Data Import : : CHEAT SHEET

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

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

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

OTHER TYPES OF DATA

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

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

Save Data

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

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

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

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

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

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

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

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

Read Tabular Data - These functions share the common arguments:

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

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

A	B	C
1	2	3
4	5	NA

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

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

A	B	C
1	2	3
4	5	NA

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

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

A	B	C
1	2	3
4	5	NA

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

a b c
1 2 3
4 5 NA

A	B	C
1	2	3
4	5	NA

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

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

USEFUL ARGUMENTS

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

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

A	B	C
1	2	3
4	5	NA

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

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

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

1	2	3
4	5	NA

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

A	B	C
1	2	3

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

A	B	C
NA	2	3
4	5	NA

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

Read Non-Tabular Data

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

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

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

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

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

Data types

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

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

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

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

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

2. Use a col_ function to guide parsing.

- **col_guess()** - the default
- **col_character()**
- **col_double()**, **col_euro_double()**
- **col_datetime(**format = ""**)** Also **col_date(**format = ""**)**, **col_time(**format = ""**)**
- **col_factor(**levels, ordered = FALSE**)**
- **col_integer()**
- **col_logical()**
- **col_number()**, **col_numeric()**
- **col_skip()**

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

3. Else, read in as character vectors then parse with a parse_ function.

- **parse_guess()**
- **parse_character()**
- **parse_datetime()** Also **parse_date()** and **parse_time()**
- **parse_double()**
- **parse_factor()**
- **parse_integer()**
- **parse_logical()**
- **parse_number()**

x$A <- parse_number(x$A)

Tibbles - an enhanced data frame

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

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

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

tibble display

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

A large table to display

data frame display

- Control the default appearance with options:

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

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

CONSTRUCT A TIBBLE IN TWO WAYS

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

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 data frame to tibble.

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

is_tibble(x) Test whether x is a tibble.

Tidy Data with tidyr

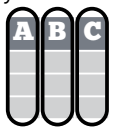
Tidy data is a way to organize tabular data. It provides a consistent data structure across packages.

A table is tidy if:

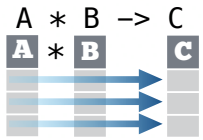
Each **variable** is in its own **column**

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

Tidy data:



Makes variables easy to access as vectors



Preserves cases during vectorized operations

Reshape Data - change the layout of values in a table

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

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

gather() moves column names into a **key** column, gathering the column values into a single **value** column.

table4a

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

→

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

key value

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

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

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

table2

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

→

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

key value

spread(table2, type, count)

Handle Missing Values

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

x

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

→

x1	x2
A	1
D	3

drop_na(x, x2)

fill(data, ..., .direction = c("down", "up")**)**
Fill in NA's in … columns with most recent non-NA values.

x

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

→

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

fill(x, x2)

replace_na(data, replace = list(), ...**)**
Replace NA's by column.

x

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

→

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

replace_na(x, list(x2 = 2))

Expand Tables - quickly create tables with combinations of values

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

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

Split Cells

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

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

Separate each cell in a column to make several columns.

table3

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

→

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

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

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

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

table3

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

→

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

separate_rows(table3, rate)

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

Collapse cells across several columns to make a single column.

table5

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

→

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

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

Data Transformation with dplyr : : CHEAT SHEET

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

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

&

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

pipes

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

Summarise Cases

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

summary function

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

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

VARIATIONS

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

Group Cases

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

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

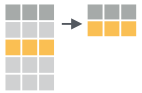
group_by(.data, ..., add = FALSE)
Returns copy of table grouped by …
g_iris <- group_by(iris, Species)

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

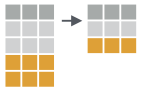
Manipulate Cases

EXTRACT CASES

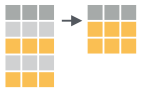
Row functions return a subset of rows as a new table.



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

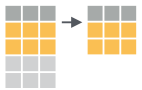


distinct(.data, ..., .keep_all = FALSE) Remove rows with duplicate values.
distinct(iris, Species)



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

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



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

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

Logical and boolean operators to use with filter()

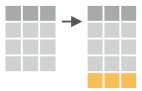
<	<=	is.na()	%in%	|	xor()
>	>=	!is.na()	!	&	

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

ARRANGE CASES

arrange(.data, …) Order rows by values of a column 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(faithful, eruptions = 1, waiting = 1)

Manipulate Variables

EXTRACT VARIABLES

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

pull(.data, var = -1) Extract column values as a vector. Choose by name or index.
pull(iris, Sepal.Length)

select(.data, …)
Extract columns as a table. Also **select_if()**.
select(iris, Sepal.Length, Species)

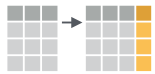
Use these helpers with select (),
e.g. select(iris, starts_with("Sepal"))

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

MAKE NEW VARIABLES

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

vectorized function

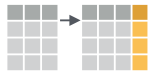


mutate(.data, …)
Compute new column(s).
mutate(mtcars, gpm = 1/mpg)

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

mutate_all(.tbl, .funs, …) Apply funs to every column. Use with **funs()**. Also **mutate_if()**.
mutate_all(faithful, funs(log(.), log2(.)))
mutate_if(iris, is.numeric, funs(log(.)))

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



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

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

Vector Functions

TO USE WITH MUTATE ()

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

vectorized function

OFFSETS

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

CUMULATIVE AGGREGATES

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

RANKINGS

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

MATH

+, - , *, /, ^, %/%, %% - arithmetic ops
log(), log2(), log10() - logs
<, <=, >, >=, !=, == - logical comparisons
dplyr::**between()** - x >= left & x <= right
dplyr::**near()** - safe == for floating point numbers

MISC

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

Summary Functions

TO USE WITH SUMMARISE ()

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

summary function

COUNTS

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

LOCATION

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

LOGICALS

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

POSITION/ORDER

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

RANK

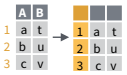
quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

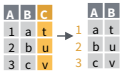
IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

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.



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

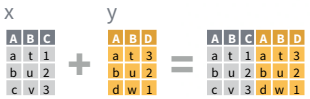


column_to_rownames()
Move col in row names.
column_to_rownames(a, var = "C")

Also **has_rownames()**, **remove_rownames()**

Combine Tables

COMBINE VARIABLES



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

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

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

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

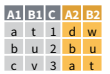
right_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),…)
Join matching values from x to y.

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

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

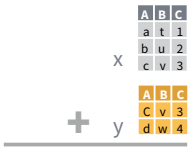
Use **by = c("col1", "col2", …)** to specify one or more common columns to match on.
left_join(x, y, by = "A")

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"))

COMBINE CASES



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

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

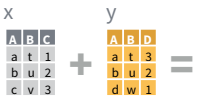
intersect(x, y, …)
Rows that appear in both x and y.

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).

EXTRACT ROWS



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

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

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

Data 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.

required

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

Not required, sensible defaults supplied

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

aesthetic mappings | data | geom

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

last_plot() Returns the last plot

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

Geoms

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

GRAPHICAL PRIMITIVES

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

a + geom_blank()
(Useful for expanding limits)

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

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

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

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

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

LINE SEGMENTS

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

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

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

ONE VARIABLE continuous

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

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

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

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

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

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

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

discrete

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

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

TWO VARIABLES

continuous x , continuous y

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

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

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

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

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

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

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

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

discrete x , continuous y

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

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

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

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

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

discrete x , discrete y

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

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

continuous bivariate distribution

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

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

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

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

continuous function

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

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

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

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

visualizing error

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

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

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

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

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

maps

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

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

THREE VARIABLES

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

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

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

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

Stats An alternative way to build a layer

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

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

geom to use | stat function | geommappings

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

variable created by stat

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

e + stat_identity(na.rm = TRUE)

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

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

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

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

e + stat_unique()

Scales

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

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

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

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

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

GENERAL PURPOSE SCALES

Use with most aesthetics

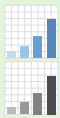
scale_*_continuous() - map cont' values to visual ones
scale_*_discrete() - map discrete values to visual ones
scale_*_identity() - use data values **as** visual ones
scale_*_manual(values = c()) - map discrete values to manually chosen visual ones
scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - treat data values as dates.
scale_*_datetime() - treat data x values as date times. Use same arguments as scale_x_date(). See ?strptime for label formats.

X & Y LOCATION SCALES

Use with x or y aesthetics (x shown here)

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

COLOR AND FILL SCALES (DISCRETE)

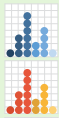


n <- d + geom_bar(aes(fill = fl))

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

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

COLOR AND FILL SCALES (CONTINUOUS)



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

o + scale_fill_distiller(palette = "Blues")

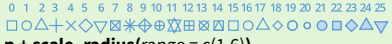
o + scale_fill_gradient(low="red", high="yellow")

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

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

SHAPE AND SIZE SCALES

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



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

Coordinate Systems

r <- d + geom_bar()

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

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

r + coord_flip()
xlim, ylim
Flipped Cartesian coordinates

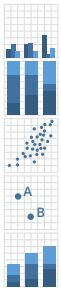
r + coord_polar(theta = "x", direction=1)
theta, start, direction
Polar coordinates

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

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

Position Adjustments

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



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

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

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

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

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

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

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

Themes

r + theme_bw()
White background with grid lines

r + theme_gray()
Grey background (default theme)

r + theme_dark()
dark for contrast

r + theme_classic()
r + theme_light()
r + theme_linedraw()
r + theme_minimal()
Minimal themes
r + theme_void()
Empty theme

Faceting

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

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

t + facet_grid(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 labels

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

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

Use scale functions to update legend labels

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

geom to place | manual values for geom's aesthetics

Legends

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

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

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

Zooming

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

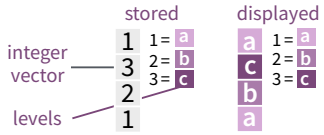
With clipping (removes unseen data points)
t + xlim(0, 100) **+ ylim**(10, 20)
t + scale_x_continuous(limits = c(0, 100)) +
scale_y_continuous(limits = c(0, 100))

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 values 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) Count the number of values with each level. *fct_count(f)*

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

Combine Factors

fct_c(…) Combine factors with different levels.
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).
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 = iris, Sepal.Width ~ fct_reorder(Species, Sepal.Width))

fct_reorder2(.f, .x, .y, .fun = last2, ..., .desc = TRUE) Reorder levels by their final values when plotted with two other variables.
ggplot(data = iris, aes(Sepal.Width, Sepal.Length, color = fct_reorder2(Species, Sepal.Width, Sepal.Length))) + 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, ...) Collapse levels into manually defined groups.
fct_collapse(f, x = c("a", "b"))

fct_lump(f, n, prop, w = NULL, other_level = "Other", ties.method = c("min", "average", "first", "last", "random", "max")) Lump together least/most common levels into a single level. Also **fct_lump_min**.
fct_lump(f, n = 1)

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)))

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

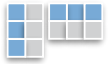
layer_input() Input layer

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

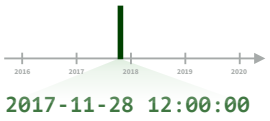
A callback is a set of functions to be applied at given stages of the training procedure. You can use callbacks to get a view on internal states and statistics of the model during training.

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

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 wide variety of input formats.

`2017-11-28T14:02:00` **ymd_hms**(), **ymd_hm**(), **ymd_h**(). *ymd_hms("2017-11-28T14:02:00")*

`2017-22-12 10:00:00` **ydm_hms**(), **ydm_hm**(), **ydm_h**(). *ydm_hms("2017-22-12 10:00:00")*

`11/28/2017 1:02:03` **mdy_hms**(), **mdy_hm**(), **mdy_h**(). *mdy_hms("11/28/2017 1:02:03")*

`1 Jan 2017 23:59:59` **dmy_hms**(), **dmy_hm**(), **dmy_h**(). *dmy_hms("1 Jan 2017 23:59:59")*

`20170131` **ymd**(), **ydm**(). *ymd(20170131)*

`July 4th, 2000` **mdy**(), **myd**(). *mdy("July 4th, 2000")*

`4th of July '99` **dmy**(), **dym**(). *dmy("4th of July '99")*

`2001: Q3` **yq**() Q for quarter. *yq("2001: Q3")*

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

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

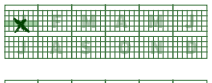
`2018-01-31 11:59:59` **month**(x, label, abbr) Month. *month(dt)*

`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)*



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

quarter(x, with_year = FALSE) Quarter. *quarter(dt)*

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

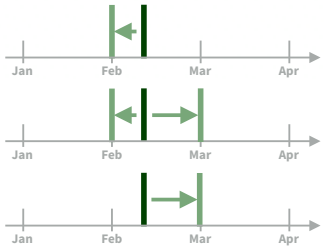
am(x) Is it in the am? *am(dt)*
pm(x) Is it in the pm? *pm(dt)*

dst(x) Is it daylight savings? *dst(d)*

leap_year(x) Is it a leap year? *leap_year(d)*

update(object, ..., simple = FALSE) *update(dt, mday = 2, hour = 1)*

Round Date-times



floor_date(x, unit = "second") Round down to nearest unit. *floor_date(dt, unit = "month")*

round_date(x, unit = "second") Round to nearest unit. *round_date(dt, unit = "month")*

ceiling_date(x, unit = "second", change_on_boundary = NULL) Round up to nearest unit. *ceiling_date(dt, unit = "month")*

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

Stamp Date-times

stamp() Derive a template from an example string and return a new function that will apply the template to date-times. Also **stamp_date**() and **stamp_time**().

1. Derive a template, create a function
   sf <- stamp("Created Sunday, Jan 17, 1999 3:34")
2. Apply the template to dates
   sf(ymd("2010-04-05"))
   ## [1] "Created Monday, Apr 05, 2010 00:00"

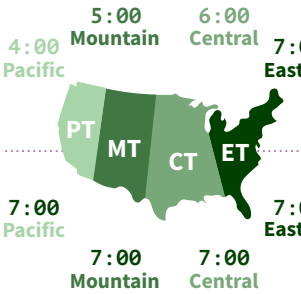
Tip: use a date with day > 12

Time Zones

R recognizes ~600 time zones. Each encodes the time zone, Daylight Savings Time, and historical calendar variations for an area. R assigns *one* time zone per vector.

Use the **UTC** time zone to avoid Daylight Savings.

OlsonNames() Returns a list of valid time zone names. *OlsonNames()*



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

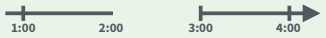
force_tz(time, tzone = "") Get the **same clock time** in a new time zone (a new date-time). *force_tz(dt, "US/Pacific")*

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

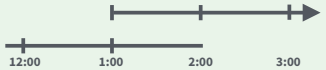
Math with date-times relies on the **timeline**, which behaves inconsistently. Consider how the timeline behaves during:

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")



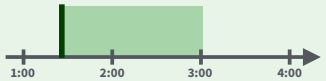
The end of daylight savings (fall back)
lap <- ymd_hms("2018-11-04 00:30:00",tz="US/Eastern")



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

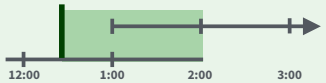
Periods track changes in clock times, which ignore time line irregularities.

nor + minutes(90)



gap + minutes(90)

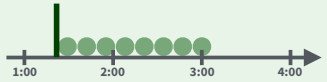
lap + minutes(90)



leap + years(1)

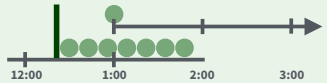
Durations track the passage of physical time, which deviates from clock time when irregularities occur.

nor + dminutes(90)



gap + dminutes(90)

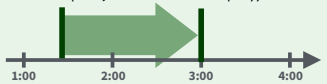
lap + dminutes(90)



leap + dyears(1)

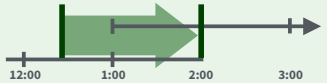
Intervals represent specific intervals of the timeline, bounded by start and end date-times.

interval(nor, nor + minutes(90))

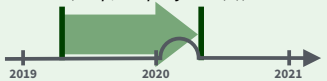


interval(gap, gap + minutes(90))

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.
dweeks(x = 1) 604800x seconds.
ddays(x = 1) 86400x seconds.
dhours(x = 1) 3600x seconds.
dminutes(x = 1) 60x seconds.
dseconds(x = 1) x seconds.
dmilliseconds(x = 1) x 10^{-3} seconds.
dmicroseconds(x = 1) x 10^{-6} seconds.
dnanoseconds(x = 1) x 10^{-9} seconds.
dpicoseconds(x = 1) x 10^{-12} seconds.

duration(num = NULL, units = "second", ...) An automation friendly duration constructor. *duration(5, unit = "years")*

as.duration(x, …) Coerce a timespan to a duration. Also **is.duration**(), **is.difftime**(). *as.duration(i)*

make_difftime(x) Make difftime with the specified number of units. *make_difftime(99999)*

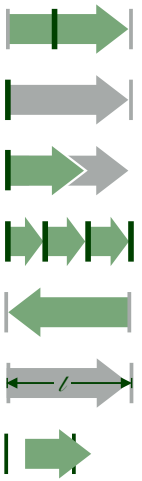
INTERVALS

Divide an interval by a duration to determine its physical length, divide 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)      ## 2017-01-01 UTC--2017-11-28 UTC
j <- d %--% ymd("2017-12-31")            ## 2017-11-28 UTC--2017-12-31 UTC
```



a **%within%** b Does interval or date-time *a* fall within interval *b*? *now() %within% i*

int_start(int) Access/set the start date-time of an interval. Also **int_end**(). *int_start(i) <- now(); int_start(i)*

int_aligns(int1, int2) Do two intervals share a boundary? Also **int_overlaps**(). *int_aligns(i, j)*

int_diff(times) Make the intervals that occur between the date-times in a vector. *v <-c(dt, dt + 100, dt + 1000); int_diff(v)*

int_flip(int) Reverse the direction of an interval. Also **int_standardize**(). *int_flip(i)*

int_length(int) Length in seconds. *int_length(i)*

int_shift(int, by) Shifts an interval up or down the timeline by a timespan. *int_shift(i, days(-1))*

as.interval(x, start, …) Coerce a timespans to an interval with the start date-time. Also **is.interval**(). *as.interval(days(1), start = now())*

Package Development: : CHEAT SHEET

Package Structure

A package is a convention for organizing files into directories.

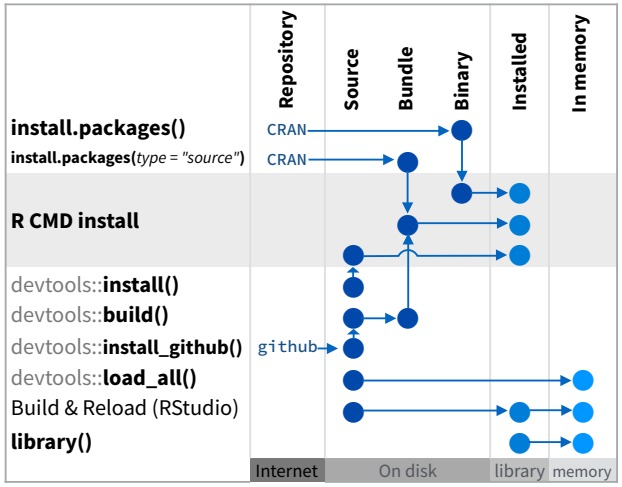
This sheet shows how to work with the 7 most common parts of an R package:

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.

- Use roxygen comments to document each function beside its definition
- Document the name of each exported data set
- Include helpful examples for each function

WORKFLOW

1. Add roxygen comments in your .R files
2. Convert roxygen comments into documentation with one of:

   devtools::**document()**
   Converts roxygen comments to .Rd files and places them in man/. Builds NAMESPACE.

   Ctrl/Cmd + Shift + D (Keyboard Shortcut)

3. Open help pages with **?** to preview documentation
4. Repeat

.Rd FORMATTING TAGS

```
\emph{italic text}
\strong{bold text}
\code{function(args)}
\pkg{package}

\dontrun{code}
\dontshow{code}
\donttest{code}

\deqn{a + b (block)}
\eqn{a + b (inline)}

\email{name@@foo.com}
\href{url}{display}
\url{url}

\link[=dest]{display}
\linkS4class{class}
\code{\link{function}}
\code{\link[package]{function}}

\tabular{lcr}{
  left \tab centered \tab right \cr
  cell \tab cell     \tab cell  \cr
}
```

ROXYGEN2

The **roxygen2** package lets you write documentation inline in your .R files with a shorthand syntax. devtools implements roxygen2 to make documentation.

- Add roxygen documentation as comment lines that begin with **#'**.
- Place comment lines directly above the code that defines the object documented.
- Place a roxygen **@** tag (right) after **#'** to supply a specific section of documentation.
- Untagged lines will be used to generate a title, description, and details section (in that order)

```
#' Add together two numbers.
#'
#' @param x A number.
#' @param y A number.
#' @return The sum of \code{x} and \code{y}.
#' @examples
#' add(1, 1)
#' @export
add <- function(x, y) {
  x + y
}
```

COMMON ROXYGEN TAGS

@aliases	@inheritParams	**@seealso**	
@concepts	@keywords	@format	
@describeIn	**@param**	@source	data
@examples	@rdname	@include	
@export	@**return**	@slot	S4
@family	@section	@field	RC

Add Data (data/)

The data/ directory allows you to include data with your package.

- Save data as .Rdata files (suggested)
- Store data in one of **data/**, **R/Sysdata.rda**, **inst/extdata**
- Always use **LazyData: true** in your DESCRIPTION file.

devtools::**use_data()**
Adds a data object to data/
(R/Sysdata.rda if **internal = TRUE**)

devtools::**use_data_raw()**
Adds an R Script used to clean a data set to data-raw/.
Includes data-raw/ on .Rbuildignore.

Store data in

- **data/** to make data available to package users
- **R/sysdata.rda** to keep data internal for use by your functions.
- **inst/extdata** to make raw data available for loading and parsing examples. Access this data with **system.file()**

Organize (NAMESPACE)

The NAMESPACE file helps you make your package self-contained: it won't interfere with other packages, and other packages won't interfere with it.

- Export functions for users by placing **@export** in their roxygen comments
- Import objects from other packages with **package::object** (recommended) or **@import**, **@importFrom**, **@importClassesFrom**, **@importMethodsFrom** (not always recommended)

WORKFLOW

1. Modify your code or tests.
2. Document your package (devtools::**document()**)
3. Check NAMESPACE
4. Repeat until NAMESPACE is correct

SUBMIT YOUR PACKAGE

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

Teach (vignettes/)

vignettes/ holds documents that teach your users how to solve real problems with your tools.

- Create a vignettes/ directory and a template vignette with

  devtools::**use_vignette()**
  Adds template vignette as vignettes/my-vignette.Rmd.
- Append YAML headers to your vignettes (like right)
- Write the body of your vignettes in R Markdown (rmarkdown.rstudio.com)

```
---
title: "Vignette Title"
author: "Vignette Author"
date: "`r Sys.Date()`"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  \usepackage[utf8]{inputenc}
---
```

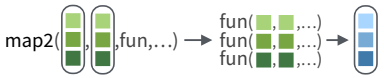
RStudio

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

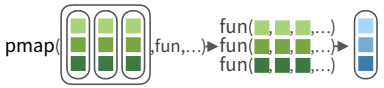
Apply Functions

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

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



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



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

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

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

OUTPUT

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

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

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

SHORTCUTS - within a purrr function:

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

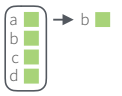
~ .x becomes **function(x) x**, e.g. *map(l, ~ 2 +.x)* becomes *map(l, function(x) 2 + x)*

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

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

Work with Lists

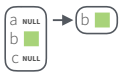
FILTER LISTS



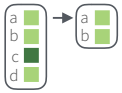
pluck(.x, ..., .default=NULL) Select an element by name or index, *pluck(x,"b")* ,or its attribute with **attr_getter**. *pluck(x,"b",attr_getter("n"))*

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

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



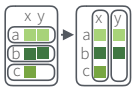
compact(.x, .p = identity) Drop empty elements. *compact(x)*



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

RESHAPE LISTS

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



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

SUMMARISE LISTS

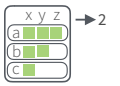
every(.x, .p, …) Do all elements pass a test? *every(x, is.character)*

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

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

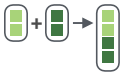
detect(.x, .f, ..., .right=FALSE, .p) Find first element to pass. *detect(x, is.character)*

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



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

JOIN (TO) LISTS



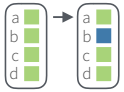
append(x, values, after = length(x)) Add to end of list. *append(x, list(d = 1))*

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

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

TRANSFORM LISTS

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



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

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

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

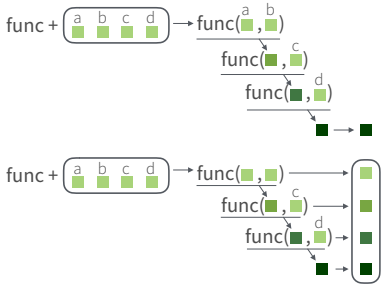
WORK WITH LISTS

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

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

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

Reduce Lists



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

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

Modify function behavior

compose() Compose multiple functions.

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

rerun() Rerun expression n times.

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

partial() Create a version of a function that has some args preset to values.

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

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

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

Nested Data

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

"cell" contents

nested data frame

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

n_iris

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

n_iris$data[[1]]

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

n_iris$data[[2]]

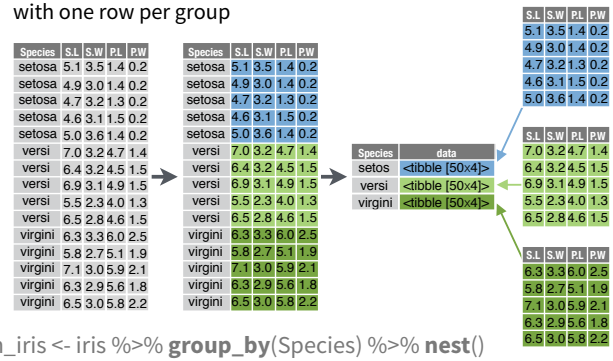
Sepal.L	Sepal.W	Petal.L	Petal.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8
6.5	3.0	5.8	2.2

n_iris$data[[3]]

Use a nested data frame to:

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

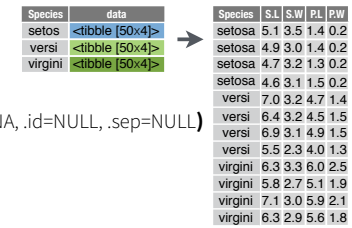
Use a two step process to create a nested data frame:
1. Group the data frame into groups with **dplyr::group_by()**
2. Use **nest()** to create a nested data frame with one row per group



n_iris <- iris %>% **group_by**(Species) %>% **nest**()

tidyr::**nest**(data, ..., .key = data)
For grouped data, moves groups into cells as data frames.

Unnest a nested data frame with **unnest()**:

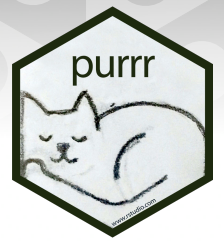


n_iris %>% **unnest**()

tidyr::**unnest**(data, ..., .drop = NA, .id=NULL, .sep=NULL)
Unnests a nested data frame.

List Column Workflow

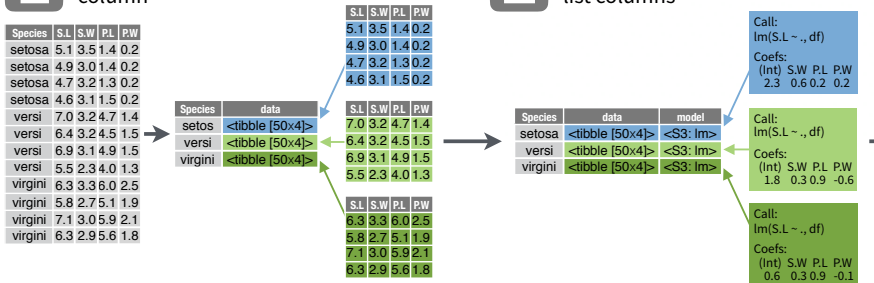
Nested data frames use a **list column**, a list that is stored as a column vector of a data frame. A typical **workflow** for list columns:



1 **Make** a list column

2 **Work with** list columns

3 **Simplify** the list column



n_iris <- iris %>%
group_by(Species) %>%
nest()

mod_fun <- function(df)
lm(Sepal.Length ~ ., data = df)

m_iris <- n_iris %>%
mutate(model = **map**(data, mod_fun))

b_fun <- function(mod)
coefficients(mod)[[1]]

m_iris %>% **transmute**(Species,
beta = **map_dbl**(model, b_fun))

1. MAKE A LIST COLUMN - You can create list columns with functions in the **tibble** and **dplyr** packages, as well as **tidyr**'s nest()

tibble::**tribble**(…)
Makes list column when needed

tribble(~max, ~seq,
3, 1:3,
4, 1:4,
5, 1:5)

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

tibble::**tibble**(…)
Saves list input as list columns
tibble(max = c(3, 4, 5), seq = list(1:3, 1:4, 1:5))

tibble::**enframe**(x, name="name", value="value")
Converts multi-level list to tibble with list cols
enframe(list('3'=1:3, '4'=1:4, '5'=1:5), 'max', 'seq')

dplyr::**mutate**(.data, …) Also **transmute**()
Returns list col when result returns list.
mtcars %>% **mutate**(seq = **map**(cyl, seq))

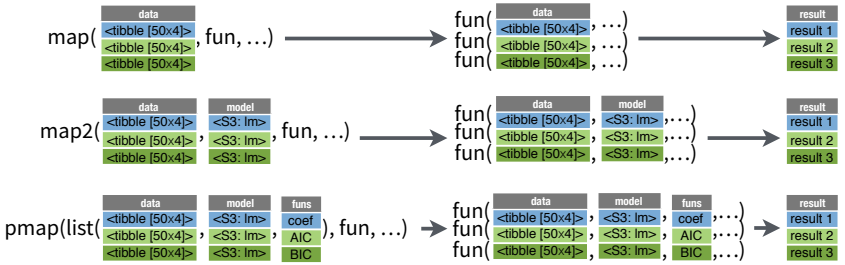
dplyr::**summarise**(.data, …)
Returns list col when result is wrapped with **list()**
mtcars %>% group_by(cyl) %>%
summarise(q = **list**(quantile(mpg)))

2. WORK WITH LIST COLUMNS - Use the purrr functions **map()**, **map2()**, and **pmap()** to apply a function that returns a result element-wise to the cells of a list column. **walk()**, **walk2()**, and **pwalk()** work the same way, but return a side effect.

purrr::**map**(.x, .f, ...)
Apply .f element-wise to .x as .f(.x)
n_iris %>% **mutate**(n = **map**(data, dim))

purrr::**map2**(.x, .y, .f, ...)
Apply .f element-wise to .x and .y as .f(.x, .y)
m_iris %>% **mutate**(n = **map2**(data, model, list))

purrr::**pmap**(.l, .f, ...)
Apply .f element-wise to vectors saved in .l
m_iris %>%
mutate(n = **pmap**(list(data, model, data), list))



3. SIMPLIFY THE LIST COLUMN (into a regular column)

Use the purrr functions **map_lgl()**, **map_int()**, **map_dbl()**, **map_chr()**, as well as tidyr's **unnest()** to reduce a list column into a regular column.

purrr::**map_lgl**(.x, .f, ...)
Apply .f element-wise to .x, return a logical vector
n_iris %>% **transmute**(n = **map_lgl**(data, is.matrix))

purrr::**map_int**(.x, .f, ...)
Apply .f element-wise to .x, return an integer vector
n_iris %>% **transmute**(n = **map_int**(data, nrow))

purrr::**map_dbl**(.x, .f, ...)
Apply .f element-wise to .x, return a double vector
n_iris %>% **transmute**(n = **map_dbl**(data, nrow))

purrr::**map_chr**(.x, .f, ...)
Apply .f element-wise to .x, return a character vector
n_iris %>% **transmute**(n = **map_chr**(data, nrow))

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.

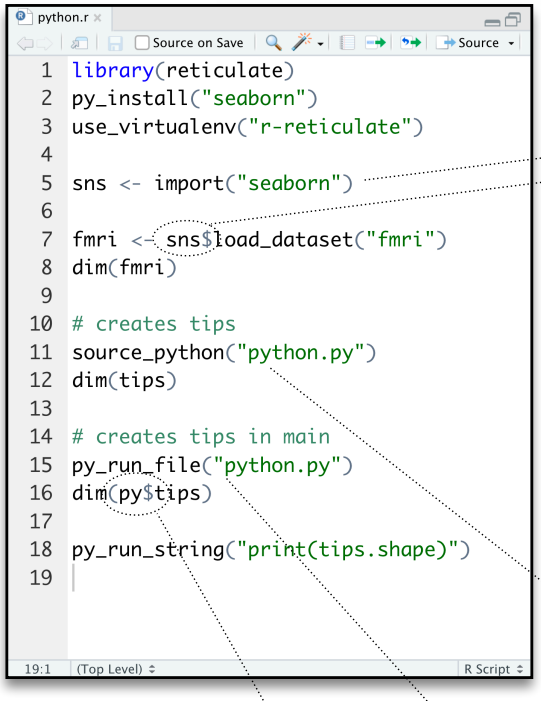
Begin Python chunks with **```{python}**. Chunk options like **echo**, **include**, etc. all work as expected.

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 code

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

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

iterate(..., convert = FALSE) 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 or higher.

Syntax highlighting for Python scripts and chunks

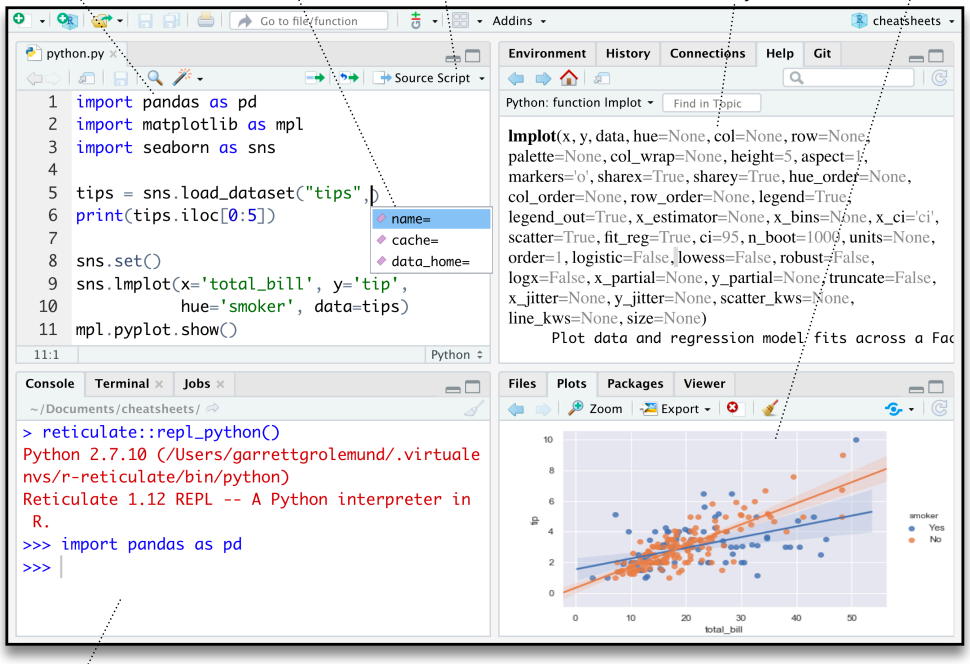
Tab completion for Python functions and objects (and Python modules imported in R scripts)

Source Python scripts.

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

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

matplotlib plots display in plots pane.

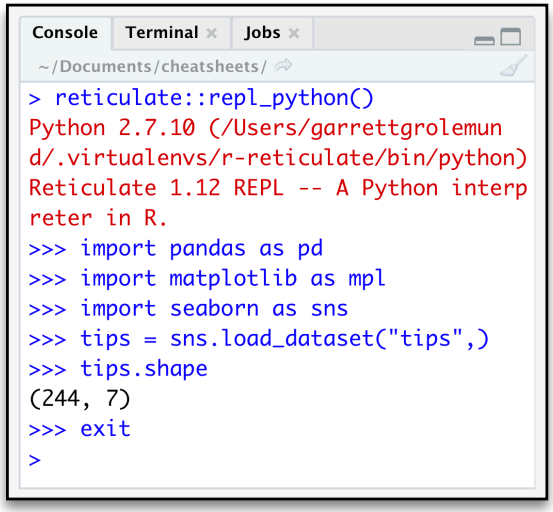


A Python REPL opens in the console when you run Python code with a keyboard shortcut. Type **exit** to close.

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)) 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

- **py_discover_config**() Return all detected versions of Python. Use **py_config** to check which version has been loaded. *py_config()*
- **py_available**(initialize = FALSE) Check if Python is available on your system. Also **py_module_available**, **py_numpy_module.** *py_available()*
- **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) Create a new virtualenv. *virtualenv_create("r-pandas")*
- **conda_create**(envname, packages = NULL, conda = "auto") Create a new Conda env. *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 = "r-reticulate", method = c("auto", "virtualenv", "conda"), conda = "auto", ...) Installs Python packages into a Python env named "r-reticulate". *py_install("pandas")*
- **virtualenv_install**(envname, packages, ignore_installed = FALSE) Install a package within a virtualenv. *virtualenv_install("r-pandas", packages = "pandas")*
- **virtualenv_remove**(envname, packages = NULL, confirm = interactive()) Remove individual packages or an entire virtualenv. *virtualenv_remove("r-pandas", packages = "pandas")*
- **conda_install**(envname, packages, forge = TRUE, pip = FALSE, pip_ignore_installed = TRUE, conda = "auto") Install a package within a Conda env. *conda_install("r-pandas", packages = "plotly")*
- **conda_remove**(envname, packages = NULL, conda = "auto") Remove individual packages or an entire Conda env. *conda_remove("r-pandas", packages = "plotly")*

Suggest an env to use

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**...

R Markdown : : CHEAT SHEET

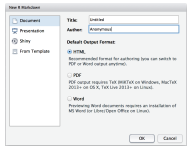
What is R Markdown?

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

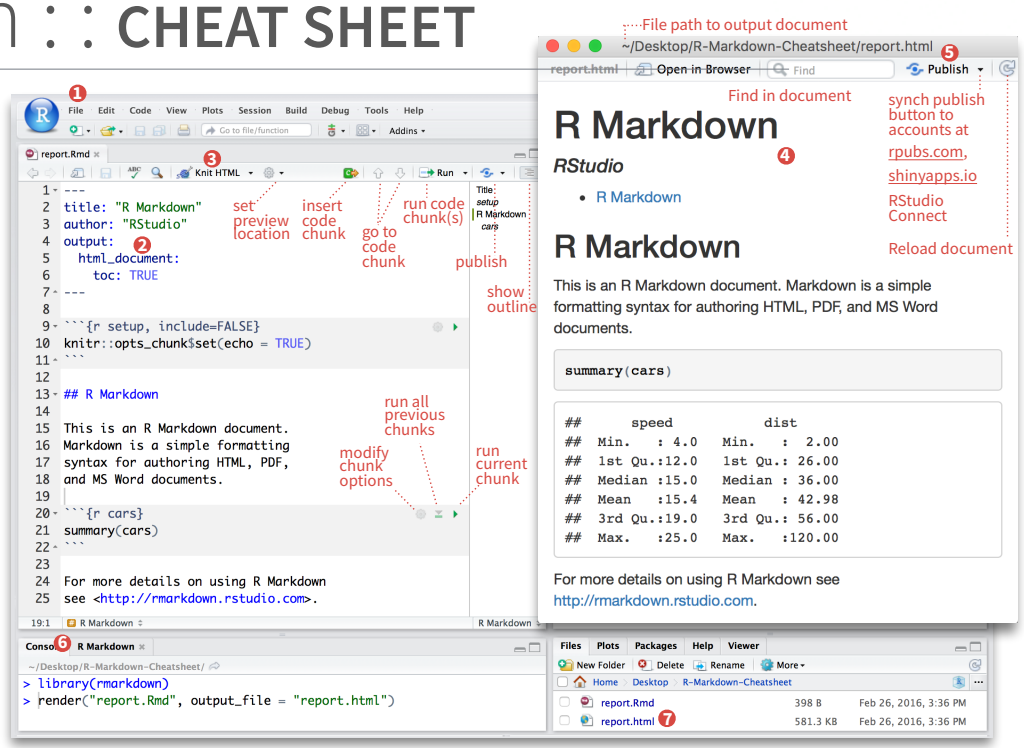
Reproducible Research • At the click of a button, or the type of a command, you can rerun the code in an R Markdown file to reproduce your work and export the results as a finished report.

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

Workflow



1. **Open a new .Rmd file** at File ▶ New File ▶ R Markdown. Use the wizard that opens to pre-populate the file with a template
2. **Write document** by editing template
3. **Knit document to create report**; use knit button or **render()** to knit
4. **Preview Output** in IDE window
5. **Publish** (optional) to web server
6. **Examine build log** in R Markdown console
7. **Use output file** that is saved along side .Rmd



.rmd Structure

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

At start of file

Between lines of `---`

Text
Narration formatted with markdown, mixed with:

Code Chunks
Chunks of embedded code. Each chunk:

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

ends with ```` ``` ````

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

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

Parameters

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

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

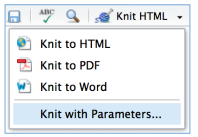
```
---
params:
  n: 100
  d: !r Sys.Date()
---
```

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

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

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

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



render

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

input - file to render **output_format**	**output_options** - List of render options (as in YAML)	**output_file** **output_dir**	**params** - list of params to use	**envir** - environment to evaluate code chunks in	**encoding** - of input file

Interactive Documents

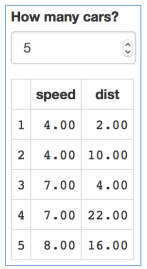
Turn your report into an interactive Shiny document in 4 steps

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

```
---
output: html_document
runtime: shiny
---

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

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



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

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

Embed code with knitr syntax

INLINE CODE

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

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

CODE CHUNKS

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

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

➡

```
getRversion()
## [1] '3.2.3'
```

GLOBAL OPTIONS

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

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

IMPORTANT CHUNK OPTIONS

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

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

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

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

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

dependson - chunk dependencies for caching (default = NULL)

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

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

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

eval - Run code in chunk (default = TRUE)

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

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

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

highlight - highlight source code (default = TRUE)

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

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

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

tidy - tidy code for display (default = FALSE)

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

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

Pandoc's Markdown

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

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

$$E = mc^{2}$$

> block quote

# Header1 {#anchor}

## Header 2 {#css_id}

### Header 3 {.css_class}

#### Header 4

##### Header 5

###### Header 6

<!--Text comment-->

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

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

![Caption](smallorb.png)

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

* item 2

  Continued (indent 4 spaces)

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

(@) A list whose numbering

continues after

(@) an interruption

Term 1

:  Definition 1

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

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

***

A footnote [^1]

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

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

$$E = mc^2$$

> block quote

Header1

Header 2

Header 3

Header 4

Header 5

Header 6

HTML ignored in pdfs

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

Caption

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

  Continued (indent 4 spaces)

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(@) an interruption

Term 1

Definition 1

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

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

A footnote [1]

1. Here is the footnote. ↩

Set render options with YAML

When you render, R Markdown

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

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

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

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

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

Indent 2 spaces — Indent 4 spaces

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

html tabsets

Use tablet css class to place sub-headers into tabs

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

Tabset

Tab 1 | Tab 2

text 1
End tabset

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

Create a Reusable Template

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

template.yaml

```
---
name: My Template
—
```

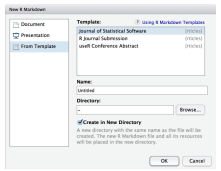


Table Suggestions

Several functions format R data into tables

Table with kable

eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62

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

Table with xtable

Table with stargazer

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

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

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

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

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

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

Citations and Bibliographies

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

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

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

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

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

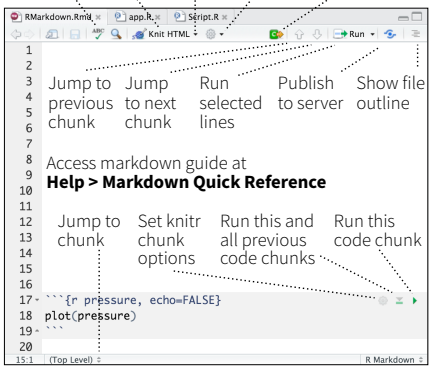
```
Smith cited (Joe Smith 2004).
Smith cited without author (2004).
Joe Smith (2004) cited in line.
```

RStudio IDE : : CHEAT SHEET

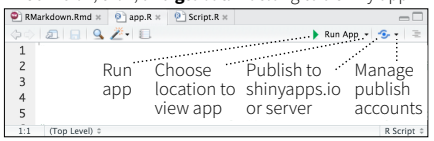
Documents and Apps

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

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

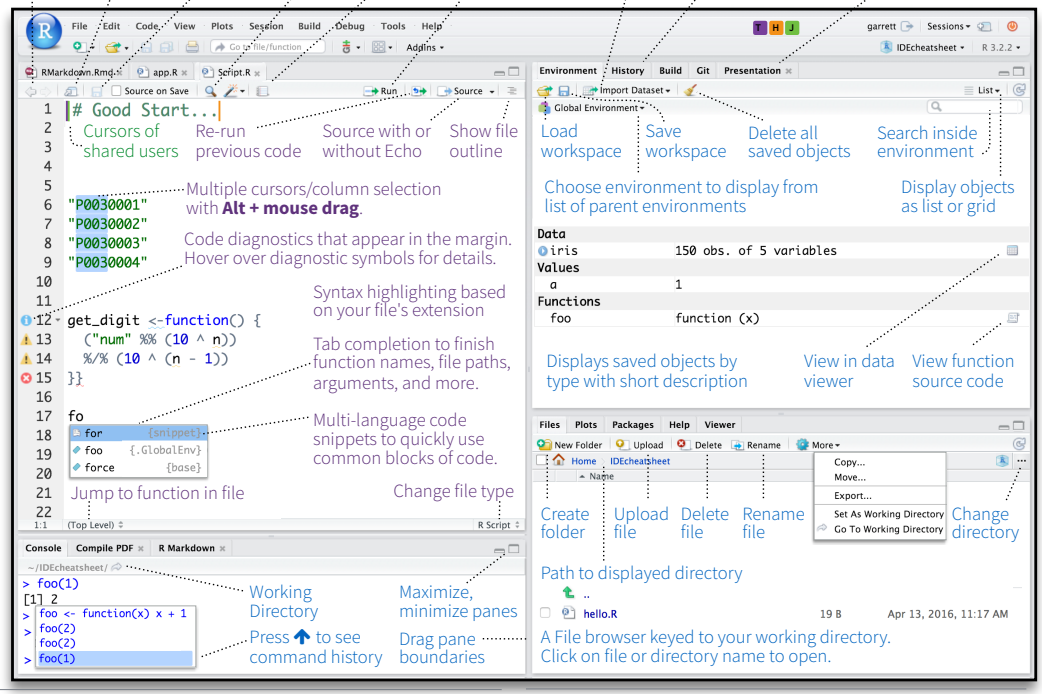


RStudio recognizes that files named **app.R**, **server.R**, **ui.R**, and **global.R** belong to a shiny app



Write Code

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

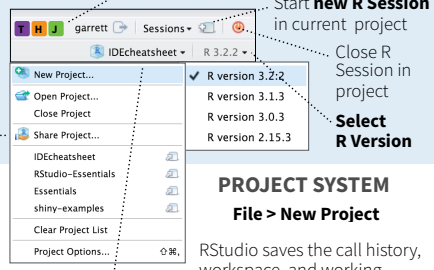


R Support

Import data with wizard | History of past commands to run/copy | Display .RPres slideshows **File > New File > R Presentation**

Pro Features

Share Project with Collaborators | Active shared collaborators

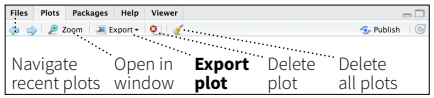


PROJECT SYSTEM

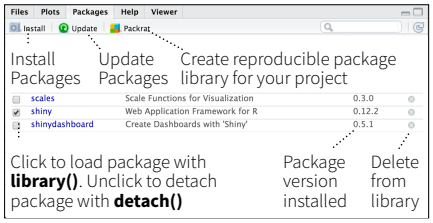
File > New Project

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

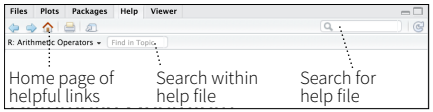
RStudio opens plots in a dedicated Plots pane



GUI Package manager lists every installed package

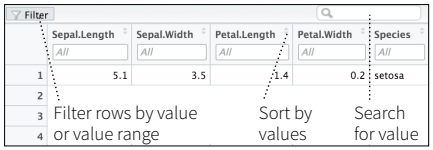


RStudio opens documentation in a dedicated Help pane



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

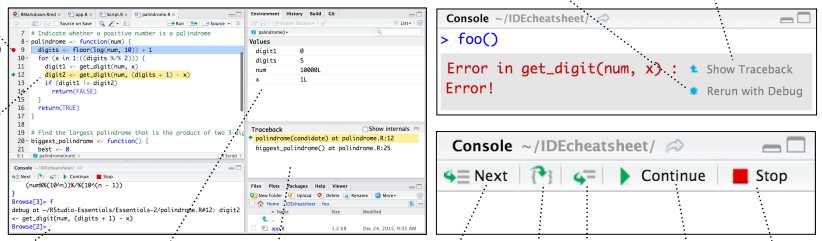
View(<data>) opens spreadsheet like view of data set



Debug Mode

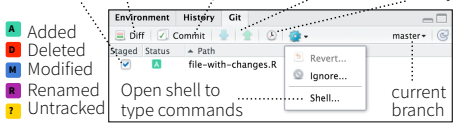
Open with **debug(), browser(),** or a breakpoint. RStudio will open the debugger mode when it encounters a breakpoint while executing code.

Launch debugger mode from origin of error | Open traceback to examine the functions that R called before the error occurred



Version Control with Git or SVN

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

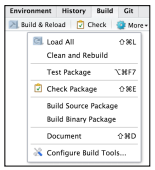


Package Writing

File > New Project > New Directory > R Package

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

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



1 LAYOUT

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

2 RUN CODE

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

3 NAVIGATE CODE

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

4 WRITE CODE

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

WHY RSTUDIO SERVER PRO?

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

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

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

5 DEBUG CODE

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

6 VERSION CONTROL

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

7 MAKE PACKAGES

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

8 DOCUMENTS AND APPS

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

RStudio

Shiny : : CHEAT SHEET

Basics

A **Shiny** app is a web page (**UI**) connected to a computer running a live R session (**Server**)

Users can manipulate the UI, which will cause the server to update the UI's displays (by running R code).

APP TEMPLATE

Begin writing a new app with this template. Preview the app by running the code at the R command line.

```
library(shiny)
ui <- fluidPage()
server <- function(input, output){}
shinyApp(ui = ui, server = server)
```

- **ui** - nested R functions that assemble an HTML user interface for your app
- **server** - a function with instructions on how to build and rebuild the R objects displayed in the UI
- **shinyApp** - combines `ui` and `server` into an app. Wrap with **runApp()** if calling from a sourced script or inside a function.

SHARE YOUR APP

The easiest way to share your app is to host it on shinyapps.io, a cloud based service from RStudio

1. Create a free or professional account at **http://shinyapps.io**
2. Click the **Publish** icon in the RStudio IDE or run:
   rsconnect::deployApp("<path to directory>"**)**

Build or purchase your own Shiny Server
at www.rstudio.com/products/shiny-server/

Building an App

Complete the template by adding arguments to fluidPage() and a body to the server function.

Add inputs to the UI with *Input() functions

Add outputs with *Output() functions

Tell server how to render outputs with R in the server function. To do this:

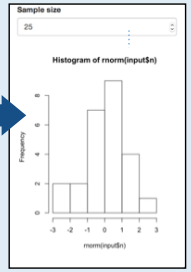
1. Refer to outputs with **output$<id>**
2. Refer to inputs with **input$<id>**
3. Wrap code in a **render*()** function before saving to output

```
library(shiny)

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

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

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



Save your template as **app.R**. Alternatively, split your template into two files named **ui.R** and **server.R**.

```
library(shiny)
ui <- fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)
server <- function(input, output) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}
shinyApp(ui = ui, server = server)
```

```
# ui.R
fluidPage(
  numericInput(inputId = "n",
    "Sample size", value = 25),
  plotOutput(outputId = "hist")
)
```

ui.R contains everything you would save to ui.

```
# server.R
function(input, output) {
  output$hist <- renderPlot({
    hist(rnorm(input$n))
  })
}
```

server.R ends with the function you would save to server.

No need to call **shinyApp()**.

Save each app as a directory that holds an **app.R** file (or a **server.R** file and a **ui.R** file) plus optional extra files.

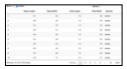
The directory name is the name of the app
(optional) defines objects available to both ui.R and server.R
(optional) used in showcase mode
(optional) data, scripts, etc.
(optional) directory of files to share with web browsers (images, CSS, .js, etc.) Must be named "**www**"

Launch apps with `runApp(<path to directory>)`

Outputs -

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

works with



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

renderImage(expr, env, quoted, deleteFile) — **imageOutput**(outputId, width, height, click, dblclick, hover, hoverDelay, inline, hoverDelayType, brush, clickId, hoverId)

renderPlot(expr, width, height, res, …, env, quoted, func) — **plotOutput**(outputId, width, height, click, dblclick, hover, hoverDelay, inline, hoverDelayType, brush, clickId, hoverId)

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

renderTable(expr,…, env, quoted, func) — **tableOutput**(outputId)

foo

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

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

Inputs

collect values from the user

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

Action — **actionButton**(inputId, label, icon, …)

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

Choice 1 / Choice 2 / Choice 3 — **checkboxGroupInput**(inputId, label, choices, selected, inline)

Check me — **checkboxInput**(inputId, label, value)

dateInput(inputId, label, value, min, max, format, startview, weekstart, language)

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

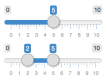
Choose File — **fileInput**(inputId, label, multiple, accept)

1 — **numericInput**(inputId, label, value, min, max, step)

••••••• — **passwordInput**(inputId, label, value)

Choice A / Choice B / Choice C — **radioButtons**(inputId, label, choices, selected, inline)

Choice 1 / Choice 1 / Choice 2 — **selectInput**(inputId, label, choices, selected, multiple, selectize, width, size) (also selectizeInput())



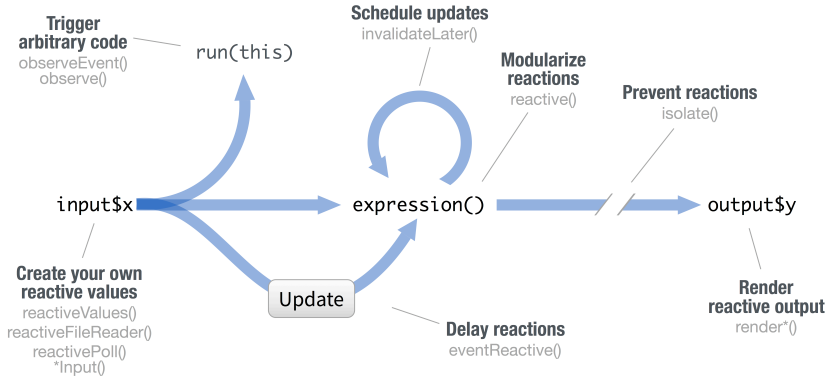
sliderInput(inputId, label, min, max, value, step, round, format, locale, ticks, animate, width, sep, pre, post)

Apply Changes — **submitButton**(text, icon) (Prevents reactions across entire app)

Enter text — **textInput**(inputId, label, value)

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

```
# example snippets


ui <- fluidPage(
 textInput("a","","A")
)


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

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

reactiveValues(...)

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

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

RENDER REACTIVE OUTPUT

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 textOutput("b")
)

server <-
function(input,output){
 output$b <-
  renderText({
   input$a
  })
}

shinyApp(ui, server)
```

render*() functions
(see front page)

Builds an object to display. Will rerun code in body to rebuild the object whenever a reactive value in the code changes.

Save the results to **output$<outputId>**

PREVENT REACTIONS

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 textOutput("b")
)

server <-
function(input,output){
 output$b <-
  renderText({
   isolate({input$a})
  })
}

shinyApp(ui, server)
```

isolate(expr)

Runs a code block. Returns a **non-reactive** copy of the results.

TRIGGER ARBITRARY CODE

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 actionButton("go","Go")
)

server <-
function(input,output){
 observeEvent(input$go,{
   print(input$a)
  })
}


shinyApp(ui, server)
```

observeEvent(eventExpr, handlerExpr, event.env, event.quoted, handler.env, handler.quoted, labe, suspended, priority, domain, autoDestroy, ignoreNULL)

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

MODULARIZE REACTIONS

```
ui <- fluidPage(
 textInput("a","","A"),
 textInput("z","","Z"),
 textOutput("b"))

server <-
function(input,output){
 re <- reactive({

paste(input$a,input$z)})
 output$b <- renderText({
   re()
  })
}
shinyApp(ui, server)
```

reactive(x, env, quoted, label, domain)

Creates a **reactive expression** that

- **caches** its value to reduce computation
- can be called by other code
- notifies its dependencies when it ha been invalidated

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

DELAY REACTIONS

```
library(shiny)

ui <- fluidPage(
 textInput("a","","A"),
 actionButton("go","Go"),
 textOutput("b")
)

server <-
function(input,output){
 re <- eventReactive(
  input$go,{input$a})
 output$b <- renderText({
   re()
  })
}

shinyApp(ui, server)
```

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

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

UI - An app's UI is an HTML document.

Use Shiny's functions to assemble this HTML with R.

```
fluidPage(
  textInput("a","")
)
## <div class="container-fluid">
##   <div class="form-group shiny-input-container">
##     <label for="a"></label>
##     <input id="a" type="text"
##       class="form-control" value=""/>
##   </div>
## </div>
```

Returns HTML

HTML

Add static HTML elements with **tags**, a list of functions that parallel common HTML tags, e.g. **tags$a()**. Unnamed arguments will be passed into the tag; named arguments will become tag attributes.

tags$a	tags$data	tags$h6	tags$nav	tags$span
tags$abbr	tags$datalist	tags$head	tags$noscript	tags$strong
tags$address	tags$dd	tags$header	tags$object	tags$style
tags$area	tags$del	tags$hgroup	tags$ol	tags$sub
tags$article	tags$details	tags$hr	tags$optgroup	tags$summary
tags$aside	tags$dfn	tags$HTML	tags$option	tags$sup
tags$audio	tags$div	tags$i	tags$output	tags$table
tags$b	tags$dl	tags$iframe	tags$p	tags$tbody
tags$base	tags$dt	tags$img	tags$param	tags$td
tags$bdi	tags$em	tags$input	tags$pre	tags$textarea
tags$bdo	tags$embed	tags$ins	tags$progress	tags$tfoot
tags$blockquote	tags$eventsource	tags$kbd	tags$q	tags$th
tags$body	tags$fieldset	tags$keygen	tags$ruby	tags$thead
tags$br	tags$figcaption	tags$label	tags$rp	tags$time
tags$button	tags$figure	tags$legend	tags$rt	tags$title
tags$canvas	tags$footer	tags$li	tags$s	tags$tr
tags$caption	tags$form	tags$link	tags$samp	tags$track
tags$cite	tags$h1	tags$mark	tags$script	tags$u
tags$code	tags$h2	tags$map	tags$section	tags$ul
tags$col	tags$h3	tags$menu	tags$select	tags$var
tags$colgroup	tags$h4	tags$meta	tags$small	tags$video
tags$command	tags$h5	tags$meter	tags$source	tags$wbr

The most common tags have wrapper functions. You do not need to prefix their names with **tags$**

```
ui <- fluidPage(
  h1("Header 1"),
  hr(),
  br(),
  p(strong("bold")),
  p(em("italic")),
  p(code("code")),
  a(href="", "link"),
  HTML("<p>Raw html</p>")
)
```

CSS

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>"))
```

JS

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>"))
```

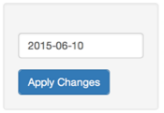
IMAGES

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.

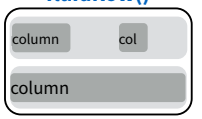
```
wellPanel(dateInput("a", ""),
          submitButton()
)
```



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

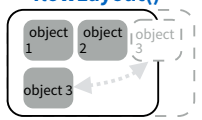
Organize panels and elements into a layout with a layout function. Add elements as arguments of the layout functions.

fluidRow()



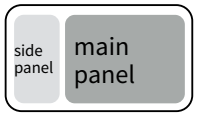

```
ui <- fluidPage(
 fluidRow(column(width = 4),
   column(width = 2, offset = 3)),
 fluidRow(column(width = 12))
)
```

flowLayout()



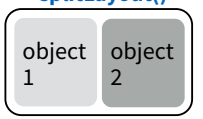

```
ui <- fluidPage(
 flowLayout( # object 1,
             # object 2,
             # object 3
 )
)
```

sidebarLayout()



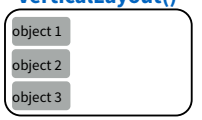

```
ui <- fluidPage(
 sidebarLayout(
  sidebarPanel(),
  mainPanel()
 )
)
```

splitLayout()




```
ui <- fluidPage(
 splitLayout( # object 1,
              # object 2
 )
)
```

verticalLayout()



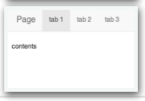

```
ui <- fluidPage(
 verticalLayout( # object 1,
                 # object 2,
                 # object 3
 )
)
```

Layer tabPanels on top of each other, and navigate between them, with:

```
ui <- fluidPage( tabsetPanel(
   tabPanel("tab 1", "contents"),
   tabPanel("tab 2", "contents"),
   tabPanel("tab 3", "contents"))
)
```


```
ui <- fluidPage( navlistPanel(
   tabPanel("tab 1", "contents"),
   tabPanel("tab 2", "contents"),
   tabPanel("tab 3", "contents"))
)
```


```
ui <- navbarPage(title = "Page",
   tabPanel("tab 1", "contents"),
   tabPanel("tab 2", "contents"),
   tabPanel("tab 3", "contents"))
```



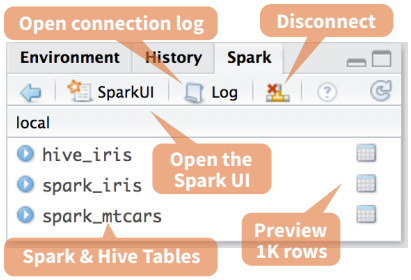
Data Science in Spark with Sparklyr : : CHEAT SHEET

Intro

sparklyr is an R interface for Apache Spark™, it provides a complete **dplyr** backend and the option to query directly using **Spark SQL** statement. With sparklyr, you can orchestrate distributed machine learning using either **Spark's MLlib** or **H2O** Sparkling Water.

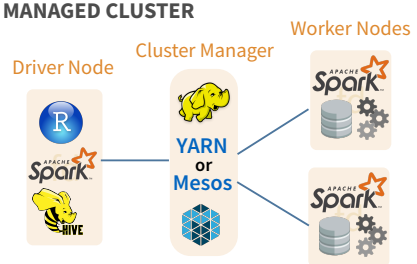
Starting with **version 1.044, RStudio Desktop, Server and Pro include integrated support for the sparklyr package**. You can create and manage connections to Spark clusters and local Spark instances from inside the IDE.

RStudio Integrates with sparklyr

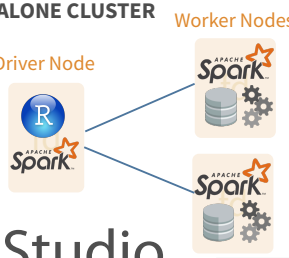


Cluster Deployment

MANAGED CLUSTER



STAND ALONE CLUSTER



Data Science Toolchain with Spark + sparklyr

Import
- Export an R DataFrame
- Read a file
- Read existing Hive table

Tidy
- dplyr verb
- Direct Spark SQL (DBI)
- SDF function (Scala API)

Understand

Transform
Transformer function

Visualize
Collect data into R for plotting

Wrangle

Model
- Spark MLlib
- H2O Extension

Communicate
- Collect data into R
- Share plots, documents, and apps

R for Data Science, Grolemund & Wickham

Getting Started

LOCAL MODE (No cluster required)

1. Install a local version of Spark: **spark_install ("2.0.1")**
2. Open a connection **sc <- spark_connect (master = "local")**

ON A MESOS MANAGED CLUSTER

1. Install RStudio Server or Pro on one of the existing nodes
2. Locate path to the cluster's Spark directory
3. Open a connection **spark_connect(master="[mesos URL]", version = "1.6.2", spark_home = [Cluster's Spark path])**

USING LIVY (Experimental)

1. The Livy REST application should be running on the cluster
2. Connect to the cluster **sc <- spark_connect(method = "livy", master = "http://host:port")**

ON A YARN MANAGED CLUSTER

1. Install RStudio Server or RStudio Pro 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. Open a connection **spark_connect(master="yarn-client", version = "1.6.2", spark_home = [Cluster's Spark path])**

ON A SPARK STANDALONE CLUSTER

1. Install RStudio Server or RStudio Pro 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())**

Tuning Spark

EXAMPLE CONFIGURATION

```
config <- spark_config()
config$spark.executor.cores <- 2
config$spark.executor.memory <- "4G"
sc <- spark_connect (master="yarn-client",
config = config, version = "2.0.1")
```

IMPORTANT TUNING PARAMETERS with defaults

- spark.yarn.am.cores
- spark.yarn.am.memory *512m*
- spark.network.timeout *120s*
- spark.executor.memory *1g*
- spark.executor.cores *1*
- spark.executor.instances
- spark.executor.extraJavaOptions
- spark.executor.heartbeatInterval *10s*
- sparklyr.shell.executor-memory
- sparklyr.shell.driver-memory

Using sparklyr

A brief example of a data analysis using Apache Spark, R and sparklyr in local mode

```
library(sparklyr); library(dplyr); library(ggplot2);
library(tidyr);
set.seed(100)
```
Install Spark locally

```
spark_install("2.0.1")
```
Connect to local version

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

import_iris <- copy_to(sc, iris, "spark_iris",
  overwrite = TRUE)
```
Copy data to Spark memory

```
partition_iris <- sdf_partition(
  import_iris,training=0.5, testing=0.5)
```
Partition data

```
sdf_register(partition_iris,
c("spark_iris_training","spark_iris_test"))
```
Create a hive metadata for each partition

```
tidy_iris <- tbl(sc,"spark_iris_training") %>%
  select(Species, Petal_Length, Petal_Width)

model_iris <- tidy_iris %>%
  ml_decision_tree(response="Species",
  features=c("Petal_Length","Petal_Width"))
```
Spark ML Decision Tree Model

```
test_iris <- tbl(sc,"spark_iris_test")
```
Create reference to Spark table

```
pred_iris <- sdf_predict(
  model_iris,  test_iris) %>%
  collect
```
Bring data back into R memory for plotting

```
pred_iris %>%
  inner_join(data.frame(prediction=0:2,
  lab=model_iris$model.parameters$labels)) %>%
  ggplot(aes(Petal_Length, Petal_Width, col=lab)) +
  geom_point()

spark_disconnect(sc)
```
Disconnect

Reactivity

COPY A DATA FRAME INTO SPARK

sdf_copy_to(sc, iris, "spark_iris")

sdf_copy_to(sc, x, name, memory, repartition, overwrite**)**

IMPORT INTO SPARK FROM A FILE

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()**

SPARK SQL COMMANDS

DBI::**dbWriteTable**(sc, "spark_iris", iris)

DBI::**dbWriteTable(**conn, name, value**)**

FROM A TABLE IN HIVE

my_var <- **tbl_cache**(sc, name= "hive_iris")

tbl_cache(sc, name, force = TRUE**)**
Loads the table into memory

my_var <- **dplyr::tbl**(sc, name= "hive_iris")

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

Wrangle

SPARK SQL VIA DPLYR VERBS

Translates into Spark SQL statements

```
my_table <- my_var %>%
  filter(Species=="setosa") %>%
  sample_n(10)
```

DIRECT SPARK SQL COMMANDS

my_table <- DBI::**dbGetQuery**(sc , "SELECT * FROM iris LIMIT 10")

DBI::**dbGetQuery(**conn, statement**)**

SCALA API VIA SDF FUNCTIONS

sdf_mutate(.data)
Works like dplyr mutate function

sdf_partition(x, ..., weights = NULL, seed = sample (.Machine$integer.max, 1)**)**
sdf_partition*(x, training = 0.5, test = 0.5)*

sdf_register(x, name = NULL**)**
Gives a Spark DataFrame a table name

sdf_sample(x, fraction = 1, replacement = TRUE, seed = NULL**)**

sdf_sort(x, columns**)**
Sorts by >=1 columns in ascending order

sdf_with_unique_id(x, id = "id"**)**

sdf_predict(object, newdata**)**
Spark DataFrame with predicted values

ML TRANSFORMERS

ft_binarizer(my_table,input.col="Petal_Length", output.col="petal_large", threshold=1.2)

Arguments that apply to all functions:
x, input.col = NULL, output.col = NULL

ft_binarizer(threshold = 0.5**)**
Assigned values based on threshold

ft_bucketizer(splits**)**
Numeric column to discretized column

ft_discrete_cosine_transform(inverse = FALSE**)**
Time domain to frequency domain

ft_elementwise_product(scaling.col**)**
Element-wise product between 2 cols

ft_index_to_string()
Index labels back to label as strings

ft_one_hot_encoder()
Continuous to binary vectors

ft_quantile_discretizer(n.buckets=5L**)**
Continuous to binned categorical values

ft_sql_transformer(sql**)**

ft_string_indexer(params = NULL**)**
Column of labels into a column of label indices.

ft_vector_assembler()
Combine vectors into single row-vector

Visualize & Communicate

DOWNLOAD DATA TO R MEMORY

r_table <- **collect**(my_table)
plot(Petal_Width~Petal_Length, data=r_table)

dplyr::**collect(**x**)**
Download a Spark DataFrame to an R DataFrame

sdf_read_column(x, column**)**
Returns contents of a single column to R

SAVE FROM SPARK TO FILE SYSTEM

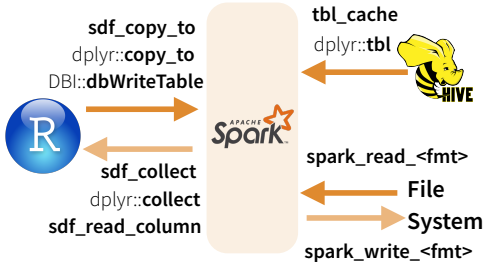
Arguments that apply to all functions: x, path

CSV **spark_read_csv(** header = TRUE, delimiter = ",", quote = "\"", escape = "\\", charset = "UTF-8", null_value = NULL**)**

JSON **spark_read_json(**mode = NULL**)**

PARQUET **spark_read_parquet(**mode = NULL**)**

Reading & Writing from Apache Spark



Extensions

Create an R package that calls the full Spark API & provide interfaces to Spark packages.

CORE TYPES

spark_connection() Connection between R and the Spark shell process

spark_jobj() Instance of a remote Spark object

spark_dataframe() Instance of a remote Spark DataFrame object

CALL SPARK FROM R

invoke() Call a method on a Java object

invoke_new() Create a new object by invoking a constructor

invoke_static() Call a static method on an object

MACHINE LEARNING EXTENSIONS

ml_create_dummy_variables()
ml_prepare_dataframe()
ml_prepare_response_features_intercept()
ml_options()
ml_model()

Model (MLlib)

ml_decision_tree(my_table, response = "Species", features = c("Petal_Length" , "Petal_Width"))

ml_als_factorization(x, user.column = "user", rating.column = "rating", item.column = "item", rank = 10L, regularization.parameter = 0.1, iter.max = 10L, ml.options = ml_options()**)**

ml_decision_tree(x, response, features, max.bins = 32L, max.depth = 5L, type = c("auto", "regression", "classification"), ml.options = ml_options()**)** Same options for: **ml_gradient_boosted_trees**

ml_generalized_linear_regression(x, response, features, intercept = TRUE, family = gaussian(link = "identity"), iter.max = 100L, ml.options = ml_options()**)**

ml_kmeans(x, centers, iter.max = 100, features = dplyr::tbl_vars(x), compute.cost = TRUE, tolerance = 1e-04, ml.options = ml_options()**)**

ml_lda(x, features = dplyr::tbl_vars(x), k = length(features), alpha = (50/k) + 1, beta = 0.1 + 1, ml.options = ml_options()**)**

ml_linear_regression(x, response, features, intercept = TRUE, alpha = 0, lambda = 0, iter.max = 100L, ml.options = ml_options()**)**
Same options for: **ml_logistic_regression**

ml_multilayer_perceptron(x, response, features, layers, iter.max = 100, seed = sample(.Machine$integer.max, 1), ml.options = ml_options()**)**

ml_naive_bayes(x, response, features, lambda = 0, ml.options = ml_options()**)**

ml_one_vs_rest(x, classifier, response, features, ml.options = ml_options()**)**

ml_pca(x, features = dplyr::tbl_vars(x), ml.options = ml_options()**)**

ml_random_forest(x, response, features, max.bins = 32L, max.depth = 5L, num.trees = 20L, type = c("auto", "regression", "classification"), ml.options = ml_options()**)**

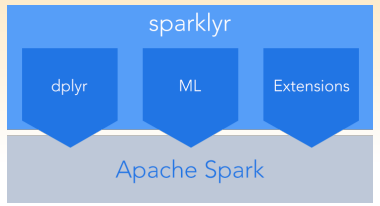
ml_survival_regression(x, response, features, intercept = TRUE,censor = "censor", iter.max = 100L, ml.options = ml_options()**)**

ml_binary_classification_eval(predicted_tbl_spark, label, score, metric = "areaUnderROC"**)**

ml_classification_eval(predicted_tbl_spark, label, predicted_lbl, metric = "f1"**)**

ml_tree_feature_importance(sc, model**)**

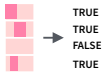
sparklyr is an R interface for Apache Spark



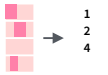
String manipulation with stringr : : **CHEAT SHEET**

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

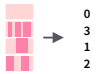
Detect Matches



str_detect(string, **pattern**) Detect the presence of a pattern match in a string.
str_detect(fruit, "a")



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

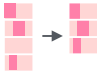


str_count(string, **pattern**) Count the number of matches in a string.
str_count(fruit, "a")

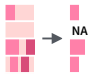
str_locate(string, **pattern**) Locate the positions of pattern matches in a string. Also **str_locate_all**. *str_locate(fruit, "a")*

Subset Strings

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



str_subset(string, **pattern**) Return only the strings that contain a pattern match.
str_subset(fruit, "b")

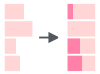


str_extract(string, **pattern**) Return the first pattern match found in each string, as a vector. Also **str_extract_all** to return every pattern match. *str_extract(fruit, "[aeiou]")*

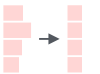
str_match(string, **pattern**) Return the first pattern match found in each string, as a matrix with a column for each ( ) group in pattern. Also **str_match_all**.
str_match(sentences, "(a|the) ([^]+)")

Manage Lengths

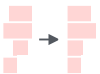
str_length(string) The width of strings (i.e. number of code points, which generally equals the number of characters). *str_length(fruit)*



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



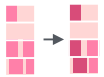
str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "...") Truncate the width of strings, replacing content with ellipsis.
str_trunc(fruit, 3)



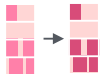
str_trim(string, side = c("both", "left", "right")) Trim whitespace from the start and/or end of a string. *str_trim(fruit)*

Mutate Strings

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



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



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

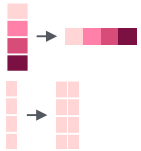
str_to_lower(string, locale = "en")[1] Convert strings to lower case.
str_to_lower(sentences)

str_to_upper(string, locale = "en")[1] Convert strings to upper case.
str_to_upper(sentences)

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

Join and Split

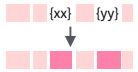
str_c(..., sep = "", collapse = NULL) Join multiple strings into a single string.
str_c(letters, LETTERS)



str_c(..., sep = "", **collapse = NULL**) Collapse a vector of strings into a single string.
str_c(letters, collapse = "")

str_dup(string, times) Repeat strings times times. *str_dup(fruit, times = 2)*

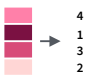
str_split_fixed(string, **pattern**, n) Split a vector of strings into a matrix of substrings (splitting at occurrences of a pattern match). Also **str_split** to return a list of substrings.
str_split_fixed(fruit, " ", n=2)



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")

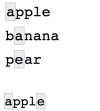
Order Strings



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

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

Helpers



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

str_view(string, **pattern**, match = NA) View HTML rendering of first regex match in each string. *str_view(fruit, "[aeiou]")*

str_view_all(string, **pattern**, match = NA) View HTML rendering of all regex matches.
str_view_all(fruit, "[aeiou]")

str_wrap(string, width = 80, indent = 0, exdent = 0) Wrap strings into nicely formatted paragraphs. *str_wrap(sentences, 20)*

[1] See bit.ly/ISO639-1 for a complete list of locales.

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:]

. , : ; ? ! \ | / ` = * + - ^
_ ~ " ' [ ] { } ( ) < > @ # $

[: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
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
Z

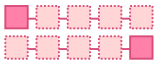
ALTERNATES

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

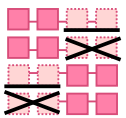
anchor <- function(rx) str_view_all("aaa", rx)



regexp	matches	example	
^a	start of string	anchor("^a")	aaa
a**$**	end of string	anchor("a$")	aaa

LOOK AROUNDS

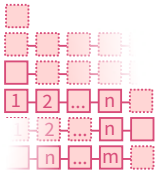
look <- function(rx) str_view_all("bacad", rx)



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

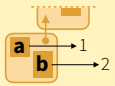
Tidy evaluation with rlang : : **CHEAT SHEET**

Vocabulary

Tidy Evaluation (Tidy Eval) is not a package, but a framework for doing non-standard evaluation (i.e. delayed evaluation) that makes it easier to program with tidyverse functions.

pi

Symbol - a name that represents a value or object stored in R. *is_symbol(expr(pi))*



Environment - a list-like object that binds symbols (names) to objects stored in memory. Each env contains a link to a second, **parent** env, which creates a chain, or search path, of environments. *is_environment(current_env())*

rlang::**caller_env**(n = 1) Returns calling env of the function it is in.

rlang::**child_env**(.parent, ...) Creates new env as child of .parent. Also **env**.

rlang::**current_env**() Returns execution env of the function it is in.

1

Constant - a bare value (i.e. an atomic vector of length 1). *is_bare_atomic(1)*

abs (**1**)

Call object - a vector of symbols/constants/calls that begins with a function name, possibly followed by arguments. *is_call(expr(abs(1)))*

pi — code
3.14 — result

Code - a sequence of symbols/constants/calls that will return a result if evaluated. Code can be:

1. Evaluated immediately (**Standard Eval**)
2. Quoted to use later (**Non-Standard Eval**)

is_expression(expr(pi))

e
a + b

Expression - an object that stores quoted code without evaluating it. is_*expression(expr(a + b))*

q
a + b, a b

Quosure- an object that stores both quoted code (without evaluating it) and the code's environment. *is_quosure(quo(a + b))*

a b rlang::**quo_get_env**(quo) Return the environment of a quosure.

a b rlang::**quo_set_env**(quo, expr) Set the environment of a quosure.

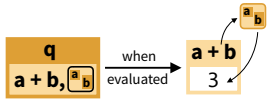
a + b rlang::**quo_get_expr**(quo) Return the expression of a quosure.

Expression Vector - a list of pieces of quoted code created by base R's *expression* and *parse* functions. Not to be confused with **expression**.

Quoting Code

Quote code in one of two ways (if in doubt use a quosure):

QUOSURES



Quosure- An expression that has been saved *with an environment* (aka a closure).

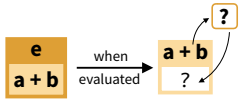
A quosure can be evaluated later in the stored environment to return a predictable result.

rlang::**quo**(expr) Quote contents as a quosure. Also **quos** to quote multiple expressions. *a <- 1; b <- 2; q <- quo(a + b); qs <- quos(a, b)*

rlang::**enquo**(arg) Call from within a function to quote what the user passed to an argument as a quosure. Also **enquos** for multiple args.
quote_this < - function(x) enquo(x)
quote_these < - function(…) enquos(…)

rlang::**new_quosure**(expr, env = caller_env()) Build a quosure from a quoted expression and an environment.
new_quosure(expr(a + b), current_env())

EXPRESSION



Quoted Expression - An expression that has been saved by itself.

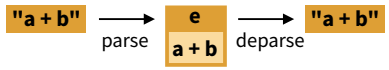
A quoted expression can be evaluated later to return a result that will depend on the environment it is evaluated in

rlang::**expr**(expr) Quote contents. Also **exprs** to quote multiple expressions. *a <- 1; b <- 2; e <- expr(a + b); es <- exprs(a, b, a + b)*

rlang::**enexpr**(arg) Call from within a function to quote what the user passed to an argument. Also **enexprs** to quote multiple arguments.
quote_that < - function(x) enexpr(x)
quote_those < - function(…) enexprs(…)

rlang::**ensym**(x) Call from within a function to quote what the user passed to an argument as a symbol, accepts strings. Also **ensyms**.
quote_name < - function(name) ensym(name)
quote_names < - function(…) ensyms(…)

Parsing and Deparsing



Parse - Convert a string to a saved expression.

rlang::**parse_expr**(x) Convert a string to an expression. Also **parse_exprs**, **sym**, **parse_quo**, **parse_quos**. e<-*parse_expr("a+b")*

Deparse - Convert a saved expression to a string.

rlang::**expr_text**(expr, width = 60L, nlines = Inf) Convert expr to a string. Also **quo_name**. *expr_text(e)*

Building Calls

rlang::**call2**(.fn, ..., .ns = NULL) Create a call from a function and a list of args. Use **exec** to create and then evaluate the call. (See back page for **!!!**) *args <- list(x = 4, base = 2)*

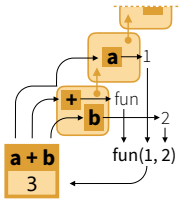
log (x = **4** , base = **2**)

2

call2("log", x = 4, base = 2)
call2("log", !!!args)

exec("log", x = 4, base = 2)
exec("log", !!!args)

Evaluation



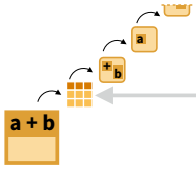
To evaluate an expression, R :

1. Looks up the symbols in the expression in the active environment (or a supplied one), followed by the environment's parents
2. Executes the calls in the expression

The result of an expression depends on which environment it is evaluated in.

QUOTED EXPRESSION

rlang::**eval_bare**(expr, env = parent.frame()) Evaluate expr in env. *eval_bare(e, env =.GlobalEnv)*



a <- 1; b <- 2
*p <- quo(**.data$**a + **!!**b)*
mask <- tibble(a = 5, b = 6)
eval_tidy(p, data = mask)

QUOSURES (and quoted exprs)

rlang::**eval_tidy**(expr, data = NULL, env = caller_env()) Evaluate expr in env, using data as a **data mask**. Will evaluate quosures in their stored environment. *eval_tidy(q)*

Data Mask - If data is non-NULL, eval_tidy inserts data into the search path before env, matching symbols to names in data.

Use the pronoun **.data$** to force a symbol to be matched in data, and **!!** (see back) to force a symbol to be matched in the environments.

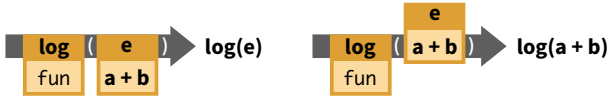
Quasiquotation (!!, !!!, :=)

QUOTATION

Storing an expression without evaluating it.
e <- expr(a + b)

QUASIQUOTATION

Quoting *some* parts of an expression while evaluating and then inserting the results of others (**unquoting** others).
e <- expr(a + b)

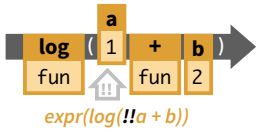


rlang provides **!!**, **!!!**, and **:=** for doing quasiquotation.

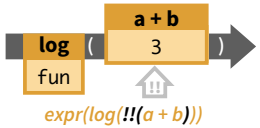
!!, **!!!**, and **:=** are not functions but syntax (symbols recognized by the functions they are passed to). Compare this to how

. is used by magrittr::**%>%()**
. is used by stats::**lm()**
.x is used by purrr::**map()**, and so on.

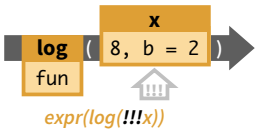
!!, **!!!**, and **:=** are only recognized by some rlang functions and functions that use those functions (such as tidyverse functions).



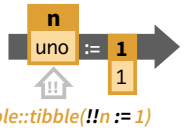
!! Unquotes the symbol or call that follows. Pronounced "unquote" or "bang-bang." *a <- 1; b <- 2*
expr(log(!!a + b))



Combine **!!** with **()** to unquote a longer expression.
a <- 1; b <- 2
expr(log(!!(a + b)))



!!! Unquotes a vector or list and splices the results as arguments into the surrounding call. Pronounced "unquote splice" or "bang-bang-bang."
x <- list(8, b = 2)
expr(log(!!!x))



:= Replaces an = to allow unquoting within the name that appears on the left hand side of the =. Use with **!!**
n <- expr(uno)
tibble::tibble(!!n := 1)

Programming Recipes

Quoting function- A function that quotes any of its arguments internally for delayed evaluation in a chosen environment. You must take **special steps to program safely** with a quoting function.

How to spot a quoting function?
A function quotes an argument if the argument returns an error when run on its own.

Many tidyverse functions are quoting functions: e.g. **filter**, **select**, **mutate**, **summarise**, etc.

dplyr::filter(cars, **speed = = 25**)

speed	dist
1	25
85	

speed == 25
Error!

PROGRAM WITH A QUOTING FUNCTION

```
data_mean <- function(data, var) {
  require(dplyr)
  var <- rlang::enquo(var)                    1
  data %>%
    summarise(mean = mean(!!var))             2
}
```

1. Capture user argument that will be quoted with rlang::**enquo**.
2. Unquote the user argument into the quoting function with **!!**.

PASS MULTIPLE ARGUMENTS TO A QUOTING FUNCTION

```
group_mean <- function(data, var, …) {
  require(dplyr)
  var <- rlang::enquo(var)
  group_vars <- rlang::enquos(…)              1
  data %>%
    group_by(!!!group_vars) %>%               2
    summarise(mean = mean(!!var))
}
```

1. Capture user arguments that will be quoted with rlang::**enquos**.
2. Unquote splice the user arguments into the quoting function with **!!!**.

PASS TO ARGUMENT NAMES OF A QUOTING FUNCTION

```
named_m <- function(data, var, name) {
  require(dplyr)
  var <- rlang::enquo(var)
  name <- rlang::ensym(name)                  1
  data %>%
    summarise(!!name := mean(!!var))          2
}
```

1. Capture user argument that will be quoted with rlang::**ensym**.
2. Unquote the name into the quoting function with **!!** and **:=**.

MODIFY USER ARGUMENTS

```
my_do <- function(f, v, df) {
  f <- rlang::enquo(f)                        1
  v <- rlang::enquo(v)
  todo <- rlang::quo((!!f)(!!v))              2
  rlang::eval_tidy(todo, df)                  3
}
```

1. Capture user arguments with rlang::**enquo**.
2. **Unquote** user arguments into a new expression or quosure to use
3. **Evaluate** the new expression/ quosure instead of the original argument

APPLY AN ARGUMENT TO A DATA FRAME

```
subset2 <- function(df, rows) {
  rows <- rlang::enquo(rows)                  1
  vals <- rlang::eval_tidy(rows, data = df)
  df[vals, , drop = FALSE]                    2
}
```

1. Capture user argument with rlang::**enquo**.
2. Evaluate the argument with rlang::**eval_tidy**. Pass the data frame to **data** to use as a data mask.
3. **Suggest** in your documentation that your users use the **.data** and **.env** pronouns.

PASS CRAN CHECK

```
#' @importFrom rlang .data                    1
mutate_y <- function(df) {
  dplyr::mutate(df, y = .data$a +1)           2
}
```

Quoted arguments in tidyverse functions can trigger an **R CMD check** NOTE about undefined global variables. To avoid this:

1. Import rlang::**.data** to your package, perhaps with the roxygen2 tag **@importFrom rlang .data**
2. Use the **.data$** pronoun in front of variable names in tidyverse functions

WRITE A FUNCTION THAT RECOGNIZES QUASIQUOTATION (!!,!!!,:=)

1. Capture the quasiquotation-aware argument with rlang::**enquo**.
2. Evaluate the arg with rlang::**eval_tidy**.

```
add1 <- function(x) {
  q <- rlang::enquo(x)                        1
  rlang::eval_tidy(q) + 1                     2
}
```

Base R
Cheat Sheet

Getting Help

Accessing the help files

?mean
Get help of a particular function.
help.search('weighted mean')
Search the help files for a word or phrase.
help(package = 'dplyr')
Find help for a package.

More about an object

str(iris)
Get a summary of an object's structure.
class(iris)
Find the class an object belongs to.

Using Packages

install.packages('dplyr')
Download and install a package from CRAN.

library(dplyr)
Load the package into the session, making all its functions available to use.

dplyr::select
Use a particular function from a package.

data(iris)
Load a built-in dataset into the environment.

Working Directory

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

setwd('C://file/path')
Change the current working directory.

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

Vectors

Creating Vectors

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

Vector Functions

sort(x)
Return x sorted.
rev(x)
Return x reversed.
table(x)
See counts of values.
unique(x)
See unique values.

Selecting Vector Elements

By Position

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

By Value

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

Named Vectors

`x['apple']`	Element with name 'apple'.

Programming

For Loop

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

Example

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

While Loop

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

Example

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

If Statements

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

Example

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

Functions

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

Example

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

Reading and Writing Data

Also see the **readr** package.

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

Conditions

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

Types

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

`as.logical`	`TRUE, FALSE, TRUE`	Boolean values (TRUE or FALSE).
`as.numeric`	`1, 0, 1`	Integers or floating point numbers.
`as.character`	`'1', '0', '1'`	Character strings. Generally preferred to factors.
`as.factor`	`'1', '0', '1', levels: '1', '0'`	Character strings with preset levels. Needed for some statistical models.

Maths Functions

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

Variable Assignment

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

The Environment

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

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

Matrices

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


`m[2, ]` - Select a row


`m[ , 1]` - Select a column


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

`t(m)`
Transpose

`m %*% n`
Matrix Multiplication

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

Lists

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

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

Also see the **dplyr** package.

Data Frames

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

x	y
1	a
2	b
3	c

List subsetting


`df$x`


`df[[2]]`

Understanding a data frame

`View(df)` See the full data frame.

`head(df)` See the first 6 rows.

Matrix subsetting


`df[ , 2]`


`df[2, ]`

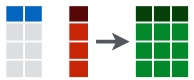

`df[2, 2]`

`nrow(df)`
Number of rows.

`ncol(df)`
Number of columns.

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

`cbind` - Bind columns.



`rbind` - Bind rows.

Strings

Also see the **stringr** package.

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

Factors

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

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

Statistics

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

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

`summary`
Get more detailed information out a model.

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

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

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

`aov`
Analysis of variance.

Distributions

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

Plotting

Also see the **ggplot2** package.


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


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


`hist(x)`
Histogram of x.

Dates

See the **lubridate** package.

caret Package

Cheat Sheet

Specifying the Model

Possible syntaxes for specifying the variables in the model:

```
train(y ~ x1 + x2, data = dat, ...)
train(x = predictor_df, y = outcome_vector, ...)
train(recipe_object, data = dat, ...)
```

- `rfe`, `sbf`, `gafs`, and `safs` only have the `x/y` interface.
- The `train` formula method will **always** create dummy variables.
- The `x/y` interface to `train` will not create dummy variables (but the underlying model function might).

Remember to:

- Have column names in your data.
- Use factors for a classification outcome (not 0/1 or integers).
- Have valid R names for class levels (not "0"/"1")
- Set the random number seed prior to calling `train` repeatedly to get the same resamples across calls.
- Use the `train` option `na.action = na.pass` if you will being imputing missing data. Also, use this option when predicting new data containing missing values.

To pass options to the underlying model function, you can pass them to `train` via *the ellipses*:

```
train(y ~ ., data = dat, method = "rf",
      # options to `randomForest`:
      importance = TRUE)
```

Parallel Processing

The `foreach` package is used to run models in parallel. The `train` code does not change but a "`do`" package must be called first.

```
# on MacOS or Linux
library(doMC)
registerDoMC(cores=4)
```

```
# on Windows
library(doParallel)
cl <- makeCluster(2)
registerDoParallel(cl)
```

The function `parallel::detectCores` can help too.

Preprocessing

Transformations, filters, and other operations can be applied to the *predictors* with the `preProc` option.

```
train(, preProc = c("method1", "method2"), ...)
```

Methods include:

- `"center"`, `"scale"`, and `"range"` to normalize predictors.
- `"BoxCox"`, `"YeoJohnson"`, or `"expoTrans"` to transform predictors.
- `"knnImpute"`, `"bagImpute"`, or `"medianImpute"` to impute.
- `"corr"`, `"nzv"`, `"zv"`, and `"conditionalX"` to filter.
- `"pca"`, `"ica"`, or `"spatialSign"` to transform groups.

`train` determines the order of operations; the order that the methods are declared does not matter.

The `recipes` package has a more extensive list of preprocessing operations.

Adding Options

Many `train` options can be specified using the `trainControl` function:

```
train(y ~ ., data = dat, method = "cubist",
      trControl = trainControl(<options>))
```

Resampling Options

`trainControl` is used to choose a resampling method:

```
trainControl(method = <method>, <options>)
```

Methods and options are:

- `"cv"` for K-fold cross-validation (`number` sets the # folds).
- `"repeatedcv"` for repeated cross-validation (`repeats` for # repeats).
- `"boot"` for bootstrap (`number` sets the iterations).
- `"LGOCV"` for leave-group-out (`number` and `p` are options).
- `"LOO"` for leave-one-out cross-validation.
- `"oob"` for out-of-bag resampling (only for some models).
- `"timeslice"` for time-series data (options are `initialWindow`, `horizon`, `fixedWindow`, and `skip`).

Performance Metrics

To choose how to summarize a model, the `trainControl` function is used again.

```
trainControl(summaryFunction = <R function>,
             classProbs = <logical>)
```

Custom R functions can be used but `caret` includes several: `defaultSummary` (for accuracy, RMSE, etc), `twoClassSummary` (for ROC curves), and `prSummary` (for information retrieval). For the last two functions, the option `classProbs` must be set to TRUE.

Grid Search

To let `train` determine the values of the tuning parameter(s), the `tuneLength` option controls how many values **per tuning** parameter to evaluate.

Alternatively, specific values of the tuning parameters can be declared using the `tuneGrid` argument:

```
grid <- expand.grid(alpha = c(0.1, 0.5, 0.9),
                    lambda = c(0.001, 0.01))

train(x = x, y = y, method = "glmnet",
      preProc = c("center", "scale"),
      tuneGrid = grid)
```

Random Search

For tuning, `train` can also generate random tuning parameter combinations over a wide range. `tuneLength` controls the total number of combinations to evaluate. To use random search:

```
trainControl(search = "random")
```

Subsampling

With a large class imbalance, `train` can subsample the data to balance the classes them prior to model fitting.

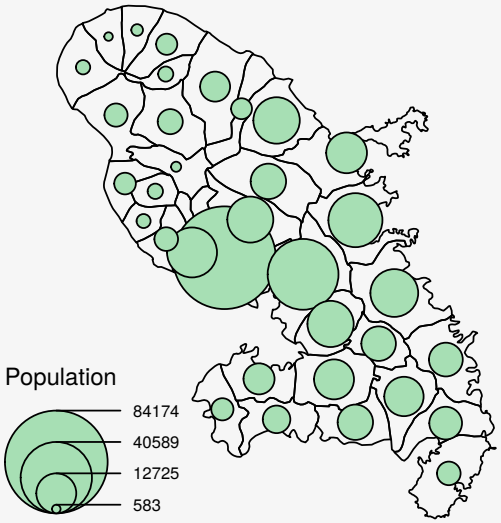
```
trainControl(sampling = "down")
```

Other values are `"up"`, `"smote"`, or `"rose"`. The latter two may require additional package installs.

Thematic maps with cartography : : **CHEAT SHEET**

Use cartography with spatial objects from sf or sp packages to create thematic maps.

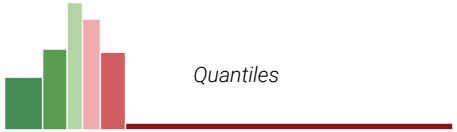
```
library(cartography)
library(sf)
mtq <- st_read("martinique.shp")
plot(st_geometry(mtq))
propSymbolsLayer(x = mtq, var = "P13_POP",
 legend.title.txt = "Population",
 col = "#a7dfb4")
```



Classification

Available methods are: quantile, equal, q6, fisher-jenks, mean-sd, sd, geometric progression...

```
bks1 <- getBreaks(v = var, nclass = 6,
 method = "quantile")
bks2 <- getBreaks(v = var, nclass = 6,
 method = "fisher-jenks")
pal <- carto.pal("green.pal",3, "wine.pal", 3)
hist(var, breaks = bks1, col = pal)
```




```
hist(var, breaks = bks2, col = pal)
```

Symbology

In most functions the x argument should be an sf object. sp objects are handled through spdf and df arguments.

Choropleth
```
choroLayer(x = mtq, var = "myvar",
 method = "quantile", nclass = 8)
```

Typology
```
typoLayer(x = mtq, var = "myvar")
```

Proportional Symbols
```
propSymbolsLayer(x = mtq, var = "myvar",
 inches = 0.1, symbols = "circle")
```

Colorized Proportional Symbols (relative data)
```
propSymbolsChoroLayer(x = mtq, var = "myvar",
 var2 = "myvar2")
```

Colorized Proportional Symbols (qualitative data)
```
propSymbolsTypoLayer(x = mtq, var = "myvar",
 var2 = "myvar2")
```

Double Proportional Symbols
```
propTrianglesLayer(x = mtq, var1 = "myvar",
 var2 = "myvar2")
```

OpenStreetMap Basemap (see rosm package)
```
tiles <- getTiles(x = mtq, type = "osm")
tilesLayer(tiles)
```

Isopleth (see SpatialPosition package)
```
smoothLayer(x = mtq, var = "myvar",
 typefct = "exponential", span = 500,
 beta = 2)
```

Discontinuities
```
discLayer(x = mtq.borders, df = mtq,
 var = "myvar", threshold = 0.5
```

Flows
```
propLinkLayer(x = mtq_link, df = mtq_df,
 var = "fij")
```

Dot Density
```
dotDensityLayer(x = mtq, var = "myvar")
```

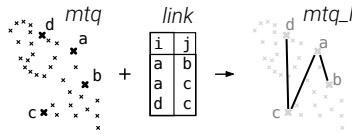
Labels
```
labelLayer(x = mtq, txt = "myvar",
 halo = TRUE, overlap = FALSE)
```

Transformations

Polygons to Grid
```
mtq_grid <- getGridLayer(x = mtq, cellsize = 3.6e+07,
  type = "hexagonal", var = "myvar")
```

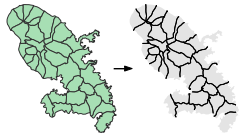
Grids layers can be used by choroLayer() or propSymbolsLayer().

Points to Links
```
mtq_link <- getLinkLayer(x = mtq, df = link)
```



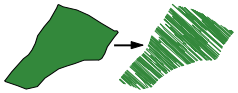
Links layers can be used by *LinkLayer().

Polygons to Borders
```
mtq_border <- getBorders(x = mtq)
```



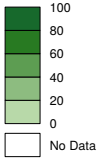
Borders layers can be used by discLayer() function

Polygons to Pencil Lines
```
mtq_pen <- getPencilLayer(x = mtq)
```



Legends

legendChoro()




```
legendChoro(pos = "topleft",
 title.txt = "legendChoro()",
 breaks = c(0,20,40,60,80,100),
 col = carto.pal("green.pal", 5),
 nodata = TRUE, nodata.txt = "No Data")
```

legendTypo()


```
legendTypo(title.txt = "legendTypo()",
 col = c("peru", "skyblue", "gray77"),
 categ = c("type 1", "type 2", "type 3"),
 nodata = FALSE)
```

legendCirclesSymbols()


```
legendCirclesSymbols(var = c(10,100),
 title.txt = "legendCirclesSymbols()",
 col = "#a7dfb4ff", inches = 0.3)
```

See also legendSquaresSymbols(), legendBarsSymbols(), legendGradLines(), legendPropLines() and legendPropTriangles().

Map Layout

North Arrow:
```
north(pos = "topright")
```

Scale Bar:
```
barscale(size = 5)
```

Full Layout:
```
layoutLayer(
 title = "Martinique",
 tabtitle = TRUE,
 frame = TRUE,
 author = "Author",
 sources = "Sources",
 north = TRUE,
 scale = 5)
```

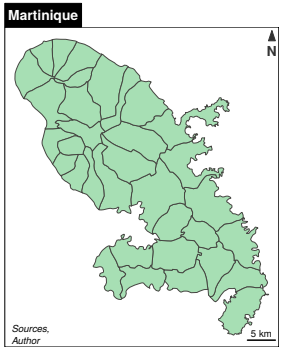
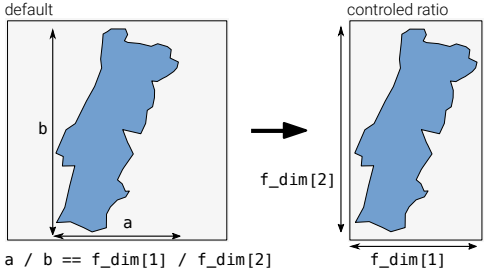


Figure Dimensions

Get figure dimensions based on the dimension ratio of a spatial object, figure margins and output resolution.

```
f_dim <- getFigDim(x = sf_obj, width = 500,
  mar = c(0,0,0,0))
png("fig.png", width = 500, height = f_dim[2])
par(mar = c(0,0,0,0))
plot(sf_obj, col = "#729fcf")
dev.off()
```



Color Palettes

```
carto.pal(pal1 = "blue.pal", n1 = 5,
 pal2 = sand.pal, n2 = 3)
```

```
display.carto.all(n = 8)
```

Data Transformation with data.table : : CHEAT SHEET

Basics

data.table is an extremely fast and memory efficient package for transforming data in R. It works by converting R's native data frame objects into data.tables with new and enhanced functionality. The basics of working with data.tables are:

dt[i, j, by]

Take data.table **dt**,
subset rows using **i**
and manipulate columns with **j**,
grouped according to **by**.

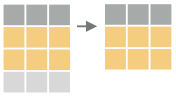
data.tables are also data frames – functions that work with data frames therefore also work with data.tables.

Create a data.table

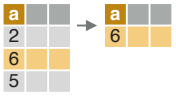
data.table(a = c(1, 2), b = c("a", "b")**)** – create a data.table from scratch. Analogous to data.frame().

setDT(df**)*** or **as.data.table(**df**)** – convert a data frame or a list to a data.table.

Subset rows using i



dt[**1:2**,] – subset rows based on row numbers.



dt[**a > 5**,] – subset rows based on values in one or more columns.

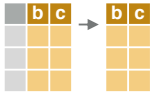
LOGICAL OPERATORS TO USE IN i

<	<=	is.na()	%in%	|	**%like%**
>	>=	!is.na()	!	&	**%between%**

Manipulate columns with j

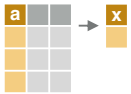
EXTRACT

dt[, **c(2)**] – extract columns by number. Prefix column numbers with "-" to drop.



dt[, **.(b, c)**] – extract columns by name.

SUMMARIZE

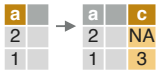


dt[, **.(x = sum(a))**] – create a data.table with new columns based on the summarized values of rows.

Summary functions like mean(), median(), min(), max(), etc. can be used to summarize rows.

COMPUTE COLUMNS*

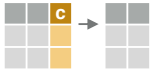
dt[, **c := 1 + 2**] – compute a column based on an expression.



dt[**a == 1**, **c := 1 + 2**] – compute a column based on an expression but only for a subset of rows.

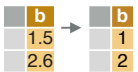
dt[, **`:=`(c = 1 , d = 2)**] – compute multiple columns based on separate expressions.

DELETE COLUMN



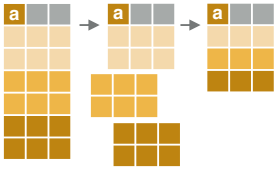
dt[, **c := NULL**] – delete a column.

CONVERT COLUMN TYPE



dt[, **b := as.integer(b)**] – convert the type of a column using as.integer(), as.numeric(), as.character(), as.Date(), etc..

Group according to by



dt[, j, **by = .(a)**] – group rows by values in specified columns.

dt[, j, **keyby = .(a)**] – group *and simultaneously sort* rows by values in specified columns.

COMMON GROUPED OPERATIONS

dt[, **.(c = sum(b))**, **by = a**] – summarize rows within groups.

dt[, **c := sum(b)**, **by = a**] – create a new column and compute rows within groups.

dt[, **.SD[1]**, **by = a**] – extract first row of groups.

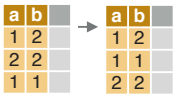
dt[, **.SD[.N]**, **by = a**] – extract last row of groups.

Chaining

dt[…**][**…**]** – perform a sequence of data.table operations by *chaining* multiple "[]".

Functions for data.tables

REORDER

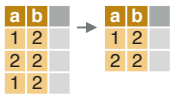


setorder(dt, a, **-**b**)** – reorder a data.table according to specified columns. Prefix column names with "**-**" for descending order.

* SET FUNCTIONS AND :=

data.table's functions prefixed with "set" and the operator ":=" work without "<-" to alter data without making copies in memory. E.g., the more efficient "setDT(df)" is analogous to "df <- as.data.table(df)".

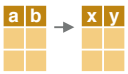
UNIQUE ROWS



unique(dt, by = c("a", "b")**)** – extract unique rows based on columns specified in "by". Leave out "by" to use all columns.

uniqueN(dt, by = c("a", "b")**)** – count the number of unique rows based on columns specified in "by".

RENAME COLUMNS



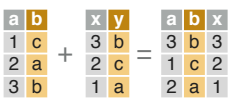
setnames(dt, c("a", "b"), c("x", "y")**)** – rename columns.

SET KEYS

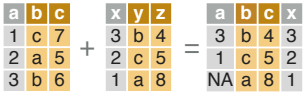
setkey(dt, a, b**)** – set keys to enable fast repeated lookup in specified columns using "dt[.(value),]" or for merging without specifying merging columns using "dt_a[dt_b]".

Combine data.tables

JOIN

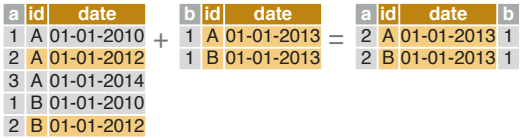


dt_a[dt_b, **on = .(b = y)**] – join data.tables on rows with equal values.



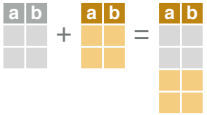
dt_a[dt_b, **on = .(b = y, c > z)**] – join data.tables on rows with equal *and unequal* values.

ROLLING JOIN

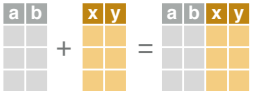


dt_a[dt_b, **on = .(id = id, date = date), roll = TRUE**] – join data.tables on matching rows in id columns but only keep the most recent preceding match with the left data.table according to date columns. "roll = -Inf" reverses direction.

BIND



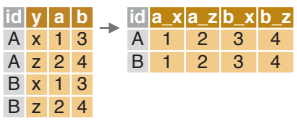
rbind(dt_a, dt_b**)** – combine rows of two data.tables.



cbind(dt_a, dt_b**)** – combine columns of two data.tables.

Reshape a data.table

RESHAPE TO WIDE FORMAT

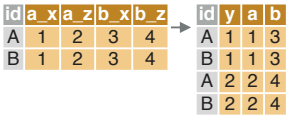


dcast(dt,
id ~ y,
value.var = c("a", "b")**)**

Reshape a data.table from long to wide format.

dt	A data.table.
id ~ y	Formula with a LHS: ID columns containing IDs for multiple entries. And a RHS: columns with values to spread in column headers.
value.var	Columns containing values to fill into cells.

RESHAPE TO LONG FORMAT



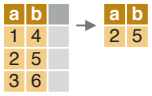
melt(dt,
id.vars = c("id"),
measure.vars = patterns("^a", "^b"),
variable.name = "y",
value.name = c("a", "b")**)**

Reshape a data.table from wide to long format.

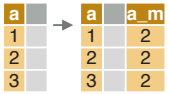
dt	A data.table.
id.vars	ID columns with IDs for multiple entries.
measure.vars	Columns containing values to fill into cells (often in pattern form).
variable.name, value.name	Names of new columns for variables and values derived from old headers.

Apply function to cols.

APPLY A FUNCTION TO MULTIPLE COLUMNS



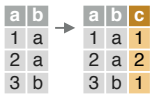
dt[, **lapply(.SD, mean)**, **.SDcols = c("a", "b")**] – apply a function – e.g. mean(), as.character(), which.max() – to columns specified in .SDcols with lapply() and the .SD symbol. Also works with groups.



cols <- c("a")
dt[, **paste0(cols, "_m") := lapply(.SD, mean)**, **.SDcols = cols**] – apply a function to specified columns and assign the result with suffixed variable names to the original data.

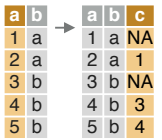
Sequential rows

ROW IDS



dt[, **c := 1:.N**, **by = b**] – within groups, compute a column with sequential row IDs.

LAG & LEAD



dt[, **c := shift(a, 1)**, **by = b**] – within groups, duplicate a column with rows *lagged* by specified amount.

dt[, **c := shift(a, 1, type = "lead")**, **by = b**] – within groups, duplicate a column with rows *leading* by specified amount.

read & write files

IMPORT

fread("file.csv"**)** – read data from a flat file such as .csv or .tsv into R.

fread("file.csv", select = c("a", "b")**)** – read specified columns from a flat file into R.

EXPORT

fwrite(dt, "file.csv"**)** – write data to a flat file from R.

DeclareDesign: : CHEAT SHEET

Model

What is your model of the world, including how outcomes respond to interventions in the world?

Population

Define the size of the population, hierarchical structure (if any), and background variables.

Simple dataset with no background variables

```
pop <- declare_population(N = 100)
pop()
```

Simple dataset with background variables

```
declare_population(N = 100,
                   X = rnorm(N))
```

Two-level dataset

```
declare_population(
  schools =
    add_level(N = 10,
              funding = rnorm(N)),
  students =
    add_level(N = 100,
              scores = rnorm(N))
)
```

Outcomes

Outcomes that depend on a treatment (Z)

Using a formula

```
declare_potential_outcomes(
  Y ~ .5 * Z + rnorm(N))
```

As separate variables

```
declare_potential_outcomes(
  Y_Z_0 = rnorm(N),
  Y_Z_1 = Y_Z_0 + .5)
```

Outcomes that do not depend on treatment

```
declare_potential_outcomes(
  Y = rnorm(N))
```

Inquiry

What is the research question you want to answer?

Causal inquiries

```
declare_estimand(
  ATE = mean(Y_Z_1 - Y_Z_0))
```

Descriptive inquiries

```
declare_estimand(
  Y_median = median(Y))
```

Conditional estimands

```
declare_estimand(
  LATE = mean(Y_Z_1 - Y_Z_0),
  subset = complier == TRUE)
```

Data Strategy

How will you generate data to answer your inquiry?

Sampling

```
declare_sampling(n = 100)

declare_sampling(
  strata_n = 20,
  strata = urban_area)
```

Treatment assignment

```
declare_assignment(m = 100)

declare_assignment(
  clusters = villages,
  m = 10)
```

Answer Strategy

How will you generate an answer to your inquiry?

OLS with robust standard errors

```
declare_estimator(
  Y ~ Z, model = lm_robust)
```

2SLS instrumental variables regression with robust SEs

```
declare_estimator(
  Y ~ D | Z, model = iv_robust)
```

Difference-in-means

```
declare_estimator(
  Y ~ Z,
  model = difference_in_means)
```

DeclareDesign is a software implementation of the MIDA framework, according to which research designs have a **M**odel of the world, an **I**nquiry about that model, a **D**ata strategy that generates information about the world, and an **A**nswer strategy that uses data to make a guess about the **I**nquiry. Declared designs can be "diagnosed" to calculate the properties of the design such as power and bias using Monte Carlo simulation.

All `declare_*` functions return *functions*. Most functions take a data.frame and return a data.frame.

Design Declaration

Put together all the steps into a declared design using the + operator

```
design <-
  declare_population(N = 200, X = rnorm(N)) +
  declare_potential_outcomes(Y ~ .5 * Z + X) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_sampling(n = 100) +
  declare_assignment(m = 50) +
  declare_estimator(Y ~ Z, model = lm_robust)
```

```
draw_data(design)
draw_estimates(design)
get_estimates(design, data = real_data)
draw_estimands(design)
run_design(design)
summary(design)
compare_designs(design_1, design_2)
```

Design Diagnosis

Diagnose the properties of your design

```
diagnosis <- diagnose_design(
  design, sims = 100, bootstrap_sims = 100)
```

```
summary(diagnosis)
get_diagnosands(diagnosis)
get_simulations(diagnosis)
```

Custom diagnosands

```
diagnose_design(
  design,
  diagnosands = declare_diagnosands(
    sig_pos = mean(p.value < .05 & estimate > 0)))
```

estimatr : : CHEAT SHEET

OLS with lm_robust()

`lm_robust()` is `lm()` with robust SEs. HC2 is the default.

```
lm_robust(mpg ~ hp, data = mtcars)
lm_robust(mpg ~ hp, se_type = "HC1",
          data = mtcars)
lm_robust(mpg ~ hp, se_type = "classical",
          data = mtcars)
```

Indicate `clusters` to get clustered SEs. CR2 is the default.

```
lm_robust(mpg ~ hp, clusters = carb,
          data = mtcars)
lm_robust(mpg ~ hp, clusters = carb,
          se_type = "stata", data = mtcars)
```

Fixed effects two ways:

```
# FEs as "dummies"
lm_robust(mpg ~ hp + as.factor(am),
          data = mtcars)

# "Absorbing" FEs (substantially faster)
lm_robust(mpg ~ hp,
          fixed_effects = ~ am,
          data = mtcars)
```

post-estimation commands:

```
fit <- lm_robust(mpg ~ hp, data = mtcars)
summary(fit)
print(fit)
tidy(fit)
vcov(fit)
confint(fit)
nobs(fit)
predict(fit, newdata = mtcars)
```

2SLS with iv_robust()

`iv_robust()` is `AER::ivreg()` with robust SEs.

```
iv_robust(mpg ~ hp | am, data = mtcars)
iv_robust(mpg ~ hp | am,
          clusters = carb, data = mtcars)
```

Two-group estimators

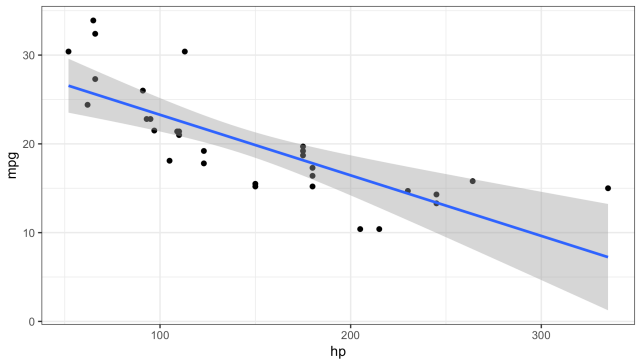
`difference_in_means()` and `horvitz_thompson()` compare two groups

```
difference_in_means(mpg ~ am, data = mtcars)
horvitz_thompson(mpg ~ am, data = mtcars)
```

ggplot2 integration

Use robust variance estimates for drawing confidence intervals:

```
library(ggplot2)
ggplot(mtcars, aes(mpg, hp)) +
  geom_point() +
  stat_smooth(method = "lm_robust") +
  theme_bw()
```



Multiple models

Same outcome, different subsets:

```
library(tidyverse)
mtcars %>%
  split(.$cyl) %>%
  map(~lm_robust(mpg ~ hp, data = .)) %>%
  map(tidy) %>%
  bind_rows(.id = "cyl")
```

Different outcomes, same subset:

```
c("mpg", "disp") %>%
  map(~formula(paste0(., " ~ hp"))) %>%
  map(~lm_robust(., data = mtcars)) %>%
  map(tidy) %>%
  bind_rows
```

Extras

```
# Lin (2013) covariate adjustment
lm_lin(mpg ~ am, covariates = ~ hp,
       data = mtcars)

# regression tables with texreg
fit <- lm_robust(mpg ~ hp, data = mtcars)
texreg::texreg(fit, include.ci = FALSE)
```

estimatr-to-Stata dictionary

estimatr	Stata
`lm_robust(y ~ z, data = dat)`	`reg y z, vce(hc2)`
`lm_robust(y ~ z, clusters = cl, se_type = "stata", data = dat)`	`reg y z, vce(cluster cl)`
`lm_robust(mpg ~ hp, fixed_effects = ~ am, se_type = "stata", data = mtcars)`	`areg mpg hp, absorb(am) vce(robust)`
`iv_robust(mpg ~ hp | am, se_type = "HC1", data = mtcars)`	`ivregress 2sls mpg (hp = am), vce(robust) small`

estimatr is part of the DeclareDesign suite of packages for designing, implementing, and analyzing social science research designs.

The *eurostat* package

R tools to access open data from Eurostat database

Search and download

Data in the Eurostat database is stored in tables. Each table has an identifier, a short table_code, and a description (e.g. *tsdtr420* - People killed in road accidents).
Key eurostat functions allow to find the table_code, download the eurostat table and polish labels in the table.

Find the table code

The **search_eurostat(pattern, ...)** function scans the directory of Eurostat tables and returns codes and descriptions of tables that match pattern.

```
library("eurostat")
query <- search_eurostat("road", type = "table")
query[1:3,1:2]
##                                 title     code
## 1          Goods transport by road ttr00005
## 2   People killed in road accidents tsdtr420
## 3 Enterprises with broadband access tin00090
```

Download the table

The **get_eurostat(id, time_format = "date", filters = "none", type = "code", cache = TRUE, ...)** function downloads the requested table from the *Eurostat bulk download facility* or from *The Eurostat Web Services JSON API* (if **filters** are defined). Downloaded data is cached (if **cache=TRUE**). Additional arguments define how to read the time column (**time_format**) and if table dimensions shall be kept as codes or converted to labels (**type**).

```
dat <- get_eurostat(id="tsdtr420", time_format="num")
head(dat)
##     unit    sex    geo  time values
## 1     NR      T     AT  1999   1079
## 2     NR      T     BE  1999   1397
## 3     NR      T     CZ  1999   1455
## 4     NR      T     DK  1999    514
## 5     NR      T     EL  1999   2116
## 6     NR      T     ES  1999   5738
```

Add labels

The **label_eurostat(x, lang = "en", ...)** gets definitions for Eurostat codes and replace them with labels in given language ("en", "fr" or "de").

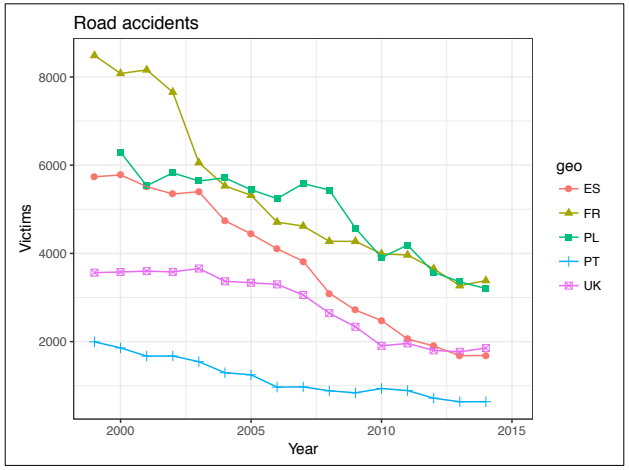
```
dat <- label_eurostat(dat)
head(dat)
##     unit    sex            geo  time values
## 1 Number  Total        Austria  1999   1079
## 2 Number  Total        Belgium  1999   1397
## 3 Number  Total Czech Republic  1999   1455
## 4 Number  Total        Denmark  1999    514
## 5 Number  Total         Greece  1999   2116
## 6 Number  Total          Spain  1999   5738
```

eurostat and plots

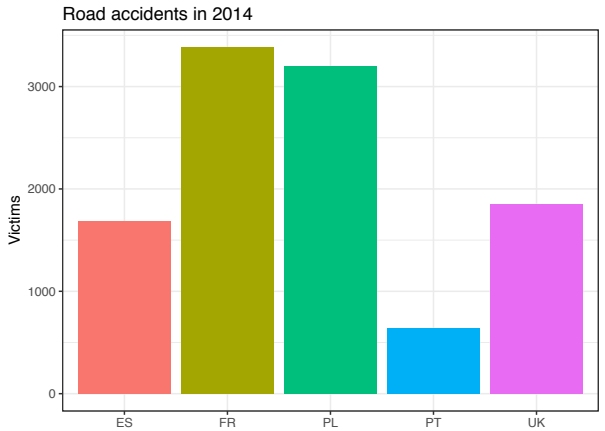
The **get_eurostat()** function returns tibbles in the long format. Packages **dplyr** and **tidyr** are well suited to transform these objects. The **ggplot2** package is well suited to plot these objects.

```
t1 <- get_eurostat("tsdtr420", filters =
            list(geo = c("UK", "FR", "PL", "ES", "PT")))

library("ggplot2")
ggplot(t1, aes(x = time, y = values, color = geo,
               group = geo, shape = geo)) +
  geom_point(size = 2) +
  geom_line() + theme_bw() +
  labs(title="Road accidents", x = "Year", y = "Victims")
```




```
library("dplyr")
t2 <- t1 %>% filter(time == "2014-01-01")
ggplot(t2, aes(geo, values, fill=geo)) +
  geom_bar(stat = "identity") + theme_bw() +
  theme(legend.position = "none")+
  labs(title="Road accidents in 2014", x="", y="Victims")
```



eurostat and maps

Fetch and process data

There are three function to work with geospatial data from GISCO. The **get_eurostat_geospatial()** returns preprocessed spatial data as sp-objects or as data frames. The **merge_eurostat_geospatial()** both downloads and merges the geospatial data with a preloaded tabular data. The **cut_to_classes()** is a wrapper for **cut()** - function and is used for categorizing data for maps with tidy labels.

```
library("eurostat")
library("dplyr")

fertility <- get_eurostat("demo_r_frate3")  %>%
  filter(time == "2014-01-01") %>%
  mutate(cat = cut_to_classes(values, n=7, decimals=1))

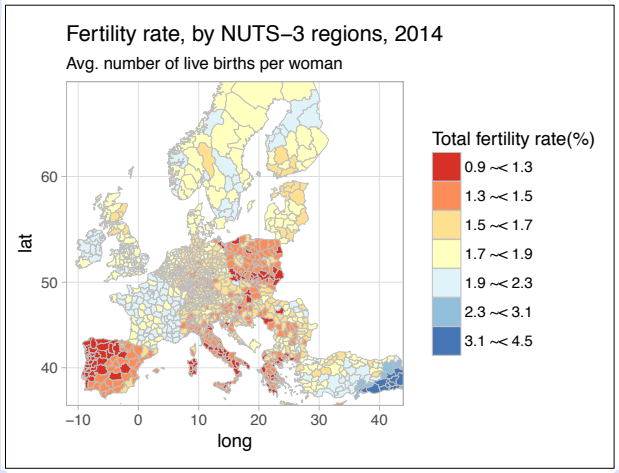
mapdata <-  merge_eurostat_geodata(fertility,
              resolution = "20")

head(select(mapdata,geo,values,cat,long,lat,order,id))
##     geo values         cat     long      lat order id
## 1 AT124   1.39 1.3 ~< 1.5 15.54245 48.90770   214 10
## 2 AT124   1.39 1.3 ~< 1.5 15.75363 48.85218   215 10
## 3 AT124   1.39 1.3 ~< 1.5 15.88763 48.78511   216 10
## 4 AT124   1.39 1.3 ~< 1.5 15.81535 48.69270   217 10
## 5 AT124   1.39 1.3 ~< 1.5 15.94094 48.67173   218 10
## 6 AT124   1.39 1.3 ~< 1.5 15.90833 48.59815   219 10
```

Draw a cartogram

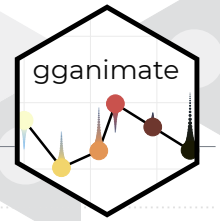
The object returned by **merge_eurostat_geospatial()** are ready to be plotted with ggplot2 package. The **coord_map()** function is useful to set the projection while **labs()** adds annotations o the plot.

```
library("ggplot2")
ggplot(mapdata, aes(x = long, y = lat, group = group))+
  geom_polygon(aes(fill=cat), color="grey", size = .1)+
  scale_fill_brewer(palette = "RdYlBu") +
  labs(title="Fertility rate, by NUTS-3 regions, 2014",
       subtitle="Avg. number of live births per woman",
       fill="Total fertility rate(%)") + theme_light()+
  coord_map(xlim=c(-12,44), ylim=c(35,67))
```



This onepager presents the **eurostat** package
Leo Lahti, Janne Huovari, Markus Kainu, Przemyslaw Biecek 2014-2017 package version 2.2.43 URL: *https://github.com/rOpenGov/eurostat*

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)
```

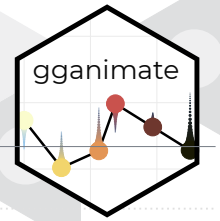
... and we're cycling between **seven** views. Seven is the number of steps in the transition, so the view is changing when the points are static, and visa versa. Views are determined by what data is in the current frame.

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

GWAS Catalog access with gwasrapidd

Introduction

The **GWAS Catalog** is a service provided by the EMBL-EBI and NHGRI that offers a manually curated and freely available database of published genome-wide association studies (GWAS).

The GWAS Catalog data provided by the **RESTful API** is organized around four core entities:

- **studies**
- **associations**
- **variants**
- **traits**

Get GWAS Catalog Entities

gwasrapidd facilitates the access to the Catalog via the RESTful API, allowing you to programmatically retrieve data directly into R. Each of the four entities is mapped to an S4 object of a class of the same name.

Search by	Example	S	A	V	T
study_id	"GCST000858"	●	●	●	●
association_id	"24300113"	●	●	●	●
variant_id	"rs12752552"	●	●	●	
efo_id	"EFO_0005543"	●	●	●	●
pubmed_id	"21626137"	●	●	●	●
user_requested	TRUE	●			
full_pvalue_set	FALSE	●			
efo_uri	"http://www.ebi.ac.uk/efo/EFO_0004761"	●			●
genomic_range	list(chromosome = "22", start = 1L, end = 15473564L)			●	
gene_name	"BRCA1"			●	
efo_trait	"lung adenocarcinoma"	●	●	●	●
reported_trait	"Breast cancer"	●		●	
cytogenetic_band	"1p36.33"			●	

S4 Representation of GWAS Catalog Entities

S4 class studies

The **studies** object consists of eight slots, each a table (tibble). Each study is an observation (row) in the studies table — main table. All tables have the column study_id as primary key.

For details about the studies S4 class: `class?studies`.

studies
- study_id
- reported_trait
- initial_sample_size
- replication_sample_size
- gxe
- gxg
- snp_count
- qualifier
- imputed
- pooled
- study_design_comment
- full_pvalue_set
- user_requested

genotyping_techs
- study_id
- genotyping technology

platforms
- study_id
- manufacturer

ancestries
- study_id
- ancestry_id
- type
- number_of_individuals

ancestral_groups
- study_id
- ancestry_id
- ancestral_group

countries_of_recruitment
- study_id
- ancestry_id
- country_name
- major_area
- region

countries_of_origin
- study_id
- ancestry_id
- country_name
- major_area
- region

publications
- study_id
- pubmed_id
- publication_date
- publication
- title
- author_fullname
- author_orcid

S4 class associations

The **associations** object consists of six slots, each a table (tibble). Each association is an observation (row) in the associations table — main table. All tables have the column association_id as primary key.

For details about the associations S4 class: `class?associations`.

associations
- association_id
- pvalue
- pvalue_description
- pvalue_mantissa
- pvalue_exponent
- multiple_snp_haplotype
- snp_interaction
- snp_type
- standard_error
- range
- or_per_copy_number
- beta_number
- beta_unit
- beta_direction
- beta_description
- last_mapping_date
- last_update_date

loci
- association_id
- locus_id
- haplotype_snp_count
- description

risk_alleles
- association_id
- locus_id
- variant_id
- risk_allele
- risk_frequency
- genome_wide
- limited_list

genes
- association_id
- locus_id
- gene_name

ensembl_ids
- association_id
- locus_id
- gene_name
- ensembl_id

entrez_ids
- association_id
- locus_id
- gene_name
- entrez_id

S4 class variants

The **variants** object consists of four slots, each a table (tibble). Each variant is an observation (row) in the variants table — main table. All tables have the column variant_id as primary key.

For details about the variants S4 class: `class?variants`.

variants
- variant_id
- merged
- functional_class
- chromosome_name
- chromosome_position
- chromosome_region
- last_update_date

genomic_contexts
- variant_id
- gene_name
- chromosome_name
- chromosome_position
- distance
- is_closest_gene
- is_intergenic
- is_upstream
- is_downstream
- source
- mapping_method

ensembl_ids
- variant_id
- gene_name
- ensembl_id

entrez_ids
- variant_id
- gene_name
- entrez_id

S4 class traits

The **traits** object consists of one slot only, a table (tibble) of GWAS Catalog EFO traits. Each EFO trait is an observation (row) in the traits table — main table.

For details about the traits S4 class: `class?traits`.

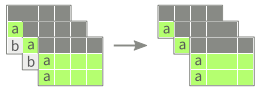
traits
- efo_id
- trait
- uri

Manipulate Cases

Get a **studies** object **s** of two GWAS studies:

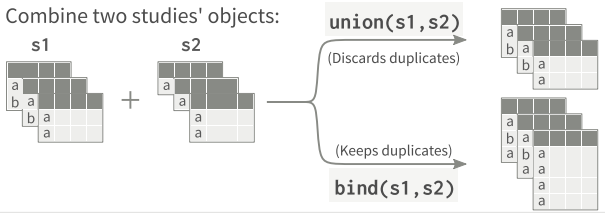
```
s <- get_studies(study_id = c('a', 'b'))
```

Subset object **s** by either identifier or position using `[`:



```
s['a'] # Subset by identifier
s[1] # Subset by position
```

Combine two studies' objects:



h2o: : CHEAT SHEET

Dataset Operations

DATA IMPORT / EXPORT

h2o.uploadFile: Upload a file into H2O from a client-side path, and parse it.

h2o.downloadCSV: Download a H2O dataset to a client-side CSV file.

h2o.importFile: Import a file into H2O from a server-side path, and parse it.

h2o.exportFile: Export an H2O Data Frame to a server-side file.

h2o.parseRaw: Parse a raw data file.

NATIVE R TO H2O COERCION

as.h2o: Convert a R object to an H2O object

H2O TO NATIVE R COERCION

as.data.frame: Check if an object is a data frame, and coerce it if possible.

DATA GENERATION

h2o.createFrame: Creates a data frame in H2O with real-valued, categorical, integer, and binary columns specified by the user, with optional randomization.

h2o.runif: Produce a vector of random uniform numbers.

h2o.interaction: Create interaction terms between categorical features of an H2O Frame.

h2o.target_encode_apply: Target encoding map to an H2O Data Frame, which can improve performance of supervised learning models for high cardinality categorical columns.

DATA SAMPLING / SPLITTING

h2o.splitFrame: Split an existing H2O dataset according to user-specified ratios.

MISSING DATA HANDLING

h2o.impute: Impute a column of data using the mean, median, or mode.

h2o.insertMissingValues: Replaces a user-specified fraction of entries in an H2O dataset with missing values.

h2o.na_omit: Remove Rows With NAs.

General Operations

SUBSCRIPTING

Subscripting example to pull (/push) pieces from (/to) a H2O Parsed Data object.

Selection	Value Assignation
x[j] ## column J	x[i] <- value
x[i, j]	x[i, j, ...] <- value
x[[i]]	x[[i]] <- value
x$name	x$i <- value

SUBSETTING

h2o.head, h2o.tail: Object's Start or End.

DATA ATTRIBUTES

h2o.names: Return column names for an H2O Frame. Also: **h2o.colnames**

names<-: Set the row or column names of a H2O Frame. Also: **colnames<-**

h2o.dim: Retrieve object dimensions.

h2o.length: Length of vector, list or factor.

h2o.nrow: Number of H2O Frame rows.

h2o.ncol: Number of H2O Frame columns.

h2o.anyFactor: Check if an H2O Frame object has any categorical data columns.

is.factor, is.character, is.numeric: Check Column's Data Type.

DATA TYPE COERCION: Convert to:

h2o.asfactor, as.factor: Factor.

h2o.as_date, as.Date: Date.

h2o.ascharacter, as.character: Character.

h2o.asnumeric, as.numeric: Numeric.

BASIC DATA MANIPULATION

c: Combine Values into a Vector or List.

h2o.cbind; h2o.rbind: Combine a sequence of H2O datasets by column (cbind) or rows (rbind).

h2o.merge: Merges 2 H2OFrames.

h2o.arrange: Sorts an H2OFrame by columns.

ELEMENT INDEX SELECTION

h2o.which: True Condition's Row Numbers

CONDITIONAL VALUE SELECTION

h2o.ifelse: Apply conditional statements to numeric vectors in an H2O Frame.

Math Operations

(math) vectorized function

MATH

h2o.abs: Compute the absolute value of x.

h2o.sqrt: Principal Square Root of x, √x.

h2o.ceiling: Take a single numeric argument x and return a numeric vector containing the smallest integers not less than the corresponding elements of x.

h2o.floor: Take a single numeric argument x and return a numeric vector containing the largest integers not greater than the corresponding elements of x.

h2o.trunc: Take a single numeric argument x and return a numeric vector containing the integers formed by truncating the values in x toward 0.

h2o.log: Compute natural logarithms. See also: **h2o.log10, h2o.log2, h2o.log1p**

h2o.exp: Compute the exponential function

h2o.cos, h2o.cosh, h2o.acos, h2o.sin, h2o.tan, h2o.tanh, Math: ?groupGeneric

sign: Return a vector with the signs of the corresponding elements of x (the sign of a real number is 1, 0, or -1 if the number is positive, zero, or negative, respectively).

&& (Vectorized AND), **||** (Vectorized OR), **!x, %in%,** Ops: **+, -, *, /, ^, %%, %/%, ==, !=, <, <=, >=, >, &, |, !**

CUMULATIVE

h2o.cummax: Vector of the cumulative maxima of the elements of the argument.

h2o.cummin: Vector of the cumulative minima of the elements of the argument.

h2o.cumprod: Vector of the cumulative products of the elements of the argument.

h2o.cumsum: Vector of the cumulative sums of the elements of the argument.

PRECISION

h2o.round: Round values to the specified number of decimal places. The default is 0.

h2o.signif: Round values to the specified number of significant digits.

Group By Summaries

(group by) summary function

nrow: Count the number of rows.

max: All input argument's Maximum.

min: All input argument's Minimum.

sum: All argument values Sum.

mean: (Trimmed) arithmetic mean.

sd: Calculate the standard deviation of a column of continuous real valued data.

var: Compute the variance of x.

Generic Summaries

NON-GROUP_BY SUMMARIES

h2o.median: Calculate the median of x.

h2o.range: Input argument's Min/Max Vector

h2o.cor: Correlation Matrix of H2O Frames.

h2o.quantile: Obtain and display quantiles for an H2O Frame Column.

h2o.hist: Compute a histogram over a numeric H2O Frame Column.

h2o.prod: Product of all arguments values.

h2o.any: Given a set of logical vectors, determine if at least one of the values is true.

h2o.all: Given a set of logical vectors, determine if all of the values are true.

NON-GROUP_BY SUMMARIES: GENERIC

h2o.summary: Produce result summaries of the results of various model fitting functions.

Aggregations

ROW / COLUMN AGGREGATION

By Rows or By Cols

apply: Apply a function over an H2O parsed data object (an array) margins.

GROUP BY AGGREGATION

h2o.group_by: Apply an aggregate function to each group of an H2O dataset.

TABULATION

h2o.table: Use the cross-classifying factors to build a table of counts at each combination of factor levels.

h2o: : CHEAT SHEET

Data Modeling

MODEL TRAINING: SUPERVISED LEARNING

h2o.deeplearning: Perform Deep Learning Neural Networks on an H2OFrame.

h2o.gbm: Build Gradient Boosted Regression Trees or Classification Trees.

h2o.glm: Fit a Generalized Linear Model, specified by a response variable, a set of predictors, and the error distribution.

h2o.naiveBayes: Compute Naive Bayes classification probabilities on an H2O Frame.

h2o.randomForest: Perform Random Forest Classification on an H2O Frame.

h2o.xgboost: Build an Extreme Gradient Boosted Model using the XGBoost backend.

h2o.stackedEnsemble: Build a stacked ensemble (aka. Super Learner) using the specified H2O base learning algorithms.

h2o.automl: Automates the Supervised Machine Learning Model Training Process: Automatically Trains and Cross-validates a set of Models, and trains a Stacked Ensemble.

MODEL TRAINING: UNSUPERVISED LEARNING

h2o.prcomp: Perform Principal Components Analysis on the given H2O Frame.

h2o.kmeans: Perform k-means Clustering on the given H2O Frame.

h2o.anomaly: Detect anomalies in a H2O Frame using a H2O Deep Learning Model with Auto-Encoding.

h2o.deepfeatures: Extract the non-linear features from a H2O Frame using a H2O Deep Learning Model.

h2o.glrm: Builds a Generalized Low Rank Decomposition of an H2O Frame.

h2o.svd: Singular value decomposition of an H2O Frame using the power method.

h2o.word2vec: Trains a word2vec model on a String column of an H2O data frame.

SURVIVAL MODELS: TIME-TO-EVENT

h2o.coxph: Trains a Cox Proportional Hazards Model (CoxPH) on an H2O Frame.

GRID SEARCH

h2o.grid: Efficient method to build multiple models with different hyperparameters.

h2o.getGrid: Get a grid object from H2O distributed K/V store.

MODEL SCORING

h2o.predict: Obtain predictions from various fitted H2O model objects.

h2o.scoreHistory: Get Model Score History.

MODEL METRICS

h2o.make_metrics: Given predicted values (target for regression, class-1 probabilities, or binomial or per-class probabilities for multinomial), compute a model metrics object.

GENERAL MODEL HELPER

h2o.performance: Evaluate the predictive performance of a Supervised Learning Regression or Classification Model via various metrics. Set **xval = TRUE** for retrieving the training cross-validation metrics.

REGRESSION MODEL HELPER

h2o.mse: Display the mean squared error calculated from "Predicted Responses" and "Actual (Reference) Responses". Set **xval = TRUE** for retrieving the cross-validation MSE.

CLASSIFICATION MODEL HELPERS

h2o.accuracy: Get Model Accuracy metric.

h2o.auc: Retrieve the AUC (area under ROC curve). Set **xval = TRUE** for retrieving the cross-validation AUC.

h2o.confusionMatrix: Display prediction errors for classification data ("Predicted" vs "Reference : Real Values").

h2o.hit_ratio_table: Retrieve the Hit Ratios. Set **xval = TRUE** for retrieving the cross-validation Hit Ratio.

CLUSTERING MODEL HELPER

h2o.betweenss: Get the between cluster Sum of Squares.

h2o.centers: Retrieve the Model Centers.

PREDICTOR VARIABLE IMPORTANCE

h2o.varimp: Retrieve the variable importance

h2o.varimp_plot: Plot Variable Importances.

Data Munging

GENERAL COLUMN MANIPULATION

is.na: Display missing elements.

FACTOR LEVEL MANIPULATIONS

h2o.levels: Display a list of the unique values found in a categorical data column.

h2o.relevel: Reorders levels of an H2O factor, similarly to standard R's relevel.

h2o.setLevels: Set Levels of H2O Factor.

NUMERIC COLUMN MANIPULATIONS

h2o.cut: Convert H2O Numeric Data to Factor by breaking it into Intervals.

CHARACTER COLUMN MANIPULATIONS

h2o.strsplit: "String Split": Splits the given factor column on the input split.

h2o.tolower: Convert the characters of a character vector to lower case.

h2o.toupper: Convert the characters of a character vector to upper case.

h2o.trim: "Trim spaces": Remove leading and trailing white space.

h2o.gsub: Match a pattern & replace ***all*** instances (occurrences) of the matched pattern with the replacement string globally.

h2o.sub: Match a pattern & replace the ***first*** instance (occurrence) of the matched pattern with the replacement string.

DATE MANIPULATIONS

h2o.month: Convert Milliseconds to Months in H2O Datasets (Scale: 0 to 11).

h2o.year: Convert Milliseconds to Years in H2O Datasets, indexed starting from 1900.

h2o.day: Convert Milliseconds to Day of Month in H2O Datasets (Scale: 1 to 31).

h2o.hour: Convert Milliseconds to Hour of Day in H2O Datasets (Scale: 0 to 23).

h2o.dayOfWeek: Convert Milliseconds to Day of Week in a H2OFrame (Scale: 0 to 6)

MATRIX OPERATIONS

%*%: Multiply two conformable matrices.

t: Returns the transpose of an H2OFrame.

Cluster Operations

H2O KEY VALUE STORE ACCESS

h2o.assign: Assign H2O hex.keys to R objects.

h2o.getFrame: Get H2O dataset Reference.

h2o.getModel: Get H2O model reference.

h2o.ls: Display a list of object keys in the running instance of H2O.

h2o.rm: Remove specified H2O Objects from the H2O server, but not from the R environment.

h2o.removeAll: Remove All H2O Objects from the H2O server, but not from the R environment.

H2O MODEL IMPORT / EXPORT

h2o.loadModel: Load H2OModel from disk.

h2o.saveModel: Save H2OModel object to disk.

h2o.download_pojo: Download the Scoring POJO (Plain Old Java Object) of an H2O Model.

h2o.download_mojo: Download the model in MOJO format.

H2O CLUSTER CONNECTION

h2o.init: Connect to a running H2O instance using all CPUs on the host.

h2o.shutdown: Shut down the specified H2O instance. All data on the server will be lost!

H2O CLUSTER INFORMATION

h2o.clusterInfo: Display the name, version, uptime, total nodes, total memory, total cores and health of a cluster running H2O.

h2o.clusterStatus: Retrieve information on the status of the cluster running H2O.

H2O LOGGING

h2o.clearLog: Clear all H2O R command and error response logs from the local disk.

h2o.downloadAllLogs: Download all H2O log files to the local disk.

h2o.logAndEcho: Write a message to the H2O Java log file and echo it back.

h2o.openLog: Open existing logs of H2O R POST commands and error responses on disk.

h2o.getLogPath: Get the file path for the H2O R command and error response logs.

h2o.startLogging: Begin logging H2O R POST commands and error responses.

h2o.stopLogging: Stop logging H2O R POST commands and error responses.

How Big is Your Graph?

An R Cheat Sheet

Introduction

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

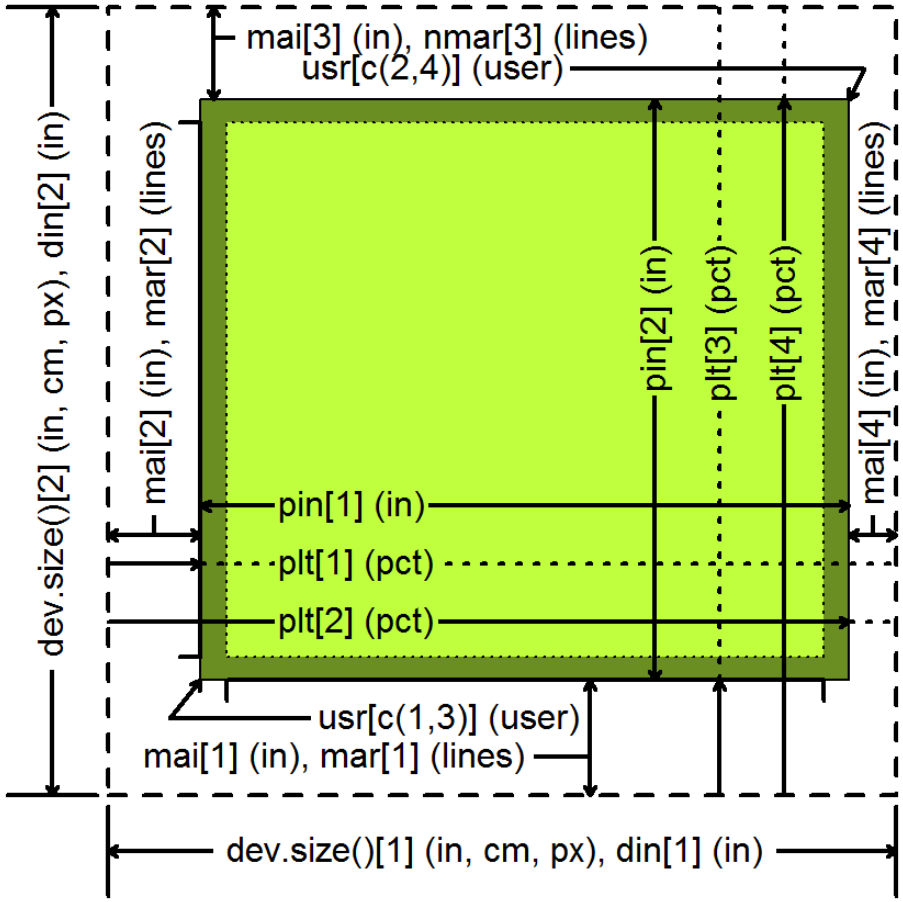
Your graphics device

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

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

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

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



Your plot margins

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

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

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

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

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

Your plotting region

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

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

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

Your x-y coordinates

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

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

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

Getting a square graph

par("pty")

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

Converting units

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

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

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

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

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

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

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

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

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

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

Panels

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

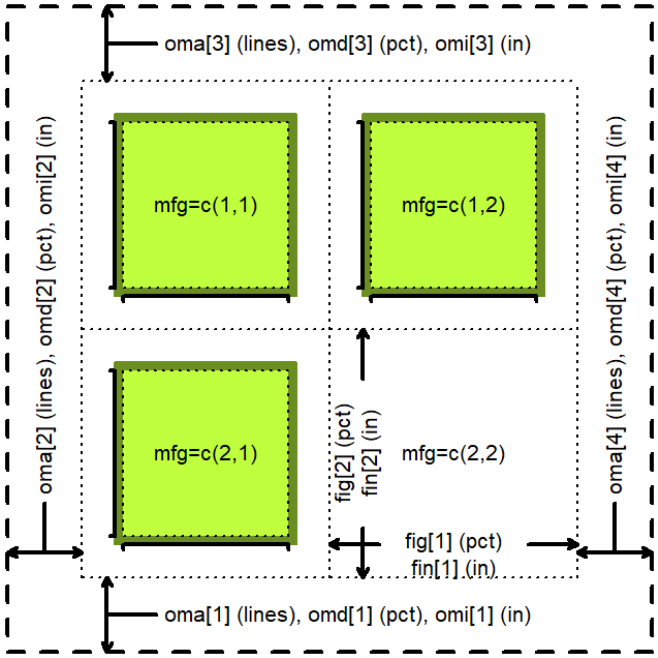
If you display multiple plots within a single graphics window (e.g., with the **mfrow** or **mfcol** arguments of **par** or with the **layout** function), then the **fig** and **fin** arguments will tell you the size of the current subplot window in percent or inches, respectively.

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

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

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

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



Character and string sizes

strheight()

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

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

strwidth()

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

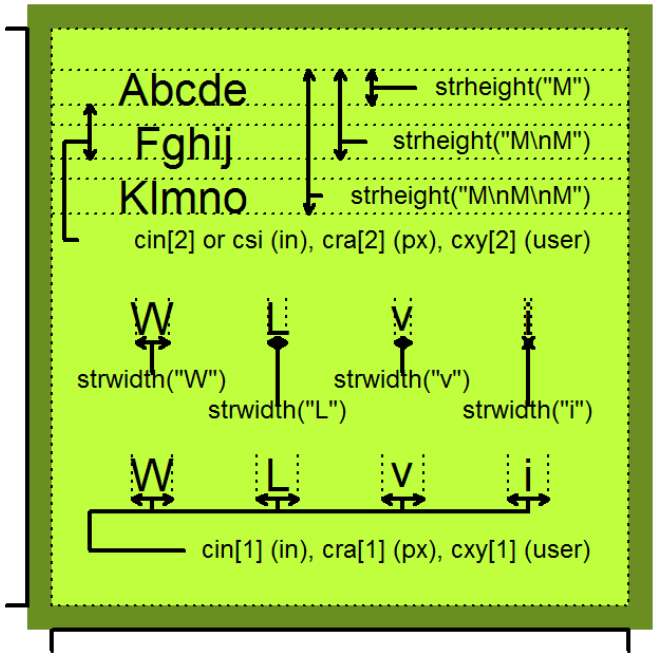
par("cin") *(r.o.)* (width, height) in inches
par("csi") *(r.o.)* height in inches
par("cra") *(r.o.)* (width, height) in pixels
par("cxy") *(r.o.)* (width, height) in xy coordinates

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

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

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

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



If your fonts are too big or too small

Fixing this takes a bit of trial and error.

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

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

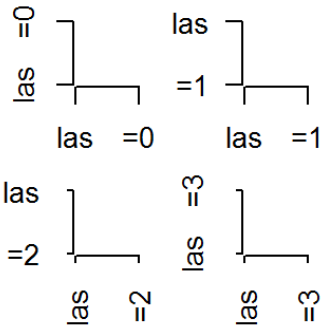
3. Use the **cex** argument to increase or decrease the relative size of your fonts.

If your axes don't fit

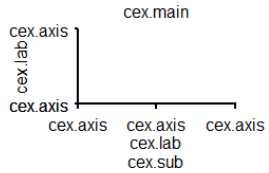
There are several possible solutions.

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

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



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



Leaflet Cheat Sheet

Leaflet for R

an open-source JavaScript library for mobile-friendly interactive maps

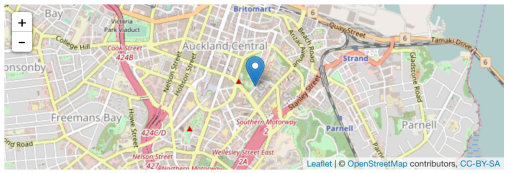
Quick Start

Installation

Use **install.packages("leaflet")** to installize the package or directly from Github *devtools::install_github("rstudio/leaflet")*.

First Map

```
m <- leaflet() %>%      # leaflet works with the pipe operator
  addTiles() %>%        # setup the default OpenStreetMap map tiles
  addMarkers(lng = 174.768, lat = -36.852, popup = "The birthplace of R")
                        # add a single point layer
m
```



Map Widget

Initialization

m <- leaflet(options = leafletOptions(...))

center	Initial geographic center of the map
zoom	Initial map zoom level
minZoom	Minimum zoom level of the map
maxZoom	Maximum zoom level of the map

Map Methods

m %>% setView(lng, lat, zoom, options = list())
Set the view of the map (center and zoom level)

m %>% fitBounds(lng1, lat1, lng2, lat2)
Fit the view into the rectangle [lng1, lat1] - [lng2, lat2]

m %>% clearBounds()
Clear the bound, automatically determine from the map elements

Data Object

Both **leaflet()** and the **map** layers have an optional data parameter that is designed to receive spatial data with the following formats:

Base R — *The arguments of all layers take normal R objects:*

```
df <- data.frame(lat = ..., lng = ... )
leaflet(df) %>% addTiles() %>% addCircles()
```

sp *package* — library(sp) *Useful functions:*

```
SpatialPoints, SpatialLines, SpatialPolygons, ...
```

maps *package* — library(maps) *Build a map of states with colors:*

```
mapStates <- map("state", fill = TRUE, plot = FALSE)
leaflet(mapStates) %>% addTiles() %>%
  addPolygons(fillColor = topo.colors(10, alpha = NULL), stroke = FALSE)
```

Markers

Use markers to call out points, express locations with latitude/longitude coordinates, appear as icons or as circles.
Data come from vectors or assigned data frame, or **sp** package objects.

Icon Markers

Regular Icons: default and simple

addMarkers(lng, lat, popup, label) *add basic icon markers*

makeIcon/icons (iconUrl, iconWidth, iconHeight, iconAnchorX, iconAnchorY, shadowUrl, shadowWidth, shadowHeight, ...) *customize marker icons*

iconList() *create a list of icons*

Awesome Icons: customizable with colors and icons

addAwesomeMarkers, makeAwesomeIcon, awesomeIcons, awesomeIconList

Marker Clusters: option of addMarters()

clusterOptions = markerClusterOptions()
freezeAtZoom Freeze the cluster at assigned zoom level

Circle Markers

addCircleMarkers(color, radius, stroke, opacity, ...)
Customize their color, radius, stroke, opacity

Popups and Labels

addPopups(lng, lat, ...content..., options) *Add standalone popups*
options = popupOptions(closeButton=FALSE)

addMarkers(..., popup, ...) *Show popups with markers or shapes*

addMarkers(..., label, labelOptions...) *Show labels with markers or shapes*
labelOptions = labelOptions(noHide, textOnly, textsize, direction, style)

addLabelOnlyMarkers() *Add labels without markers*

Lines and Shapes

Polygons and Polylines

addPolygons(color, weight=1, smoothFactor=0.5, opacity=1.0, fillOpacity=0.5, fillColor= ~colorQuantile("YlOrRd", ALAND)(ALAND), highlightOptions, ...)

highlightOptions(color, weight=2, bringToFront=TRUE) *highlight shapes*

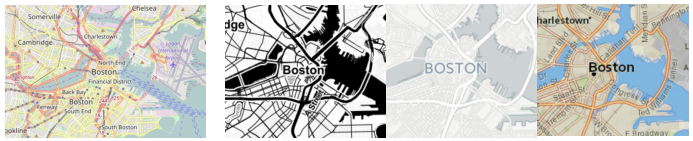
Use **rmapshaper::ms_simplify** to simplify complex shapes

Circles **addCircles**(lng, lat, weight=1, radius, ...)

Rectangles **addRectangles**(lng1, lat1, lng2, lat2, fillColor="transparent", ...)

Basemaps

addTiles() providers$Stamen.Toner, CartoDB.Positron, Esri.NatGeoWorldMap



Default Tiles — Third-Party Tiles **addProviderTiles()**

Use **addTiles()** to add a custom map tile URL template, use **addWMSTiles()** to add WMS (Web Map Service) tiles

GeoJSON and TopoJSON

There are two options to use the GeoJSON/TopoJSON data.

* To read into **sp** objects with the **geojsonio** or **rgdal** package:
geojsonio::geojson_read(...,what="sp") *rgdal::readOGR(...,"OGRGeoJSON")*
* Or to use the **addGeoJSON()** and **addTopoJSON()** functions:
addTopoJSON/addGeoJSON(... weight, color, fill, opacity, fillOpacity...)
Styles can also be tuned separately with a *style: {...}* object.

Other packages including **RJSONIO** and **jsonlite** can help fast parse or generate the data needed.

Shiny Integration

To integrate a Leaflet map into an app:
* In the UI, call **leafletOutput**("name")
* On the server side, assign a **renderLeaflet**(...) call to the output
* Inside the **renderLeaflet** expression, return a Leaflet map object

Modification

To modify an existing map or add incremental changes to the map, you can use **leafletProxy()**. This should be performed in an observer on the server side.

Other useful functions to edit your map:

fitBounds(0, 0, 11, 11) *similar to setView*
fit the view to within these bounds

addCircles(1:10, 1:10, layerId = LETTERS[1:10])
create circles with layerIds of "A", "B", "C"...

removeShape(c("B", "F")) *remove some of the circles*

clearShapes() *clear all circles (and other shapes)*

Inputs/Events

Object Events

Object event names generally use this pattern:
input$*MAPID_OBJCATEGORY_EVENTNAME*.
Triger an event changes the value of the Shiny input at this variable.
Valid values for *OBJCATEGORY* are *marker*, *shape*, *geojson* and *topojson*.
Valid values for *EVENTNAME* are *click*, *mouseover* and *mouseout*.

All of these events are set to either *NULL* if the event has never happened, or a *list()* that includes:
* lat The latitude of the object, if available; otherwise, the mouse cursor
* lng The longitude of the object, if available; otherwise, the mouse cursor
* id The layerId, if any

GeoJSON events also include additional properties:
* featureId The feature ID, if any
* properties The feature properties

Map Events

input$*MAPID*_click *when the map background or basemap is clicked*
value -- a list with lat and lng

input$*MAPID*_bounds *provide the lat/lng bounds of the visible map area*
value -- a list with north, east, south and west

input$*MAPID*_zoom *an integer indicates the zoom level*

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Adapted from Rstudio materials https://rstudio.github.io/leaflet/ 2017/05/01

Machine Learning Modelling in R : : CHEAT SHEET

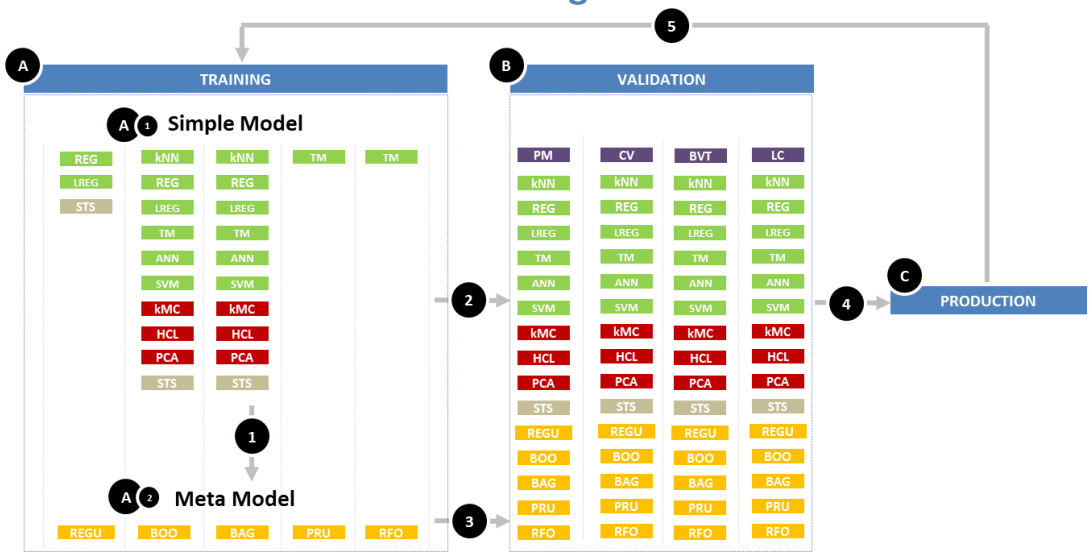
Supervised & Unsupervised Learning

	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
SUPERVISED LEARNING	NBC Naïve Bayes classifier	A classification technique based on Bayes' Theorem with an assumption of independence among predictors. In simple terms, a Naive Bayes classifier assumes that the presence of a particular feature in a class is unrelated to the presence of any other feature	e1071::naiveBayes	naiveBayes(class ~ ., data = x)
	kNN k–Nearest Neighbours	A non-parametric method used for classification and regression. In both cases, the input consists of the k closest training examples in the feature space. The output depends on whether k-NN is used for classification or regression	class::knn	knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
	REG Linear Regression	Model the linear relationship between a scalar dependant variable *Y* and one or more explanatory variables (or independent variables) denoted *X*	stats::lm	lm(dist ~ speed, data=cars)
	LREG Logistic Regression	Used to predict a binary outcome (1 / 0, Yes / No, True / False) given a set of independent variables.	stats::glm	glm(Y ~ ., family = binomial (link = 'logit'), data = X)
	TM Tree-Based Models	The idea is to consecutively divide (branch) the training dataset based on the input features until an assignment criterion with respect to the target variable into a "data bucket" (leaf) is reached	rpart::rpart	rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
	ANN Artificial Neural Network	Neural networks are built from units called perceptrons. Perceptrons have one or more inputs, an activation function and an output. An ANN model is built up by combining perceptrons in structured layers.	neuralnet::neuralnet	neuralnet(f,data=train_,hidden=c(5,3),linear.output=T)
	SVM Support Vector Machine	A data classification method that separates data using hyperplanes	e1071::svm	svm(formula, data = NULL, ..., subset, na.action = na.omit, scale = TRUE)
UNSUPERVISED LEARNING	PCA Principal Component Analysis	A procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.	stats::prcomp stats::princomp FactoMineR::PCA ade4::dudi.pca amap::acp	**stats** : prcomp(formula, data = NULL, subset, na.action, ...) **stats** : princomp(formula, data = NULL, subset, na.action, ...) **FactoMineR** : PCA(decathlon, quanti.sup = 11:12, quali.sup=13) **ade4** : dudi.pca(deug$tab, center = deug$cent, scale = FALSE, scan = FALSE) **amap** : acp(lubisch)
	kMC k-Mean Clustering	Aims at partitioning *n* observations into *k* clusters in which each observation belongs to the cluster with the nearest mean	stats::kmeans	kmeans(x, centers, iter.max = 10, nstart = 1, algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"), trace=FALSE)
	HCL Hierarchical Clustering	An approach which builds a hierarchy from the bottom-up, and doesn't require the number of clusters to be specified beforehand.	stats::hclust	hclust(d, method = "complete", members = NULL)

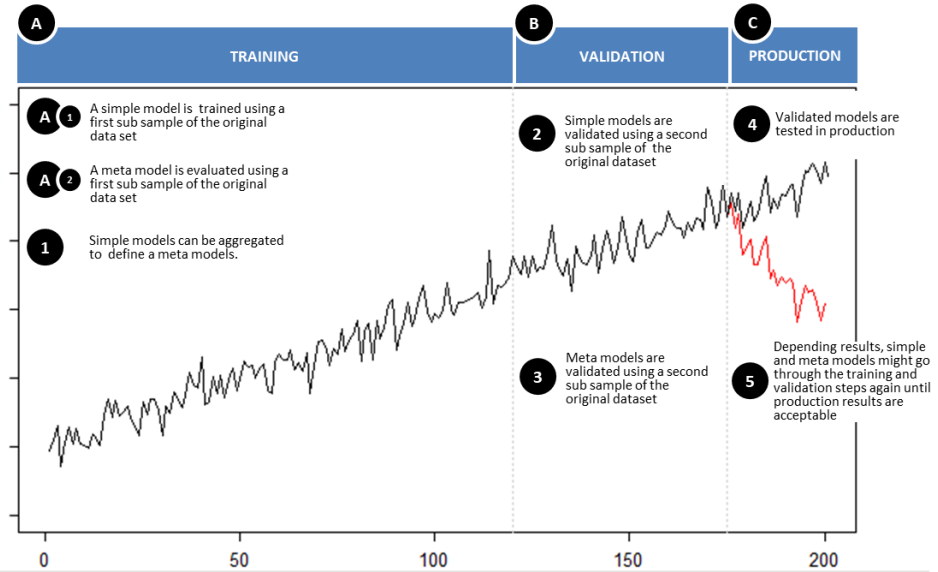
Meta-Algorithm, Time Series & Model Validation

	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
META ALGORITHM	REGU Regularisation L1 (Lasso) L2 (Ridge)	Regularization adds a penalty on the different parameters of a model to reduce the freedom of the model. Hence, the model will be less likely to fit the noise of the training data and will improve the generalization abilities of the model	glmnet::glmnet	**L1 :** glmnet(myMatrixA, myMatrixB , family = "gaussian", alpha = 1) **L2 :** glmnet(myMatrixA, myMatrixB , family = "gaussian", alpha = 0)
	BOO Boosting	A process of iteratively refining, e.g. by reweighting, of estimated regression and classification functions (though it has primarily been applied to the latter), in order to improve predictive ability.	**Parametric model** - mboost::glmboost	glmboost(Yen ~ ., data = curr1[trnidxs,])
	BAG Bagging	Bagging is a way to increase the power of a predictive statistical model by taking multiple random samples (with replacement) of the training data set, and using each of them to construct a separate model and separate predictions for the original test set	**All models**: foreach **Tree models**: ipred::bagging	**foreach :** d <- data.frame(x=1:10, y=rnorm(10)) s <- foreach(d=iter(d, by='row'), .combine=rbind) %dopar%d identical(s, d) **ipred :** bagging(formula, data, subset, na.action=na.rpart, \dots)
	PRU Pruning	Pruning is a technique that reduces the size of decision tree by removing sections of the tree that provide little power to classify instances. Pruning reduces the complexity of the final classifier and hence improves predictive accuracy by reducing overfitting	rpart::prune	prune(x, cp = 0.1)
	RFO Random Forrest	An ensemble learning method for classification, regression and other tasks, that operate by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean prediction (regression)	randomForest::randomForest	randomForest(X ~ . , data = Y , subset = mySub)
TIME SERIES	STS Lead-lag analysis, Auto-correlation, Spectral analysis, Time series clustering, Seasonality, Trend....	Random sampling of observations for training and testing a model can be an issue when faced with a times dimension. Random sampling may either destroy serial correlation properties in the data which we would like to exploit	stats xts forecast spectral TTR	**Auto-correlation**: acf(x, lag.max = NULL, type = c("correlation", "covariance", "partial")) **Spectral Analysis**: spec.pgram(myTs, spans = NULL) **Seasonal Decomposition of Time Series** - stl(x, s.window = 7, t.window = 50, t.jump = 1) .....
MODEL VALIDATION	PM Performance metrics	Depends on the problem: • **Regression**: squared errors, outliers, error rate... • **Classification**: Accuracy, precision, recall, F-score...	**Regression**-stats::outlierTest, stats:: qqPlot .... **Classification**-ROCR:: **Tree**: caret:: confusionMatrix	**Regresion**: fit <- lm(Y~X,data=myData) outlierTest(fit) qqPlot(fit, main="QQ Plot")
	BVT Biais-Variance Tradeoff	• Simple models with few parameters are easier to compute but may lead to poorer fits (**high bias**). • Complex models may provide more accurate fits but may over-fit the data (**high variance**)	Tailored to the analysis	Tailored to the analysis
	CV Cross validation	Cross validation compares the test performances of different model realisations with different sets or values of parameters	caret::createDataPartition caret::createFolds	createDataPartition(classes, p = 0.8, list = FALSE)
	LC Learning Curves	Learning curves plot a model's training and test errors, or the chosen performance metric, depending on the training set size	caret:: learing_curve_dat	learing_curve_dat(dat, outcome = NULL, proportion = (1:10)/10, test_prop = 0, verbose = TRUE, ...)

Standard Modelling Workflow



Time Series View



Intro stats with `mosaic`

ggformula version

Loading packages

```
library(mosaic)
```

Essential R syntax

Names in R are case sensitive

Function and arguments

```
rflip(10)
```

Optional arguments

```
rflip(10, prob = 0.8)
```

Assignment

```
x <- rflip(10, prob = 0.8)
```

Getting help on any function

```
help(mean)
```

Arithmetic operations

`+ - * /`	basic operations
`^`	exponentiation
`( )`	grouping
`sqrt(x)`	square root
`abs(x)`	absolute value
`log10(x)`	logarithm, base 10
`log(x)`	natural logarithm, base e
`exp(x)`	exponential function e^x
`factorial(k)`	$k! = k(k-1)\ ...\ 1$

Logical operators

`==`	is equal to (note double equal sign)
`!=`	is not equal to
`<`	is less than
`<=`	is less than or equal to
`>`	is greater than
`>=`	is greater than or equal to
`&`	`A & B` ("A and B") is `TRUE` if both `A` and `B` are `TRUE`
`|`	`A | B` ("A or B") is `TRUE` if one or both of `A` and `B` are `TRUE`
`%in%`	inclusion; for example `"C" %in% c("A", "B")` is `FALSE`

Formula interface

Use for graphics, statistics, inference, and modeling operations.

```
goal(y ~ x, data = mydata)
```

Read as "Calculate `goal` for `y` using `mydata` "broken down by" `x`, or "modeled by" `x`.

```
mean(age ~ sex, data = HELPrct)
```

For graphics:

```
goal(y ~ x | z, data = mydata,
  color = ~ w)
```

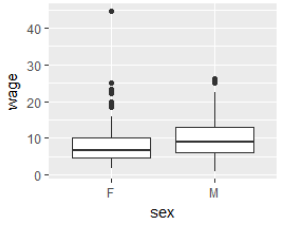
`y` : y-axis variable (*optional*)

`x` : x-axis variable (*required*)

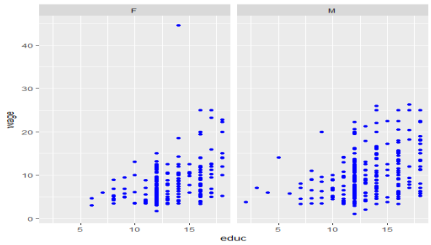
`z` : panel-by variable (*optional*)

`w` : color-by formula (*optional*)

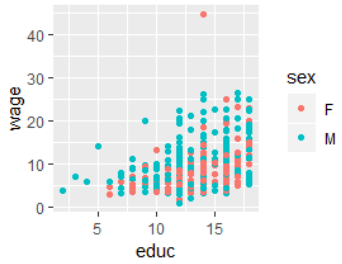
```
gf_boxplot(wage ~ sex,
   data = CPS85)
```




```
gf_point(wage ~ educ | sex,
  data = CPS85, color = "blue")
```




```
gf_point(wage ~ educ,
  data = CPS85, color = ~ sex)
```



Examining data

Print short summary of all variables

```
inspect(HELPrct)
```

Number of rows and columns

```
dim(HELPrct)
nrow(HELPrct)
ncol(HELPrct)
```

Print first rows or last rows

```
head(KidsFeet)
tail(KidsFeet, 10)
```

Names of variables

```
names(HELPrct)
```

One categorical variable

Counts by category

```
tally(~ sex, data = HELPrct)
```

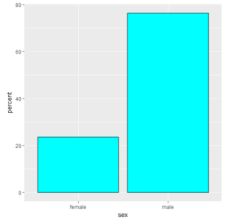
Percentages by category

```
tally(~ sex, data = HELPrct,
  format = "percent")
```

Bar graph of percentages

```
gf_percents(~ sex,
  data = HELPrct, fill = "cyan",
  color = "black")
```

`



Tests and confidence intervals

Exact test

```
result1 <-
  binom.test(~ homeless ==
  "homeless", data = HELPrct)
```

Approximate test (large samples)

```
result2 <-
  prop.test(~ homeless ==
  "homeless", data = HELPrct,
  alternative = "less",
  p = 0.4)
```

Extract confidence intervals and p-values

```
confint(result1)
pval(result2)
```

One quantitative variable

Make output more readable

```
options(digits = 3)
```

Compute summary statistics

```
mean(~ cesd, data = HELPrct)
```

Other summary statistics work similarly

```
median()  iqr()  max()  min()
fivenum()  sd()  var()  sum()
```

Table of summary statistics

```
favstats(~ cesd, data = HELPrct)
```

Summary statistics by group

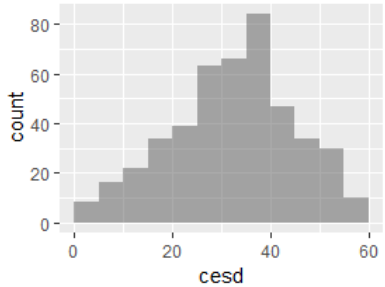
```
favstats(cesd ~ sex,
  data = HELPrct)
```

Quantiles

```
quantile(~ cesd, data = HELPrct,
  prob = c(0.25, 0.5, 0.8))
```

Histogram

```
gf_histogram(~ cesd,
  data = HELPrct, binwidth = 5,
  center = 2.5)
```



Normal probability plot

```
gf_qq(~ cesd, data = HELPrct)
```

Density plot

```
gf_dens(~ cesd, data = HELPrct,
  color = "blue", size = 1.25)
```

One-sample t-test

```
result <- t_test(~ cesd,
  data = HELPrct, mu = 34)
```

Extract confidence intervals and p-values

```
confint(result)
pval(result)
```

Paired t-test

```
t_test(extra ~ group,
  data = sleep, paired = TRUE)
```


Adapted from *A Student's Guide to R* by NJ Horton, R Pruim & DT Kaplan • Updated: 08/18

Data wrangling

Drop, rename, or reorder variables

```
df <- select(HELPrct,
  c(id, age, gender = sex))
```

Create new variables from existing ones

```
KidsFeet <- mutate(KidsFeet,
  width_in = 0.394 * width)
```

Extract specific rows from data

```
girls_feet <- filter(KidsFeet,
  sex == "G")
```

Sort data rows by value in column

```
df <- arrange(KidsFeet, length)
```

Compute summary statistics by group

```
group_by(KidsFeet, sex) %>%
  summarize(mean_width =
    mean(width))
```

For more, see Tidyverse cheatsheet

Importing data

Import data from file or URL

```
MustangPrice <-
  read.file("C:/MustangPrice.csv")
```

Note: R uses *forward* slashes in file paths

```
kidsfeet <-
  read.file("http://www.mosaic-
  web.org/go/datasets/kidsfeet.csv")
```

Randomization and simulation

Fix random number sequence

```
set.seed(42)
```

Toss coins

```
rflip(10) # default prob is 0.5
```

Do something repeatedly

```
do(5) * rflip(10, prob = 0.75)
```

Draw a simple random sample

```
sample(LETTERS, 10)
deal(Cards, 5) # poker hand
```

Resample with replacement

```
Small <- sample(KidsFeet, 10)
resample(Small)
```

Random permutation (shuffling)

```
shuffle(Cards)
```

Random values from distributions

```
rbinom(5, size = 10, prob = 0.7)
rnorm(5, mean = 10, sd = 2)
```

Two categorical variables

Contingency table with margins

```
tally(~ substance + sex,
  data = HELPrct, margins = TRUE)
```

Percentages by column

```
tally(~ sex | substance,
  data = HELPrct,
  format = "percent")
```

Mosaic plot

```
my_tbl <- tally(substance ~ sex,
  data = HELPrct)
mosaicplot(my_tbl, color = TRUE)
```

Test for proportions (approximate)

```
prop.test(homeless ~ sex,
  success = "homeless",
  data = HELPrct)
```

Distributions

Normal distribution function

```
pnorm(13, mean = 10, sd = 2)
```

Normal distribution function with graph

```
xpnorm(1.645, mean = 0, sd = 1)
```

Normal distribution quantiles

```
qnorm(0.95) # mean = 0, sd = 1
```

Normal distribution quantiles with graph

```
xqnorm(0.85, mean = 10, sd = 2)
```

Binomial density function ("size" means *n*)

```
dbinom(5, size = 8, prob = 0.65)
```

Binomial distribution function

```
pbinom(5, size = 8, prob = 0.65)
```

Central portion of distribution

```
cdist("norm", 0.95)
cdist("t", c(0.90, 0.99), df = 5)
```

Plotting distributions

```
plotDist("binom", size = 8,
  prob = 0.65, xlim = c(-1, 9))
plotDist("norm", mean = 10,
  sd = 2)
```

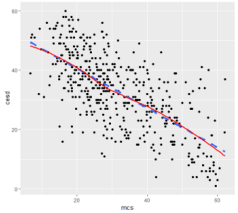
Two quantitative variables

Correlation coefficient

```
cor(cesd ~ mcs, data = HELPrct)
```

Scatterplot with regression line and smooth

```
gf_point(cesd ~ mcs,
         data = HELPrct) %>%
  gf_lm(size = 1.5, linetype =
    "dashed") %>%
  gf_smooth(color = "red")
```



Simple linear regression

```
cesdmodel <- lm(cesd ~ mcs,
  data = HELPrct)
msummary(cesdmodel)
```

Prediction

```
lm_fun <- makeFun(cesdmodel)
lm_fun(mcs = 35)
```

Extract useful quantities

```
anova(cesdmodel)
coef(cesdmodel)
confint(cesdmodel)
rsquared(cesdmodel)
```

Diagnostics; plot residuals

```
gf_dhistogram(~resid(cesdmodel))
gf_qq(~resid(cesdmodel))
```

Diagnostics; plot residuals vs. fitted

```
gf_point(resid(cesdmodel) ~
    fitted(cesdmodel)) %>%
  gf_lm(size = 2)
```

Categorical response, quantitative predictor

Logistic regression

```
logit_mod <- glm(homeless ~ age,
  data = HELPrct,
  family = binomial)
msummary(logit_mod)
```

Odds ratios and confidence intervals

```
exp(coef(logit_mod))
exp(confint(logit_mod))
```

Quantitative response, categorical predictor

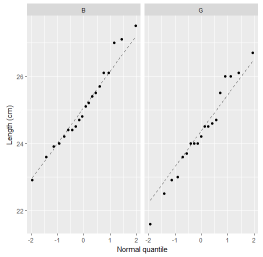
Two-level predictor: two-sample *t* test

Numeric summaries

```
favstats(~length | sex,
  data = KidsFeet)
```

Graphic summaries

```
gf_qq(~ length | sex,
      data =  KidsFeet) %>%
  gf_qqline() %>%
  gf_labs(x = "Normal quantile",
          y = "Length (cm)")
```



Two-sample *t*-test and confidence interval

```
result <- t_test(cesd ~ sex,
  data = HELPrct)
result # view results
confint(result)
pval(result)
```

More than two levels (Analysis of variance)

Numeric and graphic summaries

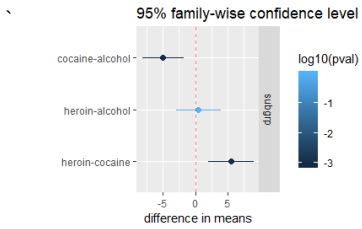
```
favstats(cesd ~ substance,
  data = HELPrct)
gf_boxplot(cesd ~ substance,
  data = HELPrct)
```

Fit and summarize model

```
mod <- lm(age ~ substance,
  data = HELPrct)
anova(mod)
```

Which differences are significant?

```
mplot(TukeyHSD(mod))
```



Adapted from *A Student's Guide to R* by NJ Horton, R Pruim & DT Kaplan • Updated: 08/18

nardl Package

An R package to estimate the nonlinear cointegrating autoregressive distributed lag model

Specifying the Model

Possible syntaxes for specifying the variables in the model:

- **nardl with fixed p and q lags**

nardl(fod~inf,p,q,data=fod,ic="aic",maxlags = FALSE,graph = FALSE,case=3)

- **Auto selected lags (maxlags=TRUE)**

nardl(fod~inf,data=fod,ic="aic",maxlags = TRUE,graph = FALSE,case=3)

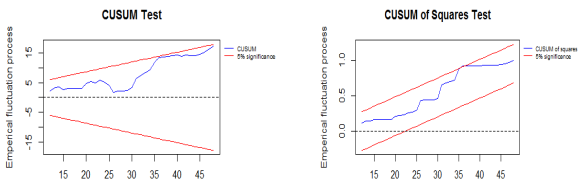
The formula:

- y~x | z1+z2….
- y the dependent variable
- x the decomposed variable (this package version can't assume more than one decomposed variable)
- z1+z2+… independent variables
- Data is the dataframe
- p number of lags of the dependent variable
- q number of lags of the independent variables
- ic : c("aic","bic","ll","R2") criteria model selection
- maxlags if TRUE auto lags selection
- case case number 3 for (unrestricted intercert, no trend) and 5 (unrestricted intercept, unrestricted trend), 1 2 and 4 not supported

Cusum and CusumQ plot

Cusum and CusumQ plot (graph=TRUE)

nardl(food~inf,data=fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)



Cointegration bounds test

pssbounds(obs, fstat, tstat = NULL, case, k)

pssbounds specification include:

- Case case number 3 for (unrestricted intercert, no trend) and 5 (unrestricted intercept, unrestricted trend), 1 2 and 4 not supported
- fstat represent the value of the F-statistic
- obs represent the number of observation
- k number of regressors appearing in lag levels

Example:

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

pssbounds(case=reg$case,fstat=reg$fstat,obs=reg$obs,k=reg$k)

LM test for serial correlation

LM test for serial correlation

bp2(object, nlags, fill = NULL, type = c("F", "Chi2"))

- **Methods and options are:**
- object fitted lm model
- nlags positive integer number of lags
- fill starting values for the lagged residuals in the auxiliary regression. By default 0.
- type Fisher or Chisquare statistics

Example :

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

bp2(regfit,regnp,fill=0,type="F")

Lagrange multiplier test

Lagrange multiplier test for conditional heteroscedasticity of Engle (1982), as described by Tsay (2005, pp. 101-102)

ArchTest(x, lags = 12, demean = FALSE)

- **Methods and options are:**
- x numeric vector
- lags positive integer number of lags.
- demaen logical: If TRUE, remove the mean before computing the test statistic.

Example :

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)
x<-reg$selresidu
nlag<-reg$np
ArchTest(x,lags=nlag)

Dynamic multipliers plot

Dynamic multiplier plot

plotmplier(model, np, k, h)

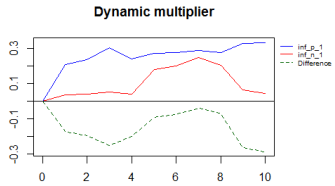
Methods and options are:

- model the fitted model
- np the selected number of lags
- k number of decomposed independent variables
- h is the horizon over which multipliers will be computed

Example

reg<-nardl(food~inf,p=4,q=4,fod,ic="aic",maxlags = FALSE,graph = TRUE,case=3)

plotmplier(reg,reg$np,1,10)



pssbounds

pssbound function display the necessary critical values to conduct the Pesaran, Shin and Smith 2001 bounds test for cointegration. See http://andyphilips.github.io/pssbounds/.

pssbounds(obs, fstat, tstat = NULL, case, k)

Methods and options are:

- obs number of observations
- fstat value of the F-statistic
- tstat value of the t-statistic
- case case number
- k number of regressors appearing in lag levels

Example

reg<-nardl(food~inf,fod,ic="aic",maxlags = TRUE,graph = TRUE,case=3)

pssbounds(case=reg$case,fstat=reg$fstat,obs=reg$obs,k=reg$k)

F-stat concludes I(1) and cointegrating, t-stat concludes I(0).

Parallel Computing :: **CHEAT SHEET**

Splitting :

Splitting a code by :

1. **Task** (different tasks on same data)
2. **Data** (one task on different data)

Hardware needs :

CPU (+2 cores)

RAM (shared memory vs distributed memory)

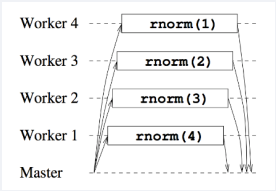
2 ideas in parallel computing :

1. **Map-Reduced Models :**
(distributed data; physically on different devices)
- **Hadoop**
- **Spark**

R Packages:
- sparklyr, iotools
- pbdr (programming with big data in R)

2. **Master - Worker Models :**
(M tasks on C cores; usually 1 < C << M)

R Packages:
- snow, snowFT, snowfal
- foreach
- future, future.apply



Not always parallel computing:

stop/start cluster takes time
overhead (communication time b/w master and workers ; not good for repeatedly sending big data!

Sequential vs Parallel:

```
library(microbenchmark)
microbenchmark( FUN1(…), FUN2(…),
times = 10)
```

parallel.R : core package

```
library(parallel)
ncores <- detectCores(logical=F) # physical cores
cl <- makeCluster(ncores)
clusterApply(cl, x = c(…), fun = FUN) # FUN(x,…)
stopCluster(cl)
```

Initialization of workers :

```
clusterCall(cl,FUN)  # calls FUN on workers
clusterEvalQ(cl, exp) # eval an exp. on workers
## clusterEvalQ(cl, library(foo))
clusterExport(cl, varlist) # varlist on workers
## clusterExport(cl, c("mean")) where mean = 10
```

Data Chunk on workers :

1. generated on workers

```
# clusterApply(cl,x, FUN) e.g FUN(){ rnorm()}
```

2. generated on master and pass to workers

```
# ind <- splitIndices(200, 5)
# clusterApply(cl, ind, FUN)
# (-) : not efficient in Big Data : heavy
```

3. chunk on workers # copy of original Data on all workers

```
# clusterExport(cl, M)        e.g. M is a matrix
# clusterApply(cl, x, FUN)    FUN contains subset M
```

foreach.R : Sequential

```
library(foreach)          # by default return a list
foreach(n = rep(5,3), m = 10^(0:2)) %do% FUN(n,m)
foreach(n, .packages = "X") %do% FUN(n)
# FUN needs package X to be run
foreach(n, .export = c("Y") ) %do% FUN(n,b=Y)
# FUN needs outside object/function "Y"
foreach(n,.combine = rbind) %do% FUN(n) #row bind
foreach(n,.combine = '+') %do% FUN(n) #rbind + colSum
foreach(n,.combine = c) %do% FUN(n) # vector
foreach(n,.combine = c) %:% when(n > 2) %do% FUN(n)
```

future.R : asynchronously

```
library(future) (variables run as soon as created)
plan(multicore)
# plans : sequential, cluster, multicore, multiprocess
x %<-% mean(rnorm(100))
y %<-% mean(rnorm(100))
```

future.apply.R : parallel _apply

```
library(future.apply) (parallel _apply functions)
plan(multicore)     # can be other plans
future_apply(n,FUN),future_lapply(…),future_sapply(…)
```

foreach.R : Parallel

```
needs backend packages support parallel computing
• doParallel(parallel.R),doFuture (future.R),doSEQ
```

doParallel.R : backend of foreach

```
library(doParallel)
cl <- makeCluster(ncores)     # ncores = 2,3,…
registerDoParallel(cl)     # register the backend
foreach(…) %dopar% FUN(…)
```

doFuture.R : backend of foreach

```
library(doFuture)
registerDoFuture()
plan(cluster , workers = 3) # can be other plans
foreach(…) %dopar% FUN(…)
```

Load Balancing: for uneven task times

```
clusterApplyLB(cl,x,FUN) # not for small task time
clusterApply(cl, x = splitIndices(10,2), FUN)
library(itertools)
foreach(s=isplitVector(1:10,chunks =2))%dopar% FUN
# e.g. FUN = sapply(s,"*",100)
future_sapply(…, future.scheduling = 1)
```

quanteda Cheat Sheet

Quantitative Analysis of Textual Data

General syntax

- **corpus_*** manage text collections/metadata
- **tokens_*** create/modify tokenized texts
- **dfm_*** create/modify doc-feature matrices
- **fcm_*** work with co-occurrence matrices
- **textstat_*** calculate text-based statistics
- **textmodel_*** fit (un-)supervised models
- **textplot_*** create text-based visualizations

Consistent grammar:

- **object()** constructor for the object type
- **object_verb()** inputs & returns object type

Extensions

quanteda works well with these companion packages:

- **readtext**: an easy way to read text data
- **spacyr**: NLP using the spaCy library
- **quanteda.corpora**: additional text corpora
- **stopwords**: multilingual stopword lists in R

Create a corpus from texts (corpus_*)

Read texts (txt, pdf, csv, doc, docx, json, xml)

```
my_texts <- readtext::readtext("~/link/to/path/*")
```

Construct a corpus from a character vector

```
x <- corpus(data_char_ukimmig2010, text_field = "text")
```

Explore a corpus

```
summary(data_corpus_inaugural, n = 2)
# Corpus consisting of 58 documents, showing 2 documents:
#            Text Types Tokens Sentences Year  President FirstName
# 1789-Washington   625   1538        23 1789 Washington    George
# 1793-Washington    96    147         4 1793 Washington    George
#
# Source:  Gerhard Peters and John T. Woolley. The American Presidency Project.
# Created: Tue Jun 13 14:51:47 2017
# Notes:   http://www.presidency.ucsb.edu/inaugurals.php
```

Extract or add document-level variables

```
party <- docvars(data_corpus_inaugural, "Party")
docvars(x, "serial_number") <- 1:ndoc(x)
```

Bind or subset corpora

```
corpus(x[1:5]) + corpus(x[7:9])
corpus_subset(x, Year > 1990)
```

Change units of a corpus

```
corpus_reshape(x, to = c("sentences", "paragraphs"))
```

Segment texts on a pattern match

```
corpus_segment(x, pattern, valuetype, extract_pattern = TRUE)
```

Take a random sample of corpus texts

```
corpus_sample(x, size = 10, replace = FALSE)
```

Extract features (dfm_*; fcm_*)

Create a document-feature matrix (dfm) from a corpus

```
x <- dfm(data_corpus_inaugural,
         tolower = TRUE, stem = FALSE, remove_punct = TRUE,
         remove = stopwords("english"))

head(x, n = 2, nf = 4)
## Document-feature matrix of: 2 documents, 4 features (41.7% sparse).
##                  features
## docs              fellow-citizens senate house representatives
##   1789-Washington               1      1     2               2
##   1793-Washington               0      0     0               0
```

Create a dictionary

```
dictionary(list(negative = c("bad", "awful", "sad"),
                positive = c("good", "wonderful", "happy")))
```

Apply a dictionary

```
dfm_lookup(x, dictionary = data_dictionary_LSD2015)
```

Select features

```
dfm_select(x, dictionary = data_dictionary_LSD2015)
```

Randomly sample documents or features

```
dfm_sample(x, what = c("documents", "features"))
```

Weight or smooth the feature frequencies

```
dfm_weight(x, type = "prop") | dfm_smooth(x, smoothing = 0.5)
```

Sort or group a dfm

```
dfm_sort(x, margin = c("features", "documents", "both"))
dfm_group(x, groups = "President")
```

Combine identical dimension elements of a dfm

```
dfm_compress(x, margin = c("both", "documents", "features"))
```

Create a feature co-occurrence matrix (fcm)

```
x <- fcm(data_corpus_inaugural, context = "window", size = 5)
```

fcm_compress/remove/select/toupper/tolower are also available

Useful additional functions

Locate keywords-in-context

```
kwic(data_corpus_inaugural, "america*")
```

Utility functions

texts(corpus)	*Show texts of a corpus*
ndoc(corpus/dfm/tokens)	*Count documents/features*
nfeat(corpus/dfm/tokens)	*Count features*
summary(corpus/dfm)	*Print summary*
head(corpus/dfm)	*Return first part*
tail(corpus/dfm)	*Return last part*

Tokenize a set of texts (tokens_*)

Tokenize texts from a character vector or corpus

```
x <- tokens("Powerful tool for text analysis.",
            remove_punct = TRUE, stem = TRUE)
```

Convert sequences into compound tokens

```
myseqs <- phrase(c("powerful", "tool", "text analysis"))
tokens_compound(x, myseqs)
```

Select tokens

```
tokens_select(x, c("powerful", "text"), selection = "keep")
```

Create ngrams and skipgrams from tokens

```
tokens_ngrams(x, n = 1:3)
tokens_skipgrams(toks, n = 2, skip = 0:1)
```

Convert case of tokens

```
tokens_tolower(x) | tokens_topupper(x)
```

Stem the terms in an object

```
tokens_wordstem(x)
```

Calculate text statistics (textstat_*)

Tabulate feature frequencies from a dfm

```
textstat_frequency(x) | topfeatures(x)
```

Identify and score collocations from a tokenized text

```
toks <- tokens(c("quanteda is a pkg for quant text analysis",
                 "quant text analysis is a growing field"))
textstat_collocations(toks, size = 3, min_count = 2)
```

Calculate readability of a corpus

```
textstat_readability(data_corpus_inaugural, measure = "Flesch")
```

Calculate lexical diversity of a dfm

```
textstat_lexdiv(x, measure = "TTR")
```

Measure distance or similarity from a dfm

```
textstat_simil(x, "2017-Trump", method = "cosine")
textstat_dist(x, "2017-Trump", margin = "features")
```

Calculate keyness statistics

```
textstat_keyness(x, target = "2017-Trump")
```

Fit text models based on a dfm (textmodel_*)

Correspondence Analysis (CA)

```
textmodel_ca(x, threads = 2, sparse = TRUE, residual_floor = 0.1)
```

Naïve Bayes classifier for texts

```
textmodel_nb(x, y = training_labels, distribution = "multinomial")
```

Wordscores text model

```
refscores <- c(seq(-1.5, 1.5, .75), NA))
textmodel_wordscores(data_dfm_lbgexample, refscores)
```

Wordfish Poisson scaling model

```
textmodel_wordfish(dfm(data_corpus_irishbudget2010), dir = c(6,5))
```

Textmodel methods: `predict()`, `coef()`, `summary()`, `print()`

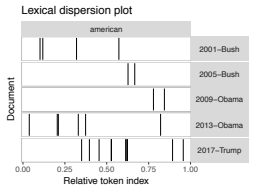
Plot features or models (textplot_*)

Plot features as a wordcloud

```
data_corpus_inaugural %>%
  corpus_subset(President == "Obama") %>%
  dfm(remove = stopwords("english")) %>%
  textplot_wordcloud()
```

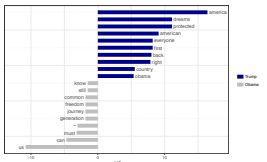
Plot the dispersion of key word(s)

```
data_corpus_inaugural %>%
  corpus_subset(Year > 1945) %>%
  kwic("american") %>%
  textplot_xray()
```



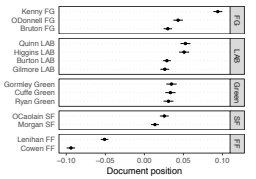
Plot word keyness

```
data_corpus_inaugural %>%
  corpus_subset(President %in%
                  c("Obama", "Trump")) %>%
  dfm(groups = "President",
      remove = stopwords("english")) %>%
  textstat_keyness(target = "Trump") %>%
  textplot_keyness()
```



Plot Wordfish, Wordscores or CA models

```
textplot_scale1d(scaling_model,
  groups = party,
  margin = "documents")
```



Convert dfm to a non-quanteda format

```
convert(x, to = c("lda", "tm", "stm", "austin", "topicmodels",
                  "lsa", "matrix", "data.frame"))
```

by **Stefan Müller** and **Kenneth Benoit** • *mullers@tcd.ie*, *kbenoit@lse.ac.uk*

Learn more at: http://quanteda.io • updated: 11/18

randomizr: : CHEAT SHEET

Two Arm Trials

Simple random assignment is like flipping coins for each unit separately.

```
simple_ra(N = 100, prob = 0.5)
```

Complete random assignment allocates a fixed number of units to each condition.

```
complete_ra(N = 100, m = 50)
complete_ra(N = 100, prob = 0.5)
```

Block random assignment conducts complete random assignment separately for groups of units.

```
blocks <- rep(c("A", "B", "C"),
              c(50, 100, 200))

# defaults to half of each block
block_ra(blocks = blocks)

# can change with block_m
block_ra(blocks = blocks,
         block_m = c(20, 30, 40))
```

Cluster random assignment allocates whole groups of units to conditions together.

```
clusters <- rep(letters, times = 1:26
cluster_ra(clusters = clusters)
```

Block and cluster random assignment conducts cluster random assignment separately for groups of clusters.

```
clusters <- rep(letters, times = 1:26)
blocks <- rep(paste0("block_", 1:5),
              c(15, 40, 65, 90, 141))
block_and_cluster_ra(blocks = blocks,
                     clusters = clusters)
```

Multi Arm Trials

Set the number of arms with `num_arms` or with `conditions`.

```
complete_ra(N = 100, num_arms = 3)
complete_ra(N = 100, conditions = c("control",
"placebo", "treatment"))
```

The `*_each` arguments in randomizr functions specify design parameters for each arm separately.

```
complete_ra(N = 100, m_each = c(20, 30, 50))
complete_ra(N = 100,
            prob_each = c(0.2, 0.3, 0.5))
```

If the design is the **same** for all blocks, use `prob_each`:

```
blocks <- rep(c("A", "B","C"),
              c(50, 100, 200))
block_ra(blocks = blocks,
         prob_each = c(.1, .1, .8))
```

If the design is **different** in different blocks, use `block_m_each` or `block_prob_each`:

```
block_m_each <- rbind(c(10, 20, 20),
                      c(30, 50, 20),
                      c(50, 75, 75))
block_ra(blocks = blocks,
         block_m_each = block_m_each)

block_prob_each <- rbind(c(.1, .1, .8),
                         c(.2, .2, .6),
                         c(.3, .3, .4))
block_ra(blocks = blocks,
         block_prob_each = block_prob_each)
```

If `conditions` is numeric, the output will be **numeric**.

If `conditions` is not numeric, the output will be a **factor** with levels in the order provided to conditions.

```
complete_ra(N = 100, conditions = -2:2)
complete_ra(N = 100, conditions = c("A", "B"))
```

Declaration

Learn about assignment procedures by "declaring" them with `declare_ra()`

```
declaration <-
  declare_ra(N = 100, m_each = c(30, 30, 40))

declaration # print design information
```

Conduct a random assignment:

```
conduct_ra(declaration)
```

Obtain observed condition probabilities (useful for inverse probability weighting if probabilities of assignment are not constant)

```
Z <- conduct_ra(declaration)
obtain_condition_probabilities(declaration, Z)
```

Sampling

All assignment functions have sampling analogues: Sampling is identical to a two arm trial where the treatment group is sampled.

Assignment	Sampling
`simple_ra()`	`simple_rs()`
`complete_ra()`	`complete_rs()`
`block_ra()`	`strata_rs()`
`cluster_ra()`	`cluster_rs()`
`block_and_cluster_ra()`	`strata_and_cluster_rs()`
`declare_ra()`	`declare_rs()`
`conduct_ra()`	`draw_rs()`

Stata

A Stata version of randomizr is available, with the same arguments but different syntax:

```
ssc install randomizr
set obs 100
complete_ra, m(50)
```

randomizr is part of the DeclareDesign suite of packages for designing, implementing, and analyzing social science research designs.

Basic Regular Expressions in R

Cheat Sheet

Character Classes

[[:digit:]] or \\d	Digits; `[0-9]`
\\D	Non-digits; `[^0-9]`
[[:lower:]]	Lower-case letters; `[a-z]`
[[:upper:]]	Upper-case letters; `[A-Z]`
[[:alpha:]]	Alphabetic characters; `[A-z]`
[[:alnum:]]	Alphanumeric characters `[A-z0-9]`
\\w	Word characters; `[A-z0-9_]`
\\W	Non-word characters
[[:xdigit:]] or \\x	Hexadec. digits; `[0-9A-Fa-f]`
[[:blank:]]	Space and tab
[[:space:]] or \\s	Space, tab, vertical tab, newline, form feed, carriage return
\\S	Not space; `[^[:space:]]`
[[:punct:]]	Punctuation characters; `!"#$%&'()*+,-./:;<=>?@[]^_`{|}~`
[[:graph:]]	Graphical characters; `[[:alnum:][:punct:]]`
[[:print:]]	Printable characters; `[[:alnum:][:punct:]\\s]`
[[:cntrl:]] or \\c	Control characters; `\n`, `\r` etc.

Special Metacharacters

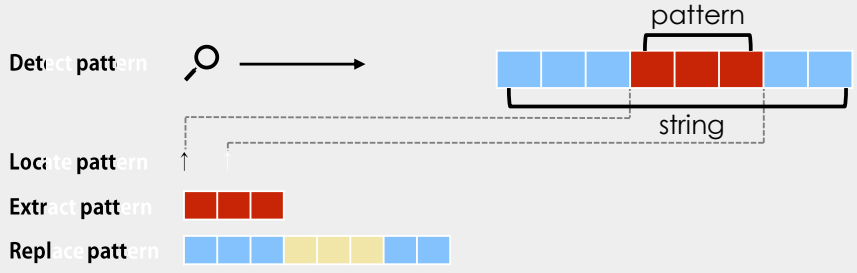
\n	New line
\r	Carriage return
\t	Tab
\v	Vertical tab
\f	Form feed

Lookaraounds and Conditionals*

(?=)	Lookahead (requires PERL = TRUE), e.g. `(?=yx)`: position followed by 'xy'
(?!)	Negative lookahead (PERL = TRUE); position NOT followed by pattern
(?<=)	Lookbehind (PERL = TRUE), e.g. `(?<=yx)`: position following 'xy'
(?<!)	Negative lookbehind (PERL = TRUE); position NOT following pattern
?(if)then	If-then-condition (PERL = TRUE); use lookaheads, optional char. etc in if-clause
?(if)then|else	If-then-else-condition (PERL = TRUE)

*see, e.g. http://www.regular-expressions.info/lookaround.html
http://www.regular-expressions.info/conditional.html

Functions for Pattern Matching




```
> string <- c("Hiphopopotamus", "Rhymenoceros", "time for bottomless lyrics")
> pattern <- "t.m"
```

Detect Patterns

grep(pattern, string)
`[1] 1 3`

grep(pattern, string, value = TRUE)
`[1] "Hiphopopotamus"`
`[2] "time for bottomless lyrics"`

grepl(pattern, string)
`[1] TRUE FALSE TRUE`

stringr::str_detect(string, pattern)
`[1] TRUE FALSE TRUE`

Locate Patterns

regexpr(pattern, string)
find starting position and length of first match

gregexpr(pattern, string)
find starting position and length of all matches

stringr::**str_locate(string, pattern)**
find starting and end position of first match

stringr::**str_locate_all(string, pattern)**
find starting and end position of all matches

Splitting Strings using a Pattern

strsplit(string, pattern) or stringr::**str_split(string, pattern)**

Extract Patterns

regmatches(string, regexpr(pattern, string))
extract first match `[1] "tam" "tim"`

regmatches(string, gregexpr(pattern, string))
extract all matches, outputs a list
`[[1]] "tam" [[2]] character(0) [[3]] "tim" "tom"`

stringr::**str_extract(string, pattern)**
extract first match `[1] "tam" NA "tim"`

stringr::**str_extract_all(string, pattern)**
extract all matches, outputs a list

stringr::**str_extract_all(string, pattern, simplify = TRUE)**
extract all matches, outputs a matrix

stringr::**str_match(string, pattern)**
extract first match + individual character groups

stringr::**str_match_all(string, pattern)**
extract all matches + individual character groups

Replacing Patterns

sub(pattern, replacement, string)
replace first match

gsub(pattern, replacement, string)
replace all matches

stringr::**str_replace(string, pattern, replacement)**
replace first match

stringr::**str_replace_all(string, pattern, replacement)**
replace all matches

Character Classes and Groups

.	Any character except \n
|	Or, e.g. `(a|b)`
[…]	List permitted characters, e.g. `[abc]`
[a-z]	Specify character ranges
[^…]	List excluded characters
(…)	Grouping, enables back referencing using \\N where N is an integer

Anchors

^	Start of the string
$	End of the string
\\b	Empty string at either edge of a word
\\B	NOT the edge of a word
\\<	Beginning of a word
\\>	End of a word

Quantifiers

*	Matches at least 0 times
+	Matches at least 1 time
?	Matches at most 1 time; optional string
{n}	Matches exactly n times
{n,}	Matches at least n times
{n,m}	Matches between n and m times

General Modes

By default R uses *extended* regular expressions. You can switch to *PCRE regular expressions* using `PERL = TRUE` for base or by wrapping patterns with `perl()` for stringr.

All functions can be used with literal searches using `fixed = TRUE` for base or by wrapping patterns with `fixed()` for stringr.

All base functions can be made case insensitive by specifying `ignore.cases = TRUE`.

Escaping Characters

Metacharacters (`. * +` etc.) can be used as literal characters by escaping them. Characters can be escaped using \\ or by enclosing them in `\\Q...\\E`.

Case Conversions

Regular expressions can be made case insensitive using `(?i)`. In backreferences, the strings can be converted to lower or upper case using `\\L` or `\\U` (e.g. `\\L\\1`). This requires `PERL = TRUE`.

Greedy Matching

By default the asterisk * is greedy, i.e. it always matches the longest possible string. It can be used in lazy mode by adding `?`, i.e. `*?`.

Greedy mode can be turned off using `(?U)`. This switches the syntax, so that `(?U)a*` is lazy and `(?U)a*?` is greedy.

Note

Regular expressions can conveniently be created using e.g. the packages rex or rebus.

Updated: 10/18

Spatial manipulation with sf: : CHEAT SHEET

The sf package provides a set of tools for working with geospatial vectors, i.e. points, lines, polygons, etc.

Geometric confirmation

st_contains(x, y, ...) Identifies if x is within y (i.e. point within polygon)

st_covered_by(x, y, ...) Identifies if x is completely within y (i.e. polygon completely within polygon)

st_covers(x, y, ...) Identifies if any point from x is outside of y (i.e. polygon outside polygon)

st_crosses(x, y, ...) Identifies if any geometry of x have commonalities with y

st_disjoint(x, y, ...) Identifies when geometries from x do not share space with y

st_equals(x, y, ...) Identifies if x and y share the same geometry

st_intersects(x, y, ...) Identifies if x and y geometry share any space

st_overlaps(x, y, ...) Identifies if geometries of x and y share space, are of the same dimension, but are not completely contained by each other

st_touches(x, y, ...) Identifies if geometries of x and y share a common point but their interiors do not intersect

st_within(x, y, ...) Identifies if x is in a specified distance to y

Geometric operations

st_boundary(x) Creates a polygon that encompasses the full extent of the geometry

st_buffer(x, dist, nQuadSegs) Creates a polygon covering all points of the geometry within a given distance

st_centroid(x, ..., of_largest_polygon) Creates a point at the geometric centre of the geometry

st_convex_hull(x) Creates geometry that represents the minimum convex geometry of x

st_line_merge(x) Creates linestring geometry from sewing multi linestring geometry together

st_node(x) Creates nodes on overlapping geometry where nodes do not exist

st_point_on_surface(x) Creates a point that is guarenteed to fall on the surface of the geometry

st_polygonize(x) Creates polygon geometry from linestring geometry

st_segmentize(x, dfMaxLength, ...) Creates linesting geometry from x based on a specified length

st_simplify(x, preserveTopology, dTolerance) Creates a simplified version of the geometry based on a specified tolerance

Geometry creation

st_triangulate(x, dTolerance, bOnlyEdges) Creates polygon geometry as triangles from point geometry

st_voronoi(x, envelope, dTolerance, bOnlyEdges) Creates polygon geometry covering the envolope of x, with x at the centre of the geometry

st_point(x, c(numeric vector), dim = "XYZ") Creating point geometry from numeric values

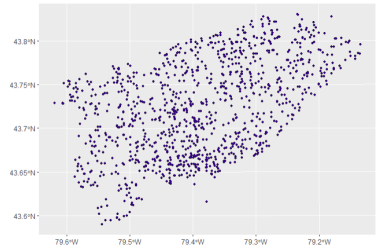
st_multipoint(x = matrix(numeric values in rows), dim = "XYZ") Creating multi point geometry from numeric values

st_linestring(x = matrix(numeric values in rows), dim = "XYZ") Creating linestring geometry from numeric values

st_multilinestring(x = list(numeric matricesin rows), dim = "XYZ") Creating multi linestring geometry from numeric values

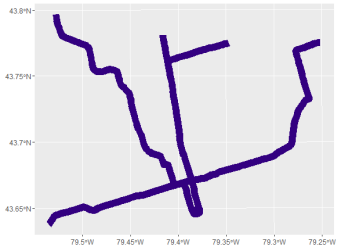
st_polygon(x = list(numeric matrices in rows), dim = "XYZ") Creating polygon geometry from numeric values

st_multipolygon(x = list(numeric matrices in rows), dim = "XYZ") Creating multi polygon geometry from numeric values



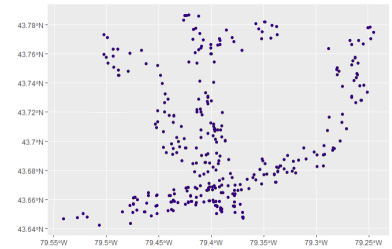
```
ggplot() +
  geom_sf(data = schools)
```

+



```
ggplot() +
  geom_sf(data = subway)
```

=>



```
ggplot() +
  geom_sf(data = st_intersection(schools, st_buffer(subway, 1000)))
```

This cheatsheet presents the sf package [Edzer Pebesma 2018] in version 0.6.3. See https://github.com/r-spatial/sf for more details.

Spatial manipulation with sf: : CHEAT SHEET

The sf package provides a set of tools for working with geospatial vectors, i.e. points, lines, polygons, etc.

Geometry operations

st_contains(x, y, ...) Identifies if x is within y (i.e. point within polygon)

st_crop(x, y, ..., xmin, ymin, xmax, ymax) Creates geometry of x that intersects a specified rectangle

st_difference(x, y) Creates geometry from x that does not intersect with y

st_intersection(x, y) Creates geometry of the shared portion of x and y

st_sym_difference(x, y) Creates geometry representing portions of x and y that do not intersect

st_snap(x, y, tolerance) Snap nodes from geometry x to geometry y

st_union(x, y, ..., by_feature) Creates multiple geometries into a a single geometry, consisiting of all geometry elements

Geometric measurement

st_area(x) Calculate the surface area of a polygon geometry based on the current coordinate reference system

st_distance(x, y, ..., dist_fun, by_element, which) Calculates the 2D distance between x and y based on the current coordinate system

st_length(x) Calculates the 2D length of a geometry based on the current coordinate system

Misc operations

st_as_sf(x, ...) Create a sf object from a non-geospatial tabular data frame

st_cast(x, to, ...) Change x geometry to a different geometry type

st_coordinates(x, ...) Creates a matrix of coordinate values from x

st_crs(x, ...) Identifies the coordinate reference system of x

st_join(x, y, join, FUN, suffix, ...) Performs a spatial left or inner join between x and y

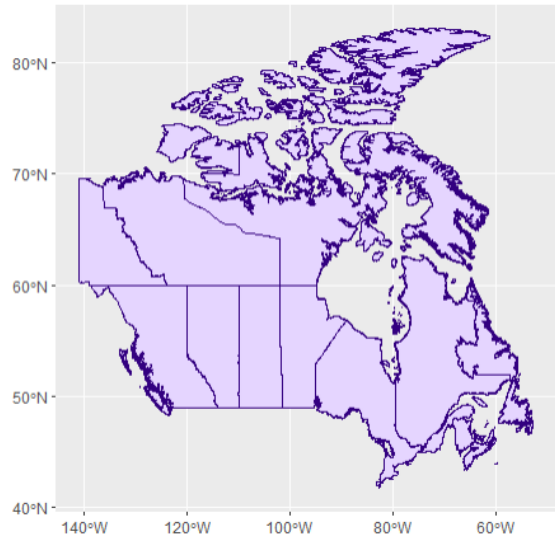
st_make_grid(x, cellsize, offset, n, crs, what) Creates rectangular grid geometry over the bounding box of x

st_nearest_feature(x, y) Creates an index of the closest feature between x and y

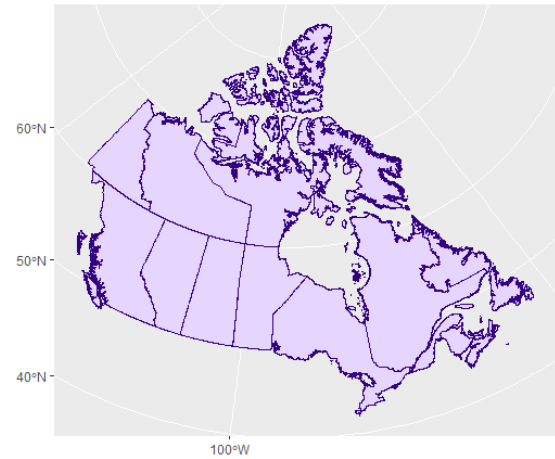
st_nearest_points(x, y, ...) Returns the closest point between x and y

st_read(dsn, layer, ...) Read file or database vector dataset as a sf object

st_transform(x, crs, ...) Convert coordinates of x to a different coordinate reference system




```
ggplot() +
  geom_sf(data = cdn) +
  coord_sf(crs = st_crs(4326))
```




```
ggplot() +
  geom_sf(data = cdn) +
  coord_sf(crs = st_crs(3347))
```

Data & Variable Transformation with sjmisc Cheat Sheet

sjmisc complements dplyr, and helps with data transformation tasks and recoding *variables*.

sjmisc works together seamlessly with dplyr and pipes. All functions are designed to support labelled data.

Design Philosophy

The design of sjmisc functions follows the tidyverse-approach: first argument is always the data (either a *data frame* **or** *vector*), followed by variable names to be processed by the functions.

The returned object for each function *equals the type of the data-argument*.

Vector input

- If the data-argument is a *vector*, functions return a *vector*.

rec(mtcars$carb, rec = "1,2=1; 3,4=2; else=3")

Data frame input

- If the data-argument is a *data frame*, functions return a *data frame*.

rec(mtcars, carb, rec = "1,2=1; 3,4=2; else=3")

The …-ellipses Argument

Apply functions to a single variable, selected variables or to a complete data frame.

Variable selection is powered by dplyr::select(): Separate variables with comma, or use dplyr select-helpers to select variables, e.g. *?rec*:

```
rec(mtcars, one_of(c("gear", "carb")),
    rec = "min:3=1; 4:max=2")

rec(mtcars, gear, carb, rec = "min:3=1; 4:max=2")
```

Descriptives and Summaries

Most of the sjmisc functions (including recode-functions) also work on grouped data frames:

```
library(dplyr)
efc %>%
  group_by(e16sex, c172code) %>%
  frq(e42dep)
```

Frequency Tables

frq(x, ..., sort.frq = c("none", "asc", "desc"), weight.by = NULL, auto.grp = NUL)

Print frequency tables of (labelled) vectors. Uses variable labels as table header.

data(efc); frq(efc, e42dep, c161sex)

Use this data set in examples!

flat_table(data, ..., margin = c("counts", "cell", "row", "col"), digits = 2, show.values = FALSE)

Print contingency tables of (labelled) vectors. Uses value labels.

flat_table(efc, e42dep, c172code, e16sex)

count_na(x, ...)

Print frequency table of tagged NA values.

```
library(haven); x <- labelled(c(1:3,
tagged_na("a",  "a", "z")), labels =
c("Refused" = tagged_na("a"), "N/A" =
tagged_na("z")))
count_na(x)
```

Descriptive Summary

descr(x, ..., max.length = NULL)

Descriptive summary of data frames, including variable labels in output.

descr(efc, contains("cop"), max.length = 20)

Finding Variables in a Data Frame

Use find_var() to search for variables by names, value or variable labels. Returns vector/data frame.

```
# variables with "cop" in n
find_var(efc, pattern = "cop", out = "df")

# variables with "level" in names and value labels
find_var(efc, "level", search = "name_value")
```

Recode and Transform Variables

Recode functions add a *suffix* to new variables, so original variables are preserved.

By default, original input data frame and new created variables are returned. Use *append = FALSE* to return the recoded variables only.

rec(x, ..., rec, as.num = TRUE, var.label = NULL, val.labels = NULL, append = TRUE, suffix = "_r")

Recode values, return result as numeric, character or categorical (factor).

rec(mtcars, carb, rec = "1,2=1; 3,4=2; else=3")

dicho(x, ..., dich.by = "median", as.num = FALSE, var.label = NULL, val.labels = NULL, append = TRUE, suffix = "_d")

Dichotomise variable by median, mean or specific value.

dicho(mtcars, disp)

split_var(x, ..., n, as.num = FALSE, val.labels = NULL, var.label = NULL, inclusive = FALSE, append = TRUE, suffix = "_g")

Split variable into equal sized groups. Unlike dplyr::ntile(), does not split original categories into different values (see examples in ?split_var).

split_var(mtcars, mpg, disp, n = 3)

group_var(x, ..., size = 5, as.num = TRUE, right.interval = FALSE, n = 30, append = TRUE, suffix = "_gr")

Split variable into groups with equal value range, or into a max. # of groups (value range per group is adjusted to match # of groups).

group_var(mtcars, mpg, disp, size = 5)
group_var(mtcars, mpg, size = "auto", n = 4)

std(x, ..., robust = "sd", include.fac = FALSE, append = TRUE, suffix = "_z")

Z-standardise variables. Also center().

std(efc, e17age, c160age)

recode_to(x, ..., lowest = 0, highest = -1, append = TRUE, suffix = "_r0")

Shift ("renumber") c

recode_to(mtcars$gear)

Summarise Variables and Cases

The summary functions mostly mimic base R equivalents, but are designed to work together with pipes and dplyr.

row_sums(x, ..., na.rm = TRUE, var = "rowsums", append = FALSE)

Row sums of data frames.

row_sums(efc, c82cop1:c90cop9)

row_means(x, ..., n, var = "rowmeans", append = FALSE)

Row means, for at least n valid (non-NA) values.

row_means(efc, c82cop1:c90cop9, n = 7)

row_count(x, ..., count, var = "rowcount", append = FALSE)

Row-wise count # of values in data frames. Also col_count().

row_count(efc, c82cop1:c90cop9, count = 2)

Other Useful Functions

- add_columns() and replace_columns() to combine data frames, but either replace or preserve existing columns.
- set_na() and replace_na() to convert regular into missing values, or vice versa. replace_na() also replaces specific tagged NA values only.
- remove_var() and var_rename() to remove variables from data frames, or rename variables.
- group_str() to group similar string values. Useful for variables with similar, but not identically spelled string values tha
- merge_df() to full join data frames and preserve value and variable labels.
- to_long() to gather multiple columns in data frames from wide into long format.

Use with %>% and dplyr

```
# use sjmisc-functions in pipes
mtcars %>% select(gear, carb) %>%
  rec(rec = "min:3=1; 4:max=2")

# use sjmisc-function inside mutate
mtcars %>% select(gear, carb) %>% mutate(
  carb2 = rec(carb, re
  gear2 = rec(gear, re
```

Creating Survival Plots

Informative and Elegant with *survminer*

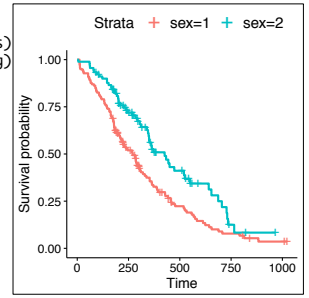
Survival Curves

The **ggsurvplot()** function creates **ggplot2** plots from **survfit** objects.

```
library("survival")
fit <- survfit(Surv(time,status)
               ~ sex, data = lung)

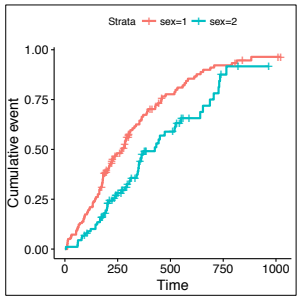
class(fit)
## [1] "survfit"

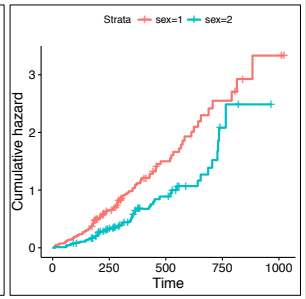
library("survminer")
ggsurvplot(fit, data = lung)
```



Use the **fun** argument to set the transformation of the survival curve. E.g. **"event"** for cumulative events, **"cumhaz"** for the cumulative hazard function or **"pct"** for survival probability in percentage.

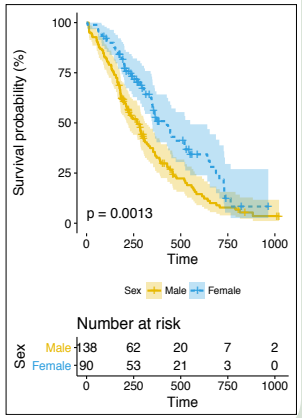
```
ggsurvplot(fit, data = lung, fun = "event")
ggsurvplot(fit, data = lung, fun = "cumhaz")
```





With lots of graphical parameters you have full control over look and feel of the survival plots; position and content of the legend; additional annotations like p-value, title, subtitle.

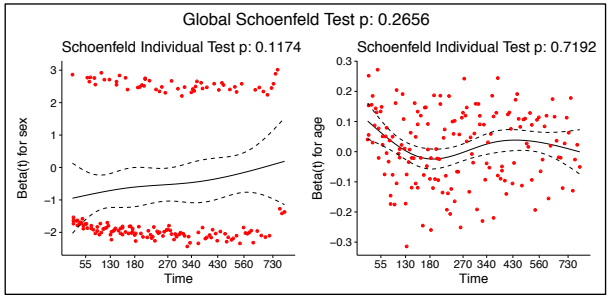
```
ggsurvplot(fit, data = lung,
     conf.int = TRUE,
     pval = TRUE,
     fun = "pct",
     risk.table = TRUE,
     size = 1,
     linetype = "strata",
     palette = c("#E7B800",
                 "#2E9FDF"),
     legend = "bottom",
     legend.title = "Sex",
     legend.labs = c("Male",
                     "Female"))
```



Diagnostics of Cox Model

The function **cox.zph()** from **survival** package may be used to test the proportional hazards assumption for a Cox regression model fit. The graphical verification of this assumption may be performed with the function **ggcoxzph()** from the **survminer** package. For each covariate it produces plots with scaled Schoenfeld residuals against the time.

```
library("survival")
fit <- coxph(Surv(time, status) ~ sex + age, data = lung)
ftest <- cox.zph(fit)
ftest
##            rho chisq     p
## sex     0.1236 2.452 0.117
## age    -0.0275 0.129 0.719
## GLOBAL      NA 2.651 0.266
library("survminer")
ggcoxzph(ftest)
```



The function **ggcoxdiagnostics()** plots different types of residuals as a function of time, linear predictor or observation id. The type of residual is selected with **type** argument. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta"', "dfbetas", and "scaledsch".

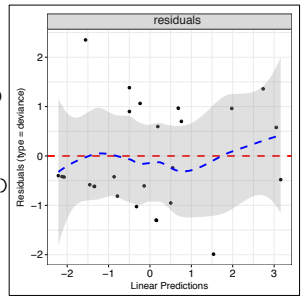
The **ox.scale** argument defines what shall be plotted on the OX axis. Possible values are "linear.predictions", "observation.id", "time".

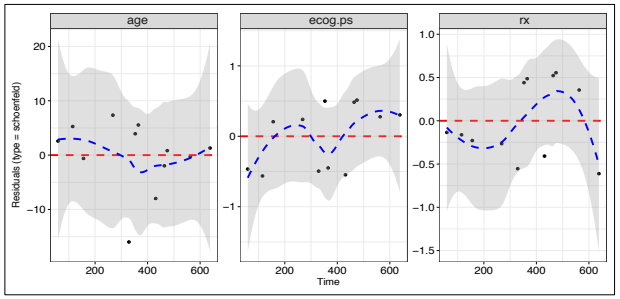
Logical arguments **hline** and **sline** may be used to add horizontal line or smooth line to the plot.

```
library("survival")
library("survminer")
fit <- coxph(Surv(time, status) ~
             sex + age, data = lung)

ggcoxdiagnostics(fit,
      type = "deviance",
      ox.scale = "linear.predictions")

ggcoxdiagnostics(fit,
      type = "schoenfeld",
      ox.scale = "time")
```





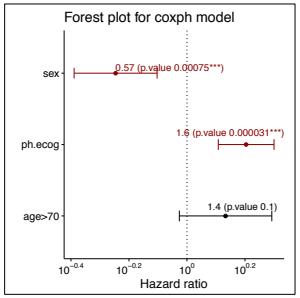
Summary of Cox Model

The function **ggforest()** from the **survminer** package creates a forest plot for a Cox regression model fit. Hazard ratio estimates along with confidence intervals and p-values are plotter for each variable.

```
library("survival")
library("survminer")
lung$age <- ifelse(lung$age > 70, ">70","<= 70")
fit <- coxph( Surv(time, status) ~ sex + ph.ecog + age, data = lung)
fit

## Call:
## coxph(formula = Surv(time, status) ~ sex+ph.ecog+age, data=lung)
##
##            coef exp(coef) se(coef)     z       p
## sex     -0.567     0.567    0.168 -3.37 0.00075
## ph.ecog  0.470     1.600    0.113  4.16 3.1e-05
## age>70   0.307     1.359    0.187  1.64 0.10175
##
## Likelihood ratio test=31.6  on
## n= 227, number of events= 164

ggforest(fit)
```



The function **ggcoxadjustedcurves()** from the **survminer** package plots Adjusted Survival Curves for Cox Proportional Hazards Model. Adjusted Survival Curves show how a selected factor influences survival estimated from a Cox model.

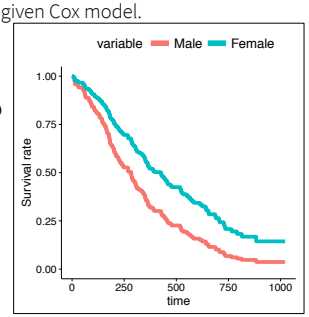
Note that these curves differ from Kaplan Meier estimates since they present expected ssurvival based on given Cox model.

```
library("survival")
library("survminer")

lung$sex <- ifelse(lung$sex == 1,
                   "Male", "Female")

fit <- coxph(Surv(time, status) ~
             sex + ph.ecog + age,
             data = lung)

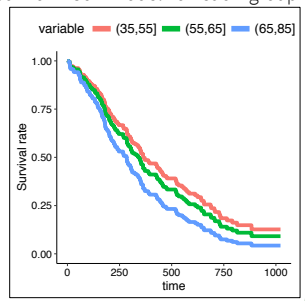
ggcoxadjustedcurves(fit, data=lung,
             variable=lung$sex)
```



Note that it is not necessary to include the grouping factor in the Cox model. Survival curves are estimated from Cox model for each group defined by the factor independently.

```
lung$age3 <- cut(lung$age,
                 c(35,55,65,85))

ggcoxadjustedcurves(fit, data=lung,
             variable=lung$age3)
```



This onepager presents the **survminer** package [Alboukadel Kassambara, Marcin Kosinski 2017] in version 0.3.
See *https://github.com/kassambara/survminer/* for more details.

R Syntax Comparison : : **CHEAT SHEET**

Dollar sign syntax

```
goal(data$x, data$y)
```

SUMMARY STATISTICS:

one continuous variable:
```
mean(mtcars$mpg)
```

one categorical variable:
```
table(mtcars$cyl)
```

two categorical variables:
```
table(mtcars$cyl, mtcars$am)
```

one continuous, one categorical:
```
mean(mtcars$mpg[mtcars$cyl==4])
mean(mtcars$mpg[mtcars$cyl==6])
mean(mtcars$mpg[mtcars$cyl==8])
```

PLOTTING:

one continuous variable:
```
hist(mtcars$disp)

boxplot(mtcars$disp)
```

one categorical variable:
```
barplot(table(mtcars$cyl))
```

two continuous variables:
```
plot(mtcars$disp, mtcars$mpg)
```

two categorical variables:
```
mosaicplot(table(mtcars$am, mtcars$cyl))
```

one continuous, one categorical:
```
histogram(mtcars$disp[mtcars$cyl==4])
histogram(mtcars$disp[mtcars$cyl==6])
histogram(mtcars$disp[mtcars$cyl==8])

boxplot(mtcars$disp[mtcars$cyl==4])
boxplot(mtcars$disp[mtcars$cyl==6])
boxplot(mtcars$disp[mtcars$cyl==8])
```

WRANGLING:

subsetting:
```
mtcars[mtcars$mpg>30, ]
```

making a new variable:
```
mtcars$efficient[mtcars$mpg>30] <- TRUE
mtcars$efficient[mtcars$mpg<30] <- FALSE
```

Formula syntax

```
goal(y~x|z, data=data, group=w)
```

SUMMARY STATISTICS:

one continuous variable:
```
mosaic::mean(~mpg, data=mtcars)
```

one categorical variable:
```
mosaic::tally(~cyl, data=mtcars)
```

two categorical variables:
```
mosaic::tally(cyl~am, data=mtcars)
```

one continuous, one categorical:
```
mosaic::mean(mpg~cyl, data=mtcars)
```

tilde

PLOTTING:

one continuous variable:
```
lattice::histogram(~disp, data=mtcars)

lattice::bwplot(~disp, data=mtcars)
```

one categorical variable:
```
mosaic::bargraph(~cyl, data=mtcars)
```

two continuous variables:
```
lattice::xyplot(mpg~disp, data=mtcars)
```

two categorical variables:
```
mosaic::bargraph(~am, data=mtcars, group=cyl)
```

one continuous, one categorical:
```
lattice::histogram(~disp|cyl, data=mtcars)

lattice::bwplot(cyl~disp, data=mtcars)
```

The variety of R syntaxes give you many ways to "say" the same thing

read **across** the cheatsheet to see how different syntaxes approach the same problem

Tidyverse syntax

```
data %>% goal(x)
```

SUMMARY STATISTICS:

one continuous variable:
```
mtcars %>% dplyr::summarize(mean(mpg))
```

one categorical variable:
```
mtcars %>% dplyr::group_by(cyl) %>%
dplyr::summarize(n())
```

the pipe

two categorical variables:
```
mtcars %>% dplyr::group_by(cyl, am) %>%
dplyr::summarize(n())
```

one continuous, one categorical:
```
mtcars %>%  dplyr::group_by(cyl) %>%
  dplyr::summarize(mean(mpg))
```

PLOTTING:

one continuous variable:
```
ggplot2::qplot(x=mpg, data=mtcars, geom = "histogram")

ggplot2::qplot(y=disp, x=1, data=mtcars, geom="boxplot")
```

one categorical variable:
```
ggplot2::qplot(x=cyl, data=mtcars, geom="bar")
```

two continuous variables:
```
ggplot2::qplot(x=disp, y=mpg, data=mtcars, geom="point")
```

two categorical variables:
```
ggplot2::qplot(x=factor(cyl), data=mtcars, geom="bar") +
       facet_grid(.~am)
```

one continuous, one categorical:
```
ggplot2::qplot(x=disp, data=mtcars, geom = "histogram") +
       facet_grid(.~cyl)

ggplot2::qplot(y=disp, x=factor(cyl), data=mtcars,
               geom="boxplot")
```

WRANGLING:

subsetting:
```
mtcars %>% dplyr::filter(mpg>30)
```

making a new variable:
```
mtcars <- mtcars %>%
dplyr::mutate(efficient = if_else(mpg>30,  TRUE, FALSE))
```

R Syntax Comparison : : **CHEAT SHEET**

Syntax is the set of rules that govern what code works and doesn't work in a programming language. Most programming languages offer one standardized syntax, but R allows package developers to specify their own syntax. As a result, there is a large variety of (equally valid) R syntaxes.

The three most prevalent R syntaxes are:

1. The **dollar sign syntax,** sometimes called **base R syntax**, expected by most `base` R functions. It is characterized by the use of `dataset$variablename`, and is also associated with square bracket subsetting, as in `dataset[1,2]`. Almost all R functions will accept things passed to them in dollar sign syntax.
2. The **formula syntax**, used by modeling functions like `lm()`, `lattice` graphics, and `mosaic` summary statistics. It uses the tilde (~) to connect a response variable and one (or many) predictors. Many base R functions will accept formula syntax.
3. The **tidyverse syntax** used by `dplyr`, `tidyr`, and more. These functions expect data to be the first argument, which allows them to work with the "pipe" (%>%) from the `magrittr` package. Typically, `ggplot2` is thought of as part of the tidyverse, although it has its own flavor of the syntax using plus signs (+) to string pieces together. `ggplot2` author Hadley Wickham has said the package would have had different syntax if he had written it after learning about the pipe.

Educators often try to teach within one unified syntax, but most R programmers use some combination of all the syntaxes.

Internet research tip:

If you are searching on google, StackOverflow, or another favorite online source and see code in a syntax you don't recognize:

- Check to see if the code is using one of the three common syntaxes listed on this cheatsheet
- Try your search again, using a keyword from the syntax name ("tidyverse") or a relevant package ("mosaic")

❗ Sometimes particular syntaxes work, but are considered dangerous to use, because they are so easy to get wrong. For example, passing variable names without assigning them to a named argument.

Even **more** ways to say the same thing

Even within one syntax, there are often variations that are equally valid. As a case study, let's look at the `ggplot2` syntax. `ggplot2` is the plotting package that lives within the tidyverse. If you read **down** this column, all the code here produces the same graphic.

read down this column for many pieces of code in one syntax that look different but produce the same graphic

quickplot

`qplot()` stands for quickplot, and allows you to make quick plots. It doesn't have the full power of `ggplot2`, and it uses a slightly different syntax than the rest of the package.

```
ggplot2::qplot(x=disp, y=mpg, data=mtcars, geom="point")
```

```
ggplot2::qplot(x=disp, y=mpg, data=mtcars)  ❗
```

```
ggplot2::qplot(disp, mpg, data=mtcars)  ❗ ❗
```

ggplot

To unlock the power of `ggplot2`, you need to use the `ggplot()` function (which sets up a plotting region) and add `geoms` to the plot.

```
ggplot2::ggplot(mtcars) +
    geom_point(aes(x=disp, y=mpg))
```

```
ggplot2::ggplot(data=mtcars) +
    geom_point(mapping=aes(x=disp, y=mpg))
```

plus adds layers

```
ggplot2::ggplot(mtcars, aes(x=disp, y=mpg)) +
    geom_point()
```

```
ggplot2::ggplot(mtcars, aes(x=disp)) +
    geom_point(aes(y=mpg))
```

ggformula

The "third and a half way" to use the formula syntax, but get ggplot2-style graphics

```
ggformula::gf_point(mpg~disp, data= mtcars)
```

formulas in base plots

Base R plots will also take the formula syntax, although it's not as commonly used

```
plot(mpg~disp, data=mtcars)
```

The teachR's : : CHEAT SHEET

Getting ready to teach some R? Use our cheat sheet to **prepare**, **teach** and **debrief**

DRAFT v0.1

Before the course (design)

Use these to prepare your lecture/course:

Who are your learners? (Persona Analysis)
(change according to requirements…[1])

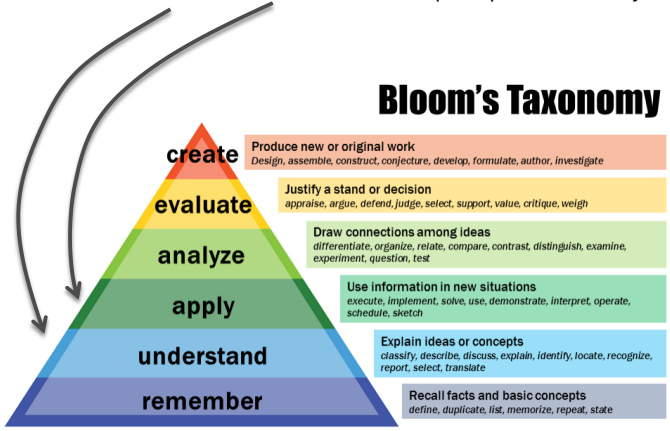
The R novice
Background: some statistics, some programming
Prior knowledge: basic R course, base R syntax
Goals: understand tidy concepts,
expose to tidyverse practices
Special needs: First successes, mitigate fears, encourage learning

The R "false expert"
Background: working with R for some time, but doesn't keep-up
Prior knowledge: been using base R syntax, loops, and functions
Goals: strengthen tidyverse familiarity, apply dplyr workflow
Special needs: switch from obsolete methods to state-of-the-art R

Define goals using Bloom's Taxonomy [2]

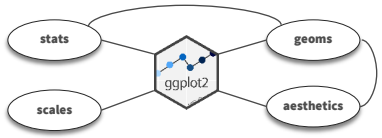
Design your classes to move your learners "up the pyramid"
Keep "realistic goals" for each persona

For example (R shiny – novice):
Learners will **describe** and **demonstrate** the principles of reactivity



Design your lecture using Conceptual maps

Keep the number of elements small (up to ~7 items), e.g.:



Write the "final exam"

How are you going to test knowledge after the lecture?
What should learners be able to answer?

Turn the concepts into slides

Add faded examples (exercises) and check-in slides

Check-ins, e.g.: multiple choice quick questions"
Faded examples = fill in the blanks, e.g.:

```
ggplot(data = ___, mapping = aes(x = ___, y = ___)) +
  geom_*() +
```

During the course (implement)

Things you can implement to improve the lecture workflow

Learners use **sticky notes** to indicate status:
Green = everything is OK/Exercise completed.
Red = help me! I ran into a problem.
Blue = I need a break.

Engage with online mini-polls during lecture
Use regular check-ins during your lecture (3-4 check-ins per hour). No one "opts-out" (everyone answers once in a while – you choose)

After the course (learn/improve)

Make sure you make the most to improve your next lecture

Use feedback to understand what went well, and what you need to improve.

Measure the time each lecture takes you (or where did you get to), so that next time your time estimates will be better

Useful tips and tricks

Useful tips for preparations

Use github to upload course materials

RMarkdown for exercises

Recommended reading materials/references for R courses:

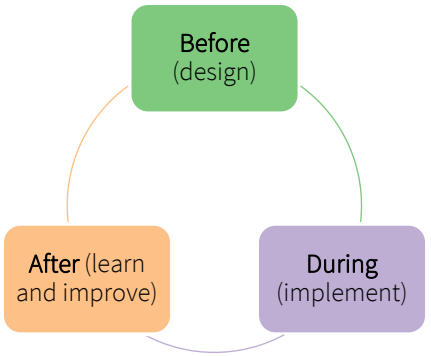
R for Data Science / Garrett Grolemund and Hadley Wickham (r4ds.had.co.nz)

Advanced R/ Hadley Wickham (adv-r.had.co.nz)

RStudio **Cheat sheets**:

https://www.rstudio.com/resources/cheatsheets/

Iterative work flow



Additional sources

[1] Dreyfus, Stuart E., and Hubert L. Dreyfus. *A five stage model of the mental activities involved in directed skill acquisition.* No. ORC-80-2. California Univ Berkeley Operations Research Center, 1980.

[2] Content downloaded from https://cft.vanderbilt.edu/guides-sub-pages/blooms-taxonomy/
(CC-BY-SA Vanderbilt University Center for Teaching)

Class Agnostic Time Series with tsbox : : CHEAT SHEET

Basics

IDEA

tsbox provides a time series toolkit which:

1. works identically with most time series **classes**
2. handles regular and irregular **frequencies**
3. **converts** between classes and frequencies

Most functions in tsbox have the same structure:

function starts with ts_

first argument is any ts-boxable object

```
a <- ts_pc(AirPassengers)
```

returns a ts-boxable obect of the same class as input

COMBINE TIME SERIES

collect time series of **all classes** and **frequencies** as multiple time series

```
ts_c(mdeaths, austres)
```

combine time series to a new, single time series (first series wins if overlapping)

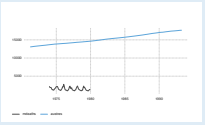
```
ts_bind(mdeaths, austres)
```

like ts_bind, but extra- and retropolate, using growth rates

```
ts_chain(mdeaths, austres)
```

PLOT AND SUMMARIZE

Plot time series of **all classes** and **frequencies**



```
ts_plot(mdeaths, austres)
ts_ggplot(mdeaths, austres)
```

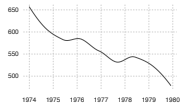
```
ts_summary(ts_c(mdeaths, austres))
```

```
      id obs    diff freq      start        end
1 mdeaths  72 1 month   12 1974-01-01 1979-12-01
2 austres  89 3 month    4 1971-04-01 1993-04-01
```

Helper Functions

Transform time series of **all classes** and **frequencies**

TRANSFORM



ts_trend(): Trend estimation based on loess

```
ts_trend(fdeaths)
```

ts_pc(), ts_pcy(), ts_pca(), ts_diff(), ts_diffy(): (annualized) Percentage change rates or differences to previous period, year

```
ts_pc(fdeaths)
```

ts_scale(): normalize mean and variance

```
ts_scale(fdeaths)
```

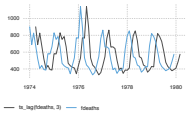
ts_index():Index, based on levels
ts_compound(): Index, based on growth rates

```
ts_index(fdeaths, base = 1976)
```

ts_seas(): seasonal adjustment using X-13

```
ts_seas(fdeaths)
```

SPAN AND FREQUENCY

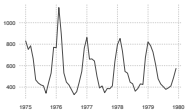


ts_lag(): Lag or lead of time series

```
ts_lag(fdeaths, 4)
```

ts_frequency(): convert to frequency

```
ts_frequency(fdeaths, "year")
```



ts_span(): filter time series for a time span.

```
ts_span(fdeaths, "1976-01-01")
ts_span(fdeaths, "-5 year")
```

Class Conversion

tsbox is built around a set of converters, which convert time series of the following **supported classes** to each other:

converter function	ts-boxable class
ts_ts()	ts, mts
ts_data.frame(), ts_df()	data.frame
ts_data.table(), ts_dt()	data.table
ts_tbl()	df_tbl, "tibble"
ts_xts()	xts
ts_zoo()	zoo
ts_tibbletime()	tibbletime
ts_timeSeries()	timeSeries
ts_tsibble()	tsibble
ts_tslist()	a list with ts objects

Time Series in data frames

LONG STRUCTURE

Default structure to store multiple time series in long data frames (or data tables, or tibbles)

```
ts_df(ts_c(fdeaths, mdeaths))
```

id	time	value
fdeaths	1974-01-01	901
fdeaths	1974-02-01	689
fdeaths	1974-03-01	827
...	...	...

AUTO-DETECT COLUMN NAMES

tsbox auto-detects a *value*-, a *time*- and zero, one or several *id*-columns. Alternatively, the *time*- and the *value*-column can be explicitly named **time** and **value**.

ts_default(): standardize column names in data frames

RESHAPE

ts_wide(): convert default long structure to wide
ts_long(): convert wide structure to default long

USE WITH PIPE

tsbox plays well with tibbles and with `%>%`, so it can be easily integrated into a dplyr/pipe workflow

```
library(dplyr)
ts_c(fdeaths, mdeaths) %>%
  ts_tbl() %>%
  ts_trend() %>%
  ts_pc()
```

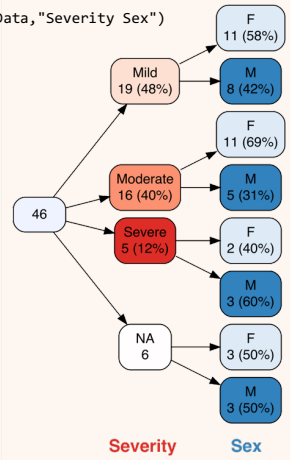
pass return value as first argument to the next function

vtree cheatsheet

Basics

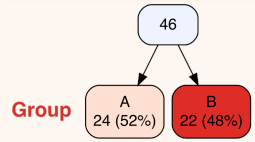
Draw a basic variable tree

```
vtree(FakeData,"Severity Sex")
```



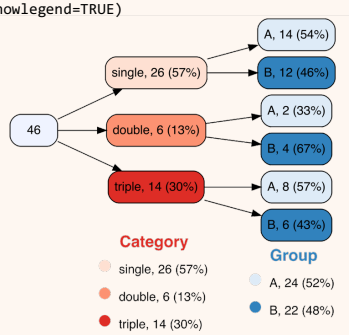
Draw the tree vertically

```
vtree(FakeData,"Group",horiz=FALSE)
```



Display a legend

```
vtree(FakeData,"Category Group",sameline=TRUE,
  showlegend=TRUE)
```



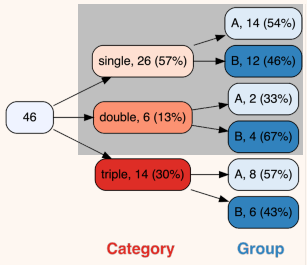
Variable specification

Modifier	Effect
prefix `is.na:`	is.na(variable)
prefix `stem:`	all REDCap variables with stem
prefix `tri:`	trichotomize in each node
`variable=`*x*	dichotomize at *x*
`variable<`*x*	dichotomize below x
`variable>`*x*	dichotomize above *x*

Pruning

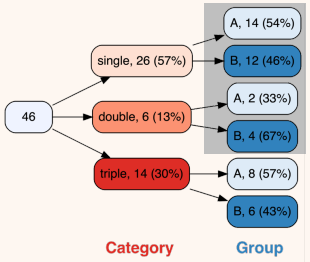
Prune single and double and their descendants

```
vtree(FakeData,"Category Group",sameline=TRUE,
  prune=list(Category=c("single","double")))
```



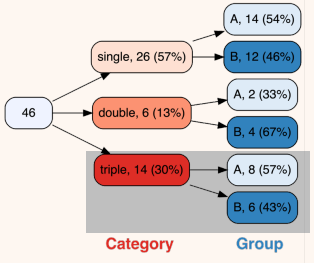
Prune nodes below single and double

```
vtree(FakeData,"Category Group",sameline=TRUE,
  prunebelow=list(Category=c("single","double")))
```



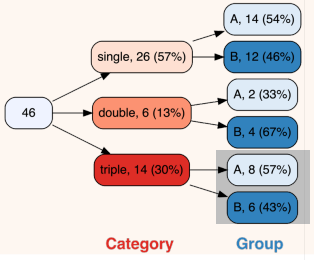
Only keep single and double and their descendants

```
vtree(FakeData,"Category Group",sameline=TRUE,
  keep=list(Category=c("single","double")))
```



Only include descendants of single and double

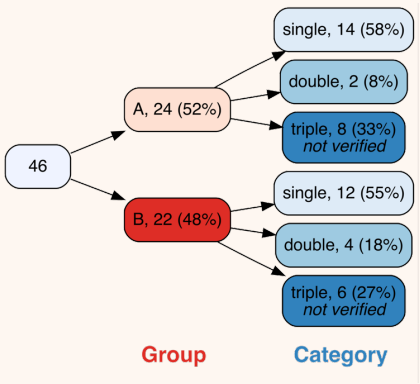
```
vtree(FakeData,"Category Group",sameline=TRUE,
  follow=list(Category=c("single","double")))
```



Text

Add text to nodes

```
vtree(FakeData,"Group Category",sameline=TRUE,
  text=list(Category=c(triple="\n*not verified*")))
```



Code	Meaning
`\n`	Line break
`*...*`	Italics
`**...**`	Bold
`^...^`	Superscript
`~...~`	Subscript
`%%red ...%%`	Make text red (or another color)

Text in a specific node ("targeted text")

```
ttext=list(Group="A",Severity="Moderate",text="hi")
```

Labeling

Parameter

Change variable labels
`labelvar=c(`
`Severity="New label for Severity")`

Change node labels for a variable
`labelnode=list(MyVar=`
`c(New="Old",New2="Old2"))`

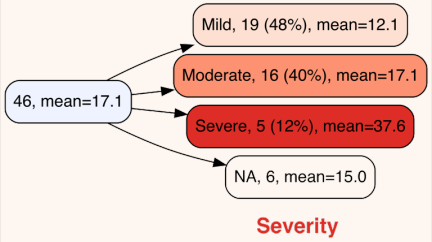
Change a specific node label
`tlabelnode=list(`
`c(Group="A",Sex="F",label="girl"))`

Font size (points) for variable names `varnamepointsize=15`
Specify an optional label for the root node `title="All patients"`
Show node labels? `shownodelabels=TRUE`
Show variable names? `showvarnames=TRUE`

Summary information

Add summary statistics to nodes

```
vtree(FakeData,"Severity",sameline=TRUE,
  summary="Score , mean=%mean%")
```



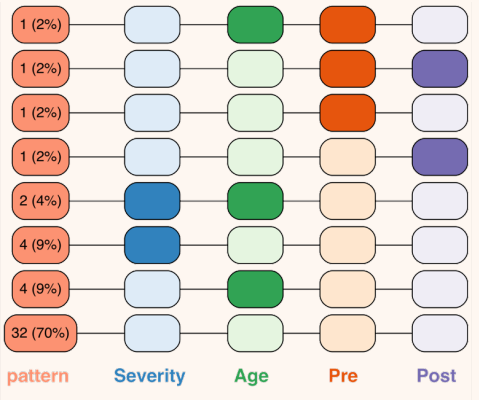
Code	Result
`%mean%`	mean
`%SD%`	standard deviation
`%min%`	minimum
`%max%`	maximum
`%pX%`	Xth percentile (e.g. p50 means the 50th percentile)
`%median%`	median, i.e. p50
`%IQR%`	IQR, i.e. p25, p75
`%npct%`	frequency and percentage
`%pct%`	just percentage
`%list%`	list of individual values, separated by commas
`%listlines%`	list of individual values, each on a separate line
`%mv%`	the number of missing values

Code	Summary information restricted to:
`%noroot%`	all nodes *except* the root
`%leafonly%`	leaf nodes
`%var=`*v*`%`	nodes of variable *v*
`%node=`*n*`%`	nodes named *n*

Checking for missing values

Show missing value patterns; dark color = missing, light = not missing

```
vtree(FakeData,"Severity Age Pre Post",check.is.na=TRUE)
```



 • Learn more at https://github.com/nbarrowman/vtree/ • package version 2.0.0 available on CRAN • updated June 1, 2019

xplain Cheat Sheet

Important Links

xplain package on CRAN	https://cran.r-project.org/web/packages/xplain/index.html
xplain web tutorial	http://www.zuckarelli.de/xplain/index.html
xplain cheat sheet	http://www.zuckarelli.de/xplain/xplain_cheatsheet.pdf
xplain on GitHub	https://www.github.com/jsugarelli/xplain

Purpose & Application

- xplain allows to **write interpretation/explanation texts** for statistical functions in the form of XML files.
- The user of the functions can read these explanations **while working on his/her specific problems**.
- xplain explanations **can react to the user's results** and provide meaningful insights related to the user's problem.
- For this, the xplain **XML files can contain R code** and can **work with the return object** of the user's function call.

```
> xplain("lm(education ~ young + income + urban)")
> Your R^2 is 0.11 which is quite low. There is a serious
risk your model is misspecified. You should reconsider the
selection of variables included in your model.
```

xplain XML files

1 <xplain>
Any valid xplain XML must be enclosed in an <xplain> block. Multiple <xplain> blocks per XML file are possible.

2 <package>
A <package> block combines all functions from the same package.

3 <function>
Within a <function> block, explanations/interpretations for the function as such or for specific elements of the return object can be provided.

4 <result>
Packages explanations/ interpretations related to one element of the function's return object.

```
<xml>
 1 <xplain>
     2 <package name = "stats">
         3 <function name = "lm">
             4 <title>This is about lm</title>
             5 <text>…</text>
             6 <result name = "coefficients">
                 4 <title>…<title>
                 5 <text>…</text>
               </result>
           </function>
       </package>
   </xplain>
</xml>
```

Not case-sensitive

5 <title>
Structures explanations with headers.

6 <text>
The actual explanations/interpretations. Can include R code with references to the function's return object.

Including R code

R code can be easily integrated into <text></text> elements:

```
<text>  !%%  R code  %%!  </text>
```

R code delimiter tags

Access the explained function's (<function name="…">) return object:

- Access the full return object with @. Example: summary(@).
- Access the current <result name="…"> item of the return object with ##. Example: mean(##).

Using placeholders

```
<define name= "placeholder" > !%%  R code  %%! </define>

</text>  Text…  !** "placeholder" **!  Text…  </text>
```

Placeholder name delimiter tags

Example:
```
<define name="s">!%% summary(@) %%!</define>
<text>And here is the summary !**s**! for your model</text>
```

Iterating through (items of) the return object

- To apply a <text> element to a whole matrix, data frame, vector or list, use the **foreach** attribute.
- Value of foreach defines what is iterated over and (for 2D structures) in which sequence; items is for lists.
- $ is a placeholder for the index of the current element.
- **Example** (shows all 1st column elements of the coefficient matrix):
<text foreach="rows">!%% @$coefficients[$,1] %%!</text>

foreach =
"rows"
"columns"
"rows, columns"
"columns, rows"
"items"

Main attributes: Overview

name	Name of the element (package, function, result).
lang	Language (ISO code) of the explanation (e.g. "EN").
level	Complexity level; integer number; cumulative, i.e. level=1 explanations will also be presented when level=2 or level=3 are called.

Attributes: Inheritance and necessity

- Elements **inherit attributes from higher-level** elements; e.g., if only one language, definition on <xplain> level suffices. Lower-level attributes overrule higher-level.
- **name** attribute required for <package>, <function> and <result> elements.
- All levels shown, if no **level** is given to xplain().

Calling xplain()

1 Direct call of xplain()

call	Call of the explained function as string
xml	Path of the XML file providing the explanations
lang	Language of the explanations to be shown (default means English)
level	Complexity level of the explanations (cumulative! Default means "all")

2 Wrapper function with xplain.getcall()

Example: lm

```
lm.xplain <- function(formula, data, subset, weights, na.action,
method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE,
singular.ok = TRUE, contrasts = NULL, offset, ...) {
  call<-xplain.getcall("lm")
  xplain(call, xml="http://www.zuckarelli.de/example_lm.xml")
}
```

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