

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  
}
```

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	Output	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.

	<code>m[2,]</code> - Select a row	<code>t(m)</code> Transpose
	<code>m[, 1]</code> - Select a column	<code>m %*% n</code> Matrix Multiplication
	<code>m[2, 3]</code> - Select an element	<code>solve(m, n)</code> Find x in: $m \cdot x = n$

Lists

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

<code>l[[2]]</code>	<code>l[1]</code>	<code>l\$x</code>	<code>l['y']</code>
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

Matrix subsetting

<code>df[, 2]</code>		<code>nrow(df)</code> Number of rows.	<code>cbind</code> - Bind columns.
<code>df[2,]</code>		<code>ncol(df)</code> Number of columns.	<code>rbind</code> - Bind rows.
<code>df[2, 2]</code>		<code>dim(df)</code> Number of columns and rows.	

Strings

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

Factors

<code>factor(x)</code>	Turn a vector into a factor. Can set the levels of the factor and the order.
<code>cut(x, breaks = 4)</code>	Turn a numeric vector into a factor by 'cutting' into sections.

Statistics

<code>lm(y ~ x, data=df)</code>	Linear model.	<code>t.test(x, y)</code>	Test for a difference between proportions.
<code>glm(y ~ x, data=df)</code>	Generalised linear model.	<code>pairwise.t.test</code>	Perform a t-test for paired data.
<code>summary</code>	Get more detailed information out a model.	<code>aov</code>	Analysis of variance.

Distributions

	Random Variates	Density Function	Cumulative Distribution	Quantile
Normal	<code>rnorm</code>	<code>dnorm</code>	<code>pnorm</code>	<code>qnorm</code>
Poisson	<code>rpois</code>	<code>dpois</code>	<code>ppois</code>	<code>qpois</code>
Binomial	<code>rbinom</code>	<code>dbinom</code>	<code>pbinom</code>	<code>qbinom</code>
Uniform	<code>runif</code>	<code>dunif</code>	<code>unif</code>	<code>qunif</code>

Plotting

<code>plot(x)</code>	Values of x in order.	<code>plot(x, y)</code>	Values of x against y.	<code>hist(x)</code>	Histogram of x.
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Dates

See the `lubridate` package.

Advanced R

Cheat Sheet

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Environment Basics

Environment – **Data structure** (with two components below) that powers lexical scoping

Create environment: `env1<-new.env()`

1. **Named list** (“Bag of names”) – each name points to an object stored elsewhere in memory.

If an object has no names pointing to it, it gets automatically deleted by the garbage collector.

- Access with: `ls('env1')`

2. **Parent environment** – used to implement lexical scoping. If a name is not found in an environment, then R will look in its parent (and so on).

- Access with: `parent.env('env1')`

Four special environments

1. **Empty environment** – ultimate ancestor of all environments
 - Parent: none
 - Access with: `emptyenv()`

2. **Base environment** - environment of the base package
 - Parent: empty environment
 - Access with: `baseenv()`

3. **Global environment** – the interactive workspace that you normally work in
 - Parent: environment of last attached package
 - Access with: `globalenv()`

4. **Current environment** – environment that R is currently working in (may be any of the above and others)
 - Parent: empty environment
 - Access with: `environment()`

Environments

Search Path

Search path – mechanism to look up objects, particularly functions.

- Access with : `search()` – lists all parents of the global environment (see Figure 1)
- Access any environment on the search path:
`as.environment('package:base')`

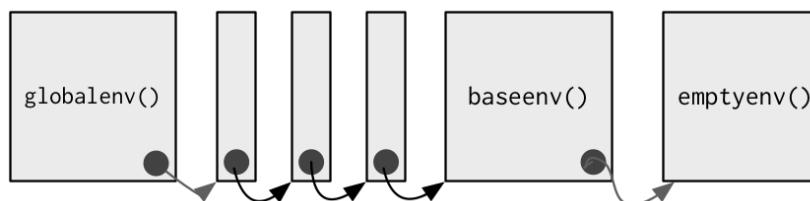


Figure 1 – The Search Path

- Mechanism : always start the search from global environment, then inside the latest attached package environment.
 - New package loading with `library()`/`require()` : new package is attached right after global environment. (See Figure 2)
 - Name conflict in two different package : functions with the same name, latest package function will get called.

`search()`:

```
'.GlobalEnv' ... 'Autoloads' 'package:base'  
library(reshape2); search()  
.GlobalEnv' 'package:reshape2' ... 'Autoloads' 'package:base'
```

NOTE: Autoloads : special environment used for saving memory by only loading package objects (like big datasets) when needed

Figure 2 – Package Attachment

Binding Names to Values

Assignment – act of binding (or rebinding) a name to a value in an environment.

1. `<-` (Regular assignment arrow) – always creates a variable in the current environment
2. `<-<` (Deep assignment arrow) - modifies an existing variable found by walking up the parent environments

Warning: If `<-<` doesn't find an existing variable, it will create one in the global environment.

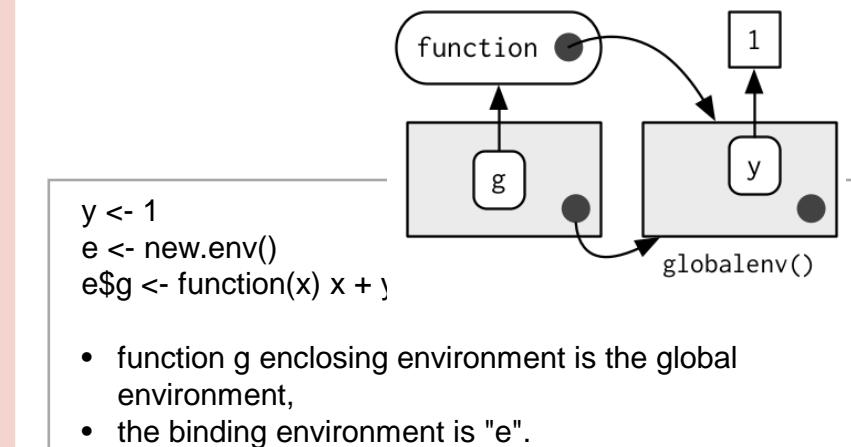
Function Environments

1. **Enclosing environment** - an environment where the function is created. It determines how function finds value.
 - Enclosing environment never changes, even if the function is moved to a different environment.
 - Access with: `environment('func1')`

2. **Binding environment** - all environments that the function has a binding to. It determines how we find the function.

- Access with: `pryr::where('func1')`

Example (for enclosing and binding environment):



3. **Execution environment** - new created environments to host a function call execution.

- Two parents :
 - I. Enclosing environment of the function
 - II. Calling environment of the function
- Execution environment is thrown away once the function has completed.

4. **Calling environment** - environments where the function was called.

- Access with: `parent.frame('func1')`
- Dynamic scoping :
 - About : look up variables in the calling environment rather than in the enclosing environment
 - Usage : most useful for developing functions that aid interactive data analysis

Data Structures

	Homogeneous	Heterogeneous
1d	Atomic vector	List
2d	Matrix	Data frame
nd	Array	

Note: R has no 0-dimensional or scalar types. Individual numbers or strings, are actually vectors of length one, NOT scalars.

Human readable description of any R data structure :

```
str(variable)
```

Every **Object** has a mode and a class

- Mode:** represents how an object is stored in memory
 - 'type' of the object from R's point of view
 - Access with: `typeof()`
- Class:** represents the object's abstract type
 - 'type' of the object from R's object-oriented programming point of view
 - Access with: `class()`

	typeof()	class()
strings or vector of strings	character	character
numbers or vector of numbers	numeric	numeric
list	list	list
data.frame	list	data.frame

Factors

- Factors are built on top of integer vectors using two attributes :

```
class(x) -> 'factor'
```

```
levels(x) # defines the set of allowed values
```

- Useful when you know the possible values a variable may take, even if you don't see all values in a given dataset.

Warning on Factor Usage:

- Factors look and often behave like character vectors, they are actually integers. Be careful when treating them like strings.
- Most data loading functions automatically convert character vectors to factors. (Use argument `stringAsFactors = FALSE` to suppress this behavior)

Object Oriented (OO) Field Guide

Object Oriented Systems

R has three object oriented systems :

- S3** is a very casual system. It has no formal definition of classes. It implements generic function OO.
 - Generic-function OO** - a special type of function called a generic function decides which method to call.

Example:	<code>drawRect(canvas, 'blue')</code>
Language:	R

- Message-passing OO** - messages (methods) are sent to objects and the object determines which function to call.

Example:	<code>canvas.drawRect('blue')</code>
Language:	Java, C++, and C#

- S4** works similarly to S3, but is more formal. Two major differences to S3 :

- Formal class definitions** - describe the representation and inheritance for each class, and has special helper functions for defining generics and methods.
- Multiple dispatch** - generic functions can pick methods based on the class of any number of arguments, not just one.

- Reference classes** are very different from S3 and S4:

- Implements message-passing OO** - methods belong to classes, not functions.
- Notation** - \$ is used to separate objects and methods, so method calls look like `canvas$drawRect('blue')`.

S3

1. About S3 :

- R's first and simplest OO system
- Only OO system used in the base and stats package
- Methods belong to functions, not to objects or classes.

2. Notation :

- `generic.class()`

<code>mean.Date()</code>	Date method for the generic - <code>mean()</code>
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3. Useful 'Generic' Operations

- Get all methods that belong to the 'mean' generic:
 - `Methods('mean')`
- List all generics that have a method for the 'Date' class :
 - `methods(class = 'Date')`

4. S3 objects

- are usually built on top of lists, or atomic vectors with attributes.
- Factor and data frame are S3 class
 - Useful operations:

Check if object is an S3 object	<code>is.object(x) & !isS4(x) or pryr::oGetType()</code>
Check if object inherits from a specific class	<code>inherits(x, 'classname')</code>
Determine class of any object	<code>class(x)</code>

Base Type (C Structure)

R base types - the internal C-level types that underlie the above OO systems.

- Includes** : atomic vectors, list, functions, environments, etc.
- Useful operation** : Determine if an object is a base type (Not S3, S4 or RC) `is.object(x)` returns FALSE

- Internal representation** : C structure (or struct) that includes :

- Contents of the object
- Memory Management Information
- Type
 - Access with: `typeof()`

Functions

Function Basics

Functions – objects in their own right

All R functions have three parts:

body()	code inside the function
formals()	list of arguments which controls how you can call the function
environment()	“map” of the location of the function’s variables (see “Enclosing Environment”)

Every operation is a function call

- +, for, if, [, \$, { ...
- x + y is the same as `+`(x, y)

Note: the backtick (`), lets you refer to functions or variables that have otherwise reserved or illegal names.

Lexical Scoping

What is Lexical Scoping?

- Looks up value of a symbol. (see “Enclosing Environment”)
- **findGlobals()** - lists all the external dependencies of a function

```
f <- function() x + 1
codetools::findGlobals(f)
> '+' 'x'

environment(f) <- emptyenv()
f()

# error in f(): could not find function "+"
```

- R relies on lexical scoping to find everything, even the + operator.

Function Arguments

Arguments – passed by reference and copied on modify

1. Arguments are matched first by exact name (perfect matching), then by prefix matching, and finally by position.
2. Check if an argument was supplied : **missing()**

```
i <- function(a, b) {
  missing(a) -> # return true or false
}
```

3. Lazy evaluation – since x is not used **stop("This is an error!")** never get evaluated.

```
f <- function(x) {
  10
}
f(stop('This is an error!')) -> 10
```

4. Force evaluation

```
f <- function(x) {
  force(x)
  10
}
```

5. Default arguments evaluation

```
f <- function(x = ls()) {
  a <- 1
  x
}
```

f() -> 'a' 'x'	ls() evaluated inside f
f(ls())	ls() evaluated in global environment

Return Values

- **Last expression evaluated or explicit return()**. Only use explicit return() when returning early.
- **Return ONLY single object**. Workaround is to return a list containing any number of objects.
- **Invisible return object value** - not printed out by default when you call the function.

```
f1 <- function() invisible(1)
```

Primitive Functions

What are Primitive Functions?

1. Call C code directly with **.Primitive()** and contain no R code

```
print(sum) :
> function (... , na.rm = FALSE) .Primitive('sum')
```

2. **formals()**, **body()**, and **environment()** are all NULL

3. Only found in base package

4. More efficient since they operate at a low level

Influx Functions

What are Influx Functions?

1. Function name comes in between its arguments, like + or -
2. All user-created infix functions must start and end with %.

```
'%+%' <- function(a, b) paste0(a, b)
'new' %+% 'string'
```

3. Useful way of providing a default value in case the output of another function is NULL:

```
'%||%' <- function(a, b) if (!is.null(a)) a else b
function_that_might_return_null() %||% default value
```

Replacement Functions

What are Replacement Functions?

1. Act like they modify their arguments in place, and have the special name xxx <-
2. Actually create a modified copy. Can use **pryr::address()** to find the memory address of the underlying object

```
second<- <- function(x, value) {
  x[2] <- value
  x
}
x <- 1:10
second(x) <- 5L
```

Subsetting

Subsetting returns a copy of the original data, NOT copy-on modified

Simplifying vs. Preserving Subsetting

1. Simplifying subsetting

- Returns the **simplest** possible data structure that can represent the output

2. Preserving subsetting

- Keeps the structure of the output the **same** as the input.
- When you use drop = FALSE, it's preserving

	Simplifying*	Preserving
Vector	x[[1]]	x[1]
List	x[[1]]	x[1]
Factor	x[1:4, drop = T]	x[1:4]
Array	x[1,] or x[, 1]	x[1, , drop = F] or x[, 1, drop = F]
Data frame	x[, 1] or x[[1]]	x[, 1, drop = F] or x[1]

Simplifying behavior varies slightly between different data types:

1. Atomic Vector

- x[[1]] is the same as x[1]

2. List

- [] always returns a list
- Use [[]] to get list contents, this returns a single value piece out of a list

3. Factor

- Drops any unused levels but it remains a factor class

4. Matrix or Array

- If any of the dimensions has length 1, that dimension is dropped

5. Data Frame

- If output is a single column, it returns a vector instead of a data frame

Data Frame Subsetting

Data Frame – possesses the **characteristics of both lists and matrices**. If you subset with a single vector, they behave like lists; if you subset with two vectors, they behave like matrices

1. Subset with a single vector : Behave like lists

```
df1[c('col1', 'col2')]
```

2. Subset with two vectors : Behave like matrices

```
df1[, c('col1', 'col2')]
```

The results are the same in the above examples, however, results are different if subsetting with only one column. (see below)

1. Behave like matrices

```
str(df1[, 'col1']) -> int [1:3]
```

- Result: the result is a vector

2. Behave like lists

```
str(df1['col1']) -> 'data.frame'
```

- Result: the result remains a data frame of 1 column

\$ Subsetting Operator

1. About Subsetting Operator

- Useful shorthand for [[combined with character subsetting

```
x$y is equivalent to x[['y', exact = FALSE]]
```

2. Difference vs. [[

- \$ does partial matching, [[does not

```
x <- list(abc = 1)
x$a -> 1      # since "exact = FALSE"
x[['a']] ->   # would be an error
```

3. Common mistake with \$

- Using it when you have the name of a column stored in a variable

```
var <- 'cyl'
x$var
# doesn't work, translated to x[['var']]
# Instead use x[[var]]
```

Examples

1. Lookup tables (character subsetting)

```
x <- c('m', 'f', 'u', 'f', 'f', 'm', 'm')
lookup <- c(m = 'Male', f = 'Female', u = NA)
lookup[x]
> m f u f f m m
> 'Male' 'Female' NA 'Female' 'Female' 'Male' 'Male'
unname(lookup[x])
> 'Male' 'Female' NA 'Female' 'Female' 'Male' 'Male'
```

2. Matching and merging by hand (integer subsetting)

Lookup table which has multiple columns of information:

```
grades <- c(1, 2, 2, 3, 1)
info <- data.frame(
  grade = 3:1,
  desc = c('Excellent', 'Good', 'Poor'),
  fail = c(F, F, T)
)
```

First Method

```
id <- match(grades, info$grade)
info[id, ]
```

Second Method

```
rownames(info) <- info$grade
info[as.character(grades), ]
```

3. Expanding aggregated counts (integer subsetting)

- Problem:** a data frame where identical rows have been collapsed into one and a count column has been added
- Solution:** rep() and integer subsetting make it easy to uncollapse the data by subsetting with a repeated row index:
rep(x, y) rep replicates the values in x, y times.

```
df1$countCol is c(3, 5, 1)
rep(1:nrow(df1), df1$countCol)
> 1 1 1 2 2 2 2 2 3
```

4. Removing columns from data frames (character subsetting)

There are two ways to remove columns from a data frame:

Set individual columns to NULL	df1\$col3 <- NULL
Subset to return only columns you want	df1[c('col1', 'col2')]

5. Selecting rows based on a condition (logical subsetting)

- This is the most commonly used technique for extracting rows out of a data frame.

```
df1[df1$col1 == 5 & df1$col2 == 4, ]
```

Subsetting continued

Boolean Algebra vs. Sets (Logical and Integer Subsetting)

1. **Using integer subsetting** is more effective when:

- You want to find the first (or last) TRUE.
- You have very few TRUEs and very many FALSEs; a set representation may be faster and require less storage.

2. **which()** - conversion from boolean representation to integer representation

```
which(c(T, F, T F)) -> 1 3
```

- Integer representation length : is always <= boolean representation length
- Common mistakes :
 - I. Use **x[which(y)]** instead of **x[y]**
 - II. **x[-which(y)]** is not equivalent to **x[!y]**

Recommendation:

Avoid switching from logical to integer subsetting unless you want, for example, the first or last TRUE value

Subsetting with Assignment

1. All subsetting operators can be combined with assignment to modify selected values of the input vector.

```
df1$col1[df1$col1 < 8] <- 0
```

2. Subsetting with nothing in conjunction with assignment :

- Why : Preserve original object class and structure

```
df1[] <- lapply(df1, as.integer)
```

Debugging, Condition Handling and Defensive Programming

Debugging Methods

1. traceback() or RStudio's error inspector

- Lists the sequence of calls that lead to the error

2. browser() or RStudio's breakpoints tool

- Opens an interactive debug session at an arbitrary location in the code

3. options(error = browser) or RStudio's "Rerun with Debug" tool

- Opens an interactive debug session where the error occurred

Error Options:

options(error = recover)

- Difference vs. 'browser': can enter environment of any of the calls in the stack

options(error = dump_and_quit)

- Equivalent to 'recover' for non-interactive mode
- Creates **last.dump.rda** in the current working directory

In batch R process :

```
dump_and_quit <- function() {  
  # Save debugging info to file  
  last.dump.rda  
  dump.frames(to.file = TRUE)  
  # Quit R with error status  
  q(status = 1)  
}  
  
options(error = dump_and_quit)
```

In a later interactive session :

```
load("last.dump.rda")  
debugger()
```

Condition Handling of Expected Errors

1. Communicating potential problems to users:

I. stop()

- Action : raise fatal error and force all execution to terminate
- Example usage : when there is no way for a function to continue

II. warning()

- Action : generate warnings to display potential problems
- Example usage : when some of elements of a vectorized input are invalid

III. message()

- Action : generate messages to give informative output
- Example usage : when you would like to print the steps of a program execution

2. Handling conditions programmatically:

I. try()

- Action : gives you the ability to continue execution even when an error occurs

II. tryCatch()

- Action : lets you specify handler functions that control what happens when a condition is signaled

```
result = tryCatch(code,  
  error = function(c) "error",  
  warning = function(c) "warning",  
  message = function(c) "message"  
)
```

Use **conditionMessage(c)** or **c\$message** to extract the message associated with the original error.

Defensive Programming

Basic principle : "fail fast", to raise an error as soon as something goes wrong

1. **stopifnot()** or use 'assertthat' package - check inputs are correct

2. **Avoid subset(), transform() and with()** - these are non-standard evaluation, when they fail, often fail with uninformative error messages.

3. **Avoid [and sapply()** - functions that can return different types of output.

- Recommendation : Whenever subsetting a data frame in a function, you should always use **drop = FALSE**

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

	<code>str_detect(string, pattern)</code> Detect the presence of a pattern match in a string. <code>str_detect(fruit, "a")</code>
	<code>str_which(string, pattern)</code> Find the indexes of strings that contain a pattern match. <code>str_which(fruit, "a")</code>
	<code>str_count(string, pattern)</code> Count the number of matches in a string. <code>str_count(fruit, "a")</code>
	<code>str_locate(string, pattern)</code> Locate the positions of pattern matches in a string. Also <code>str_locate_all</code> . <code>str_locate(fruit, "a")</code>

Subset Strings

	<code>str_sub(string, start = 1L, end = -1L)</code> Extract substrings from a character vector. <code>str_sub(fruit, 1, 3); str_sub(fruit, -2)</code>
	<code>str_subset(string, pattern)</code> Return only the strings that contain a pattern match. <code>str_subset(fruit, "b")</code>
	<code>str_extract(string, pattern)</code> Return the first pattern match found in each string, as a vector. Also <code>str_extract_all</code> to return every pattern match. <code>str_extract(fruit, "[aeiou]")</code>
	<code>str_match(string, pattern)</code> Return the first pattern match found in each string, as a matrix with a column for each () group in pattern. Also <code>str_match_all</code> . <code>str_match(sentences, "(a the) ([^]+)")</code>

Manage Lengths

	<code>str_length(string)</code> The width of strings (i.e. number of code points, which generally equals the number of characters). <code>str_length(fruit)</code>
	<code>str_pad(string, width, side = c("left", "right", "both"), pad = " ")</code> Pad strings to constant width. <code>str_pad(fruit, 17)</code>
	<code>str_trunc(string, width, side = c("right", "left", "center"), ellipsis = "...")</code> Truncate the width of strings, replacing content with ellipsis. <code>str_trunc(fruit, 3)</code>
	<code>str_trim(string, side = c("both", "left", "right"))</code> Trim whitespace from the start and/or end of a string. <code>str_trim(fruit)</code>

Mutate Strings

	<code>str_sub()</code> <- value. Replace substrings by identifying the substrings with <code>str_sub()</code> and assigning into the results. <code>str_sub(fruit, 1, 3) <- "str"</code>
	<code>str_replace(string, pattern, replacement)</code> Replace the first matched pattern in each string. <code>str_replace(fruit, "a", "-")</code>
	<code>str_replace_all(string, pattern, replacement)</code> Replace all matched patterns in each string. <code>str_replace_all(fruit, "a", "-")</code>
	<code>str_to_lower(string, locale = "en")¹</code> Convert strings to lower case. <code>str_to_lower(sentences)</code>
	<code>str_to_upper(string, locale = "en")¹</code> Convert strings to upper case. <code>str_to_upper(sentences)</code>
	<code>str_to_title(string, locale = "en")¹</code> Convert strings to title case. <code>str_to_title(sentences)</code>

Join and Split

	<code>str_c(..., sep = "", collapse = NULL)</code> Join multiple strings into a single string. <code>str_c(letters, LETTERS)</code>
	<code>str_c(..., sep = "", collapse = NULL)</code> Collapse a vector of strings into a single string. <code>str_c(letters, collapse = "")</code>
	<code>str_dup(string, times)</code> Repeat strings times times. <code>str_dup(fruit, times = 2)</code>
	<code>str_split_fixed(string, pattern, n)</code> Split a vector of strings into a matrix of substrings (splitting at occurrences of a pattern match). Also <code>str_split</code> to return a list of substrings. <code>str_split_fixed(fruit, " ", n=2)</code>
	<code>str_glue(..., .sep = "", .envir = parent.frame())</code> Create a string from strings and {expressions} to evaluate. <code>str_glue("Pi is {pi}")</code>
	<code>str_glue_data(.x, ..., .sep = "", .envir = parent.frame(), .na = "NA")</code> Use a data frame, list, or environment to create a string from strings and {expressions} to evaluate. <code>str_glue_data(mtcars, "{rownames(mtcars)} has {hp} hp")</code>

Order Strings

	<code>str_order(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...)¹</code> Return the vector of indexes that sorts a character vector. <code>x[str_order(x)]</code>
	<code>str_sort(x, decreasing = FALSE, na_last = TRUE, locale = "en", numeric = FALSE, ...)¹</code> Sort a character vector. <code>str_sort(x)</code>

Helpers

	<code>str_conv(string, encoding)</code> Override the encoding of a string. <code>str_conv(fruit, "ISO-8859-1")</code>
	<code>str_view(string, pattern, match = NA)</code> View HTML rendering of first regex match in each string. <code>str_view(fruit, "[aeiou]")</code>
	<code>str_view_all(string, pattern, match = NA)</code> View HTML rendering of all regex matches. <code>str_view_all(fruit, "[aeiou]")</code>
	<code>str_wrap(string, width = 80, indent = 0, exdent = 0)</code> Wrap strings into nicely formatted paragraphs. <code>str_wrap(sentences, 20)</code>

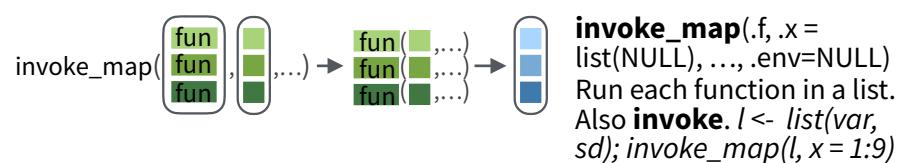
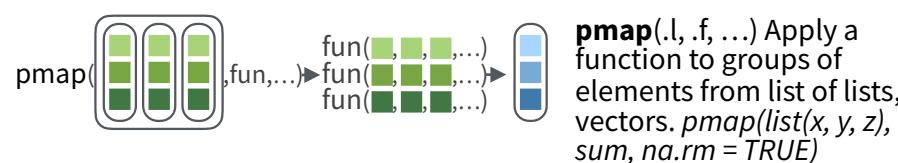
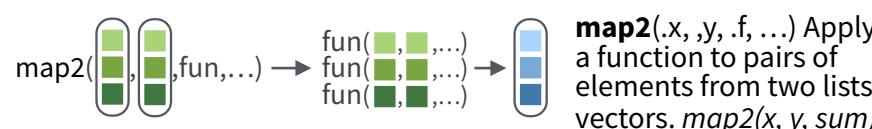
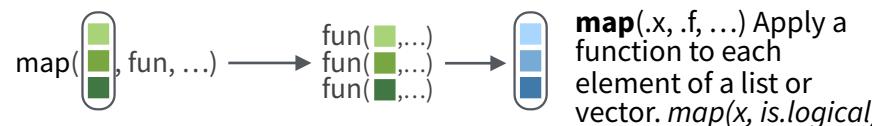
¹ See bit.ly/ISO639-1 for a complete list of locales.

Apply functions with purrr :: CHEAT SHEET



Apply Functions

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



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.

SHORTCUTS - within a purrr function:

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

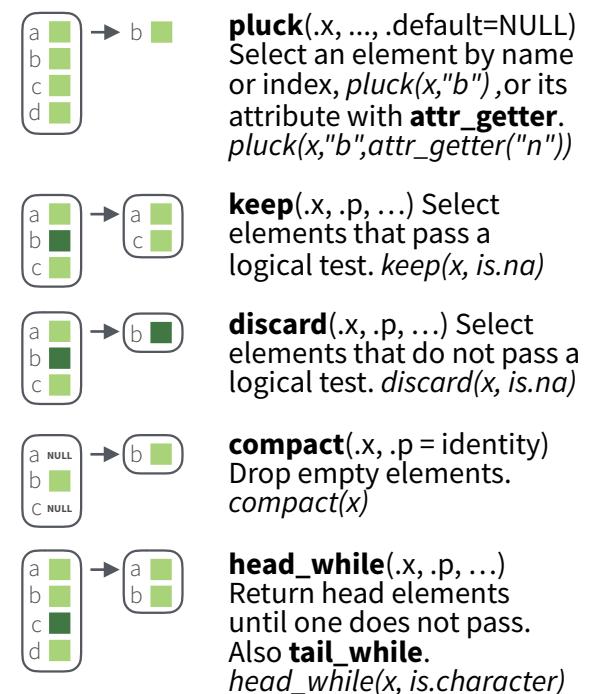
`~.x` becomes **function(x) x**, e.g. `map(l, ~2+x)` becomes `map(l, function(x) 2+x)`

function returns

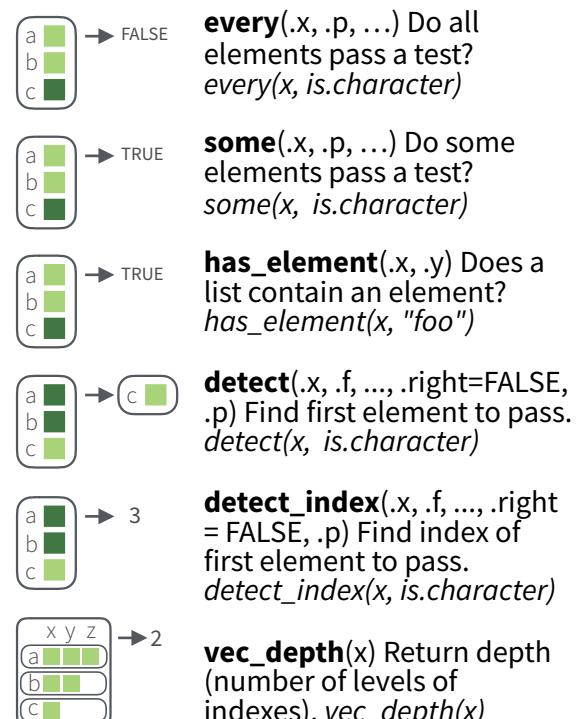
function	returns
map	list
map_chr	character vector
map_dbl	double (numeric) vector
map_dfc	data frame (column bind)
map_dfr	data frame (row bind)
map_int	integer vector
map_lgl	logical vector
walk	triggers side effects, returns the input invisibly

Work with Lists

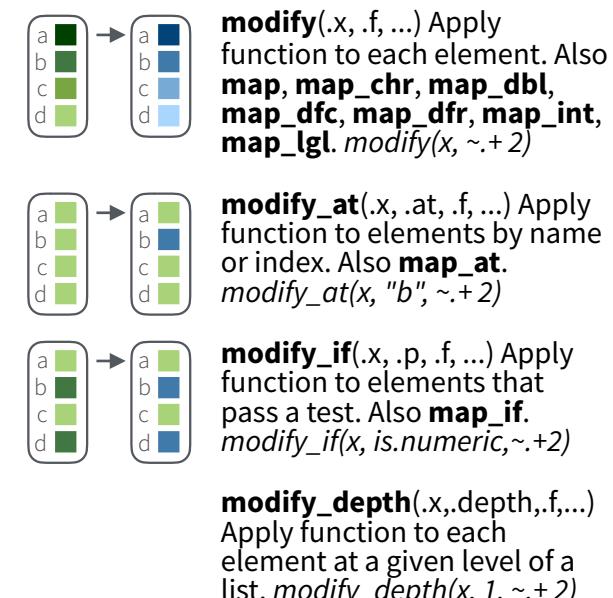
FILTER LISTS



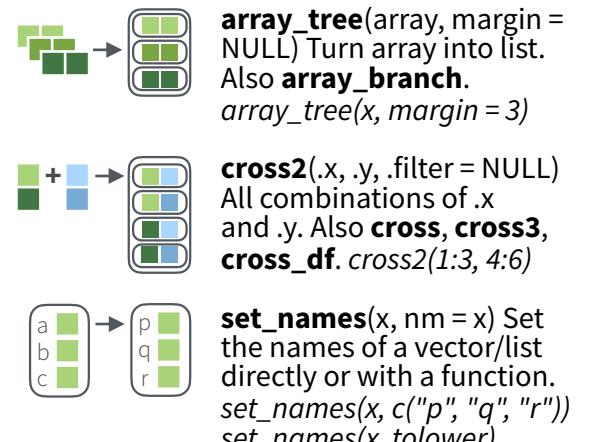
SUMMARISE LISTS



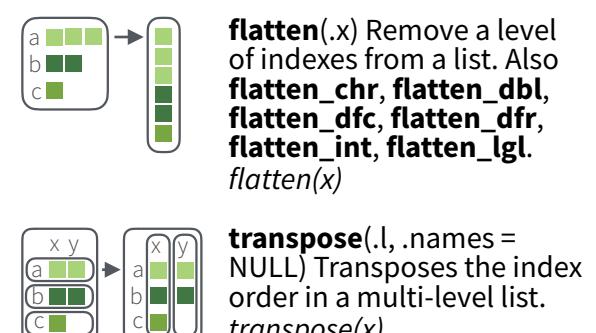
TRANSFORM LISTS



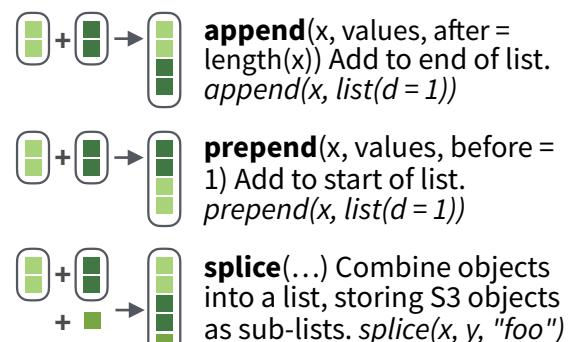
WORK WITH LISTS



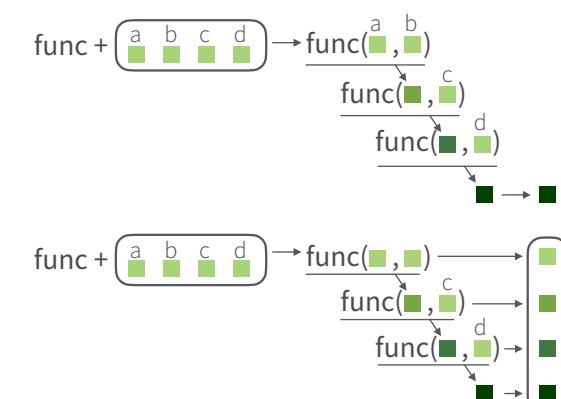
RESHAPE LISTS



JOIN (TO) LISTS



Reduce Lists



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**.

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

rerun() Rerun expression n times.

Modify function behavior

- negate()** Negate a predicate function (a pipe friendly !)
- 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).
- partial()** Create a version of a function that has some args preset to values.
- safely()** Modify func to return list of results and errors.



Nested Data

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

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

n_iris\$data[[1]]

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

n_iris

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

n_iris\$data[[2]]

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

n_iris\$data[[3]]

Use a nested data frame to:

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

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

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

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

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

tidy::nest(data, ..., .key = data)

For grouped data, moves groups into cells as data frames.

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

n_iris %>% unnest()

tidy::unnest(data, ..., .drop = NA, .id=NULL, .sep=NULL)

Unnests a nested data frame.

List Column Workflow

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

1 Make a list column

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

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

2 Work with list columns

Species	data	model
setosa	<tibble [50x4]>	<S3: lm>
versi	<tibble [50x4]>	<S3: lm>
virgini	<tibble [50x4]>	<S3: lm>

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

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

3 Simplify the list column

Species	beta
setos	2.35
versi	1.89
virgini	0.69

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

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

1. MAKE A LIST COLUMN

You can create list columns with functions in the **tibble** and **dplyr** packages, as well as **tidyR**'s **nest()**

tibble::tribble(...)

Makes list column when needed

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

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')`

2. WORK WITH LIST COLUMNS

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

purrr::map(.x, .f, ...)

Apply .f element-wise to .x as .f(x)

`n_iris %>% mutate(n = map(data, dim))`

purrr::map2(.x, .y, .f, ...)

Apply .f element-wise to .x and .y as .f(x, .y)

`m_iris %>% mutate(n = map2(data, model, list))`

purrr::pmap(.l, .f, ...)

Apply .f element-wise to vectors saved in .l

`m_iris %>%
 mutate(n = pmap(list(data, model, data), list))`

map(data, fun, ...)

map2(data, model, fun, ...)

pmap(list(data, model, fun, ...))

fun(data, ...)

fun(data, model, ...)

fun(data, model, fun, ...)

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 %>% trans`

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

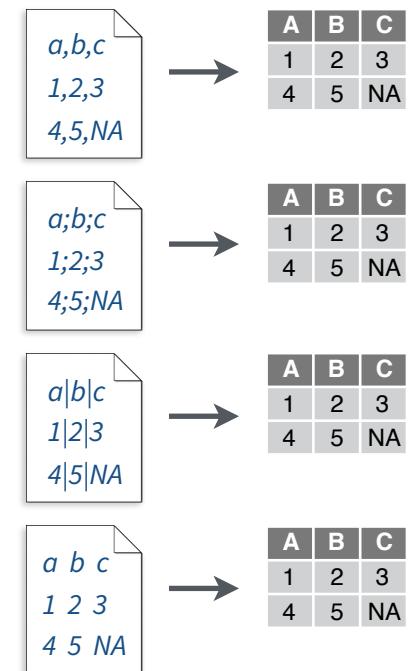
```
write_tsv(x, path, na = "NA", append = FALSE,  
          col_names = !append)
```



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())
```



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")
```

Semi-colon Delimited Files

```
read_csv2("file2.csv")
```

```
write_file(x = "a;b;c\n1;2;3\n4;5;NA", path = "file2.csv")
```

Files with Any Delimiter

```
read_delim("file.txt", delim = "|")
```

```
write_file(x = "a|b|c\n1|2|3\n4|5|NA", path = "file.txt")
```

Fixed Width Files

```
read_fwf("file.fwf", col_positions = c(1, 3, 5))
```

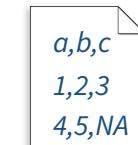
```
write_file(x = "a b c\n1 2 3\n4 5 NA", path = "file.fwf")
```

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



Example file

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

1	2	3
4	5	NA

Skip lines

```
read_csv(f, skip = 1)
```

A	B	C
1	2	3
4	5	NA

No header

```
read_csv(f, col_names = FALSE)
```

A	B	C
1	2	3
4	5	NA

Read in a subset

```
read_csv(f, n_max = 1)
```

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

Provide header

```
read_csv(f, col_names = c("x", "y", "z"))
```

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	cyl	trans
1 audi	a4	1.80	4	auto(l4)	
2 audi	a4	1.80	4	auto(l4)	
3 audi	a4	2.00	4	auto(l4)	
4 audi	a4	2.00	4	auto(l4)	
5 audi	a4	2.00	4	auto(l4)	
6 audi	a4	2.00	4	auto(l4)	
7 audi	a4	3.10	6	quattro	
8 audi	a4	3.10	6	quattro	
9 audi	a4	3.10	6	quattro	
10 audi	a4	3.10	6	quattro	
... with 224 more rows, and 3 more variables: year <int>, cyl <int>, trans <chr>					

tibble display

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

data frame display

A large table to 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. <code>tibble(x = 1:3, y = c("a", "b", "c"))</code>	Both make this tibble
tribble(...)	Construct by rows. <code>tribble(~x, ~y, 1, "a", 2, "b", 3, "c")</code>	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 tidyverse

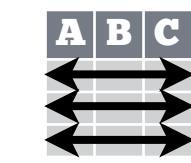
Tidy data is a way to organize tabular data. It provides a consistent data structure across packages.

A table is tidy if:



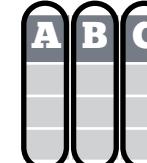
Each **variable** is in its own **column**

&



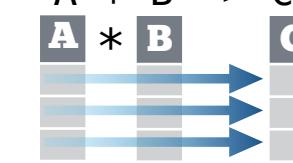
Each **observation**, or **case**, is in its own **row**

Tidy data:



Makes variables easy to access as vectors

$A * B \rightarrow C$



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
B	1999	cases	37K
B	1999	pop	172M
C	1999	cases	212K
C	1999	pop	1T
A	2000	cases	2K
A	2000	pop	20M
B	2000	cases	80K
B	2000	pop	174M
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	

`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	

`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	

`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 ...

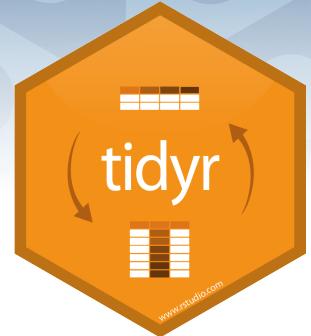
`complete(mtcars, cyl, gear, carb)`

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

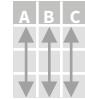
country	year	rate
A	1999	0.7K/19M
A	2000	2K/20M
B	1999	37K/172M
B	2000	80K/174M
C	1999	212K/1T
C	2000	213K/1T

country	year	cases	pop
A	1999	0.7K	19M
A	2000	2K</	

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**



`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).



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.



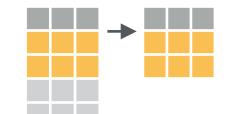
filter(.data, ...) Extract rows that meet logical criteria. `filter(iris, Sepal.Length > 7)`



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)`



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)`

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

MAKE NEW VARIABLES

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



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

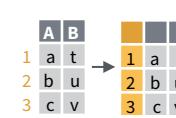
quantile() - nth quantile
min() - minimum value
max() - maximum value

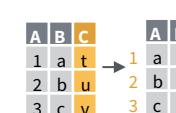
SPREAD

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

X	y	=
A B C a t 1 b u 2 c v 3	A B D a t 3 b u 2 d w 1	A B C A B D a t 1 a t 3 b u 2 b u 2 c v 3 d w 1

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.

A B C D	left_join(x, y, by = NULL,
a t 1 3 b u 2 2 c v 3 NA	copy=FALSE, suffix=c("x","y"),...)
	Join matching values from y to x.

A B C D	right_join(x, y, by = NULL, copy =
a t 1 3 b u 2 2 d w NA 1	FALSE, suffix=c("x","y"),...)
	Join matching values from x to y.

A B C D	inner_join(x, y, by = NULL, copy =
a t 1 3 b u 2 2	FALSE, suffix=c("x","y"),...)
	Join data. Retain only rows with matches.

A B C D	full_join(x, y, by = NULL,
a t 1 3 b u 2 2 d w NA 1	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

X	y	=
A B C a t 1 b u 2 c v 3	A B C C v 3 d w 4	

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

df A B C	bind_rows(..., .id = NULL)
x a t 1 x b u 2 x c v 3 z c v 3 z d w 4	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)

A B C	intersect(x, y, ...)
c v 3	Rows that appear in both x and y.

A B C	setdiff(x, y, ...)
a t 1 b u 2	Rows that appear in x but not y.

A B C	union(x, y, ...)
a t 1 b u 2 c v 3 d w 4	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

X	y	=
A B C a t 1 b u 2 c v 3	A B D a t 3 b u 2 d w 1	

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

A B C	semi_join(x, y, by = NULL, ...)
a t 1 b u 2	Return rows of x that have a match in y.
	USEFUL TO SEE WHAT WILL BE JOINED.

A B C	anti_join(x, y, by = NULL, ...)
c v 3	Return rows of x that do not have a match in y. USEFUL TO SEE WHAT WILL NOT BE JOINED.

R Markdown :: CHEAT SHEET

What is R Markdown?

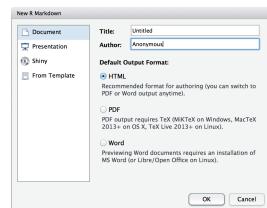


.Rmd files • An R Markdown (.Rmd) file is a record of your research. It contains the code that a scientist needs to reproduce your work along with the narration that a reader needs to understand your work.

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

The screenshot shows the RStudio interface. On the left is the R Markdown editor with the following code:

```

1 ---  
2 title: "R Markdown"  
3 author: "RStudio"  
4 output: ② html_document:  
5   toc: TRUE  
6 ---  
7  
8  
9 `r setup, include=FALSE`  
10 knitr::opts_chunk$set(echo = TRUE)  
11  
12  
13 ## R Markdown  
14  
15 This is an R Markdown document.  
16 Markdown is a simple formatting  
17 syntax for authoring HTML, PDF,  
18 and MS Word documents.  
19  
20 `r cars`  
21 summary(cars)  
22  
23  
24 For more details on using R Markdown  
see <http://rmarkdown.rstudio.com>.

```

Annotations in red highlight several features:

- ① Set preview location
- ② Insert code chunk
- ③ Run code chunk(s)
- ④ Go to code chunk
- ⑤ Publish
- ⑥ Show outline
- ⑦ Run all previous chunks
- ⑧ Modify chunk options
- ⑨ Run current chunk

The browser preview (report.html) shows the rendered content, including the R code and its output (summary(cars)). A sidebar on the right includes links to RStudio Connect and Rpubs.com.

render

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

input - file to render
output_format

output_options - List of render options (as in YAML)

output_file
output_dir

params - list of params to use

envir - environment to evaluate code chunks in

encoding - of input file

Embed code with knitr syntax

INLINE CODE

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

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

CODE CHUNKS

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

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

### GLOBAL OPTIONS

Set with knitr::opts\_chunk\$set(), e.g.

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

```

### IMPORTANT CHUNK OPTIONS

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

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

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

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

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

**dependson** - chunk dependencies for caching (default = NULL)

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

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

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

**eval** - Run code in chunk (default = TRUE)

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

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

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

**highlight** - highlight source code (default = TRUE)

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

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

**results** (default = 'markup')  
'asis' - passthrough results

'hide' - do not display results  
'hold' - put all results below all code

**tidy** - tidy code for display (default = FALSE)

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

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



## .rmd Structure



### YAML Header

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

At start of file

Between lines of ---

### Text

Narration formatted with markdown, mixed with:

### Code Chunks

Chunks of embedded code. Each chunk:

Begins with `r`

ends with ``

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

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

## Parameters

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

```

params:
 n: 100
 d: ! Sys.Date()

```

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

New Folder Delete Rename More
   
 Home Desktop R-Markdown-Cheatsheet
   
 report.Rmd 398 B Feb 26, 2016, 3:36 PM
   
 report.html 581.3 KB Feb 26, 2016, 3:36 PM

## Interactive Documents

Turn your report into an interactive Shiny document in 4 steps

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

```

output: html_document
runtime: shiny

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

```

| How many cars? |       |
|----------------|-------|
| speed          | dist  |
| 1 4.00         | 2.00  |
| 2 4.00         | 10.00 |
| 3 7.00         | 4.00  |
| 4 7.00         | 22.00 |
| 5 8.00         | 16.00 |

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

NOTE: Your report will be 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.



# 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/superscript22
~~strikethrough~~
escaped: `*` \\
endash: --, emdash: ---
equation: $A = \pi * r^2$
```

```
equation block:
```

```
$$E = mc^2$$
```

```
Plain text
End a line with two spaces
to start a new paragraph.
italics and bold
`verbatim` code
sub/superscript22
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{Text ignored in HTML}
HTML ignored in pdfs
```

```
<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
```

```
2. an interruption
```

```
Term 1
```

```
Definition 1
```

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

- slide bullet 1
- slide bullet 2

```
(>- to have bullets appear on click)
```

```
horizontal rule/slide break:
```

```

```

```
A footnote [^1]
```

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

```
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):

```

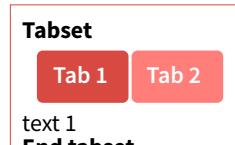
output: html_document:
 code_folding: hide
 toc_float: TRUE

Body
```

## html tabs

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
```



# 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)

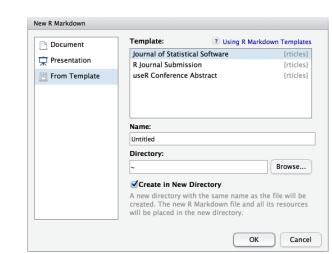
any supporting files

3. Install the package

4. Access template in wizard at File ▶ New File ▶ R Markdown template.yaml

A footnote 1

1. Here is the footnote. ↵



## sub-option

## description

|                       | html | pdf | word | odt | rtf | md | gitlab | ioslides | slidy | beamer |
|-----------------------|------|-----|------|-----|-----|----|--------|----------|-------|--------|
| citation_package      | X    |     |      |     |     |    |        |          |       |        |
| code_folding          |      | X   |      |     |     |    |        |          |       |        |
| colortheme            |      |     |      |     |     |    |        | X        |       |        |
| css                   |      |     | X    |     |     |    |        | X        | X     |        |
| dev                   |      |     |      | X   | X   | X  | X      | X        | X     | X      |
| duration              |      |     |      |     |     |    |        |          | X     |        |
| fig_caption           |      | X   | X    | X   | X   |    |        | X        | X     | X      |
| fig_height, fig_width |      | X   | X    | X   | X   | X  | X      | X        | X     | X      |
| highlight             |      |     |      |     |     |    |        | X        | X     |        |
| includes              |      |     |      |     |     |    |        | X        | X     | X      |
| incremental           |      |     |      |     |     |    |        | X        | X     | X      |
| keep_md               |      |     |      |     |     |    |        | X        | X     | X      |
| keep_tex              |      |     |      |     |     |    |        | X        |       |        |
| latex_engine          |      |     |      |     |     |    |        | X        |       |        |
| lib_dir               |      |     |      |     |     |    |        | X        |       | X      |
| mathjax               |      |     |      |     |     |    |        | X        |       | X      |
| md_extensions         |      | X   | X    | X   | X   | X  | X      | X        | X     | X      |
| number_sections       |      |     |      |     |     |    |        | X        | X     |        |
| pandoc_args           |      |     |      |     |     |    |        | X        | X     | X      |
| preserve_yaml         |      |     |      |     |     |    |        |          |       | X      |
| reference_docx        |      |     |      |     |     |    |        |          | X     |        |
| self_contained        |      |     |      |     |     |    |        | X        |       | X      |
| slide_level           |      |     |      |     |     |    |        |          |       | X      |
| smaller               |      |     |      |     |     |    |        |          |       | X      |
| smart                 |      |     |      |     |     |    |        | X        |       | X      |
| template              |      |     |      |     |     |    |        | X        | X     | X      |
| theme                 |      |     |      |     |     |    |        | X        |       | X      |
| toc                   |      |     |      |     |     |    |        | X        | X     | X      |
| toc_depth             |      |     |      |     |     |    |        | X        | X     | X      |
| toc_float             |      |     |      |     |     |    |        | X        |       |        |

# Table Suggestions

Several functions format R data into tables

| Table with kable    |      |
|---------------------|------|
| <code>erupts</code> |      |
| 1                   | 3.60 |
| 2                   | 1.80 |
| 3                   | 3.33 |
| 4                   | 2.28 |
|                     | 79   |
|                     | 54   |
|                     | 74   |
|                     | 62   |

| erupts  |       |
|---------|-------|
| waiting | 90.00 |
| 1       | 79.00 |
| 2       | 54.00 |
| 3       | 74.00 |
| 4       | 62.00 |

| Table with stargazer |       |
|----------------------|-------|
| erupts               | 79    |
| 1                    | 3.600 |
| 2                    | 1.800 |
| 3                    | 3.333 |
| 4                    | 2.283 |

`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

# RStudio IDE :: CHEAT SHEET

## Documents and Apps



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

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

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

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

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

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

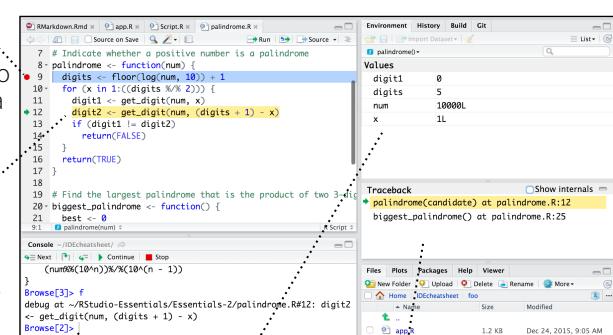
## Debug Mode

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

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

Highlighted line shows where execution has paused

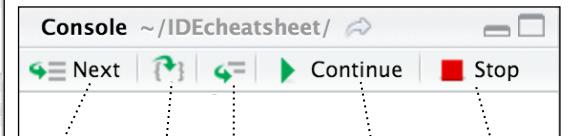
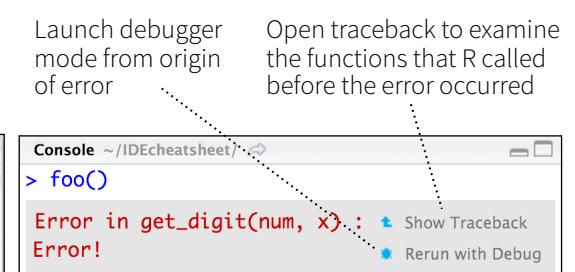
Run commands in environment where execution has paused



Examine variables in executing environment

Select function in traceback to debug

Launch debugger mode from origin of error



Step through code one line at a time

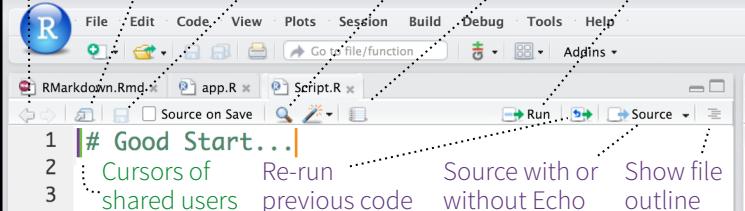
Step into and out of functions to run

Resume execution mode

Quit debug mode

## Write Code

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



Cursors of shared users   Re-run previous code   Source with or without Echo   Show file outline

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

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

Syntax highlighting based on your file's extension

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

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

Jump to function in file

Change file type

Working Directory

Press **↑** to see command history

Maximize, minimize panes

Drag pane boundaries

## R Support

**Import data** with wizard

History of past commands to run/copy

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

Load workspace

Save workspace

Delete all saved objects

Search inside environment

Choose environment to display from list of parent environments

Display objects as list or grid

Data

iris   150 obs. of 5 variables

Values

a   1

Functions

foo   function (x)

Displays saved objects by type with short description

View in data

View function source code

Files

Plots

Packages

Help

Viewer

New Folder

Upload

Delete

Rename

More

Copy...

Move...

Export...

Set As Working Directory

Go To Working Directory

Create folder

Upload file

Delete file

Rename file

Change directory

Path to displayed directory

Maximize, minimize panes

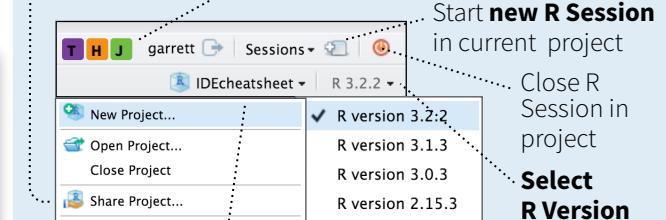
Drag pane boundaries

A File browser keyed to your working directory.

Click on file or directory name to open.

## Pro Features

**Share Project** Active shared with Collaborators



Start **new R Session** in current project

Close R Session in project

**Select R Version**

### 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



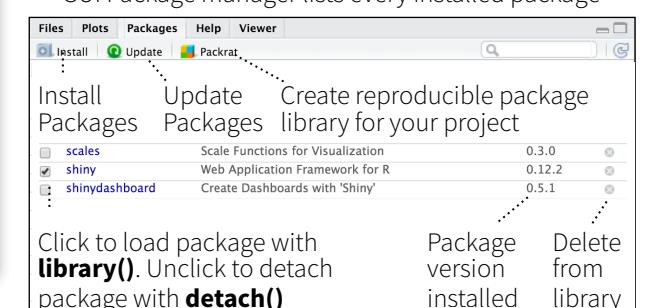
Open in recent plots

**Export plot**

Delete plot

Delete all plots

GUI Package manager lists every installed package

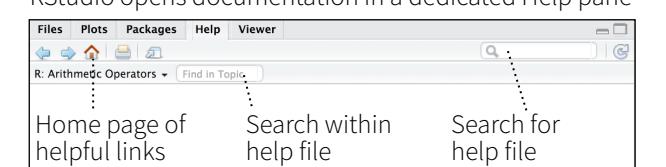


Click to load package with **library()**. Unclick to detach package with **detach()**

Package version installed

Delete from library

RStudio opens documentation in a dedicated Help pane

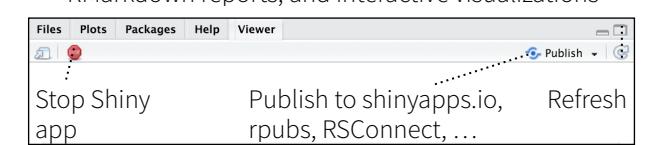


Home page of helpful links

Search within help file

Search for help file

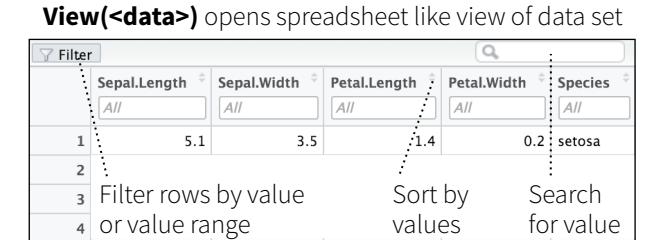
Viewer Pane displays HTML content, such as Shiny apps, RMarkdown reports, and interactive visualizations



Stop Shiny app

Publish to shinyapps.io, rpubs, RSConnect, ...

Refresh



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



Filter rows by value or value range

Sort by values

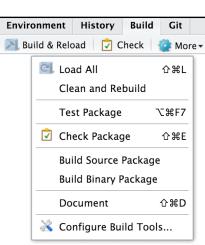
Search for value

## 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

Move focus to Source Editor  
Move focus to Console  
Move focus to Help  
Show History  
Show Files  
Show Plots  
Show Packages  
Show Environment  
Show Git/SVN  
Show Build

**Windows/Linux** **Mac**  
Ctrl+1 Ctrl+1  
Ctrl+2 Ctrl+2  
Ctrl+3 Ctrl+3  
Ctrl+4 Ctrl+4  
Ctrl+5 Ctrl+5  
Ctrl+6 Ctrl+6  
Ctrl+7 Ctrl+7  
Ctrl+8 Ctrl+8  
Ctrl+9 Ctrl+9  
Ctrl+0 Ctrl+0

## 2 RUN CODE

### Search command history

Navigate command history  
Move cursor to start of line  
Move cursor to end of line  
Change working directory

### Interrupt current command

### Clear console

Quit Session (desktop only)

### Restart R Session

Run current (retain cursor)  
Run from current to end  
Run the current function  
Source a file

### Source the current file

Source with echo

**Windows/Linux** **Mac**

**Ctrl+↑** **Cmd+↑**  
**↑/↓** **↑/↓**  
Home **Cmd+←**  
End **Cmd+→**  
Ctrl+Shift+H **Ctrl+Shift+H**

**Esc** **Esc**

**Ctrl+L** **Ctrl+L**

Ctrl+Q **Cmd+Q**

**Ctrl+Shift+F10** **Cmd+Shift+F10**

**Ctrl+Enter** **Cmd+Enter**  
Alt+Enter Option+Enter  
Ctrl+Alt+E Cmd+Option+E  
Ctrl+Alt+F Cmd+Option+F  
Ctrl+Alt+G Cmd+Option+G

**Ctrl+Shift+S** **Cmd+Shift+S**

Ctrl+Shift+Enter Cmd+Shift+Enter

## 4 WRITE CODE

### Attempt completion

Navigate candidates  
Accept candidate  
Dismiss candidates  
Undo  
Redo  
Cut  
Copy  
Paste  
Select All  
Delete Line

Select

Select Word

Select to Line Start

Select to Line End

Select Page Up/Down

Select to Start/End

Delete Word Left

Delete Word Right

Delete to Line End

Delete to Line Start

Indent

Outdent

Yank line up to cursor

Yank line after cursor

Insert yanked text

**Insert <->**

**Insert %>%**

Show help for function

Show source code

New document

New document (Chrome)

Open document

Save document

Close document

Close document (Chrome)

Close all documents

Extract function

Extract variable

Reindent lines

**(Un)Comment lines**

Reflow Comment

Reformat Selection

Select within braces

Show Diagnostics

Transpose Letters

Move Lines Up/Down

Copy Lines Up/Down

Add New Cursor Above

Add New Cursor Below

Move Active Cursor Up

Move Active Cursor Down

Find and Replace

Use Selection for Find

Replace and Find

## Windows /Linux

### Tab or Ctrl+Space

**↑/↓**  
Enter, Tab, or →  
Esc  
Ctrl+Z  
Ctrl+Shift+Z  
Ctrl+X  
Cmd+X  
Cmd+C  
Cmd+V  
Ctrl+A  
Cmd+A  
Cmd+D  
Shift+[Arrow]  
Option+Shift+ ←/→  
Alt+Shift+ ←  
Alt+Shift+ →  
Shift+PageUp/Down  
Shift+Alt+↑/↓  
Ctrl+Opt+Backspace  
Option+Delete  
Ctrl+K  
Option+Backspace  
Tab (at start of line)  
Shift+Tab  
Ctrl+U  
Ctrl+K  
Ctrl+Y  
Alt+-  
Ctrl+Shift+M  
F1  
F2  
Cmd+Shift+N  
Ctrl+Alt+Shift+N  
Ctrl+O  
Ctrl+S  
Cmd+W  
Cmd+Option+W  
Cmd+Shift+W  
Ctrl+Alt+X  
Cmd+Option+X  
Ctrl+Alt+V  
Cmd+I  
Ctrl+Shift+C  
Ctrl+Shift+/  
Ctrl+Shift+A  
Ctrl+Shift+E  
Ctrl+Shift+E  
Cmd+Shift+Opt+P  
Ctrl+T  
Option+↑/↓  
Shift+Alt+↑/↓  
Cmd+Option+↑/↓  
Ctrl+Option+Up  
Ctrl+Option+Down  
Ctrl+Option+Shift+Up  
Ctrl+Opt+Shift+Down  
Ctrl+F  
Ctrl+F3  
Ctrl+E  
Ctrl+Shift+J

## Mac

### Tab or Cmd+Space

**↑/↓**  
Enter, Tab, or →  
Esc  
Cmd+Z  
Cmd+Shift+Z  
Cmd+X  
Cmd+C  
Cmd+V  
Cmd+A  
Cmd+D  
Shift+[Arrow]  
Option+Shift+ ←/→  
Cmd+Shift+ ←  
Cmd+Shift+ →  
Shift+PageUp/Down  
Cmd+Shift+↑/↓  
Ctrl+Opt+Backspace  
Option+Delete  
Ctrl+K  
Option+Backspace  
Tab (at start of line)  
Shift+Tab  
Ctrl+U  
Ctrl+K  
Ctrl+Y  
Alt+-  
Cmd+Shift+M  
F1  
F2  
Cmd+Shift+N  
Cmd+Shift+Opt+N  
Cmd+O  
Cmd+S  
Cmd+W  
Cmd+Option+W  
Cmd+Shift+W  
Cmd+Option+X  
Cmd+Option+V  
Cmd+I  
Cmd+Shift+C  
Cmd+Shift+/  
Cmd+Shift+A  
Cmd+Shift+E  
Cmd+Shift+E  
Cmd+Shift+Opt+P  
Ctrl+T  
Option+↑/↓  
Shift+Alt+↑/↓  
Cmd+Option+↑/↓  
Ctrl+Option+Up  
Ctrl+Option+Down  
Ctrl+Option+Shift+Up  
Ctrl+Opt+Shift+Down  
Cmd+F  
Cmd+F3  
Cmd+E  
Cmd+Shift+J

## WHY RSTUDIO SERVER PRO?

RSP extends 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/](http://www.rstudio.com/products/rstudio-server-pro/)

## 5 DEBUG CODE

Toggle Breakpoint  
Execute Next Line  
Step Into Function  
Finish Function/Loop  
Continue  
Stop Debugging

## Windows/Linux Mac

Shift+F9	Shift+F9
F10	F10
Shift+F4	Shift+F4
Shift+F6	Shift+F6
Shift+F5	Shift+F5
Shift+F8	Shift+F8

## 6 VERSION CONTROL

Show diff  
Commit changes  
Scroll diff view  
Stage/Unstage (Git)  
Stage/Unstage and move to next

## Windows/Linux Mac

Ctrl+Alt+D	Ctrl+Option+D
Ctrl+Alt+M	Ctrl+Option+M
Ctrl+↑/↓	Ctrl+↑/↓
Spacebar	Spacebar
Enter	Enter

## 7 MAKE PACKAGES

Build and Reload  
**Load All (devtools)**  
**Test Package (Desktop)**  
Test Package (Web)  
Check Package  
**Document Package**

## Windows/Linux Mac

Ctrl+Shift+B	Cmd+Shift+B
<b>Ctrl+Shift+L</b>	<b>Cmd+Shift+L</b>
<b>Ctrl+Shift+T</b>	<b>Cmd+Shift+T</b>
Ctrl+Alt+F7	Cmd+Opt+F7
Ctrl+Shift+E	Cmd+Shift+E
<b>Ctrl+Shift+D</b>	<b>Cmd+Shift+D</b>

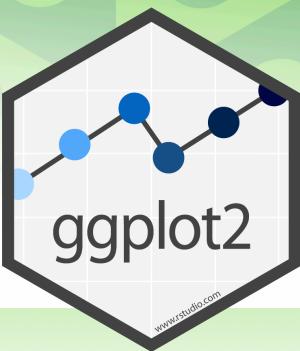
## 8 DOCUMENTS AND APPS

Preview HTML (Markdown, etc.)  
**Knit Document (knitr)**  
Compile Notebook  
Compile PDF (TeX and Sweave)  
Insert chunk (Sweave and Knitr)  
Insert code section  
Re-run previous region  
Run current document  
**Run from start to current line**  
**Run the current code section**  
Run previous Sweave/Rmd code  
Run the current chunk  
Run the next chunk  
Sync Editor & PDF Preview  
Previous plot  
Next plot  
**Show Keyboard Shortcuts**  
**Alt+Shift+K**

## Windows/Linux Mac

Ctrl+Shift+K	Cmd+Shift+K
<b>Ctrl+Shift+K</b>	<b>Cmd+Shift+K</b>
Ctrl+Shift+K	Cmd+Shift+K
Ctrl+Shift+I	Cmd+Option+I
Ctrl+Shift+R	Cmd+Shift+R
Ctrl+Shift+P	Cmd+Shift+P
Ctrl+Alt+R	Cmd+Option+R
Ctrl+Alt+P	Cmd+Option+R
Ctrl+Shift+P	Cmd+Shift+P
Ctrl+Shift+P	Cmd+Shift+P
Ctrl+Shift+P	Cmd+Shift+P
Ctrl+Alt+T	Cmd+Option+T
Ctrl+Alt+T	Cmd+Option+T
Ctrl+Alt+P	Cmd+Option+P
Ctrl+Alt+C	Cmd+Option+C
Ctrl+Alt+N	Cmd+Option+N
Ctrl+F8	Cmd+F8
Ctrl+Alt+F11	Cmd+Option+F11
Ctrl+Alt+F12	Cmd+Option+F12
Alt+Shift+K	Option+Shift+K

# Data Visualization with ggplot2 :: CHEAT SHEET



## Basics

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



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



Complete the template below to build a graph.

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

required

Not required, sensible defaults supplied

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

**aesthetic mappings** **data** **geom**

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

**last\_plot()** Returns the last plot

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

## Geoms

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

### GRAPHICAL PRIMITIVES

- a <- ggplot(economics, aes(date, unemploy))  
b <- ggplot(seals, aes(x = long, y = lat))
- a + geom\_blank()**  
(Useful for expanding limits)
- b + geom\_curve(aes(yend = lat + 1, xend=long+1, curvature=z))** - x, xend, y, yend, alpha, angle, color, curvature, linetype, size
- a + geom\_path(lineend="butt", linejoin="round", linemitre=1)**  
x, y, alpha, color, group, linetype, size
- a + geom\_polygon(aes(group = group))**  
x, y, alpha, color, fill, group, linetype, size
- b + geom\_rect(aes(xmin = long, ymin=lat, xmax=long + 1, ymax = lat + 1))** - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size
- a + geom\_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900))** - x, ymax, ymin, alpha, color, fill, group, linetype, size

### LINE SEGMENTS

- common aesthetics: x, y, alpha, color, linetype, size
- b + geom\_abline(aes(intercept=0, slope=1))**
  - b + geom\_hline(aes(yintercept = lat))**
  - b + geom\_vline(aes(xintercept = long))**

- b + geom\_segment(aes(yend=lat+1, xend=long+1))**
- b + geom\_spoke(aes(angle = 1:1155, radius = 1))**

### ONE VARIABLE continuous

- c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)
- c + geom\_area(stat = "bin")**  
x, y, alpha, color, fill, linetype, size
- c + geom\_density(kernel = "gaussian")**  
x, y, alpha, color, fill, group, linetype, size, weight
- c + geom\_dotplot()**  
x, y, alpha, color, fill
- c + geom\_freqpoly()**  
x, y, alpha, color, group, linetype, size
- c + geom\_histogram(binwidth = 5)**  
x, y, alpha, color, fill, linetype, size, weight
- c2 + geom\_qq(aes(sample = hwy))**  
x, y, alpha, color, fill, linetype, size, weight

### discrete

- d <- ggplot(mpg, aes(f1))
- 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

### 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

### 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

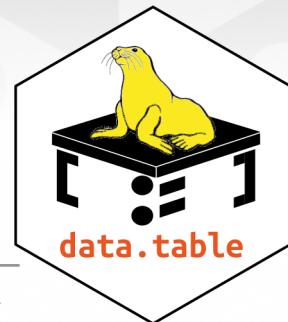
- data <- data.frame(murder = USArrests\$Murder, state = tolower(rownames(USArrests)))  
map <- map\_data("state")  
k <- ggplot(data, aes(fill = murder))

- k + geom\_map(aes(map\_id = state), map = map)**  
+ expand\_limits(x = map\$long, y = map\$lat), map\_id, alpha, color, fill, linetype, size





# 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**.

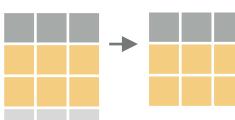
data.tables are also data frames – functions that work with data frames therefore also work with data.tables.

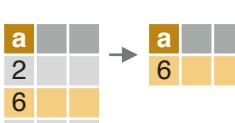
## Create a data.table

**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**

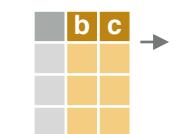
<	<=	is.na()	%in%		%like%
>	>=	!is.na()	!	&	%between%

## 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.

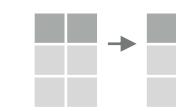
### SUMMARIZE



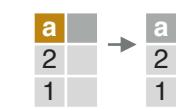
**dt[, .(x = sum(a))]** – create a data.table with new columns based on the summarized values of rows.

Summary functions like `mean()`, `median()`, `min()`, `max()`, etc. can be used to summarize rows.

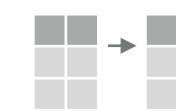
### COMPUTE COLUMNS\*



**dt[, c := 1 + 2]** – compute a column based on an expression.

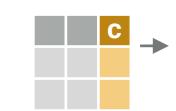


**dt[a == 1, c := 1 + 2]** – compute a column based on an expression but only for a subset of rows.



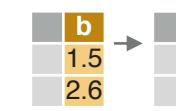
**dt[, `:=` (c = 1, d = 2)]** – compute multiple columns based on separate expressions.

### DELETE COLUMN



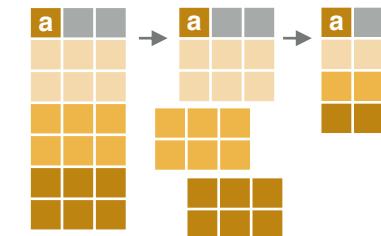
**dt[, c := NULL]** – delete a column.

### 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.

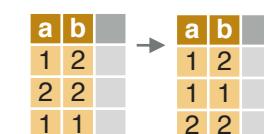
**dt[, .SD[N], by = a]** – extract last row of groups.

## 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

a	b
1	2
2	2
1	2

`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

a	b
x	y

`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

a	b
1	c
2	a
3	b

x	y
3	b
2	c
1	a

a	b	x
3	b	3
2	c	2
1	a	1

`dt_a[dt_b, on = .(b = y)]` – join data.tables on rows with equal values.

a	b	c
1	c	7
2	a	5
3	b	6

x	y	z
3	b	4
2	c	5
1	a	8

a	b	c	x
3	b	4	3
1	c	5	2
2	a	8	NA

`dt_a[dt_b, on = .(b = y, c > z)]` – join data.tables on rows with equal and unequal values.

### ROLLING JOIN

a	id	date
1	A	01-01-2010
2	A	01-01-2012
3	A	01-01-2014
1	B	01-01-2010
2	B	01-01-2012

b	id	date
1	A	01-01-2013
1	B	01-01-2013

a	id	date	b
2	A	01-01-2013	1
1	B	01-01-2013	1

`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

a	b

a	b

a	b

=

a	b

`rbind(dt_a, dt_b)` – combine rows of two data.tables.

a	b

x	y

a	b	x	y

=

a	b	x	y

`cbind(dt_a, dt_b)` – combine columns of two data.tables.

## Apply function to cols.

### APPLY A FUNCTION TO MULTIPLE COLUMNS

a	b
1	4
2	5
3	6

`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.

a	b
1	1
2	2
3	3

`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.

## Reshape a data.table

### RESHAPE TO WIDE FORMAT

id	y	a	b
A	x	1	3
A	z	2	4
B	x	1	3

`dcast(dt,`  
`id ~ y,`  
`value.var = c("a", "b"))`

Reshape a data.table from long to wide format.

`dt`  
`id ~ y`  
`value.var`

A data.table.  
Formula with a LHS: ID columns containing IDs for multiple entries. And a RHS: columns with values to spread in column headers.  
Columns containing values to fill into cells.

### RESHAPE TO LONG FORMAT

id	a	x	a	z	b	x	b	z
A	1	2	3	4	A	1	1	3
B	1	2	3	4	B	1	1	3

`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`  
`id.vars`  
`measure.vars`  
`variable.name,`  
`value.name`

A data.table.  
ID columns with IDs for multiple entries.  
Columns containing values to fill into cells (often in pattern form).  
Names of new columns for variables and values derived from old headers.

## Sequential rows

### ROW IDS

<tr

# Machine Learning Modelling in R : : CHEAT SHEET

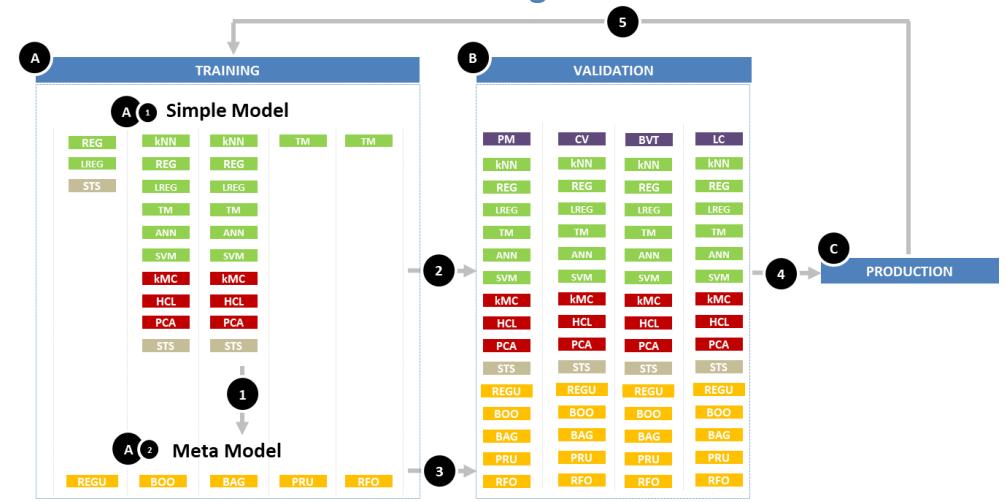
## Supervised & Unsupervised Learning

ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
NBC Naïve Bayes classifier	A classification technique based on Bayes' Theorem with an assumption of independence among predictors. In simple terms, a Naïve 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)
LRG Linear Regression	Model the linear relationship between a scalar dependent variable Y and one or more explanatory variables (or independent variables) denoted X	stats::lm	lm(dist ~ speed, data=cars)
LRC 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 data into smaller and smaller 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=(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)
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(decatlon, quanti.sup = 11:12, quali.sup = 13) ade4::dudi.pca(deugStab, center = deugCent, scale = FALSE, scan = FALSE) amap::acp(lubisch)
HAC 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(k, 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)

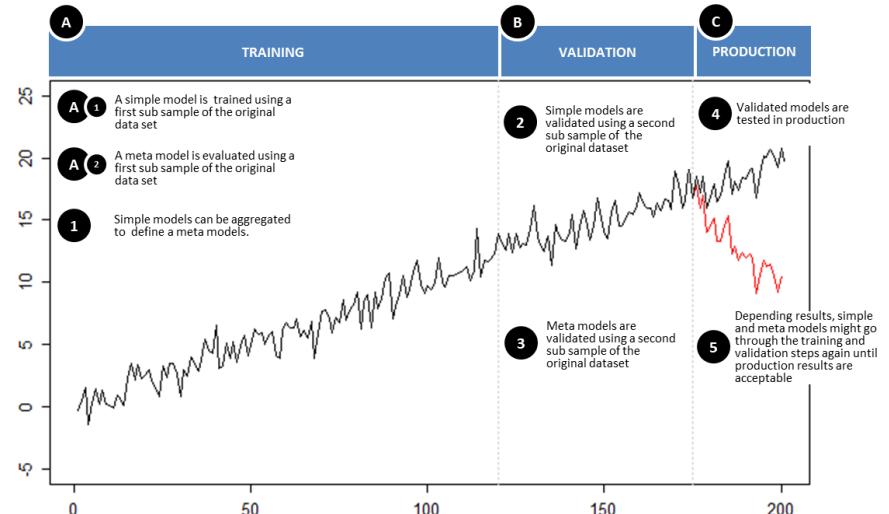
## Meta-Algorithm, Time Series & Model Validation

ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
REGU Regularisation L1 (Lasso) L2 (Ridge)	Regularisation 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.	gbm::gbm	gbmboost(Y ~ ., 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	randomForest::randomForest	foreach : d <- data.frame(x=1:10, y=rnorm(10)) s <- foreach(d=i %in% d, by=row, .combine=rbind, .id=i, .d = i) 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::rpart	prune(x, cp = 0.1)
RFO Random Forest	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)
STS Time Series	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 spectral::TTR	Auto-correlation: acf(x, lag.max = NULL, type = c("correlation", "covariance", "partial")) Spectral Analysis: spec.pgram(..., spans = NULL) Seasonal Decomposition of Time Series : stl(x, s.window = 7, t.window = 50, t.jump = 1) ....
PM Performance metrics	Depends on the problem: • Regression: squared errors, outliers, error rate... • Classification: Accuracy, precision, recall, F-score...	ROCR::ROC	Regression:stats::outlierTest, stats::qqPlot ... Classification:ROCR::ROC
JVT Bias-Variance Tradeoff	• Simple models with few parameters are easier to compute but may lead to poorer fits ( <b>high bias</b> ). • Complex models may provide more accurate fits but may over-fit the data ( <b>high variance</b> )	caret::confusionMatrix	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	Tailored to the analysis
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::learning_curve_dat	createDataPartition(classes, p = 0.8, list = FALSE) learning_curve_dat(dat, outcome = NULL, proportion = (1:10)/10, test_prop = 0, verbose = TRUE, ...)

## Standard Modelling Workflow



## Time Series View



# Machine Learning with R



## Introduction

**mlr** offers a unified interface for the basic building blocks of machine learning: tasks, learners, hyperparameters, etc.

**Tasks** contain a description of a task (classification, regression, clustering, etc.) and a data set.

**Learners** specify a machine learning algorithm (GLM, SVM, xgboost, etc.) and its parameters.

**Hyperparameters** are learner settings that can be specified directly or tuned. A **parameter set** lists the possible hyperparameters for a given learner.

**Wrapped Models** are learners that have been trained on a task and can be used to make predictions.

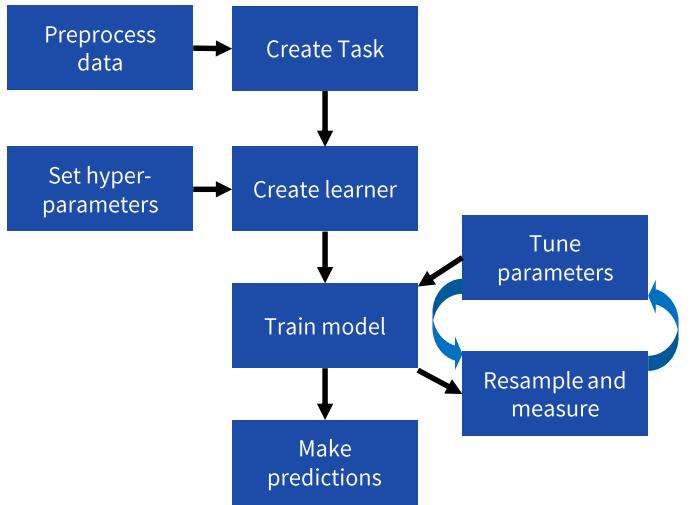
**Predictions** are the results of applying a model to either new data or the original training data.

**Measures** control how learner performance is evaluated, e.g. RMSE, LogLoss, AUC, etc.

**Resampling** estimates generalization performance by separating training data from test data. Common strategies include holdout and cross-validation.

Links: [Tutorial](#) | [CRAN](#) | [Github](#)

## mlr workflow



## Setup

### Preprocessing data

`createDummyFeatures(obj=, target=, method=, cols=)`  
Creates (0,1) flags for each non-numeric variable excluding `target`. Can be applied to entire dataset or only specific `cols`

`normalizeFeatures(obj=, target=, method=, cols=, range=, on.constant=)`  
Normalizes numerical features according to specified `method`:

- "center" (subtract mean)
- "scale" (divide by std. deviation)
- "standardize" (center and scale)
- "range" (linear scale to given range, default `range=c(0,1)`)

`mergeSmallFactorLevels(task=, cols=, min.perc=)`  
Combine infrequent factor levels into a single merged level

`summarizeColumns(obj=)` where `obj` is a data.frame or task.  
Provides type, NA, and distributional data about each column

See also `capLargeValues` `dropFeatures` `removeConstantFeatures` `summarizeLevels`

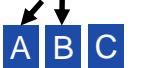
### Creating a task



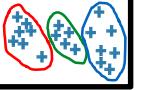
`makeClassifTask(data=, target=)`  
Classification of a target variable, with optional positive class `positive`



`makeRegrTask(data=, target=)`  
Regression on a target variable



`makeMultilabelTask(data=, target=)`  
Classification where the target can belong to more than one class per observation



`makeClusterTask(data=)`  
Unsupervised clustering on a data set



`makeSurvTask(data=, target= c("time", "event"))`  
Survival analysis with a survival time column and an event column



`makeCostSensTask(data=, costs=)`  
Cost-sensitive classification where each observation-cost pair has a specified cost

Other arguments that can be passed to a `task`:

- `weights`= Weighting vector to apply to observations
- `blocking`= Factor vector where each level indicates a block of observations that will not be split up in resampling

### Making a learner

`makeLearner(cl=, predict.type=, ..., par.vals=)`  
Choose an algorithm class to perform the task and determine what that algorithm will predict

- `cl`=name of algorithm, e.g. `"classif.xgboost"` `"regr.randomForest"` `"cluster.kmeans"`
  - `predict.type="response"` returns a prediction type that matches the source data; `"prob"` returns a predicted probability for classification problems only; `"se"` returns the standard error of the prediction for regression problems only. Only certain learners can return `"prob"` and `"se"`
  - `par.vals`= takes a list of hyperparameters and passes them to the learner; parameters can also be passed directly (...)
- You can make multiple learners at once with `makeLearners()`

mlr has integrated over 170 different learning algorithms

- Full list: `View(listLearners())` shows all learners
- Available learners for a task: `View(listLearners(task))`
- Filtered list: `View(listLearners("classif", properties=c("prob", "factors")))` shows all classification learners `"classif"` which can predict probabilities `"prob"` and handle factor inputs `"factors"`
- See also `getLearnerProperties()`

## Training & Testing

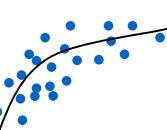
### Setting hyperparameters

`setHyperPars(learner=, ...)`  
Set the hyperparameters (settings) for each learner, if you don't want to use the defaults. You can also specify hyperparameters in the `makeLearner()` call

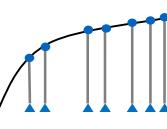


`getParamSet(learner=)`  
Show the possible universe of parameters for your learner; can take a learner directly, or a text string such as `"classif.qda"`

### Train a model and predict



`train(learner=, task=)`  
Train a model (`WrappedModel`) by applying a learner to a task. By default, the model will train on all observations. The underlying model can be extracted with `getLearnerModel()`



`predict(object=, task=, newdata=)`  
Use a trained model to make predictions on a task or dataset. The resulting `pred` object can be viewed with `View(pred)` or accessed by `as.data.frame(pred)`

### Measuring performance



`performance(pred=, measures=)`  
Calculate performance of predictions according to one or more of several measures (use `listMeasures()` for full list):

- `classif` `acc` `auc` `bac` `ber` `brier[,scaled]` `f1` `fdr` `fnr` `fpr` `gmean` `multiclass[,au1]` `aunp` `aunu` `brier` `npv` `ppv` `qsr` `ssr` `tn` `tnr` `tp` `tpr` `wkappa`
- `regr` `rsq` `expvar` `kendalltau` `mae` `mape` `medae` `medse` `mse` `msle` `rae` `rmse` `rmsle` `rrse` `rsq` `sae` `spearmanrho` `sse`
- `cluster` `db` `dunn` `G1` `G2` `silhouette`
- `multilabel` `multilabel[,f1]` `subset01` `.tpr` `.ppv` `.acc` `.hamloss`
- `costsens` `mcp` `meancosts`
- `surv` `cindex`
- `other` `featperc` `timeboth` `timelpredict` `timetrain`

For detailed performance data on classification tasks, use:

- `calculateConfusionMatrix(pred=)`
- `calculateROCMeasures(pred=)`

### Resampling a learner

`makeResampleDesc(method=, ..., stratify=)`

`method` must be one of the following:

- "CV" (cross-validation, for number of folds use `iters=`)
  - "LOO" (leave-one-out cross-validation, for folds use `iters=`)
  - "RepCV" (repeated cross-validation, for number of repetitions use `reps=`, for folds use `folds=`)
  - "Subsample" (aka Monte-Carlo cross-validation, for iterations use `iters=`, for train % use `split=`)
  - "Bootstrap" (out-of-bag bootstrap, uses `iters=`)
  - "Holdout" (for train % use `split=`)
- `stratify` keeps target proportions consistent across samples.

`makeResampleInstance(desc=, task=)` can reduce noise by ensuring the resampling is done identically every time.

`resample(learner=, task=, resampling=, measures=)`  
Train and test model according to specified resampling strategy.

mlr includes several pre-specified resample descriptions: `cv2` (2-fold cross-validation), `cv3`, `cv5`, `cv10`, `hout` (holdout with split 2/3 for training, 1/3 for testing). Convenience functions also exist to `resample()` with a specific strategy: `crossval()`, `repCV()`, `holdout()`, `subsample()`, `bootstrap00B()`, `bootstrapB632()`, `bootstrapB632plus()`

## Refining Performance

### Tuning hyperparameters

Set search space using `makeParamSet(make<type>Param())`

- `makeNumericParam(id=, lower=, upper=, trafo=)`
  - `makeIntegerParam(id=, lower=, upper=, trafo=)`
  - `makeIntegerVectorParam(id=, len=, lower=, upper=, trafo=)`
  - `makeDiscreteParam(id=, values=c(...))` (can also be used to test discrete values of numeric or integer parameters)
- `trafo` transforms the parameter output using a specified function, e.g. `lower=-2, upper=2, trafo=function(x) 10^x` would test values between 0.01 and 100, scaled exponentially
- Other acceptable parameter types include `Logical` `LogicalVector` `CharacterVector` `DiscreteVector`

Set a search algorithm with `makeTuneControl<type>()`

- `Grid(resolution=10)` Grid of all possible points
- `Random(maxit=100)` Randomly sample search space
- `MBO(budget=)` Use Bayesian model-based optimization
- `Irace(n.instances=)` Iterated racing process
- Other types: `CMAES`, `Design`, `GenSA`

Tune using `tuneParams(learner=, task=, resampling=, measures=, par.set=, control=)`

## Quickstart

### Prepare data for training and testing

```

library(mlbench)
data(Soybean)
soy = createDummyFeatures(Soybean, target="Class")
tsk = makeClassifTask(data=soy, target="Class")
ho = makeResampleInstance("Holdout", tsk)
tsk.train = subsetTask(tsk, ho$train.ind[1])
tsk.test = subsetTask(tsk, ho$test.ind[1])

```

Convert the factor inputs in the Soybean dataset into (0,1) dummy features which can be used by the XGboost algorithm. Create a task to predict the "Class" column. Create a train set with 2/3 of data and a test set with the remaining 1/3 (default).

### Create learner and evaluate performance

```

lrn = makeLearner("classif.xgboost", nrounds=10)
cv = makeResampleDesc("CV", iters=5)
res = resample(lrn, tsk.train, cv, acc)

```

Create an XGboost learner which will build 10 trees. Then test performance using 5-fold cross-validation. Accuracy should be between 0.90-0.92.

### Tune hyperparameters and retrain model

```

ps = makeParamSet(makeNumericParam("eta", 0, 1),
 makeNumericParam("lambda", 0, 200),
 makeIntegerParam("max_depth", 1, 20))
tc = makeTuneControlMBO(budget=100)
tr = tuneParams(lrn, tsk.train, cv5, acc, ps, tc)
lrn = setHyperPars(lrn, par.vals=tr$x)

```

Tune hyperparameters `eta`, `lambda`, and `max_depth` by defining a search space and using Model Based Optimization (MBO) to control the search. Then perform 100 rounds of 5-fold cross-validation, improving accuracy to ~0.93. Update the XGboost learner with the tuned hyperparameters.

```

mdl = train(lrn, tsk.train)
prd = predict(mdl, tsk.test)
calculateConfusionMatrix(prd)
mdl = train(lrn, tsk)

```

Train the model on the train set and make predictions on the test set. Show performance as a confusion matrix. Finally, re-train model on the full set to use on new data. You are now ready to go out into the real world and make 93% accurate predictions!

Legend for functions (not all parameters shown):

`function(required_parameters, optional_parameters=)`

# Configuration

mlr's default settings can be changed using `configureMlr()`:

- `show.info` Whether to show verbose output by default when training, tuning, resampling, etc. (`TRUE`)
- `on.learner.error` How to handle a learner error. `"stop"` halts execution, `"warn"` returns NAs and displays a warning, `"quiet"` returns NAs with no warning (`"stop"`)
- `on.learner.warning` How to handle a learner warning. `"warn"` displays a warning, `"quiet"` suppresses it (`"warn"`)
- `on.par.without.desc` How to handle a parameter with no description. `"stop"`, `"warn"`, `"quiet"` (`"stop"`)
- `on.par.out.of.bounds` How to handle a parameter with an out-of-bounds value. `"stop"`, `"warn"`, `"quiet"` (`"stop"`)
- `on.measure.not.applicable` How to handle a measure not applicable to a learner. `"stop"`, `"warn"`, `"quiet"` (`"stop"`)
- `show.learner.output` Whether to show learner output to the console during training (`TRUE`)
- `on.error.dump` Whether to create an error dump for crashed learners if `on.learner.error` is not set to `"stop"` (`TRUE`)

Use `getMlrOptions()` to see current settings

# Parallelization

mlr works with the `parallelMap` package to take advantage of multicore and cluster computing for faster operations. mlr automatically detects which operations are able to run in parallel.

To begin parallel operation use:

- ```
parallelStart(mode=, cpus=, level=)
```
- `mode` determines how the parallelization is performed:
 - `"local"` no parallelization applied, simply uses `mapply`
 - `"multicore"` multicore execution on a single machine, uses `parallel::mclapply`. Not available in Windows.
 - `"socket"` multicore execution in socket mode
 - `"mpi"` Snow MPI cluster on one or multiple machines using `parallel::makeCluster` and `parallel::clusterMap`
 - `"BatchJobs"` Batch queuing HPC clusters using `BatchJobs::batchMap`
 - `cpus` determines how many logical cores will be used
 - `level` controls parallelization: `"mlr.benchmark"`, `"mlr.resample"`, `"mlr.selectFeatures"`, `"mlr.tuneParams"`, `"mlr.ensemble"`

To end parallelization, use `parallelStop()`

Imputation

`impute(obj=, target=, cols=, dummy.cols=, dummy.type=)`
Applies specified logic to data frame or task containing NAs and returns an imputation description which can be used on new data

- `obj`=data frame or task on which to perform imputation
- `target`=specify target variable which will not be imputed
- `cols`=column names and logic for imputation*
- `dummy.cols`=column names to create a NA (T/F) column*
- `dummy.type`=set to `"numeric"` to use (0,1) instead of (T/F)

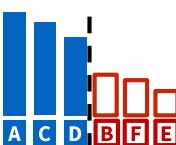
*Can also use `classes` and `dummy.classes` in place of `cols`

Imputation logic is passed to `cols` or `classes` via a list, e.g.: `cols=list(V1=imputeMean())` where `V1` is the column to which to apply the imputation, and `imputeMean()` is the imputation method. Available imputation methods include:
`imputeConst(const=)` `imputeMedian()` `imputeMode()` `imputeMin(multiplier=)` `imputeMax(multiplier=)` `imputeNormal(mean=, sd=)` `imputeHist(breaks=, use.mids=)` `imputeLearner(learner=, features=)` `impute` returns a list containing the imputed dataset or task as well as an imputation description that can be used to reapply the same imputation to new data using `reimpute`

`reimpute(obj=, desc=)` Imputes missing values on a task or dataset (`obj`) using a description (`desc`) created by `impute`

Feature Extraction

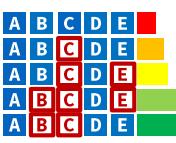
Feature filtering



`filterFeatures(task=, method=, perc=, abs=, threshold=)`
Uses a learner-agnostic feature evaluation method to rank feature importance, then includes only features in the top n percent (`perc=`), top n (`abs=`), or which meet a set performance threshold (`threshold=`).

Outputs a task with features that failed the test omitted. `method` defaults to `"randomForestSRC.rfsrc"`, but can be set to:
`"anova.test"` `"carscore"` `"cforest.importance"`
`"chi.squared"` `"gain.ratio"` `"information.gain"`
`"kruskal.test"` `"linear.correlation"` `"mrmr"` `"oneR"`
`"permutation.importance"` `"randomForest.importance"`
`"randomForestSRC.rfsrc"` `"randomForestSRC.var.select"`
`"rank.correlation"` `"relief"`
`"symmetrical.uncertainty"` `"univariate.model.score"`
`"variance"`

Feature selection



`selectFeatures(learner=, task=, resampling=, measures=, control=)`
Uses a feature selection algorithm (`control`) to resample and build a model repeatedly using different feature sets each time in order to find the best set.

Available controls include:

- `makeFeatSelControlExhaustive(max.features=)` Try every combination of features up to optional `max.features`
- `makeFeatSelControlRandom(maxit=, prob=, max.features=)` Randomly sample features with probability `prob` (default 0.5) until `maxit` (default 100) iterations; return the best one found
- `makeFeatSelControlSequential(method=, maxit=, max.features=, alpha=, beta=)` Perform an iterative search using a `method` from the following: `"sfs"` forward search, `"sbs"` backward search, `"sffs"` floating forward search, `"sfbs"` floating backward search. `alpha` indicates minimum improvement required to add a feature; `beta` indicates minimum required to remove a feature
- `makeFeatSelControlGA(maxit=, max.features=, mu=, lambda=, crossover.rate=, mutation.rate=)` Genetic algorithm trains on random feature vectors, then uses crossover on the best performers to produce 'offspring', repeated over generations. `mu` is size of parent population, `lambda` is size of children population, `crossover.rate` is probability of choosing a bit from first parent, `mutation.rate` is probability of flipping a bit (on or off)

`selectFeatures` returns a `FeatSelResult` object which contains optimal features and an optimization path. To apply feature selection result (`fsr`) to your task (`tsk`), use:
`tsk = subsetTask(tsk, features=fsr$x)`

Benchmarking

`benchmark(learners=, tasks=, resamplings=, measures=)`
Allows easy comparison of multiple learners on a single task, a single learner on multiple tasks, or multiple learners on multiple tasks. Returns a benchmark result object.

Benchmark results can be accessed with a variety of functions beginning with `getBMR<object>.AggrPerformance`
`FeatSelResults` `FilteredFeatures` `LearnerIds`
`LeanerShortNames` `Learners` `MeasureIds` `Measures`
`Models` `Performances` `Predictions` `TaskDescs` `TaskIds`
`TuneResults`

mlr contains several toy tasks which are useful for benchmarking:
`agri.task` `bc.task` `bh.task` `costiris.task` `iris.task`
`lung.task` `mtcars.task` `pid.task` `sonar.task`
`wpbc.task` `yeast.task`

Visualization

Performance

`generateThreshVsPerfData(obj=, measures=)` Measure performance at different probability cutoffs to determine optimal decision threshold for binary classification problems

- `plotThreshVsPerf(obj=)` Plot visual representation of threshold curve(s) from `ThreshVsPerfData`
- `plotROCCurves(obj=)` Plot receiver operating characteristic (ROC) curve from `ThreshVsPerfData`. Must set `measures=list(fpr, tpr)`

Residuals

- `plotResiduals(obj=)` Plots residuals for `Prediction` or `BenchmarkResult`

Learning curve

`generateLearningCurveData(learners=, task=, resampling=, percs=, measures=)` Measure performance of learner(s) trained on different percentages of task data

- `plotLearningCurve(obj=)` Plot curve showing learner performance vs. proportion of data used, uses `LearningCurveData`

Feature importance

`generateFilterValuesData(task=, method=)` Get feature importance rankings using specified filter method

- `plotFilterValues(obj=)` Plot bar chart of feature importance based on filter method using `FilterValuesData`

Hyperparameter tuning

`generateHyperParsEffectData(tune.result=)` Get the impact of different hyperparameter settings on model performance

- `plotHyperParsEffect(hyperpars.effec.t.data=, x=, y=, z=)` Create a plot showing hyperparameter impact on performance using `HyperParsEffectData`

See also:

- `plotOptPath(op=)` Display details of optimization process. Takes `<obj>$opt.path`, where `<obj>` is an object of class `tuneResult` or `featSelResult`
- `plotTuneMultiCritResult(res=)` Show pareto front for results of tuning to multiple performance measures

Partial dependence

`generatePartialDependenceData(obj=, input=)` Get partial dependence of model (`obj`) prediction over each feature of data (`input`)

- `plotPartialDependence(obj=)` Plots partial dependence of model using `PartialDependenceData`

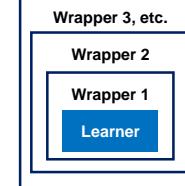
Benchmarking

- `plotBMRBoxplots(bmr=)` Distribution of performances
- `plotBMRSummary(bmr=)` Scatterplot of avg. performances
- `plotBMRanksAsBarChart(bmr=)` Rank learners in bar plot

Other

- `generateCritDifferencesData(bmr=, measure=, p.value=, test=)` Perform critical-differences test using either the Bonferroni-Dunn ("bd") or "Nemenyi" test
- `plotCritDifferences(obj=)`
- `generateCalibrationData(obj=)` Evaluate calibration of probability predictions vs. true incidence
- `plotCalibration(obj=)`

Wrappers



Wrappers fuse a learner with additional functionality. mlr treats a learner with wrappers as a single learner, and hyperparameters of wrappers can be tuned jointly with underlying model parameters. Models trained with wrappers will apply them to new data.

Preprocessing and imputation

`makeDummyFeaturesWrapper(learner=)`
`makeImputeWrapper(learner=, classes=, cols=)`
`makePreprocWrapper(learner=, train=, predict=)`
`makePreprocWrapperCaret(learner=, ...)`
`makeRemoveConstantFeaturesWrapper(learner=)`

Class imbalance

`makeOverBaggingWrapper(learner=)`
`makeSMOTEWrapper(learner=)`
`makeUndersampleWrapper(learner=)`
`makeWeightedClassesWrapper(learner=)`

Cost-sensitive learning

`makeCostSensClassifWrapper(learner=)`
`makeCostSensRegrWrapper(learner=)`
`makeCostSensWeightedPairsWrapper(learner=)`

Multilabel classification

`makeMultilabelBinaryRelevanceWrapper(learner=)`
`makeMultilabelClassifierChainsWrapper(learner=)`
`makeMultilabelDBRWrapper(learner=)`
`makeMultilabelNestedStackingWrapper(learner=)`
`makeMultilabelStackingWrapper(learner=)`

Other

`makeBaggingWrapper(learner=)`
`makeConstantClassWrapper(learner=)`
`makeDownsampleWrapper(learner=, dw.perc=)`
`makeFeatSelWrapper(learner=, resampling=, control=)`
`makeFilterWrapper(learner=, fw.perc=, fw.abs=, fw.threshold=)`
`makeMultiClassWrapper(learner=)`
`makeTuneWrapper(learner=, resampling=, par.set=, control=)`

Nested Resampling

mlr supports **nested resampling** for complex operations such as tuning and feature selection through wrappers. In order to get a good estimate of generalization performance and avoid data leakage, both an outer (for tuning/feature selection) and an inner (for the base model) resampling process are advised.

- Outer resampling can be specified in `resample` or `benchmark`
- Inner resampling can be specified in `makeTuneWrapper`, `makeFeatSelWrapper`, etc.

Ensembles

`makeStackedLearner(base.learners=, super.learner=, method=)` Combines multiple learners to create an ensemble

- `base.learners`=learners to use for initial predictions
- `super.learner`=learner to use for final prediction
- `method`=how to combine base learner predictions:
 - `"average"` simple average of all base learners
 - `"stack.nocv", "stack.cv"` train super learner on results of base learners, with or without cross-validation
 - `"hill.climb"` search for optimal weighted average
 - `"compress"` with a neural network for faster performance

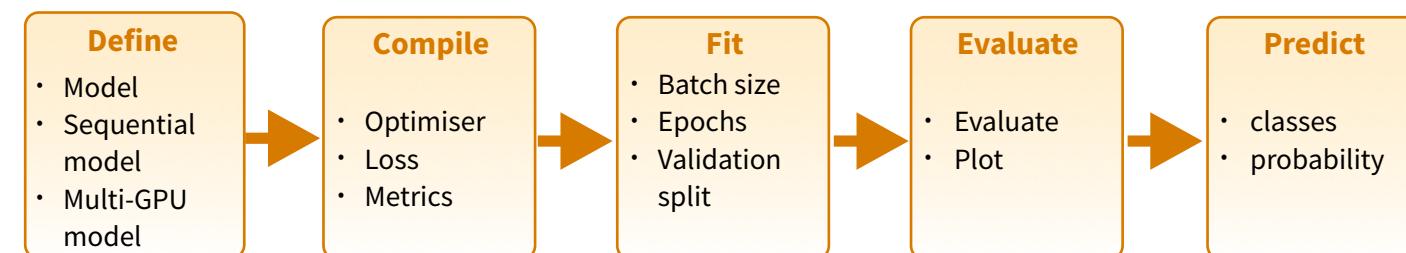
Deep Learning with Keras :: CHEAT SHEET



Intro

[Keras](#) is a high-level neural networks API developed with a focus on enabling fast experimentation. It supports multiple backends, 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.



<https://keras.rstudio.com>

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

The “Hello, World!”
of deep learning

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 on input activity



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



`layer_flatten()` Flattens an input

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`'.

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

| | |
|---|--|
|  | <code>layer_conv_1d()</code> 1D, e.g. temporal convolution |
|  | <code>layer_conv_2d_transpose()</code> Transposed 2D (deconvolution) |
|  | <code>layer_conv_2d()</code> 2D, e.g. spatial convolution over images |
|  | <code>layer_conv_3d_transpose()</code> Transposed 3D (deconvolution)
<code>layer_conv_3d()</code> 3D, e.g. spatial convolution over volumes |
|  | <code>layer_conv_lstm_2d()</code> Convolutional LSTM |
|  | <code>layer_separable_conv_2d()</code> Depthwise separable 2D |
|  | <code>layer_upsampling_1d()</code>
<code>layer_upsampling_2d()</code>
<code>layer_upsampling_3d()</code> Upsampling layer |
|  | <code>layer_zero_padding_1d()</code>
<code>layer_zero_padding_2d()</code>
<code>layer_zero_padding_3d()</code> Zero-padding layer |
|  | <code>layer_cropping_1d()</code>
<code>layer_cropping_2d()</code>
<code>layer_cropping_3d()</code> Cropping layer |

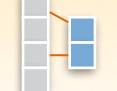
POOLING LAYERS

| | |
|---|---|
|  | <code>layer_max_pooling_1d()</code>
<code>layer_max_pooling_2d()</code>
<code>layer_max_pooling_3d()</code> Maximum pooling for 1D to 3D |
|  | <code>layer_average_pooling_1d()</code>
<code>layer_average_pooling_2d()</code>
<code>layer_average_pooling_3d()</code> Average pooling for 1D to 3D |
|  | <code>layer_global_max_pooling_1d()</code>
<code>layer_global_max_pooling_2d()</code>
<code>layer_global_max_pooling_3d()</code> Global maximum pooling |
|  | <code>layer_global_average_pooling_1d()</code>
<code>layer_global_average_pooling_2d()</code>
<code>layer_global_average_pooling_3d()</code> Global average pooling |

ACTIVATION LAYERS

| | |
|---|---|
|  | <code>layer_activation()</code> object, activation
Apply an activation function to an output |
|  | <code>layer_activation_leaky_relu()</code> Leaky version of a rectified linear unit |
|  | <code>layer_activation_parametric_relu()</code> Parametric rectified linear unit |
|  | <code>layer_activation_thresholded_relu()</code> Thresholded rectified linear unit |
|  | <code>layer_activation_elu()</code> Exponential linear unit |

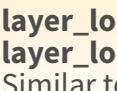
DROPOUT LAYERS

| | |
|---|---|
|  | <code>layer_dropout()</code> Applies dropout to the input |
|  | <code>layer_spatial_dropout_1d()</code>
<code>layer_spatial_dropout_2d()</code>
<code>layer_spatial_dropout_3d()</code> Spatial 1D to 3D version of dropout |

RECURRENT LAYERS

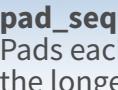
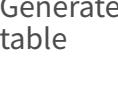
| | |
|---|---|
|  | <code>layer_simple_rnn()</code> Fully-connected RNN where the output is to be fed back to input |
|  | <code>layer_gru()</code> Gated recurrent unit - Cho et al |
|  | <code>layer_cudnn_gru()</code> Fast GRU implementation backed by CuDNN |

LOCALLY CONNECTED LAYERS

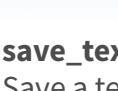
| | |
|---|--|
|  | <code>layer_locally_connected_1d()</code>
<code>layer_locally_connected_2d()</code> Similar to convolution, but weights are not shared, i.e. different filters for each patch |
|---|--|

Preprocessing

SEQUENCE PREPROCESSING

| | |
|---|---|
|  | <code>pad_sequences()</code> Pads each sequence to the same length (length of the longest sequence) |
|  | <code>skipgrams()</code> Generates skipgram word pairs |
|  | <code>make_sampling_table()</code> Generates word rank-based probabilistic sampling table |

TEXT PREPROCESSING

| | |
|---|---|
|  | <code>text_tokenizer()</code> Text tokenization utility |
|  | <code>fit_text_tokenizer()</code> Update tokenizer internal vocabulary |
|  | <code>save_text_tokenizer(); load_text_tokenizer()</code> Save a text tokenizer to an external file |
|  | <code>texts_to_sequences(); texts_to_sequences_generator()</code> Transforms each text in texts to sequence of integers |
|  | <code>texts_to_matrix(); sequences_to_matrix()</code> Convert a list of sequences into a matrix |
|  | <code>text_one_hot()</code> One-hot encode text to word indices |

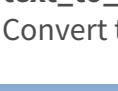
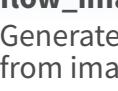
| | |
|---|--|
|  | <code>text_to_word_sequence()</code> Convert text to a sequence of words (or tokens) |
|  | |

IMAGE PREPROCESSING

| | |
|---|---|
|  | <code>image_load()</code> Loads an image into PIL format. |
|  | <code>flow_images_from_data()</code>
<code>flow_images_from_directory()</code> Generates batches of augmented/normalized data from images and labels, or a directory |
|  | <code>image_data_generator()</code> Generate minibatches of image data with real-time data augmentation. |
|  | <code>fit_image_data_generator()</code> Fit image data generator internal statistics to some sample data |
|  | <code>generator_next()</code> Retrieve the next item |

| | |
|---|--|
|  | <code>image_to_array(); image_array_resize()</code>
<code>image_array_save()</code> 3D array representation |
|---|--|

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

Data Science in Spark with sparklyr :: CHEAT SHEET

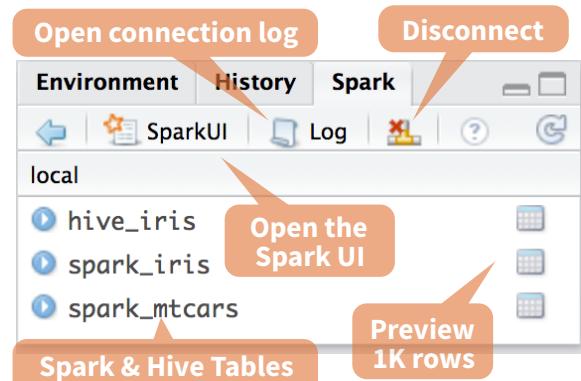


Intro

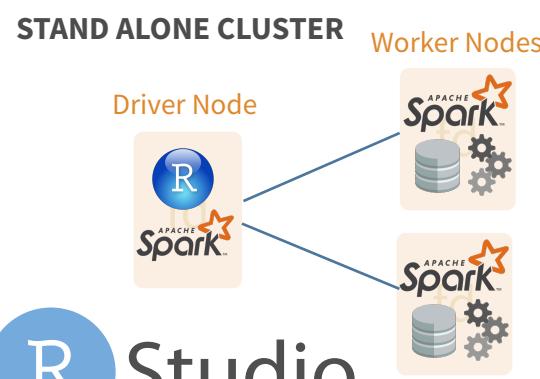
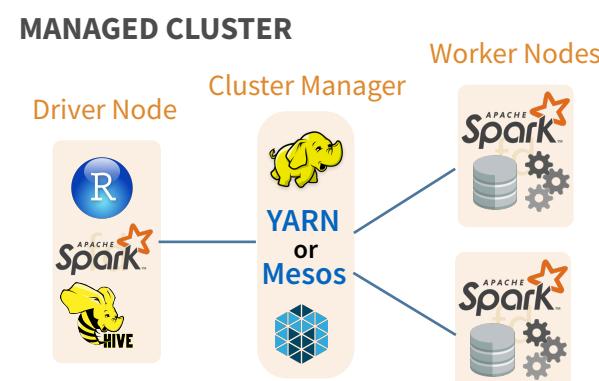
sparklyr is an R interface for Apache Spark™, it provides a complete **dplyr** backend and the option to query directly using **Spark SQL** statement. With sparklyr, you can orchestrate distributed machine learning using either **Spark's MLLib** or **H2O** Sparkling Water.

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

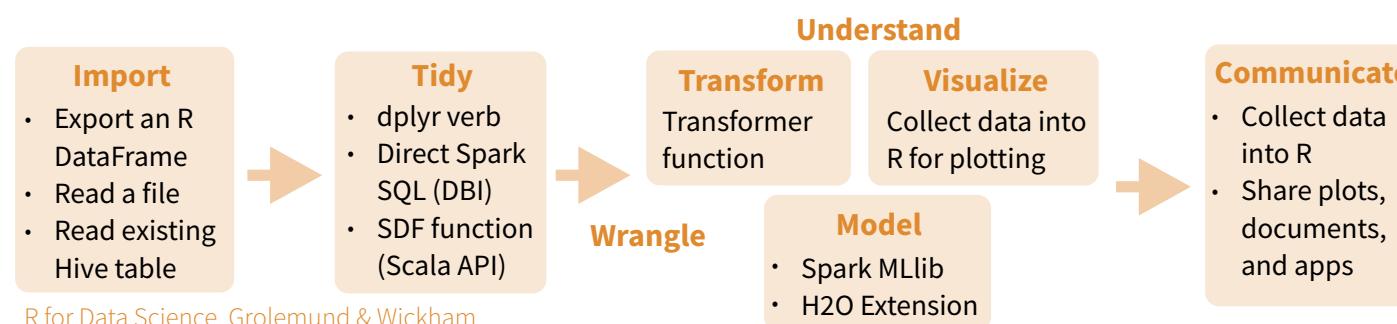


Cluster Deployment



R Studio

Data Science Toolchain with Spark + sparklyr



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, it normally is "/usr/lib/spark"
3. Open a connection
`spark_connect(master="mesos URL", version = "1.6.2", spark_home = [Cluster's Spark path])`

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)
```

Spark ML Decision Tree Model

```
model_iris <- tidy_iris %>%
  ml_decision_tree(response="Species",
  features=c("Petal_Length","Petal_Width"))
```

```
test_iris <-tbl(sc,"spark_iris_test")
```

Create reference to Spark table

```
pred_iris <- sdf_predict(
  model_iris, test_iris) %>%
  collect
```

```
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(sc, ...)`
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_vectorAssembler()`
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)`

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())`

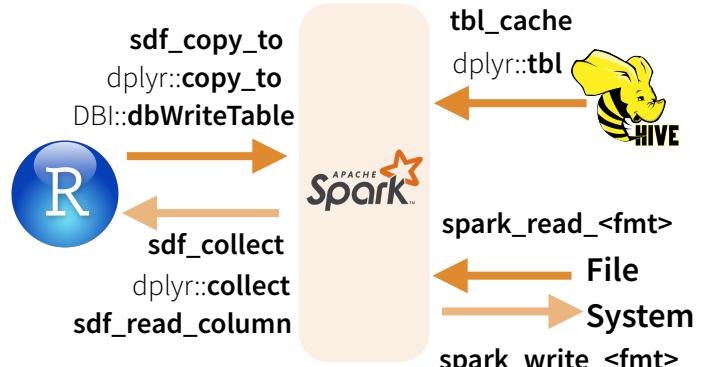
`ml_random_forest(x, response, features, max.bins = 32L, max.depth = 5L, num.trees = 20L, type = c("auto", "regression", "classification"), ml.options = ml_options())`

`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)`



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_options()`

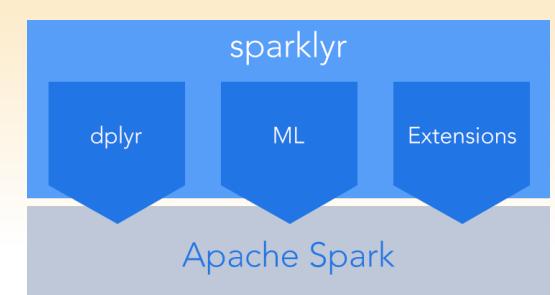
`ml_prepare_dataframe()` `ml_model()`

`ml_prepare_response_features_intercept()`

sparklyr

is an R interface
for

Apache Spark



Basic Regular Expressions in R

Cheat Sheet

Character Classes

| | |
|--|---|
| <code>[:digit:]</code> or <code>\d</code> | Digits; [0-9] |
| <code>\D</code> | Non-digits; [^0-9] |
| <code>[:lower:]</code> | Lower-case letters; [a-z] |
| <code>[:upper:]</code> | Upper-case letters; [A-Z] |
| <code>[:alpha:]</code> | Alphabetic characters; [A-z] |
| <code>[:alnum:]</code> | Alphanumeric characters [A-z0-9] |
| <code>\w</code> | Word characters; [A-z0-9_] |
| <code>\W</code> | Non-word characters |
| <code>[:xdigit:]</code> or <code>\x</code> | Hexadec. digits; [0-9A-Fa-f] |
| <code>[:blank:]</code> | Space and tab |
| <code>[:space:]</code> or <code>\s</code> | Space, tab, vertical tab, newline, form feed, carriage return |
| <code>\S</code> | Not space; [^[:space:]] |
| <code>[:punct:]</code> | Punctuation characters; !#\$%&'()*+, -./; <=>?@[]^_`{ }~ |
| <code>[:graph:]</code> | Graphical characters; [[:alnum:][:punct:]] |
| <code>[:print:]</code> | Printable characters; [[:alnum:][:punct:]\s] |
| <code>[:cntrl:]</code> or <code>\c</code> | Control characters; \n, \r etc. |

Special Metacharacters

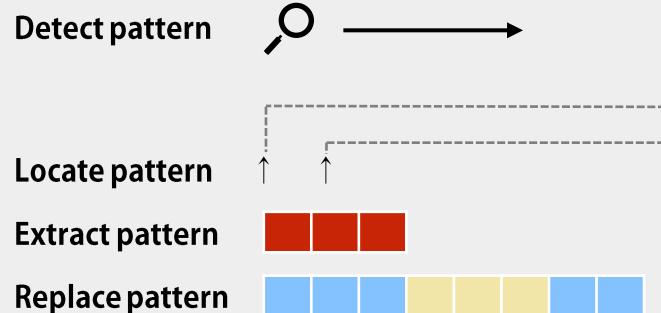
| | |
|-----------------|-----------------|
| <code>\n</code> | New line |
| <code>\r</code> | Carriage return |
| <code>\t</code> | Tab |
| <code>\v</code> | Vertical tab |
| <code>\f</code> | Form feed |

Lookarounds and Conditionals*

| | |
|-----------------------------|--|
| <code>(?=)</code> | Lookahead (requires PERL = TRUE), e.g. (?=yx): position followed by 'xy' |
| <code>(?!)</code> | Negative lookahead (PERL = TRUE); position NOT followed by pattern |
| <code>(?<=)</code> | Lookbehind (PERL = TRUE), e.g. (?<=yx): position following 'xy' |
| <code>(?<!=)</code> | Negative lookbehind (PERL = TRUE); position NOT following pattern |
| <code>?(if)then</code> | If-then-condition (PERL = TRUE); use lookaheads, optional char. etc in if-clause |
| <code>?(if)then else</code> | 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("Hipopopotamus", "Rhymenoceros", "time for bottomless lyrics")
> pattern <- "t.m"
```

Detect Patterns

```
grep(pattern, string)
[1] 1 3
grep(pattern, string, value = TRUE)
[1] "Hipopopotamus"
[2] "time for bottomless lyrics"
grepl(pattern, string)
[1] TRUE FALSE TRUE
stringr::str_detect(string, pattern)
[1] TRUE FALSE TRUE
```

Split a String using a Pattern

```
strsplit(string, pattern) or stringr::str_split(string, pattern)
```

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
```

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 |
| \B | Beginning of a word |
| \B | 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.

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 be 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 Mac OS or Linux      # on Windows
library(doMC)              library(doParallel)
registerDoMC(cores=4)       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).
- `"L0O"` 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.

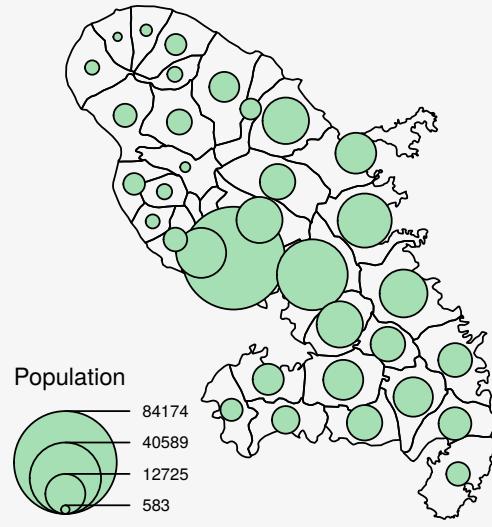
```
trainControl(sampling = "down")
```

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",
typefc = "exponential", span = 500,
beta = 2)



Discontinuities
discLayer(x = mtq.borders, df = mtq_df,
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

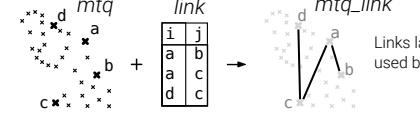
```
mtq_grid <- getGridLayer(x = mtq, cellsize = 3.6e+07,
  type = "hexagonal", var = "myvar")
```



Grids layers can be used by
choroLayer() or propSymbolsLayer().

Points to Links

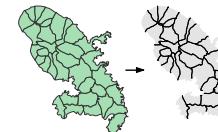
```
mtq_link <- getLinkLayer(x = mtq, df = link)
```



Links layers can be
used by *LinkLayer().

Polygons to Borders

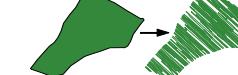
```
mtq_border <- getBorders(x = mtq)
```



Borders layers can be used by
discLayer() function

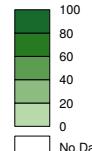
Polygons to Pencil Lines

```
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", 6),  
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()

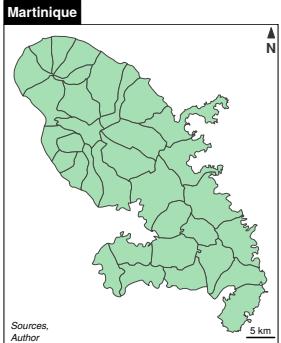


```
legendCirclesSymbols(var = c(10,100),  
title.txt = "legendCirclesSymbols()",  
col = "#a7dfb4ff", inches = 0.3)
```

See also legendSquaresSymbols(), legendBarsSymbols(),
legendGradLines(), legendPropLines() and legendPropTriangles().

Map Layout

North Arrow:
north(pos = "topright")



Scale Bar:
barscale(size = 5)

Full Layout:

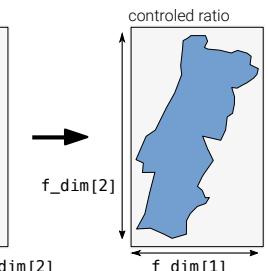
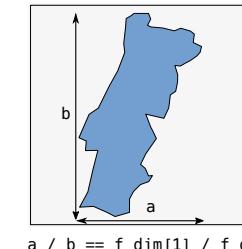
```
layoutLayer(
  title = "Martinique",
  tabtitle = TRUE,
  frame = TRUE,
  author = "Author",
  sources = "Sources",
  north = TRUE,
  scale = 5)
```

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()
```

default



Color Palettes

carto.pal(pal1 = "blue.pal", n1 = 5,
pal2 = sand.pal, n2 = 3)



display.carto.all(n = 8)



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.

| | | | |
|------------------|--------------|----------|------------------|
| x[j] ## column J | x[i] | <- value | Value Assignment |
| x[i, j] | x[i, j, ...] | <- value | |
| x[[i]] | x[[i]] | <- value | |
| x\$name | x\$i | <- value | |

Selection

Value Assignment

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:

h2o.asfactor, as.factor: Factor.

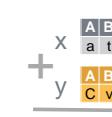
h2o.as_date, as.Date: Date.

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, \sqrt{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.

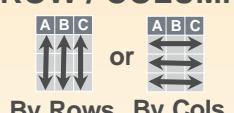
h2o.all: Given a set of logical vectors, determine if all of the values are true.

NON-GROUP_BY SUMMARIES: GENERIC

h2o.summary: Produce result summaries of the results of various model fitting functions.

Aggregations

ROW / COLUMN AGGREGATION



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.glrn: 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.



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

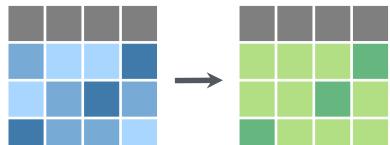
- If the data-argument is a *vector*, functions return a *vector*.



```
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's `select()`: Separate variables with comma, or use dplyr's 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 = NULL, ...)
```

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 names and variable labels  
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)
```

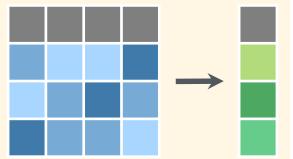
```
recode_to(x, ..., lowest = 0, highest = -1,  
  append = TRUE, suffix = "_r0")
```

Shift ("renumber") categories or values.

```
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.

```
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 that should be "merged".

- `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, rec = "1,2=0;3:8=1"),  
  gear2 = rec(gear, rec = "3=1;4:max=2"))
```

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)
```

randomizr is part of the DeclareDesign suite of packages for designing, implementing, and analyzing social science research designs.

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

```
simple_ra()
```

```
complete_ra()
```

```
block_ra()
```

```
cluster_ra()
```

```
block_and_cluster_ra()
```

```
declare_ra()
```

```
conduct_ra()
```

Sampling

```
simple_rs()
```

```
complete_rs()
```

```
strata_rs()
```

```
cluster_rs()
```

```
strata_and_cluster_rs()
```

```
declare_rs()
```

```
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)
```