producing PDF output ("pdflatex", "xelatex", or "lualatex")		X		
reference_docx/_doc	docx/pptx file containing styles to copy in the output (e.g. "file.docx", "file.pptx")			X	X
theme	Theme options (see Bootswatch and Custom Themes below)	X			
toc	Add a table of contents at start of document (TRUE or FALSE)	X	X	X	X
toc_depth	The lowest level of headings to add to table of contents (e.g. 2, 3)	X	X	X	X
toc_float	Float the table of contents to the left of the main document content (TRUE or FALSE)	X			

Use **?<output format>** to see all of a format's options, e.g. **?html_document**

Render

When you render a document, rmarkdown:

1. Runs the code and embeds results and text into an .md file with knitr.
2. Converts the .md file into the output format with Pandoc.

Save, then **Knit** to preview the document output. The resulting HTML/PDF/MS Word/etc. document will be created and saved in the same directory as the .Rmd file.

Use **rmarkdown::render()** to render/knit in the R console. See **?render** for available options.

Share

Publish on RStudio Connect

to share R Markdown documents securely, schedule automatic updates, and interact with parameters in real time.

rstudio.com/products/connect/

More Header Options

PARAMETERS

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

1. **Add parameters** in the header as sub-values of params.

```
---
params:
  state: "hawaii"
---
```

2. **Call parameters** in code using params$<name>.

```
```{r}
data <- df[, params$state]
summary(data)
```
```

3. **Set parameters** with Knit with Parameters or the params argument of **render()**.



REUSABLE TEMPLATES

1. **Create a new package** with a inst/rmarkdown/templates directory.
2. **Add a folder** containing **template.yaml** (below) and **skeleton.Rmd** (template contents).

```
---
name: "My Template"
---
```

3. **Install** the package to access template by going to **File > New R Markdown > From Template**.

BOOTSWATCH THEMES

Customize HTML documents with Bootswatch themes from the **bslib** package using the theme output option.

Use **bslib::bootswatch_themes()** to list available themes.


```
---
title: "Document Title"
author: "Author Name"
output:
  html_document:
    theme:
      bootswatch: solar
---
```

CUSTOM THEMES

Customize individual HTML elements using bslib variables. Use **?bs_theme** to see more variables.

```
---
output:
  html_document:
    theme:
      bg: "#121212"
      fg: "#E4E4E4"
      base_font:
        google: "Prompt"
---
```

More on **bslib** at **pkgs.rstudio.com/bslib/**.

STYLING WITH CSS AND SCSS

Add CSS and SCSS to your document by adding a path to a file with the **css** option in the YAML header.

```
---
title: "My Document"
author: "Author Name"
output:
  html_document:
    css: "style.css"
---
```

Apply CSS styling by writing HTML tags directly or:

- Use markdown to apply style attributes inline.

Bracketed Span
A [green]{.my-color} word.

Fenced Div
::: {.my-color}
All of these words
are green.
:::

A green word.

All of these words are green.

- Use the Visual Editor. Go to **Format > Div/Span** and add CSS styling directly with Edit Attributes.



INTERACTIVITY

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)
})
```
```



	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

Also see Shiny Prerendered for better performance. **rmarkdown.rstudio.com/authoring_shiny_prerendered**

Embed a complete app into your document with **shiny::shinyAppDir()**. More at **bookdown.org/yihui/rmarkdown/shiny-embedded.html**.

Data Science in Spark with *sparklyr* : : CHEAT SHEET

Intro

sparklyr is an R interface for Apache Spark™. ***sparklyr*** enables us to write all of our analysis code in R, but have the actual processing happen inside Spark clusters. Easily manipulate and model large-scale using R and Spark via *sparklyr.*

Import
- From R (**copy_to()**)
- Read a file (**spark_read_**)
- Read Hive table (**tbl()**)

Wrangle
- **dplyr** verb
- Feature transformer (**ft_**)
- Direct Spark SQL (**DBI**)

Visualize
- Collect result, plot in R
- Use **dbplot**

Model
- Spark MLlib (**ml_**)
- H2O Extension

Communicate
Collect results into R share using **rmarkdown**

R for Data Science, Grolemund & Wickham

Import

Import data into Spark, not R

READ A FILE INTO SPARK

Arguments that apply to all functions:
sc, name, path, options=list(), repartition=0, memory=TRUE, overwrite=TRUE

CSV	**spark_read_csv(** header = TRUE, columns=NULL, infer_schema=TRUE, delimiter = ",", quote= "\"", escape = "\\", charset = "UTF-8", null_value = NULL**)**
JSON	**spark_read_json()**
PARQUET	**spark_read_parquet()**
TEXT	**spark_read_text()**
HIVE TABLE	**spark_read_table()**
ORC	**spark_read_orc()**
LIBSVM	**spark_read_libsvm()**
JDBC	**spark_read_jdbc()**
DELTA	**spark_read_delta()**

R DATA FRAME INTO SPARK

dplyr::**copy_to(**dest, df, name**)**

FROM A TABLE IN HIVE

dplyr::**tbl(**scr, …**)** Creates a reference to the table without loading it into memory

Wrangle

DPLYR VERBS

Translates into Spark SQL statements

```
copy_to(sc, mtcars) %>%
  mutate(trm = ifelse(am == 0, "auto", "man")) %>%
  group_by(trm) %>%
  summarise_all(mean)
```

FEATURE TRANSFORMERS

ft_binarizer() - Assigned values based on threshold

ft_bucketizer() - Numeric column to discretized column

ft_count_vectorizer() - Extracts a vocabulary from document

ft_discrete_cosine_transform() - 1D discrete cosine transform of a real vector

ft_elementwise_product() - Element-wise product between 2 cols

ft_hashing_tf() - Maps a sequence of terms to their term frequencies using the hashing trick.

ft_idf() - Compute the Inverse Document Frequency (IDF) given a collection of documents

ft_imputer() - Imputation estimator for completing missing values, uses the mean or the median of the columns

ft_index_to_string() - Index labels back to label as strings

ft_interaction() - Takes in Double and Vector type columns and outputs a flattened vector of their feature interactions

ft_max_abs_scaler() - Rescale each feature individually to range [-1, 1]

ft_min_max_scaler() - Rescale each feature individually to a common range [min, max] linearly

ft_ngram() - Converts the input array of strings into an array of n-grams

ft_bucketed_random_projection_lsh()
ft_minhash_lsh() - Locality Sensitive Hashing functions for Euclidean distance and Jaccard distance (MinHash)

ft_normalizer() - Normalize a vector to have unit norm using the given p-norm

ft_one_hot_encoder()- Continuous to binary vectors

ft_pca() - Project vectors to a lower dimensional space of top k principal components

ft_quantile_discretizer() - Continuous to binned categorical values

ft_regex_tokenizer() - Extracts tokens either by using the provided regex pattern to split the text

ft_standard_scaler() - Removes the mean and scaling to unit variance using column summary statistics

ft_stop_words_remover() - Filters out stop words from input

ft_string_indexer() - Column of labels into a column of label indices.

ft_tokenizer() - Converts to lowercase and then splits it by white spaces

ft_vector_assembler() - Combine vectors into single row-vector

ft_vector_indexer() - Indexing categorical feature columns in a dataset of Vector

ft_vector_slicer() - Takes a feature vector and outputs a new feature vector with a subarray of the original features

ft_word2vec() - Word2Vec transforms a word into a code

Visualize

DPLYR + GGPLOT2

```
copy_to(sc, mtcars) %>%
  group_by(cyl) %>%
  summarise(mpg_m = mean(mpg)) %>%
  collect() %>%
  ggplot() +
    geom_col(aes(cyl, mpg_m))
```

Summarize in Spark
Collect results in R
Create plot

DBPLOT

```
copy_to(sc, mtcars) %>%
  dbplot_histogram(mpg) +
  labs(title = "Histogram of MPG")
```

dbplot_histogram(data, x, bins = 30, binwidth = NULL**)** - Calculates the histogram bins in Spark and plots in ggplot2

dbplot_raster(data, x, y, fill = n(), resolution = 100, complete = FALSE**)** - Visualize 2 continuous variables. Use instead of geom_point()

Data Science in Spark with *sparklyr* : : **CHEAT SHEET**

Modeling

REGRESSION

ml_linear_regression() - Regression using linear regression.

ml_aft_survival_regression() - Parametric survival regression model named accelerated failure time (AFT) model

ml_generalized_linear_regression() - Generalized linear regression model

ml_isotonic_regression() - Currently implemented using parallelized pool adjacent violators algorithm. Only univariate (single feature) algorithm supported

ml_random_forest_regressor() - Regression using random forests.

CLASSIFICATION

ml_linear_svc() - Classification using linear support vector machines

ml_logistic_regression() - Logistic regression

ml_multilayer_perceptron_classifier() - Classification model based on the Multilayer Perceptron.

ml_naive_bayes() - Naive Bayes Classifiers. It supports Multinomial NB which can handle finitely supported discrete data

ml_one_vs_rest() - Reduction of Multiclass Classification to Binary Classification. Performs reduction using one against all strategy.

TREE

ml_decision_tree_classifier() | ml_decision_tree() | ml_decision_tree_regressor() - Classification and regression using decision trees

ml_gbt_classifier() | ml_gradient_boosted_trees() | ml_gbt_regressor() - Binary classification and regression using gradient boosted trees

ml_random_forest_classifier() - Classification and regression using random forests.

ml_feature_importances(model,...)ml_tree_feature_importance(model) - Feature Importance for Tree Models

CLUSTERING

ml_bisecting_kmeans() - A bisecting k-means algorithm based on the paper

ml_lda() | ml_describe_topics() | ml_log_likelihood() | ml_log_perplexity() | ml_topics_matrix() - LDA topic model designed for text documents.

ml_gaussian_mixture() - Expectation maximization for multivariate Gaussian Mixture Models (GMMs)

ml_kmeans() | ml_compute_cost() - K-means clustering with support for k-means

FP GROWTH

ml_fpgrowth() | ml_association_rules() | ml_freq_itemsets() - A parallel FP-growth algorithm to mine frequent itemsets.

FEATURE

ml_chisquare_test(x,features,label) - Pearson's independence test for every feature against the label

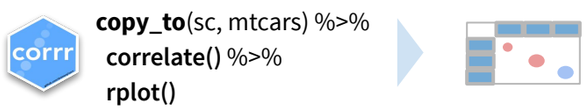
ml_default_stop_words() - Loads the default stop words for the given language

STATS

ml_summary() - Extracts a metric from the summary object of a Spark ML model

ml_corr() - Compute correlation matrix

correlate package integrates with sparklyr



RECOMMENDATION

ml_als() | ml_recommend() - Recommendation using Alternating Least Squares matrix factorization

EVALUATION

ml_clustering_evaluator() - Evaluator for clustering

ml_evaluate() - Compute performance metrics

ml_binary_classification_evaluator() | ml_binary_classification_eval() | ml_classification_eval() - A set of functions to calculate performance metrics for prediction models.

UTILITIES

ml_call_constructor() - Identifies the associated sparklyr ML constructor for the JVM

ml_model_data() - Extracts data associated with a Spark ML model

ml_standardize_formula() - Generates a formula string from user inputs, to be used in `ml_model` constructor

ml_uid() - Extracts the UID of an ML object.

Start a Spark session

YARN CLIENT

1. Install RStudio Server on one of the existing nodes, preferably an edge node
2. Locate path to the cluster's Spark Home Directory, it normally is "/usr/lib/spark"
3. Basic configuration example

```
conf <- spark_config()
conf$spark.executor.memory <- "300M"
conf$spark.executor.cores <- 2
conf$spark.executor.instances <- 3
conf$spark.dynamicAllocation.enabled<-"false"
```

4. Open a connection (some base configurations included in the example)

```
sc <- spark_connect(master = "yarn",
      spark_home = "/usr/lib/spark/",
      version = "2.1.0", config = conf)
```

YARN CLUSTER

1. Make sure to have copies of the yarn-site.xml and hive-site.xml files in the RStudio Server
2. Point environment variables to the correct paths

```
Sys.setenv(JAVA_HOME="[Path]")
Sys.setenv(SPARK_HOME ="[Path]")
Sys.setenv(YARN_CONF_DIR ="[Path]")
```

3. Open a connection

```
sc <- spark_connect(master = "yarn-cluster")
```

STANDALONE CLUSTER

1. Install RStudio Server on one of the existing nodes or a server in the same LAN
2. Install a local version of Spark:

```
spark_install (version = "2.0.1")
```

3. Open a connection

```
spark_connect(master="spark://host:port",
  version = "2.0.1",
  spark_home = spark_home_dir())
```

LOCAL MODE

No cluster required. Use for learning purposes only

1. Install a local version of Spark:

```
spark_install("2.3")
```

2. Open a connection

```
sc <- spark_connect(master="local")
```

KUBERNETES

1. Use the following to obtain the Host and Port

```
system2("kubectl", "cluster-info")
```

2. Open a connection

```
sc <- spark_connect(config =
      spark_config_kubernetes(
        "k8s://https://[HOST]>:[PORT]",
        account = "default",
        image = "docker.io/owner/repo:version",
        version = "2.3.1"))
```

MESOS

1. Install RStudio Server on one of the nodes
2. Open a connection

```
sc <- spark_connect(master="[Mesos URL]")
```

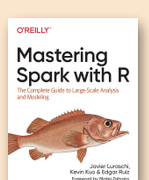
CLOUD

Databricks - spark_connect(**method = "databricks"**)

Qubole- spark_connect(**method = "qubole"**)

More Information

spark.rstudio.com



therinspark.com

REST APIs with plumber: : **CHEAT SHEET**

Introduction to REST APIs

Web APIs use **HTTP** to communicate between **client** and **server**.

HTTP

HTTP is built around a **request** and a **response**. A **client** makes a request to a **server**, which handles the request and provides a response. Requests and responses are specially formatted text containing details and data about the exchange between client and server.

REQUEST

```
curl -v "http://httpbin.org/get"

#> GET  /  get HTTP/1.1
#> Host: httpbin.org
#> User-Agent: curl/7.55.1
#> Accept: */*
#
# Request Body
```

Path · HTTP Method · Headers · HTTP Version · Message body

RESPONSE

```
#< HTTP/1.1 200 OK
#< Connection: keep-alive
#< Date: Thu, 02 Aug 2018 18:22:22 GMT
#
# Response Body
```

HTTP Version · Status code · Reason phrase · Headers · Message body

Plumber: Build APIs with R

Plumber uses special comments to turn any arbitrary R code into API endpoints. The example below defines a function that takes the **`msg`** argument and returns it embedded in additional text.

```
library(plumber)

#* @apiTitle Plumber Example API

#* Echo back the input
#* @param msg The message to echo
#* @get /echo
function(msg = "") {
  list(
    msg = paste0(
      "The message is: '", msg, "'")
  )
}
```

Plumber comments begin with #* · @ decorators define API characteristics · HTTP Method · */<path>* is used to define the location of the endpoint

Plumber pipeline

Plumber endpoints contain R code that is executed in response to an HTTP request. Incoming requests pass through a set of mechanisms before a response is returned to the client.

FILTERS

Filters can forward requests (after potentially mutating them), throw errors, or return a response without forwarding the request. Filters are defined similarly to endpoints using the **`@filter [name]`** tag. By default, filters apply to all endpoints. Endpoints can opt out of filters using the **`@preempt`** tag.

PARSER

Parsers determine how Plumber parses the incoming request body. By default Plumber parses the request body as JavaScript Object Notation (JSON). Other parsers, including custom parsers, are identified using the **`@parser [parser name]`** tag. All registered parsers can be viewed with **`registered_parsers()`**.

ENDPOINT

Endpoints define the R code that is executed in response to incoming requests. These endpoints correspond to HTTP methods and respond to incoming requests that match the defined method.

METHODS

- **`@get`** - request a resource
- **`@post`** - send data in body
- **`@put`** - store / update data
- **`@delete`** - delete resource
- **`@head`** - no request body
- **`@options`** - describe options
- **`@patch`** - partial changes
- **`@use`** - use all methods

SERIALIZER

Serializers determine how Plumber returns results to the client. By default Plumber serializes the R object returned into JavaScript Object Notation (JSON). Other serializers, including custom serializers, are identified using the **`@serializer [serializer name]`** tag. All registered serializers can be viewed with **`registered_serializers()`**.

```
library(plumber)

#* @filter log
function(req, res) {
  print(req$HTTP_USER_AGENT)
  forward()
}

#* Convert request body to uppercase
#* @preempt log
#* @parser json
#* @post /uppercase
#* @serializer json
function(req, res) {
  toupper(req$body)
}
```

Identify as filter · Filter name · Forward request · Endpoint description · Opt out of the log filter · Parser · HTTP Method · Endpoint path · Serializer

Running Plumber APIs

Plumber APIs can be run programmatically from within an R session.

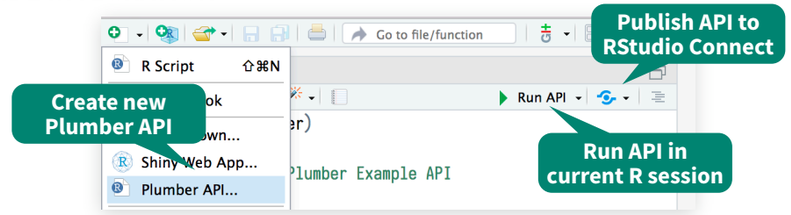
```
library(plumber)

plumb("plumber.R") %>%
  pr_run(port = 5762)
```

Path to API definition · Specify API port

This runs the API on the host machine supported by the current R session.

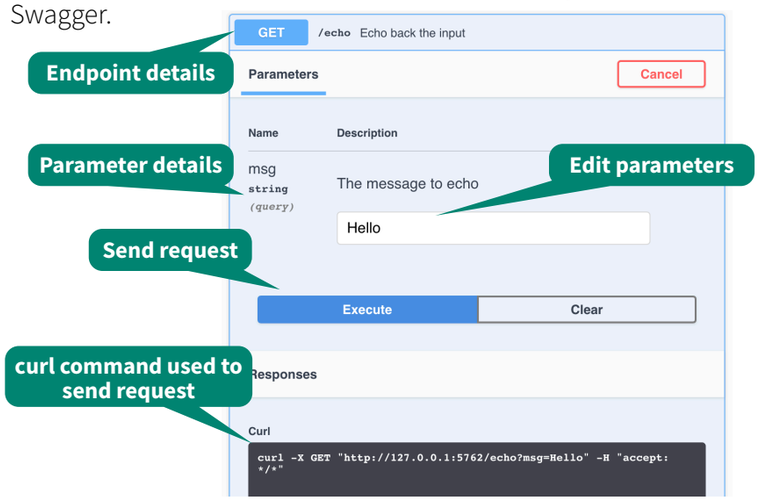
IDE INTEGRATION



Create new Plumber API · Publish API to RStudio Connect · Run API in current R session

Documentation

Plumber APIs automatically generate an OpenAPI specification file. This specification file can be interpreted to generate a dynamic user-interface for the API. The default interface is generated via Swagger.



Endpoint details · Parameter details · Edit parameters · Send request · curl command used to send request

Interact with the API

Once the API is running, it can be interacted with using any HTTP client. Note that using **`httr`** requires using a separate R session from the one serving the API.

```
(resp <- httr::GET("localhost:5762/echo?msg=Hello"))
#> Response [http://localhost:5762/echo?msg=Hello]
#>   Date: 2018-08-07 20:06
#>   Status: 200
#>   Content-Type: application/json
#>   Size: 35 B
httr::content(resp, as = "text")
#> [1] "{\"msg\":[\"The message is: 'Hello'\"]}"
```

Programmatic Plumber

Tidy Plumber

Plumber is exceptionally customizable. In addition to using special comments to create APIs, APIs can be created entirely programatically. This exposes additional features and functionality. Plumber has a convenient "tidy" interface that allows API routers to be built piece by piece. The following example is part of a standard `plumber.R` file.

```
library(plumber)

#* @plumber
function(pr) {
  pr %>%
    pr_get(path = "/echo",
           handler = function(msg = "") {
             list(msg = paste0(
               "The message is: '",
               msg,
               "'")
             )
           }) %>%
    pr_get(path = "/plot",
           handler = function() {
             rand <- rnorm(100)
             hist(rand)
           },
           serializer = serializer_png()) %>%
    pr_post(path = "/sum",
            handler = function(a, b) {
              as.numeric(a) + as.numeric(b)
            })
}
```

Use @plumber tag

Function that accepts and modifies a plumber router

"Tidy" functions for building out Plumber API

OpenAPI

Plumber automatically creates an OpenAPI specification file based on Plumber comments. This file can be further modified using `pr_set_api_spec()` with either a function that modifies the existing specification or a path to a `.yaml` or `.json` specification file.

```
library(plumber)

#* @param msg The message to echo
#* @get /echo
function(msg = "") {
  list(
    msg = paste0(
      "The message is: '", msg, "'")
  )
}

#* @plumber
function(pr) {
  pr %>%
    pr_set_api_spec(function(spec) {
      spec$paths[["/echo"]]$get$summary <-
        "Echo back the input"
      spec
    })
}
```

Function that receives and modifies the existing specification

Return the updated specification

By default, Swagger is used to interpret the OpenAPI specification file and generate the user interface for the API. Other interpreters can be used to adjust the look and feel of the user interface via `pr_set_docs()`.

RStudio

Advanced Plumber

REQUEST and RESPONSE

Plumber provides access to special `req` and `res` objects that can be passed to Plumber functions. These objects provide access to the request submitted by the client and the response that will be sent to the client. Each object has several components, the most helpful of which are outlined below:

Name	Example	Description
req		
req$pr	plumber::pr()	The Plumber router processing the request
req$body	list(a=1)	Typically the same as `argsBody`
req$argsBody	list(a=1)	The parsed body output
req$argsPath	list(c=3)	The values of the path arguments
req$argsQuery	list(e=5)	The parsed output from `req$QUERY_STRING`
req$cookies	list(cook = "a")	A list of cookies
req$REQUEST_METHOD	"GET"	The method used for the HTTP request
req$PATH_INFO	"/"	The path of the incoming HTTP request
req$HTTP_*	"HTTP_USER_AGENT"	All of the HTTP headers sent with the request
reqe$bodyRaw	charToRaw("a=1")	The `raw()` contents of the request body
res		
res$headers	list(header = "abc")	HTTP headers to include in the response
res$setHeader()	setHeader("foo", "bar")	Sets an HTTP header
res$setCookie()	setCookie("foo", "bar")	Sets an HTTP cookie on the client
res$removeCookie	removeCookie("foo")	Removes an HTTP cookie
res$body	"{\"a\":[1]}"	Serialized output
res$status	200	The response HTTP status code
res$toResponse()	toResponse()	A list of `status`, `headers`, and `body`

ASYNC PLUMBER

Plumber supports asynchronous execution via the `future` R package. This pattern allows Plumber to concurrently process multiple requests.

```
library(plumber)
future::plan("multisession")

#* @get /slow
function() {
  promises::future_promise({
    slow_calc()
  })
}
```

Set the execution plan

Slow calculation

MOUNTING ROUTERS

Plumber routers can be combined by mounting routers into other routers. This can be beneficial when building routers that involve several different endpoints and you want to break each component out into a separate router. These separate routers can even be separate files loaded using `plumb()`.

```
library(plumber)

route <- pr() %>%
  pr_get("/foo", function() "foo")

#* @plumber
function(pr) {
  pr %>%
    pr_mount("/bar", route)
}
```

Create an initial router

Mount one router into another

In the above example, the final route is `/bar/foo`.

RUNNING EXAMPLES

Some packages, like the Plumber package itself, may include example Plumber APIs. Available APIs can be viewed using `available_apis()`. These example APIs can be run with `plumb_api()` combined with `pr_run()`.

```
library(plumber)

plumb_api(package = "plumber",
          name = "01-append",
          edit = TRUE) %>%
  pr_run()
```

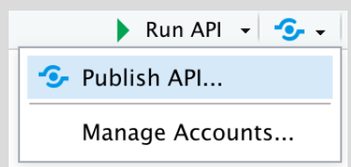
Identify the package name and API name

Optionally open the file for editing

Run the example API

Deploying Plumber APIs

Once Plumber APIs have been developed, they often need to be deployed somewhere to be useful. Plumber APIs can be deployed in a variety of different ways. One of the easiest way to deploy Plumber APIs is using RStudio Connect, which supports push button publishing from the RStudio IDE.



Deep Learning with Keras : : CHEAT SHEET

Intro

Keras is a high-level neural networks API developed with a focus on enabling fast experimentation. It supports multiple back-ends, including TensorFlow, CNTK and Theano.

TensorFlow is a lower level mathematical library for building deep neural network architectures. The `keras` R package makes it easy to use Keras and TensorFlow in R.

Define
- Model
- Sequential model
- Multi-GPU model

Compile
- Optimiser
- Loss
- Metrics

Fit
- Batch size
- Epochs
- Validation split

Evaluate
- Evaluate
- Plot

Predict
- classes
- probability

https://keras.rstudio.com

https://www.manning.com/books/deep-learning-with-r

The "Hello, World!" of deep learning

INSTALLATION

The `keras` R package uses the Python keras library. You can install all the prerequisites directly from R.

https://keras.rstudio.com/reference/install_keras.html

```
library(keras)
install_keras()
```

See ?install_keras for GPU instructions

This installs the required libraries in an Anaconda environment or virtual environment **'r-tensorflow'**.

Working with keras models

DEFINE A MODEL

keras_model() Keras Model

keras_model_sequential() Keras Model composed of a linear stack of layers

multi_gpu_model() Replicates a model on different GPUs

COMPILE A MODEL

compile(object, optimizer, loss, metrics = NULL**)** Configure a Keras model for training

FIT A MODEL

fit(object, x = NULL, y = NULL, batch_size = NULL, epochs = 10, verbose = 1, callbacks = NULL, …**)** Train a Keras model for a fixed number of epochs (iterations)

fit_generator() Fits the model on data yielded batch-by-batch by a generator

train_on_batch() test_on_batch() Single gradient update or model evaluation over one batch of samples

EVALUATE A MODEL

evaluate(object, x = NULL, y = NULL, batch_size = NULL**)** Evaluate a Keras model

evaluate_generator() Evaluates the model on a data generator

PREDICT

predict() Generate predictions from a Keras model

predict_proba() and **predict_classes()** Generates probability or class probability predictions for the input samples

predict_on_batch() Returns predictions for a single batch of samples

predict_generator() Generates predictions for the input samples from a data generator

OTHER MODEL OPERATIONS

summary() Print a summary of a Keras model

export_savedmodel() Export a saved model

get_layer() Retrieves a layer based on either its name (unique) or index

pop_layer() Remove the last layer in a model

save_model_hdf5(); load_model_hdf5() Save/ Load models using HDF5 files

serialize_model(); unserialize_model() Serialize a model to an R object

clone_model() Clone a model instance

freeze_weights(); unfreeze_weights() Freeze and unfreeze weights

CORE LAYERS

layer_input() Input layer

layer_dense() Add a densely-connected NN layer to an output

layer_activation() Apply an activation function to an output

layer_dropout() Applies Dropout to the input

layer_reshape() Reshapes an output to a certain shape

layer_permute() Permute the dimensions of an input according to a given pattern

layer_repeat_vector() Repeats the input n times

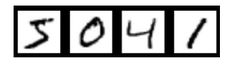
layer_lambda(object, f) Wraps arbitrary expression as a layer

layer_activity_regularization() Layer that applies an update to the cost function based input activity

layer_masking() Masks a sequence by using a mask value to skip timesteps

layer_flatten() Flattens an input

TRAINING AN IMAGE RECOGNIZER ON MNIST DATA



```
# input layer: use MNIST images
mnist <- dataset_mnist()
x_train <- mnist$train$x;  y_train <- mnist$train$y
x_test <- mnist$test$x;  y_test <- mnist$test$y

# reshape and rescale
x_train <- array_reshape(x_train, c(nrow(x_train), 784))
x_test <- array_reshape(x_test, c(nrow(x_test), 784))
x_train <- x_train / 255;  x_test <- x_test / 255

y_train <- to_categorical(y_train, 10)
y_test <- to_categorical(y_test, 10)

# defining the model and layers
model <- keras_model_sequential()
model %>%
 layer_dense(units = 256, activation = 'relu',
             input_shape = c(784)) %>%
 layer_dropout(rate = 0.4) %>%
 layer_dense(units = 128, activation = 'relu') %>%
 layer_dense(units = 10, activation = 'softmax')

# compile (define loss and optimizer)
model %>% compile(
 loss = 'categorical_crossentropy',
 optimizer = optimizer_rmsprop(),
 metrics = c('accuracy')
)

# train (fit)
model %>% fit(
 x_train, y_train,
 epochs = 30, batch_size = 128,
 validation_split = 0.2
)
model %>% evaluate(x_test, y_test)
model %>% predict_classes(x_test)
```

More layers

CONVOLUTIONAL LAYERS

layer_conv_1d() 1D, e.g. temporal convolution

layer_conv_2d_transpose()
Transposed 2D (deconvolution)

layer_conv_2d() 2D, e.g. spatial convolution over images

layer_conv_3d_transpose()
Transposed 3D (deconvolution)
layer_conv_3d() 3D, e.g. spatial convolution over volumes

layer_conv_lstm_2d()
Convolutional LSTM

layer_separable_conv_2d()
Depthwise separable 2D

layer_upsampling_1d()
layer_upsampling_2d()
layer_upsampling_3d()
Upsampling layer

layer_zero_padding_1d()
layer_zero_padding_2d()
layer_zero_padding_3d()
Zero-padding layer

layer_cropping_1d()
layer_cropping_2d()
layer_cropping_3d()
Cropping layer

POOLING LAYERS

layer_max_pooling_1d()
layer_max_pooling_2d()
layer_max_pooling_3d()
Maximum pooling for 1D to 3D

layer_average_pooling_1d()
layer_average_pooling_2d()
layer_average_pooling_3d()
Average pooling for 1D to 3D

layer_global_max_pooling_1d()
layer_global_max_pooling_2d()
layer_global_max_pooling_3d()
Global maximum pooling

layer_global_average_pooling_1d()
layer_global_average_pooling_2d()
layer_global_average_pooling_3d()
Global average pooling

ACTIVATION LAYERS

layer_activation(object, activation**)**
Apply an activation function to an output

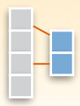
layer_activation_leaky_relu()
Leaky version of a rectified linear unit

layer_activation_parametric_relu()
Parametric rectified linear unit

layer_activation_thresholded_relu()
Thresholded rectified linear unit

layer_activation_elu()
Exponential linear unit

DROPOUT LAYERS



layer_dropout()
Applies dropout to the input

layer_spatial_dropout_1d()
layer_spatial_dropout_2d()
layer_spatial_dropout_3d()
Spatial 1D to 3D version of dropout

RECURRENT LAYERS

layer_simple_rnn()
Fully-connected RNN where the output is to be fed back to input

layer_gru()
Gated recurrent unit - Cho et al

layer_cudnn_gru()
Fast GRU implementation backed by CuDNN

layer_lstm()
Long-Short Term Memory unit - Hochreiter 1997

layer_cudnn_lstm()
Fast LSTM implementation backed by CuDNN

LOCALLY CONNECTED LAYERS

layer_locally_connected_1d()
layer_locally_connected_2d()
Similar to convolution, but weights are not shared, i.e. different filters for each patch

Preprocessing

SEQUENCE PREPROCESSING

pad_sequences()
Pads each sequence to the same length (length of the longest sequence)

skipgrams()
Generates skipgram word pairs

make_sampling_table()
Generates word rank-based probabilistic sampling table

TEXT PREPROCESSING

text_tokenizer() Text tokenization utility

fit_text_tokenizer() Update tokenizer internal vocabulary

save_text_tokenizer(); load_text_tokenizer()
Save a text tokenizer to an external file

texts_to_sequences();
texts_to_sequences_generator()
Transforms each text in texts to sequence of integers

texts_to_matrix(); sequences_to_matrix()
Convert a list of sequences into a matrix

text_one_hot() One-hot encode text to word indices

text_hashing_trick()
Converts a text to a sequence of indexes in a fixed-size hashing space

text_to_word_sequence()
Convert text to a sequence of words (or tokens)

IMAGE PREPROCESSING

image_load() Loads an image into PIL format.

flow_images_from_data()
flow_images_from_directory()
Generates batches of augmented/normalized data from images and labels, or a directory

image_data_generator() Generate minibatches of image data with real-time data augmentation.

fit_image_data_generator() Fit image data generator internal statistics to some sample data

generator_next() Retrieve the next item

image_to_array(); image_array_resize()
image_array_save() 3D array representation

Keras TensorFlow

Pre-trained models

Keras applications are deep learning models that are made available alongside pre-trained weights. These models can be used for prediction, feature extraction, and fine-tuning.

application_xception()
xception_preprocess_input()
Xception v1 model

application_inception_v3()
inception_v3_preprocess_input()
Inception v3 model, with weights pre-trained on ImageNet

application_inception_resnet_v2()
inception_resnet_v2_preprocess_input()
Inception-ResNet v2 model, with weights trained on ImageNet

application_vgg16(); application_vgg19()
VGG16 and VGG19 models

application_resnet50() ResNet50 model

application_mobilenet()
mobilenet_preprocess_input()
mobilenet_decode_predictions()
mobilenet_load_model_hdf5()
MobileNet model architecture

IMAGENET
ImageNet is a large database of images with labels, extensively used for deep learning

imagenet_preprocess_input()
imagenet_decode_predictions()
Preprocesses a tensor encoding a batch of images for ImageNet, and decodes predictions

Callbacks

A callback is a set of functions to be applied at given stages of the training procedure. You can use callbacks to get a view on internal states and statistics of the model during training.

callback_early_stopping() Stop training when a monitored quantity has stopped improving
callback_learning_rate_scheduler() Learning rate scheduler
callback_tensorboard() TensorBoard basic visualizations

RStudio

Package Development: : **CHEAT SHEET**

Package Structure

A package is a convention for organizing files into directories.

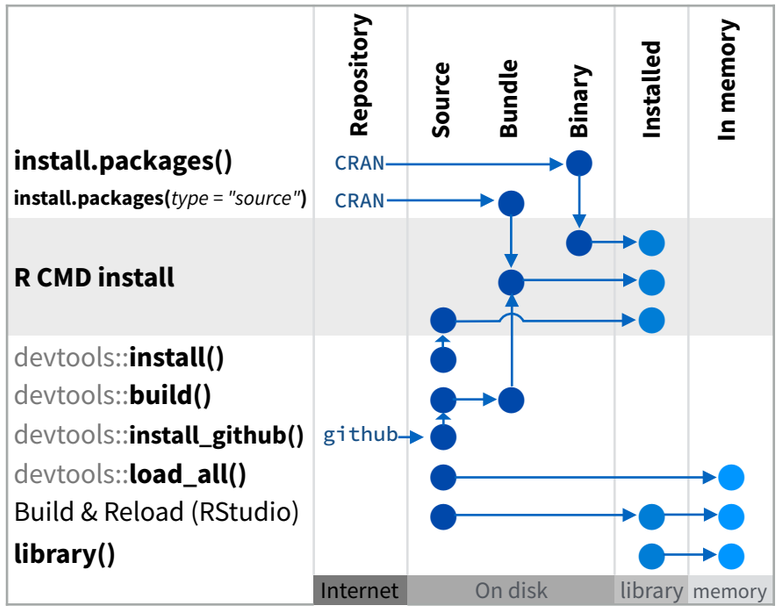
This sheet shows how to work with the 7 most common parts of an R package:

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::**use_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?

Document (man/)

man/ contains the documentation for your functions, the help pages in your package.

- [x] Use roxygen comments to document each function beside its definition
- [x] Document the name of each exported data set
- [x] 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.

- [x] Create a vignettes/ directory and a template vignette with

  devtools::**use_vignette()**

  Adds template vignette as vignettes/my-vignette.Rmd.
- [x] Append YAML headers to your vignettes (like right)
- [x] 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.

- [x] Save data as .Rdata files (suggested)
- [x] Store data in one of **data/**, **R/Sysdata.rda**, **inst/extdata**
- [x] 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.

- [x] Export functions for users by placing **@export** in their roxygen comments
- [x] 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

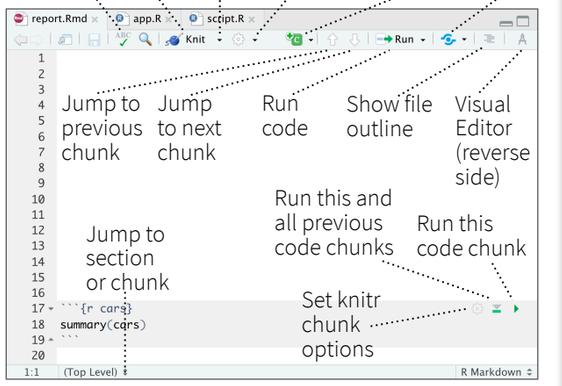
r-pkgs.had.co.nz/release.html

RStudio

RStudio IDE : : **CHEAT SHEET**

Documents and Apps

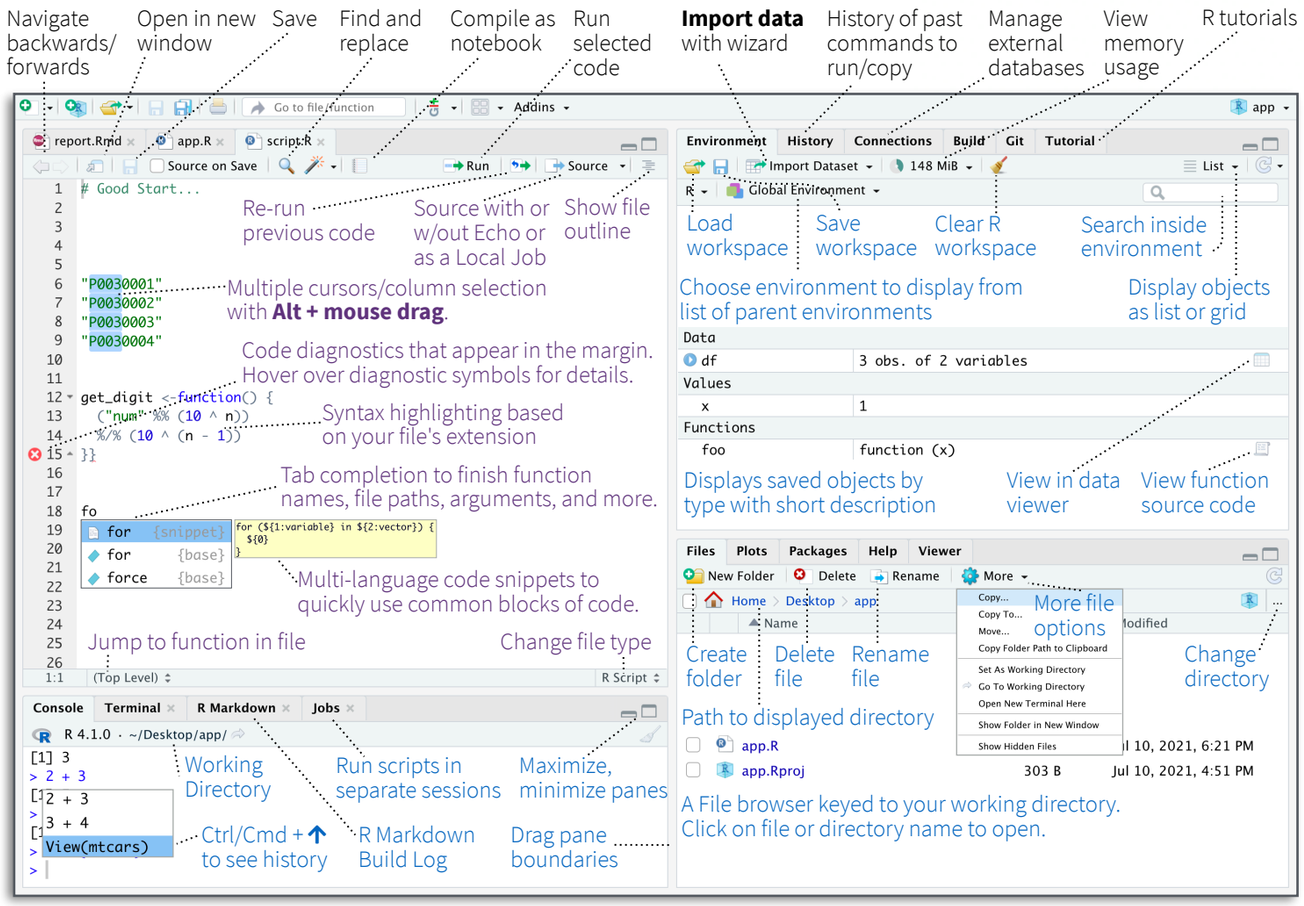
Open Shiny, R Markdown, knitr, Sweave, LaTeX, .Rd files and more in Source Pane



Access markdown guide at
Help > Markdown Quick Reference
See reverse side for more on **Visual Editor**

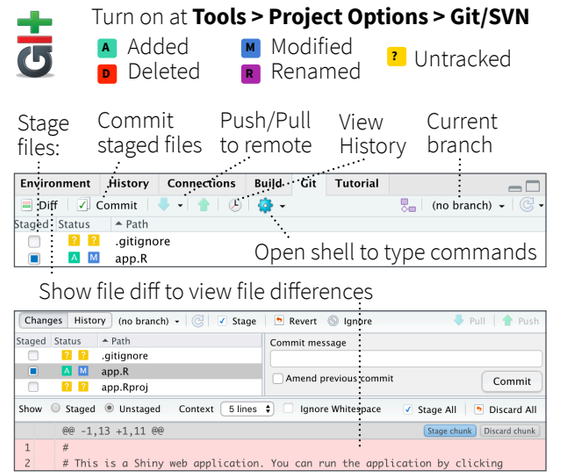
RStudio recognizes that files named **app.R**, **server.R**, **ui.R**, and **global.R** belong to a shiny app

Source Editor



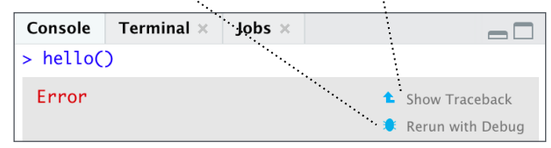
Tab Panes

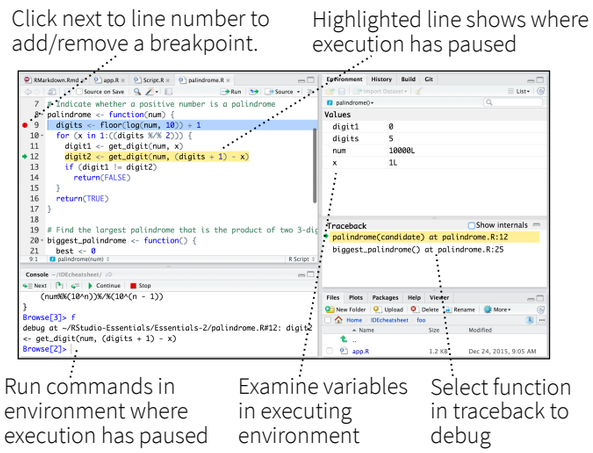
Version Control

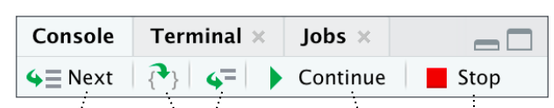


Debug Mode

Use **debug(), browser(),** or a breakpoint and execute your code to open the debugger mode.





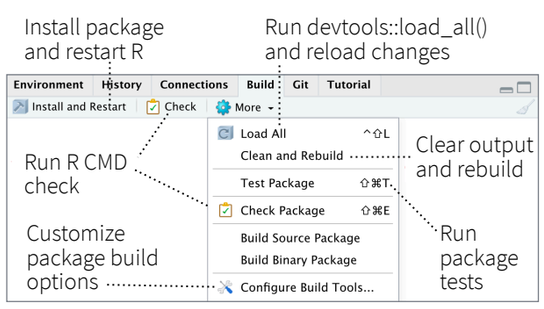


Package Development

Create a new package with
File > New Project > New Directory > R Package
Enable roxygen documentation with
Tools > Project Options > Build Tools

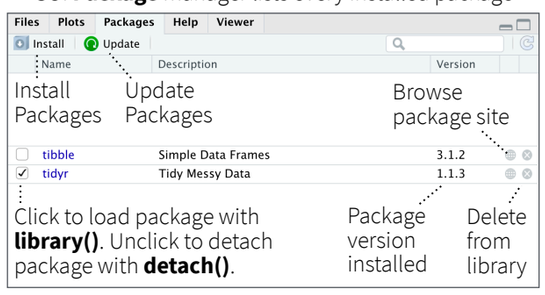
Roxygen guide at **Help > Roxygen Quick Reference**

See package information in the **Build Tab**

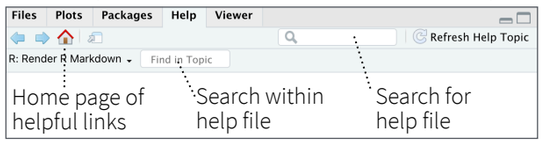


RStudio opens plots in a dedicated **Plots** pane

GUI **Package** manager lists every installed package

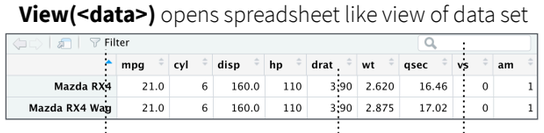


RStudio opens documentation in a dedicated **Help** pane



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

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



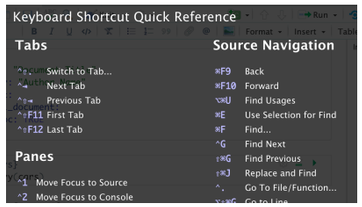
Keyboard Shortcuts

RUN CODE	Windows/Linux	Mac
Search command history	Ctrl+↑	Cmd+↑
Interrupt current command	Esc	Esc
Clear console	Ctrl+L	Ctrl+L
NAVIGATE CODE		
Go to File/Function	Ctrl+.	Ctrl+.
WRITE CODE		
Attempt completion	Tab or Ctrl+Space	Tab or Ctrl+Space
Insert <- (assignment operator)	Alt+-	Option+-
Insert %>% (pipe operator)	Ctrl+Shift+M	Cmd+Shift+M
(Un)Comment selection	Ctrl+Shift+C	Cmd+Shift+C

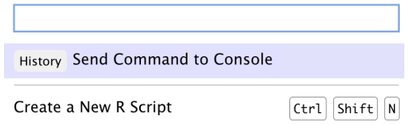
MAKE PACKAGES	Windows/Linux	Mac
Load All (devtools)	Ctrl+Shift+L	Cmd+Shift+L
Test Package (Desktop)	Ctrl+Shift+T	Cmd+Shift+T
Document Package	Ctrl+Shift+D	Cmd+Shift+D

DOCUMENTS AND APPS		
Knit Document (knitr)	Ctrl+Shift+K	Cmd+Shift+K
Insert chunk (Sweave & Knitr)	Ctrl+Alt+I	Cmd+Option+I
Run from start to current line	Ctrl+Alt+B	Cmd+Option+B
MORE KEYBOARD SHORTCUTS		
Keyboard Shortcuts Help	Alt+Shift+K	Option+Shift+K
Show Command Palette	Ctrl+Shift+P	Cmd+Shift+P

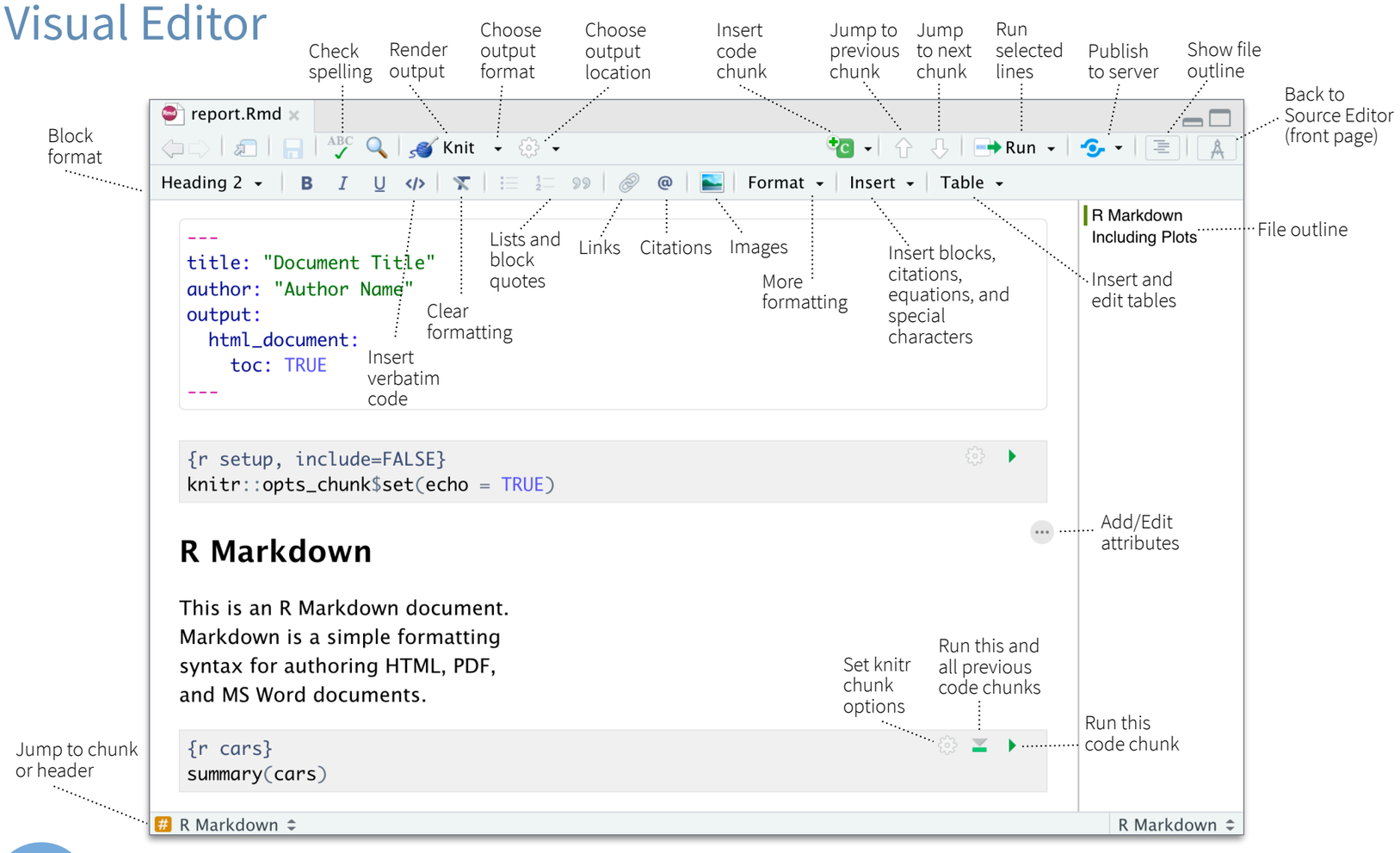
View the Keyboard Shortcut Quick Reference with **Tools > Keyboard Shortcuts** or **Alt/Option + Shift + K**



Search for keyboard shortcuts with **Tools > Show Command Palette** or **Ctrl/Cmd + Shift + P**.



Visual Editor



RStudio Workbench

WHY RSTUDIO WORKBENCH?

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

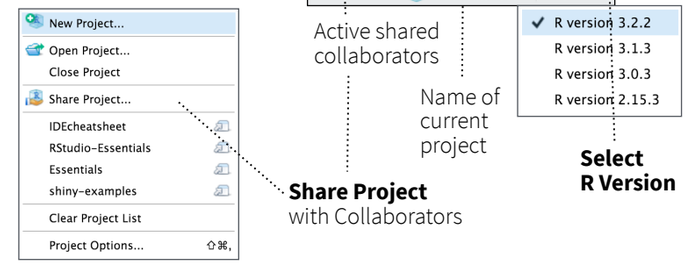
- open and run multiple R sessions at once
- tune your resources to improve performance
- administrative tools for managing user sessions
- collaborate real-time with others in shared projects
- switch easily from one version of R to a different version
- integrate with your authentication, authorization, and audit practices
- work in the RStudio IDE, JupyterLab, Jupyter Notebooks, or VS Code

Download a free 45 day evaluation at
www.rstudio.com/products/workbench/evaluation/

Share Projects

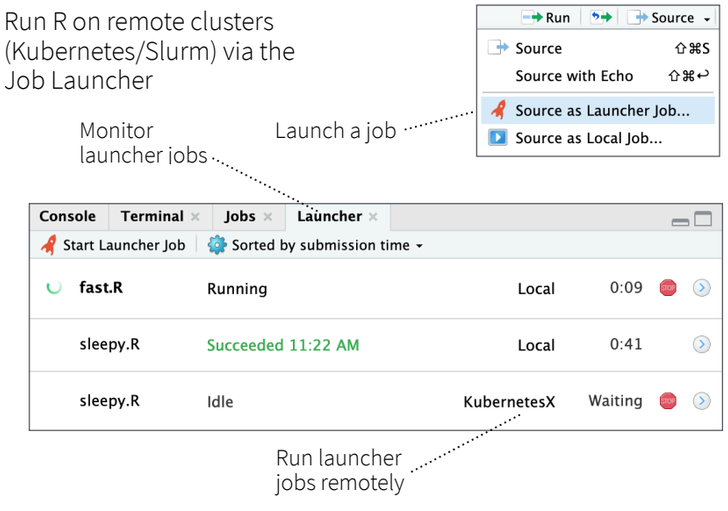
File > New Project

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



Run Remote Jobs

Run R on remote clusters (Kubernetes/Slurm) via the Job Launcher



Shiny : : CHEAT SHEET

Building an App

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).

Save your template as **app.R**. Keep your app in a directory along with optional extra files.

To generate the template, type **shinyapp** and press **Tab** in the RStudio IDE or go to **File > New Project > New Directory > Shiny Web Application**

In **ui** nest R functions to build an HTML interface

Customize the UI with **Layout Functions**

Add Inputs with ***Input()** functions

Add Outputs with ***Output()** functions

Tell the **server** how to render outputs and respond to inputs with R

Wrap code in **render*()** functions before saving to output

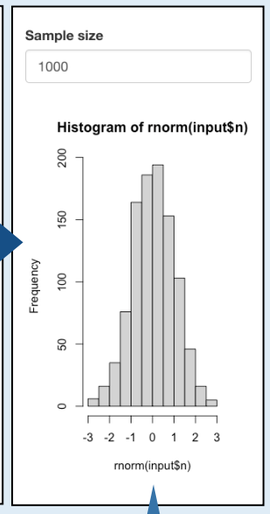
Refer to UI inputs with **input$<id>** and outputs with **output$<id>**

```
# app.R
library(shiny)

ui <- fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)

server <- function(input, output, session) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}

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



Call **shinyApp()** to combine **ui** and **server** into an interactive app!

```
app-name
  app.R
  DESCRIPTION
  README
  R/
  www/
```

The directory name is the app name

(optional) used in showcase mode

(optional) directory of supplemental .R files that are sourced automatically, must be named "**R**"

(optional) directory of files to share with web browsers (images, CSS, .js, etc.), must be named "**www**"

Launch apps stored in a directory with **runApp(**<path to directory>**)**.

See annotated examples of Shiny apps by running **runExample(**<example name>**)**. Run **runExample()** with no arguments for a list of example names.

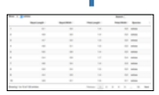
Share

Share your app in three ways:

1. **Host it on shinyapps.io**, a cloud based service from RStudio. To deploy Shiny apps:
   - Create a free or professional account at **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. **rstudio.com/products/connect/**
3. **Build your own Shiny Server** **rstudio.com/products/shiny/shiny-server/**

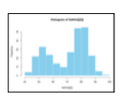
Outputs

render*() and *Output() functions work together to add R output to the UI.



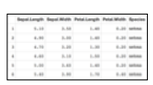
DT::**renderDataTable(**expr, options, searchDelay, callback, escape, env, quoted, outputArgs**)** — **dataTableOutput(**outputId**)**

renderImage(expr, env, quoted, deleteFile, outputArgs**)** — **imageOutput(**outputId, width, height, click, dblclick, hover, brush, inline**)**

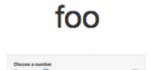


renderPlot(expr, width, height, res, …, alt, env, quoted, execOnResize, outputArgs**)** — **plotOutput(**outputId, width, height, click, dblclick, hover, brush, inline**)**

renderPrint(expr, env, quoted, width, outputArgs**)** — **verbatimTextOutput(**outputId, placeholder**)**



renderTable(expr, striped, hover, bordered, spacing, width, align, rownames, colnames, digits, na, …, env, quoted, outputArgs**)** — **tableOutput(**outputId**)**



renderText(expr, env, quoted, outputArgs, sep**)** — **textOutput(**outputId, container, inline**)**

renderUI(expr, env, quoted, outputArgs**)** — **uiOutput(**outputId, inline, container, …**)** **htmlOutput(**outputId, inline, container, …**)**

These are the core output types. See **htmlwidgets.org** for many more options.

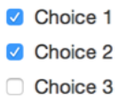
Inputs

Collect values from the user.

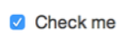
Access the current value of an input object with **input$<inputId>**. Input values are **reactive**.

actionButton(inputId, label, icon, width, …**)**

actionLink(inputId, label, icon, …**)**



checkboxGroupInput(inputId, label, choices, selected, inline, width, choiceNames, choiceValues**)**



checkboxInput(inputId, label, value, width**)**

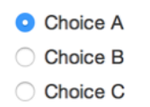
dateInput(inputId, label, value, min, max, format, startview, weekstart, language, width, autoclose, datesdisabled, daysofweekdisabled**)**

dateRangeInput(inputId, label, start, end, min, max, format, startview, weekstart, language, separator, width, autoclose**)**

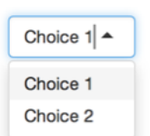
fileInput(inputId, label, multiple, accept, width, buttonLabel, placeholder**)**

numericInput(inputId, label, value, min, max, step, width**)**

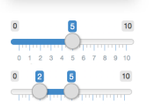
passwordInput(inputId, label, value, width, placeholder**)**



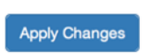
radioButtons(inputId, label, choices, selected, inline, width, choiceNames, choiceValues**)**



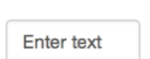
selectInput(inputId, label, choices, selected, multiple, selectize, width, size**)** Also **selectizeInput()**



sliderInput(inputId, label, min, max, value, step, round, format, locale, ticks, animate, width, sep, pre, post, timeFormat, timezone, dragRange**)**



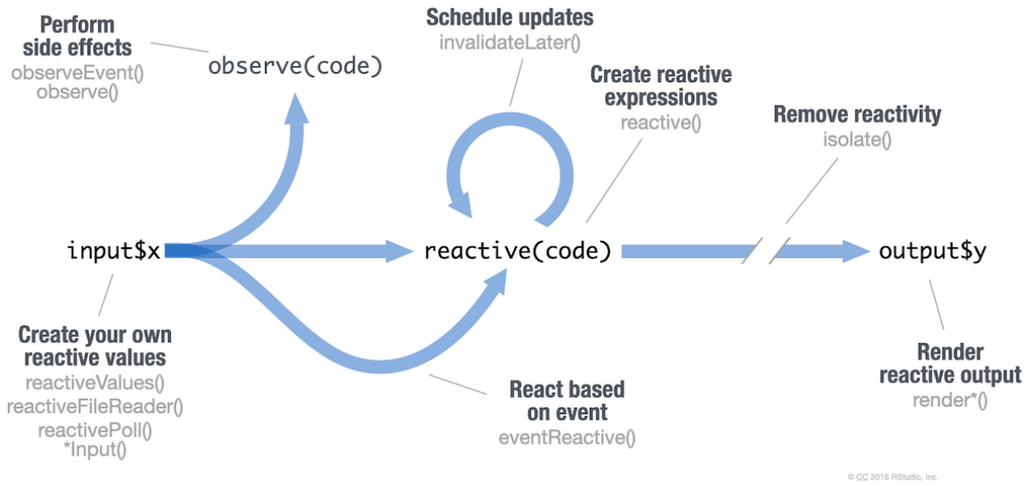
submitButton(text, icon, width**)** (Prevent reactions for entire app)



textInput(inputId, label, value, width, placeholder**)** Also **textAreaInput()**

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.`



CREATE YOUR OWN REACTIVE VALUES

```
# *Input() example
ui <- fluidPage(
 textInput("a","","A")
)
```

```
#reactiveValues example
server <-
function(input,output){
 rv <- reactiveValues()
 rv$number <- 5
}
```

***Input() functions**
(see front page)

Each input function creates a reactive value stored as **input$<inputId>**.

reactiveValues(...)
Creates a list of reactive values whose values you can set.

CREATE REACTIVE EXPRESSIONS

```
library(shiny)
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**)**

Reactive expressions:
- **cache** their value to reduce computation
- can be called elsewhere
- notify dependencies when invalidated

Call the expression with function syntax, e.g. `re()`.

REACT BASED ON EVENT

```
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()
  })
}
shinyApp(ui, server)
```

eventReactive(eventExpr, valueExpr, event.env, event.quoted, value.env, value.quoted, ..., label, domain, ignoreNULL, ignoreInit**)**

Creates reactive expression with code in 2nd argument that only invalidates when reactive values in 1st argument change.

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>**.

PERFORM SIDE EFFECTS

```
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, ..., label, suspended, priority, domain, autoDestroy, ignoreNULL, ignoreInit, once**)**

Runs code in 2nd argument when reactive values in 1st argument change. See **observe()** for alternative.

REMOVE REACTIVITY

```
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.

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.

Run **names(tags)** for a complete list.
`tags$h1("Header") -> <h1>Header</h1>`

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>")
)
```

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:

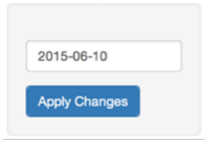
```
tags$head(tags$script(src = "<file name>"))
```

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.

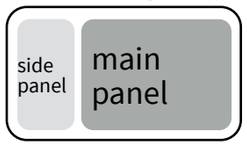
```
wellPanel(
  dateInput("a", ""),
  submitButton()
)
```



absolutePanel()
conditionalPanel()
fixedPanel()
headerPanel()
inputPanel()
mainPanel()
navlistPanel()
sidebarPanel()
tabPanel()
tabsetPanel()
titlePanel()
wellPanel()

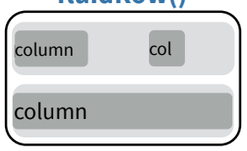
Organize panels and elements into a layout with a layout function. Add elements as arguments of the layout functions.

sidebarLayout()




```
ui <- fluidPage(
  sidebarLayout(
    sidebarPanel(),
    mainPanel()
  )
)
```

fluidRow()




```
ui <- fluidPage(
  fluidRow(column(width = 4),
           column(width = 2, offset = 3)),
  fluidRow(column(width = 12))
)
```

Also **flowLayout()**, **splitLayout()**, **verticalLayout()**, **fixedPage()**, **and fixedRow()**.

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")))
```

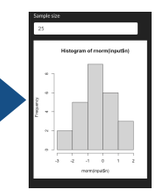
```
ui <- fluidPage( navlistPanel(
    tabPanel("tab 1", "contents"),
    tabPanel("tab 2", "contents"),
    tabPanel("tab 3", "contents")))
```

```
ui <- navbarPage(title = "Page",
    tabPanel("tab 1", "contents"),
    tabPanel("tab 2", "contents"),
    tabPanel("tab 3", "contents"))
```

Themes

Use the **bslib** package to add existing themes to your Shiny app ui, or make your own.

```
library(bslib)
ui <- fluidPage(
  theme = bs_theme(
    bootswatch = "darkly",
    ...
  )
)
```

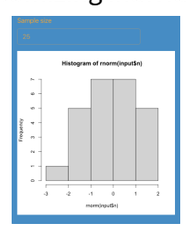


bootswatch_themes() Get a list of themes.

Build your own theme by customizing individual arguments.

bs_theme(bg = "#558AC5", fg = "#F9B02D", ...**)**

?bs_theme for a full list of arguments.



bs_themer() Place within the server function to use the interactive theming widget.