Intermediate R, Season 3

March, 2024

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# 1 About this Course

## 1.1 Curriculum

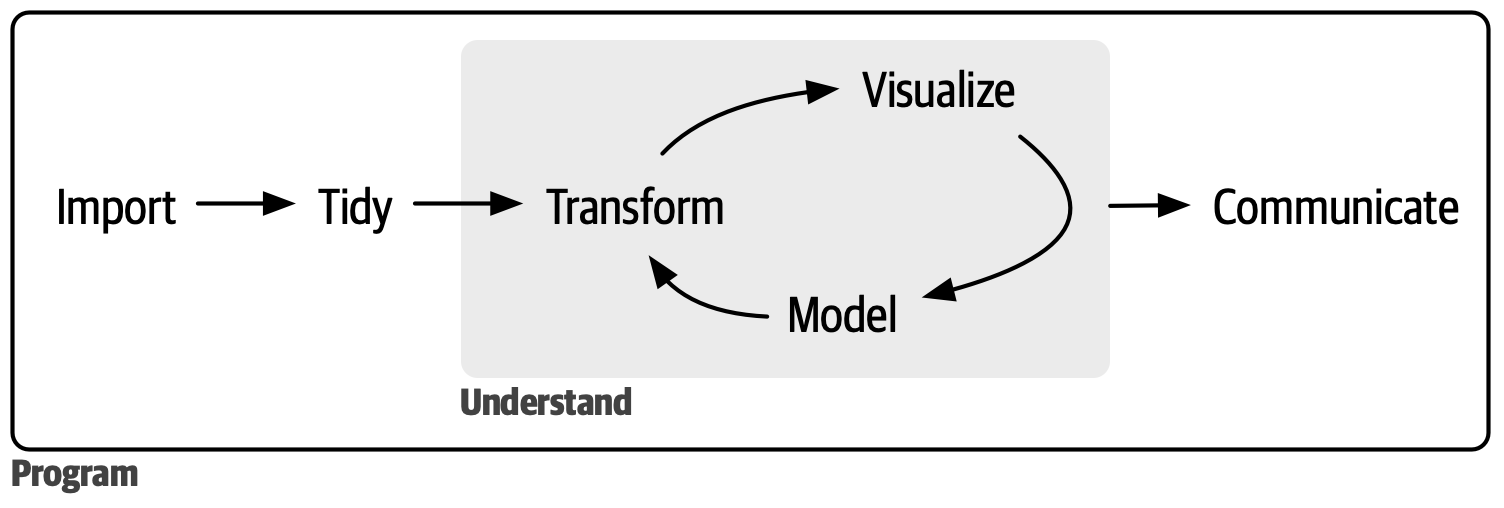
The course continues building programming fundamentals in R programming and data analysis. You will learn how to make use of complex data structures, use custom functions built by other R users, creating your own functions, and how to iterate repeated tasks that scales naturally. You will also learn how to clean messy data to a Tidy form for analysis, and conduct an end-to-end data science workflow.

## 1.2 Target Audience

The course is intended for researchers who want to continue learning the fundamentals of R programming and how to deal with messy datasets. The audience should know how to subset dataframes and vectors and conduct basic analysis, and/or have taken our [Intro to R course](https://github.com/fhdsl/Intro_to_R).

# 2 Fundamentals

## 2.1 Goals of this course

* Continue building *programming fundamentals*: how to make use of complex data structures, use custom functions built by other R users, and creating your own functions. How to iterate repeated tasks that scales naturally.
* Continue exploration of *data science fundamentals*: how to clean messy data to a Tidy form for analysis.
* Outcome: Conduct a full analysis in the data science workflow (minus model).
* 

## 2.2 Data types in R

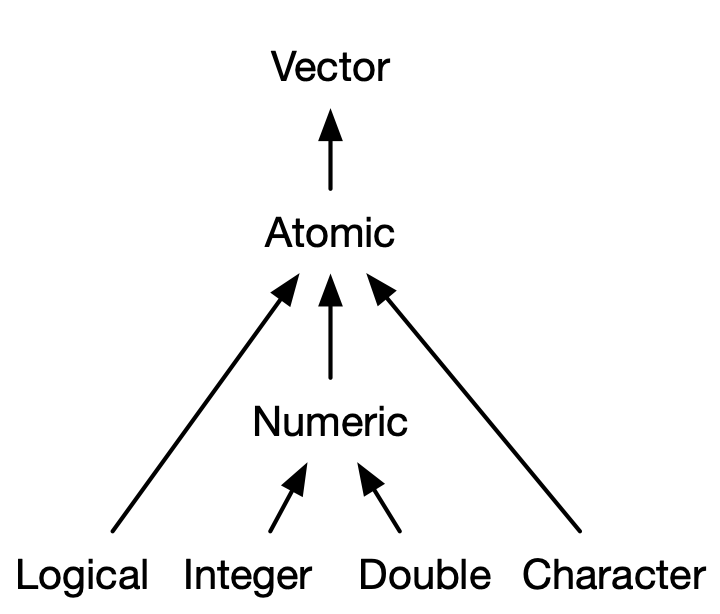
* Numeric: 18, -21, 65, 1.25
* Character: “ATCG”, “Whatever”, “948-293-0000”
* Logical: TRUE, FALSE
* Missing values: NA

## 2.3 Data structures

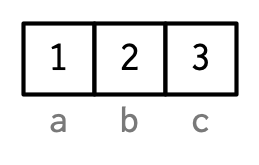
* Vector
* *Factor*
* Dataframe
* **List**
* *Matrix*

## 2.4 Vector

We know what an **(atomic) vector** is: it can contains a data type, and all elements must be the same data type.



Within the Numeric type that we are familiar with, there are more specific types: *Integer* consists of whole number values, and *Double* consists of decimal values. Most of the time we only need to consider Numeric types, but once in a while we need to be more specific.

* We can test whether a vector is a certain type with is.\_\_\_() functions, such as is.character().
* is.character(c("hello", "there"))
* ## [1] TRUE
* For NA, the test will return a vector testing each element, because NA can be mixed into other values:
* is.na(c(34, NA))
* ## [1] FALSE TRUE
* We can **coerce** vectors from one type to the other with as.\_\_\_() functions, such as as.numeric()
* as.numeric(c("23", "45"))
* ## [1] 23 45
* as.numeric(c(TRUE, FALSE))
* ## [1] 1 0
* It is common to have metadata **attributes,** such as **names,** attached to R data structures.
* x = c(1, 2, 3)  
  names(x) = c("a", "b", "c")  
  x
* ## a b c   
  ## 1 2 3
* 

We can look for more general attributes via the attributes() function:

attributes(x)

## $names  
## [1] "a" "b" "c"

### 2.4.1 Ways to subset a vector

1. Positive numeric vector
2. Negative numeric vector performs *exclusion*
3. Logical vector

### 2.4.2 Practice implicit subsetting

1. How do you subset the following vector so that it only has positive values?

data = c(2, 4, -1, -3, 2, -1, 10)

data[data > 0]

## [1] 2 4 2 10

1. How do you subset the following vector so that it has doesn’t have the character “temp”?

chars = c("temp", "object", "temp", "wish", "bumblebee", "temp")

chars[chars != "temp"]

## [1] "object" "wish" "bumblebee"

1. How do you subset the following vector so that it has no NA values?

vec\_with\_NA = c(2, 4, NA, NA, 3, NA)

vec\_with\_NA[!is.na(vec\_with\_NA)]

## [1] 2 4 3

## 2.5 Factors

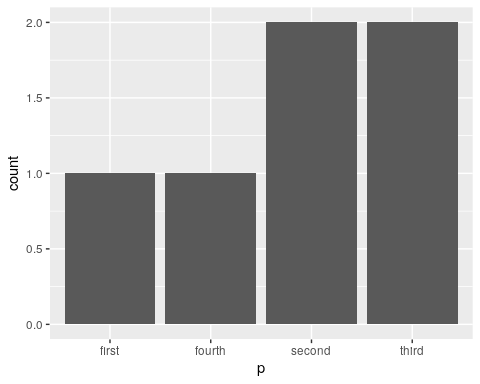
Factors are a type of vector that holds categorical information, such as sex, gender, or cancer subtype. They are useful for:

* When you know you have a fixed number of categories.
* When you want to display character vectors in a non-alphabetical order, which is common in plotting.
* Inputs for statistical models, as factors are a special type of numerical vectors.

place = factor(c("first", "third", "third", "second", "second", "fourth"))  
place

## [1] first third third second second fourth  
## Levels: first fourth second third

df = data.frame(p = place)  
ggplot(df) + geom\_bar(aes(x = p))

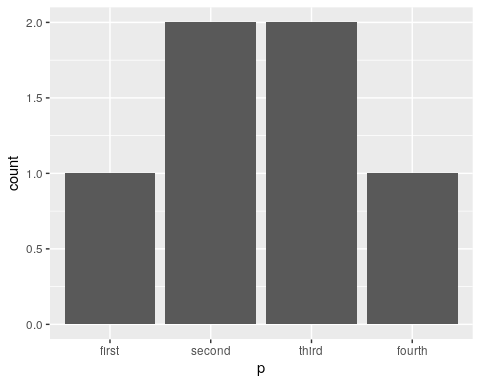


We can construct ordered factors:

place = ordered(c("first", "third", "third", "second","second", "fourth"), levels = c("first", "second", "third", "fourth"))  
place

## [1] first third third second second fourth  
## Levels: first < second < third < fourth

df = data.frame(p = place)  
ggplot(df) + geom\_bar(aes(x = p))



## 2.6 Dataframes

Usually, we load in a dataframe from a spreadsheet or a package, but we can create a new dataframe by using vectors of the same length via the data.frame() function:

df = data.frame(x = 1:3, y = c("cup", "mug", "jar"))  
attributes(df)

## $names  
## [1] "x" "y"  
##   
## $class  
## [1] "data.frame"  
##   
## $row.names  
## [1] 1 2 3

library(palmerpenguins)  
attributes(penguins)

## $class  
## [1] "tbl\_df" "tbl" "data.frame"  
##   
## $row.names  
## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18  
## [19] 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36  
## [37] 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54  
## [55] 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72  
## [73] 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90  
## [91] 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108  
## [109] 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126  
## [127] 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144  
## [145] 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162  
## [163] 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180  
## [181] 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198  
## [199] 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216  
## [217] 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234  
## [235] 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252  
## [253] 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270  
## [271] 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288  
## [289] 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306  
## [307] 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324  
## [325] 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342  
## [343] 343 344  
##   
## $names  
## [1] "species" "island" "bill\_length\_mm"   
## [4] "bill\_depth\_mm" "flipper\_length\_mm" "body\_mass\_g"   
## [7] "sex" "year"

Why are row names [undesirable](https://adv-r.hadley.nz/vectors-chap.html#rownames)?

Sometimes, data frames will be in a format called “tibble”, as shown in the penguins class names as “tbl\_df”, and “tbl”.

### 2.6.1 Subsetting dataframes

*Getting one single column:*

penguins$bill\_length\_mm

## [1] 39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42.0 37.8 37.8 41.1 38.6 34.6  
## [16] 36.6 38.7 42.5 34.4 46.0 37.8 37.7 35.9 38.2 38.8 35.3 40.6 40.5 37.9 40.5  
## [31] 39.5 37.2 39.5 40.9 36.4 39.2 38.8 42.2 37.6 39.8 36.5 40.8 36.0 44.1 37.0  
## [46] 39.6 41.1 37.5 36.0 42.3 39.6 40.1 35.0 42.0 34.5 41.4 39.0 40.6 36.5 37.6  
## [61] 35.7 41.3 37.6 41.1 36.4 41.6 35.5 41.1 35.9 41.8 33.5 39.7 39.6 45.8 35.5  
## [76] 42.8 40.9 37.2 36.2 42.1 34.6 42.9 36.7 35.1 37.3 41.3 36.3 36.9 38.3 38.9  
## [91] 35.7 41.1 34.0 39.6 36.2 40.8 38.1 40.3 33.1 43.2 35.0 41.0 37.7 37.8 37.9  
## [106] 39.7 38.6 38.2 38.1 43.2 38.1 45.6 39.7 42.2 39.6 42.7 38.6 37.3 35.7 41.1  
## [121] 36.2 37.7 40.2 41.4 35.2 40.6 38.8 41.5 39.0 44.1 38.5 43.1 36.8 37.5 38.1  
## [136] 41.1 35.6 40.2 37.0 39.7 40.2 40.6 32.1 40.7 37.3 39.0 39.2 36.6 36.0 37.8  
## [151] 36.0 41.5 46.1 50.0 48.7 50.0 47.6 46.5 45.4 46.7 43.3 46.8 40.9 49.0 45.5  
## [166] 48.4 45.8 49.3 42.0 49.2 46.2 48.7 50.2 45.1 46.5 46.3 42.9 46.1 44.5 47.8  
## [181] 48.2 50.0 47.3 42.8 45.1 59.6 49.1 48.4 42.6 44.4 44.0 48.7 42.7 49.6 45.3  
## [196] 49.6 50.5 43.6 45.5 50.5 44.9 45.2 46.6 48.5 45.1 50.1 46.5 45.0 43.8 45.5  
## [211] 43.2 50.4 45.3 46.2 45.7 54.3 45.8 49.8 46.2 49.5 43.5 50.7 47.7 46.4 48.2  
## [226] 46.5 46.4 48.6 47.5 51.1 45.2 45.2 49.1 52.5 47.4 50.0 44.9 50.8 43.4 51.3  
## [241] 47.5 52.1 47.5 52.2 45.5 49.5 44.5 50.8 49.4 46.9 48.4 51.1 48.5 55.9 47.2  
## [256] 49.1 47.3 46.8 41.7 53.4 43.3 48.1 50.5 49.8 43.5 51.5 46.2 55.1 44.5 48.8  
## [271] 47.2 NA 46.8 50.4 45.2 49.9 46.5 50.0 51.3 45.4 52.7 45.2 46.1 51.3 46.0  
## [286] 51.3 46.6 51.7 47.0 52.0 45.9 50.5 50.3 58.0 46.4 49.2 42.4 48.5 43.2 50.6  
## [301] 46.7 52.0 50.5 49.5 46.4 52.8 40.9 54.2 42.5 51.0 49.7 47.5 47.6 52.0 46.9  
## [316] 53.5 49.0 46.2 50.9 45.5 50.9 50.8 50.1 49.0 51.5 49.8 48.1 51.4 45.7 50.7  
## [331] 42.5 52.2 45.2 49.3 50.2 45.6 51.9 46.8 45.7 55.8 43.5 49.6 50.8 50.2

*I want to select columns bill\_length\_mm, bill\_depth\_mm, species, and filter for species that are “Gentoo”:*

penguins\_select = select(penguins, bill\_length\_mm, bill\_depth\_mm, species)  
penguins\_gentoo = filter(penguins\_select, species == "Gentoo")

or

penguins\_select\_2 = penguins[, c("bill\_length\_mm", "bill\_depth\_mm", "species")]  
penguins\_gentoo\_2 = penguins\_select\_2[penguins$species == "Gentoo" ,]

or

penguins\_gentoo\_2 = penguins\_select\_2[penguins$species == "Gentoo", c("bill\_length\_mm", "bill\_depth\_mm", "species")]

*I want to filter out rows that have NAs in the column bill\_length\_mm:*

penguins\_clean = filter(penguins, !is.na(bill\_length\_mm))

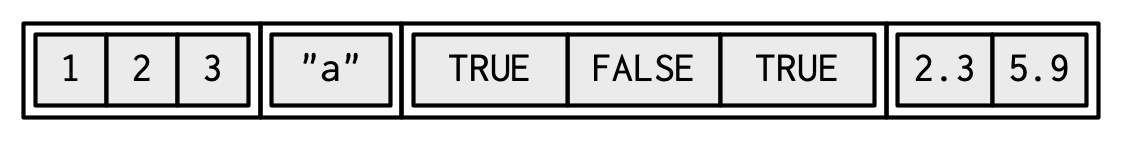
or

penguins\_clean = penguins[!is.na(penguins$bill\_depth\_mm) ,]

## 2.7 Lists

Lists operate similarly as vectors as they group data into one dimension, but each element of a list can be any data type *or data structure*!

l1 = list(  
 1:3,   
 "a",   
 c(TRUE, FALSE, TRUE),   
 c(2.3, 5.9)  
)



Unlike vectors, you access the elements of a list via the double bracket [[]]. You access a smaller list with single bracket []. (More discussion on the different uses of the bracket [here](https://stackoverflow.com/questions/1169456/the-difference-between-bracket-and-double-bracket-for-accessing-the-el).)

Here’s a [nice metaphor](https://adv-r.hadley.nz/subsetting.html#subset-single):

If list x is a train carrying objects, then x[[5]] is the object in car 5; x[4:6] is a train of cars 4-6.

l1[[1]]

## [1] 1 2 3

l1[[1]][2]

## [1] 2

Use unlist() to coerce a list into a vector. Notice all the automatic coersion that happened for the elements.

unlist(l1)

## [1] "1" "2" "3" "a" "TRUE" "FALSE" "TRUE" "2.3" "5.9"

We can give **names** to lists:

l1 = list(  
 ranking = 1:3,   
 name = "a",   
 success = c(TRUE, FALSE, TRUE),   
 score = c(2.3, 5.9)  
)  
#or  
names(l1) = c("ranking", "name", "success", "score")

And access named elements of lists via the $ operation:

l1$score

## [1] 2.3 5.9

Therefore, l1$score is the same as l1[[4]] and is the same as l1[["score"]].

A dataframe is just a named list of vectors of same length with **attributes** of (column) names and row.names.

## 2.8 Matrix

A matrix holds information of the same data type in two dimensions - it’s like a two dimensional vector. Matricies are most often used in statistical computing and matrix algebra, such as creating a design matrix. They are often created by taking a vector and reshaping it with a set number of rows and columns, or converting from a dataframe with only one data type.

my\_matrix = matrix(1:10, nrow = 2)  
my\_matrix

## [,1] [,2] [,3] [,4] [,5]  
## [1,] 1 3 5 7 9  
## [2,] 2 4 6 8 10

You access elements of a matrix similar to that of a dataframe’s indexing:

#column 3  
my\_matrix[, 3]

## [1] 5 6

#row 2  
my\_matrix[2 ,]

## [1] 2 4 6 8 10

#column 3, row 2  
my\_matrix[2, 3]

## [1] 6

# 3 Fundamentals Exercises

## 3.1 Part 1: Vectors

How do you subset the following vector to the first three elements?

measurements = c(2, 4, -1, -3, 2, -1, 10)

How do you subset the original vector so that it only has negative values?

How do you subset the following vector so that it has no NA values?

vec\_with\_NA = c(2, 4, NA, NA, 3, NA)

Consider the following logical vector some\_logicals. Convert Logical vector -> Numeric vector -> Character vector in two steps. Check that you are doing this correctly along the way by using the class() function, or is.numeric() and is.character(), on the converted data.

some\_logicals = c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE)

## 3.2 Part 2: Lists

Consider the following lists with names.

patient = list(  
 name = " ",   
 age = 34,   
 pronouns = c("he", "him", "/", "they", "them"),  
 vaccines = c("hep-B", "chickenpox", "HPV"),  
 visits = NA  
)  
  
visit1 = list(  
 symptoms = c("runny nose", "sore throat", "frustration"),  
 prescription = "recommended time off from work, rest.",  
 date = "1/1/2000"  
)  
  
visit2 = list(  
 symptoms = c("fainted", "pale complexion"),  
 prescription = "drink water and take time off work.",  
 date = "1/1/2001"  
)

Access the first element of patient via double brackets [[ ]] and modify it to a value of your choice.

Access the named element “pronouns” of patient via double bracket [[ ]] or $ and modify its value so that it doesn’t contain the “/” element. (Use your vector subsetting skills here after you access the appropriate element from the list.)

Create a new list all\_visits with elements visit1 and visit2. Yes, we’re making lists within lists!

Suppose you want to use all\_visits to access visit 1’s symptoms. You would continue the double brackets [[ ]] or $ notation: all\_visits[[1]] returns a list, so we access the first element of *that* list via all\_visits[[1]][[1]].

#all\_visits[[1]][[1]]  
  
#or  
  
#ll\_visits[[1]][["symptoms"]]  
  
#or  
  
#ll\_visits[[1]]$symptoms

How would you use all\_visits to access visit 2’s prescription?

How would you use all\_visits to access visit 2’s symptom element “pale complexion”? Remember, once you access a vector, you would go back to the single bracket [ ] to access its elements.

Finally, assign all\_visits to patient’s visits.

### 3.2.1 Part 3: Dataframes (Lists)

A dataframe is just a named list of vectors of same length with **attributes** of (column) names and row.names.

library(palmerpenguins)  
head(penguins)

## # A tibble: 6 × 8  
## species island bill\_length\_mm bill\_depth\_mm flipper\_length\_mm body\_mass\_g  
## <fct> <fct> <dbl> <dbl> <int> <int>  
## 1 Adelie Torgersen 39.1 18.7 181 3750  
## 2 Adelie Torgersen 39.5 17.4 186 3800  
## 3 Adelie Torgersen 40.3 18 195 3250  
## 4 Adelie Torgersen NA NA NA NA  
## 5 Adelie Torgersen 36.7 19.3 193 3450  
## 6 Adelie Torgersen 39.3 20.6 190 3650  
## # ℹ 2 more variables: sex <fct>, year <int>

Access the body\_mass\_g column vector of penguins via the double bracket [[ ]], treating penguins like a list, and compute the mean. Remember to use na.rm = TRUE to remove any NA values: mean(x, na.rm = TRUE)

Create a new dataframe penguins\_clean, which has no NA values in the body\_mass\_g column. You need to filter out rows that have NAs in the column bill\_length\_mm:

Now, subset penguins\_clean to each of the three species and compute their respective mean value of body\_mass\_g. Because you already got rid of NAs in body\_mass\_g, you can just use mean(x) without the extra option. How do they compare?

Finally, make a box plot of species (x-axis) vs. body\_mass\_g (y-axis) via penguins\_clean dataframe. I’ll get you started…

#ggplot(penguins\_clean) + aes(x = , y = ) + geom\_boxplot()

# 4 Data Cleaning, Part 1

## 4.1 Interpreting functions, carefully

As you become more independent R programmers, you will spend time learning about new functions on your own. We have gone over the basic anatomy of a function call back in Intro to R, but now let’s go a bit deeper to understand how a function is built and how to call them.

Recall that a function has a **function name**, **input arguments**, and a **return value**.

*Function definition consists of assigning a* ***function name*** *with a “function” statement that has a comma-separated list of named* ***function arguments****, and a* ***return expression****. The function name is stored as a variable in the global environment.*

In order to use the function, one defines or import it, then one calls it.

Example:

addFunction = function(num1, num2) {  
 result = num1 + num2   
 return(result)  
}  
result = addFunction(3, 4)

When the function is called in line 5, the variables for the arguments are reassigned to function arguments to be used within the function and helps with the modular form.

*What do you think are some valid inputs for this function?*

To see why we need the variables of the arguments to be reassigned, consider the following function that is *not* modular:

x = 3  
y = 4  
addFunction = function(num1, num2) {  
 result = x + y   
 return(result)  
}  
result = addFunction(10, -10)

Some syntax equivalents on calling the function:

addFunction(3, 4)  
addFunction(num1 = 3, num2 = 4)  
addFunction(num2 = 4, num1 = 3)

but this *could* be different:

addFunction(4, 3)

With a deeper knowledge of how functions are built, when you encounter a foreign function, you can look up its help page to understand how to use it. For example, let’s look at mean():

?mean  
  
Arithmetic Mean  
  
Description:  
  
 Generic function for the (trimmed) arithmetic mean.  
  
Usage:  
  
 mean(x, ...)  
   
 ## Default S3 method:  
 mean(x, trim = 0, na.rm = FALSE, ...)  
   
Arguments:  
  
 x: An R object. Currently there are methods for numeric/logical  
 vectors and date, date-time and time interval objects.  
 Complex vectors are allowed for ‘trim = 0’, only.  
  
 trim: the fraction (0 to 0.5) of observations to be trimmed from  
 each end of ‘x’ before the mean is computed. Values of trim  
 outside that range are taken as the nearest endpoint.  
  
 na.rm: a logical evaluating to ‘TRUE’ or ‘FALSE’ indicating whether  
 ‘NA’ values should be stripped before the computation  
 proceeds.  
  
 ...: further arguments passed to or from other methods.

Notice that the arguments trim = 0, na.rm = FALSE have default values. This means that these arguments are *optional* - you should provide it only if you want to. With this understanding, you can use mean() in a new way:

numbers = c(1, 2, NA, 4)  
mean(x = numbers, na.rm = TRUE)

## [1] 2.333333

The use of . . . (dot-dot-dot): This is a special argument that allows a function to *take any number of arguments*. This isn’t very useful for the mean() function, but it makes sense for function such as select() and filter(), and mutate(). For instance, in select(), once you provide your dataframe for the argument .data, you can pile on as many columns to select in the rest of the argument.

Usage:  
  
 select(.data, ...)  
   
Arguments:  
  
 .data: A data frame, data frame extension (e.g. a tibble), or a lazy  
 data frame (e.g. from dbplyr or dtplyr). See \_Methods\_,  
 below, for more details.  
  
 ...: <‘tidy-select’> One or more unquoted expressions separated by  
 commas. Variable names can be used as if they were positions  
 in the data frame, so expressions like ‘x:y’ can be used to  
 select a range of variables.

You will look at the function documentation on your own to see how to deal with more complex cases.

## 4.2 Recoding Data / Conditionals

It is often said that 80% of data analysis is spent on the cleaning and preparing data. Today we will start looking at common data cleaning tasks. Suppose that you have a column in your data that needs to be recoded. Since a dataframe’s column, when selected via $, is a vector, let’s start talking about recoding vectors. If we have a numeric vector, then maybe you want to have certain values to be out of bounds, or assign a range of values to a character category. If we have a character vector, then maybe you want to reassign it to a different value.

Here are popular recoding logical scenarios:

1. If: “If elements of the vector meets *condition*, then they are assigned *value*.”
2. If-else: “If elements of the vector meets *condition*, then they are assigned *value X*. Otherwise, they are assigned *value Y*.”
3. If-else\_if-else: “If elements of the vector meets *condition A*, then they are assigned *value X*. Else, if the elements of the vector meets *condition B*, they are assigned *value Y*. Otherwise, they are assigned *value Z*.”

Let’s look at a vector of grade values, as an example:

grade = c(90, 78, 95, 74, 56, 81, 102)

1. If

Instead of having the bracket [ ] notation on the right hand side of the equation, if it is on the left hand side of the equation, then we can modify a subset of the vector.

grade1 = grade  
grade1[grade1 > 100] = 100

1. If-else

grade2 = if\_else(grade > 60, TRUE, FALSE)

1. If-else\_if-else

grade3 = case\_when(grade >= 90 ~ "A",  
 grade >= 80 ~ "B",  
 grade >= 70 ~ "C",   
 grade >= 60 ~ "D",  
 .default = "F")

Let’s do it for dataframes now.

simple\_df = data.frame(grade = c(90, 78, 95, 74, 56, 81, 102),  
 status = c("case", " ", "Control", "control", "Control", "Case", "case"))

1. If

simple\_df1 = simple\_df  
simple\_df1$grade[simple\_df1$grade > 100] = 100

1. If-else

simple\_df2 = simple\_df  
simple\_df2$grade = ifelse(simple\_df2$grade > 60, TRUE, FALSE)

or

simple\_df2 = mutate(simple\_df, grade = ifelse(grade > 60, TRUE, FALSE))

1. If-else\_if-else

simple\_df3 = simple\_df  
  
simple\_df3$grade = case\_when(simple\_df3$grade >= 90 ~ "A",  
 simple\_df3$grade >= 80 ~ "B",  
 simple\_df3$grade >= 70 ~ "C",   
 simple\_df3$grade >= 60 ~ "D",  
 .default = "F")

or

simple\_df3 = mutate(simple\_df, grade = case\_when(grade >= 90 ~ "A",  
 grade >= 80 ~ "B",  
 grade >= 70 ~ "C",   
 grade >= 60 ~ "D",  
 .default = "F"))

## 4.3 Conditionals

The 3 common scenarios we looked at for recoding data is closely tied to the concept of **conditionals** in programming: *given certain conditions, you run a specific code chunk.* Given a vector’s value, assign it a different value. Or, given a value, run the following hundred lines of code. Here is what it looks like:

1. If:

if(expression\_is\_TRUE) {  
 #code goes here  
}

1. If-else:

if(expression\_is\_TRUE) {  
 #code goes here  
}else {  
 #other code goes here  
}

1. If-else\_if-else:

if(expression\_A\_is\_TRUE)   
 #code goes here  
}else if(expression\_B\_is\_TRUE) {  
 #other code goes here  
}else {  
 #some other code goes here  
}

The expression that is being tested whether it is TRUE **must be a singular logical value**, and not a logical vector. If the latter, see the recoding section for now.

Example:

nuc = "A"  
  
if(nuc == "A") {  
 nuc = "T"  
}else if(nuc == "T") {  
 nuc = "A"  
}else if(nuc == "C") {  
 nuc = "C"  
}else if(nuc == "G") {  
 nuc = "C"  
}else {  
 nuc = NA  
}  
  
nuc

## [1] "T"

Example:

my\_input = c(1, 3, 5, 7, 9)  
#my\_input = c("e", "e", "a", "i", "o")  
  
if(is.numeric(my\_input)) {  
 result = mean(my\_input)  
}else if(is.character(my\_input)) {  
 result = table(my\_input)  
}  
  
result

## [1] 5

# 5 Data Cleaning, Part 1 Exercises

## 5.1 Part 1: Looking at documentation to load in data

Suppose that you want to load in data “students.csv” in a CSV format, and you don’t know what tools to use. You decide to see whether the package “readr” can be useful to solve your problem. Where should you look?

All R packages must be stored on CRAN (Comprehensive R Archive Network), and all packages have a website that points to the reference manual (what is pulled up using the ? command), source code, vignettes examples, and dependencies on other packages. Here is [the website](https://cran.r-project.org/web/packages/readr/) for “readr”.

In the package, you find some potential functions for importing your data:

* read\_csv("file.csv") for comma-separated files
* read\_tsv("file.tsv") for tab-deliminated files
* read\_excel("example.xlsx") for excel files
* read\_excel("example.xlsx", sheet = "sheet1") for excel files with a sheet name
* read\_delim() for general-deliminated files, such as: read\_delim("file.csv", sep = ",").

After looking at the vignettes, it seems that read\_csv() is a function to try.

Let’s look at the read\_csv() function documentation, which can be accessed via ?read\_csv.

read\_csv(  
 file,  
 col\_names = TRUE,  
 col\_types = NULL,  
 col\_select = NULL,  
 id = NULL,  
 locale = default\_locale(),  
 na = c("", "NA"),  
 quoted\_na = TRUE,  
 quote = "\"",  
 comment = "",  
 trim\_ws = TRUE,  
 skip = 0,  
 n\_max = Inf,  
 guess\_max = min(1000, n\_max),  
 name\_repair = "unique",  
 num\_threads = readr\_threads(),  
 progress = show\_progress(),  
 show\_col\_types = should\_show\_types(),  
 skip\_empty\_rows = TRUE,  
 lazy = should\_read\_lazy()  
)

We see that the only *required* argument is the file variable, which is documented to be “Either a path to a file, a connection, or literal data (either a single string or a raw vector).” All the other arguments are considered *optional*, because they have a pre-allocated value in the documentation.

Load in “students.csv” via read\_csv() function as a dataframe variable students and take a look at its contents via View().

library(tidyverse)

## Warning: package 'tidyverse' was built under R version 4.0.3

## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.0 ──

## ✔ ggplot2 3.3.2 ✔ purrr 0.3.4  
## ✔ tibble 3.2.1 ✔ dplyr 1.0.2  
## ✔ tidyr 1.1.2 ✔ stringr 1.4.0  
## ✔ readr 1.4.0 ✔ forcats 0.5.0

## Warning: package 'purrr' was built under R version 4.0.5

## Warning: package 'stringr' was built under R version 4.0.3

## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()

Something looks weird here. There is only one column, and it seems that the first two entries start with “#”, and don’t fit a CSV file format. These first two entries that start with “#” likely are comments giving metadata about the file, and they should be ignore when loading in the data.

Let’s try again. Take a look at the documentation for the comment argument and give it a character value "#" with this situation. Any text after the comment characters will be silently ignored.

The column names are not very consistent . Take a look at the documentation for the col\_names argument and give it a value of [c](https://rdrr.io/r/base/c.html)("student\_id", "full\_name", "favorite\_food", "meal\_plan", "age").

Alternatively, you could have loaded the data in without col\_names option and modified the column names by accessing names(students).

For more information on loading in data, see this chapter of [R for Data Science](https://r4ds.hadley.nz/spreadsheets).

## 5.2 Part 2: Recoding data: warm-up

Consider this vector:

scores = c(23, 46, -3, 5, -1)

Recode scores so that all the negative values are 0.

Let’s look at the values of students dataframe more carefully. We will do some recoding on this small dataframe. It may feel trivial because you could do this by hand in Excel, but this is a practice on how we can scale this up with larger datasets!

Notice that some of the elements of this dataframe has proper NA values and also a character “N/A”. We want “N/A” to be a proper NA value.

Recode “N/A” to NA in the favorite\_food column:

Recode “five” to 5 in the age column:

Create a new column age\_category so that it has value “toddler” if age is < 6, and “child” if age is >= 6.

(Hint: You can create a new column via mutate, or you can directly refer to the new column via student$``age\_category.)

Create a new column favorite\_food\_numeric so that it has value 1 if favorite\_food is “Breakfast and lunch”, 2 if “Lunch only”, and 3 if “Dinner only”.

## 5.3 Part 3: Recoding data in State Cancer Profiles

Starting from this exercise, we will start building out an end-to-end analysis using [data from the National Cancer Institute’s State Cancer Profile](https://statecancerprofiles.cancer.gov/index.html):

[State Cancer Profile data] was developed with the idea to provide a geographic profile of cancer burden in the United States and reveal geographic disparities in cancer incidence, mortality, risk factors for cancer, and cancer screening, across different population subgroups.

In this analysis, we want to examine cancer incidence rates in state of Washington and make some comparisons between groups. The cancer incidence rate can be accessed at this [website](https://statecancerprofiles.cancer.gov/incidencerates/index.php), once you give input of what kind of incidence data you want to access. If you want to analyze this data in R, it takes a bit of work of exporting the data and loading it into R.

To access this data easier in R, DaSL staff built a R package cancerprof to easily load in the data. Let’s look at the package’s documentation to see how to get access to cancer incidence data.

Towards the bottom of the documentation are some useful examples to consider as starting point.

Load in data about the following population: **melanoma incidence in WA at the county level for males of all ages, all cancer stages, averaged in the past 5 years.** Store it as a dataframe variable named melanoma\_incidence

(If you are stuck, you can use the first example in the documentation.)

Take a look at the data yourself and explore it.

Let’s select a few columns of interest and give them column names that doesn’t contain spaces. We can access column names with spaces via the backtick ` symbol.

#uncomment to run!  
  
#melanoma\_incidence = select(melanoma\_incidence, County, `Age Adjusted Incidence Rate`, `Recent Trend`)  
  
#names(melanoma\_incidence) = c("County", "Age\_adjusted\_incidence\_rate", "Recent\_trend")

Take a look at the column Age\_adjusted\_incidence\_rate. It has missing data coded as “\*” (notice the space after \*). Recode “\*” as NA.

Finally, notice that the data type for Age\_adjusted\_incidence\_rate is character, if you run the function is.character() or class() on it. Convert it to a numeric data type.

# 6 Data Cleaning, Part 2

library(tidyverse)

## 6.1 Tidy Data

It is important to have standard of organizing data, as it facilitates a consistent way of thinking about data organization and building tools (functions) that make use of that standard. The principles of **Tidy data**, developed by Hadley Wickham:

1. Each variable must have its own column.
2. Each observation must have its own row.
3. Each value must have its own cell.

If we want to be technical about what variables and observations are, Hadley Wickham describes:

A dataset is a collection of **values**, usually either numbers (if quantitative) or strings (if qualitative). Every value belongs to a **variable** and an **observation**. A **variable** contains all values that measure the same underlying attribute (like height, temperature, duration) across units. An **observation** contains all values measured on the same unit (like a person, or a day, or a race) across attributes.



Figure : A tidy dataframe.

Besides a standard, Tidy data is useful because many tools in R are most effective when your data is in a Tidy format. This includes data visualization with ggplot, regression models, databases, and more. These tools assumes the values of each variable fall in their own column vector.

It seems hard to go wrong with these simple criteria of Tidy data! However, in reality, many dataframes we load in aren’t Tidy, and it’s easiest seen through counterexamples and how to fix it. Here are some common ways that data becomes un-Tidy:

1. Columns contain values of variables, rather than variables
2. Variables are stored in rows
3. Multiple variables are stored in a single column

After some clear examples, we emphasize that “Tidy” data is *subjective* to what kind of analysis you want to do with the dataframe.

### 6.1.1 1. Columns contain values, rather than variables (Long is tidy)

df = data.frame(Store = c("A", "B"),  
 Year = c(2018, 2018),  
 Q1\_Sales = c(55, 98),  
 Q2\_Sales = c(45, 70),  
 Q3\_Sales = c(22, 60),  
 Q4\_Sales = c(50, 60))  
df

## Store Year Q1\_Sales Q2\_Sales Q3\_Sales Q4\_Sales  
## 1 A 2018 55 45 22 50  
## 2 B 2018 98 70 60 60

Each observation is a store, and each observation has its own row. That looks good.

The columns “Q1\_Sales”, …, “Q4\_Sales” seem to be *values of a single variable “quarter”* of our observation. The values of “quarter” are not in a single column, but are instead in the columns.

df\_long = pivot\_longer(df, c("Q1\_Sales", "Q2\_Sales", "Q3\_Sales", "Q4\_Sales"), names\_to = "quarter", values\_to = "sales")  
df\_long

## # A tibble: 8 × 4  
## Store Year quarter sales  
## <chr> <dbl> <chr> <dbl>  
## 1 A 2018 Q1\_Sales 55  
## 2 A 2018 Q2\_Sales 45  
## 3 A 2018 Q3\_Sales 22  
## 4 A 2018 Q4\_Sales 50  
## 5 B 2018 Q1\_Sales 98  
## 6 B 2018 Q2\_Sales 70  
## 7 B 2018 Q3\_Sales 60  
## 8 B 2018 Q4\_Sales 60

Now, each observation is a store’s quarter, and each observation has its own row.

The new columns “quarter” and “sales” are variables that describes our observation, and describes our values. We’re in a tidy state!

We have transformed our data to a “**longer**” format, as our observation represents something more granular or detailed than before. Often, the original variables values will repeat itself in a “longer format”. We call the previous state of our dataframe is a “**wider**” format.

### 6.1.2 2. Variables are stored in rows (Wide is tidy)

Are all tidy dataframes Tidy in a “longer” format?

df2 = data.frame(Sample = c("A", "B"),  
 KRAS\_mutation = c(TRUE, FALSE),  
 KRAS\_expression = c(2.3, 3.9))  
df2

## Sample KRAS\_mutation KRAS\_expression  
## 1 A TRUE 2.3  
## 2 B FALSE 3.9

Each observation is a sample, and each observation has its own row. Looks good. Each variable has its own column, and no values are in columns.

What happens if we make it longer?

df2\_long = pivot\_longer(df2, c("KRAS\_mutation", "KRAS\_expression"), names\_to = "gene", values\_to = "values")  
df2\_long

## # A tibble: 4 × 3  
## Sample gene values  
## <chr> <chr> <dbl>  
## 1 A KRAS\_mutation 1   
## 2 A KRAS\_expression 2.3  
## 3 B KRAS\_mutation 0   
## 4 B KRAS\_expression 3.9

Here, each observation is a sample’s gene…type? The observation feels awkward because variables are stored in rows. Also, the column “values” contains multiple variable types: gene expression and mutation values that got coerced to numeric!

To make this dataframe wider,

df2\_long\_wide = pivot\_wider(df2\_long, names\_from = "gene", values\_from = "values")   
df2\_long\_wide$KRAS\_mutation = as.logical(df2\_long\_wide$KRAS\_mutation)  
df2\_long\_wide

## # A tibble: 2 × 3  
## Sample KRAS\_mutation KRAS\_expression  
## <chr> <lgl> <dbl>  
## 1 A TRUE 2.3  
## 2 B FALSE 3.9

We are back to our orignal form, and it was already Tidy.

### 6.1.3 3. Multiple variables are stored in a single column

table3

## # A tibble: 6 × 3  
## country year rate   
## \* <chr> <int> <chr>   
## 1 Afghanistan 1999 745/19987071   
## 2 Afghanistan 2000 2666/20595360   
## 3 Brazil 1999 37737/172006362   
## 4 Brazil 2000 80488/174504898   
## 5 China 1999 212258/1272915272  
## 6 China 2000 213766/1280428583

There seems to be two variables in the numerator and denominator of “rate” column. Let’s separate it.

separate(table3, col = "rate", into = c("count", "population"), sep = "/")

## # A tibble: 6 × 4  
## country year count population  
## <chr> <int> <chr> <chr>   
## 1 Afghanistan 1999 745 19987071   
## 2 Afghanistan 2000 2666 20595360   
## 3 Brazil 1999 37737 172006362   
## 4 Brazil 2000 80488 174504898   
## 5 China 1999 212258 1272915272  
## 6 China 2000 213766 1280428583

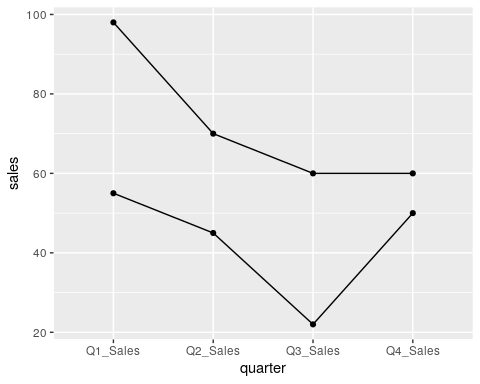
## 6.2 Uses of Tidy data

In general, many functions for analysis and visualization in R assumes that the input dataframe is Tidy. These tools assumes the values of each variable fall in their own column vector. For instance, from our first example, we can compare sales across quarters and stores.

df\_long

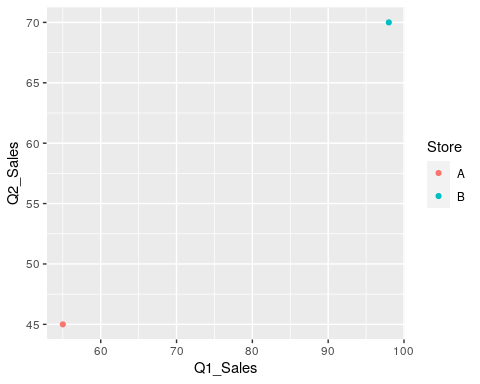
## # A tibble: 8 × 4  
## Store Year quarter sales  
## <chr> <dbl> <chr> <dbl>  
## 1 A 2018 Q1\_Sales 55  
## 2 A 2018 Q2\_Sales 45  
## 3 A 2018 Q3\_Sales 22  
## 4 A 2018 Q4\_Sales 50  
## 5 B 2018 Q1\_Sales 98  
## 6 B 2018 Q2\_Sales 70  
## 7 B 2018 Q3\_Sales 60  
## 8 B 2018 Q4\_Sales 60

ggplot(df\_long) + aes(x = quarter, y = sales, group = Store) + geom\_point() + geom\_line()



Although in its original state we can also look at sales between quarter, we can only look between two quarters at once. Tidy data encourages looking at data in the most granular scale.

ggplot(df) + aes(x = Q1\_Sales, y = Q2\_Sales, color = Store) + geom\_point()



## 6.3 Subjectivity in Tidy Data

We have looked at clear cases of when a dataset is Tidy. In reality, the Tidy state depends on what we call variables and observations.

kidney = data.frame(stone\_size = c("Small", "Large"),  
 treatment.A\_recovered = c(81, 192),  
 treatment.A\_failed = c(6, 71),  
 treatment.B\_recovered = c(234, 55),  
 treatment.B\_failed = c(36, 25))  
kidney

## stone\_size treatment.A\_recovered treatment.A\_failed treatment.B\_recovered  
## 1 Small 81 6 234  
## 2 Large 192 71 55  
## treatment.B\_failed  
## 1 36  
## 2 25

Right now, the kidney dataframe clearly has values of a variable in the column. Let’s try to make it Tidy by making it into a longer form and separating out variables that are together in a column.

kidney\_long = pivot\_longer(kidney, c("treatment.A\_recovered", "treatment.A\_failed", "treatment.B\_recovered", "treatment.B\_failed"), names\_to = "treatment\_outcome", values\_to = "count")  
  
kidney\_long = separate(kidney\_long, "treatment\_outcome", c("treatment", "outcome"), "\_")  
  
kidney\_long

## # A tibble: 8 × 4  
## stone\_size treatment outcome count  
## <chr> <chr> <chr> <dbl>  
## 1 Small treatment.A recovered 81  
## 2 Small treatment.A failed 6  
## 3 Small treatment.B recovered 234  
## 4 Small treatment.B failed 36  
## 5 Large treatment.A recovered 192  
## 6 Large treatment.A failed 71  
## 7 Large treatment.B recovered 55  
## 8 Large treatment.B failed 25

Here, each observation is a kidney stone’s treatment’s outcome type, and each observation has its own row.

The column “count” describes our observation, and describes our values. This dataframe seems reasonably Tidy.

How about this?

kidney\_long\_still = pivot\_wider(kidney\_long, names\_from = "outcome", values\_from = "count")  
kidney\_long\_still

## # A tibble: 4 × 4  
## stone\_size treatment recovered failed  
## <chr> <chr> <dbl> <dbl>  
## 1 Small treatment.A 81 6  
## 2 Small treatment.B 234 36  
## 3 Large treatment.A 192 71  
## 4 Large treatment.B 55 25

Here, each observation is a kidney stone’s treatment, and each observation has its own row.

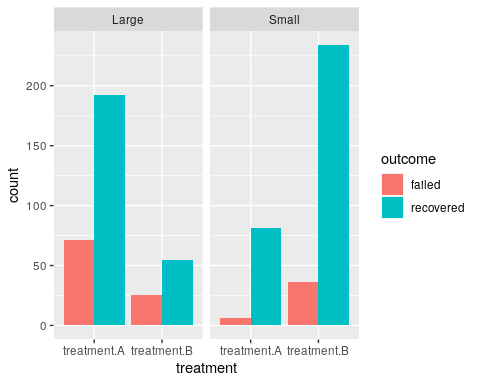
The columns “recovered” and “failed” are variables that describes our observation, and describes its corresponding values. This dataframe seems reasonably Tidy, also.

The reason why both of these versions seem Tidy is that the columns “recovered” and “failed” can be interpreted as independent variables *and* values of the variable “treatment”.

Ultimately, we decide which dataframe we prefer based on the analysis we want to do.

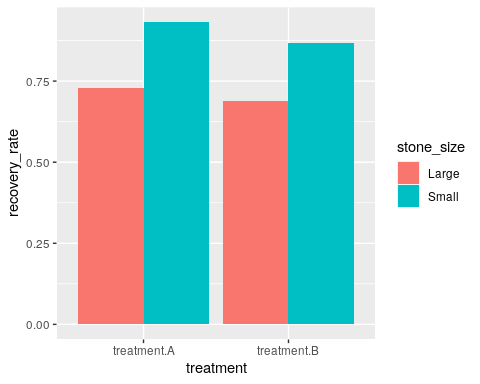
For instance, when our observation is about a kidney stone’s treatment’s outcome type, we compare it between outcome type, treatment, and stone size.

ggplot(kidney\_long) + aes(x = treatment, y = count, fill = outcome) + geom\_bar(position="dodge", stat="identity") + facet\_wrap(~stone\_size)



When our observation is about a kidney stone’s treatment’s, we compare a new variable *recovery rate* ( = recovered / (recovered + failed)) between treatment and stone size.

kidney\_long\_still = mutate(kidney\_long\_still, recovery\_rate = recovered / (recovered + failed))  
ggplot(kidney\_long\_still) + aes(x = treatment, y = recovery\_rate, fill = stone\_size) + geom\_bar(position="dodge", stat="identity")



## 6.4 References

<https://vita.had.co.nz/papers/tidy-data.html>

<https://kiwidamien.github.io/what-is-tidy-data.html>

# 7 Data Cleaning, Part 2 Exercises

# 8 Writing your first function



Figure : Function machine from algebra class.

We write functions for two main, often overlapping, reasons:

1. Following DRY (Don’t Repeat Yourself) principle: If you find yourself repeating similar patterns of code, you should write a function that executes that pattern. This saves time and the risk of mistakes.
2. Create modular structure and abstraction: Having all of your code in one place becomes increasingly complicated as your program grows. Think of the function as a mini-program that can perform without the rest of the program. Organizing your code by functions gives modular structure, as well as abstraction: you only need to know the function name, inputs, and output to use it and don’t have to worry how it works.

Some advice on writing functions:

* Code that has a well-defined set of inputs and outputs make a good function.
* A function should do only one, well-defined task.

### 8.0.1 Anatomy of a function definition

*Function definition consists of assigning a* ***function name*** *with a “function” statement that has a comma-separated list of named* ***function arguments****, and a* ***return expression****. The function name is stored as a variable in the global environment.*

In order to use the function, one defines or import it, then one calls it.

Example:

addFunction = function(argument1, argument2) {  
 result = argument1 + argument2   
 return(result)  
}  
z = addFunction(3, 4)

With function definitions, not all code runs from top to bottom. The first four lines defines the function, but the function is never run. It is called on line 5, and the lines within the function are executed.

When the function is called in line 5, the variables for the arguments are reassigned to function arguments to be used within the function and helps with the modular form. We need to introduce the concept of local and global environments to distinguish variables used only for a function from variables used for the entire program.

### 8.0.2 Local and global environments

*{ } represents variable scoping: within each { }, if variables are defined, they are stored in a* ***local environment****, and is only accessible within { }. All function arguments are stored in the local environment. The overall environment of the program is called the* ***global environment*** *and can be also accessed within { }.*

The reason of having some of this “privacy” in the local environment is to make functions modular - they are independent little tools that should not interact with the rest of the global environment. Imagine someone writing a tool that they want to give someone else to use, but the tool depends on your environment, vice versa.

### 8.0.3 A step-by-step example

Using the addFunction function, let’s see step-by-step how the R interpreter understands our code:

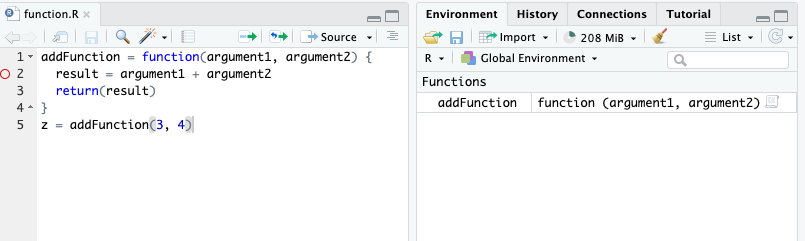


Figure : We define the function in the global environment.

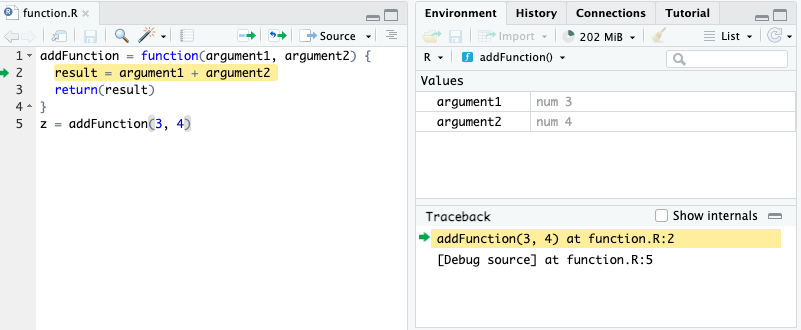


Figure : We call the function, and the function arguments 3, 4 are assigned to argument1 and argument2, respectively in the function’s local environment.

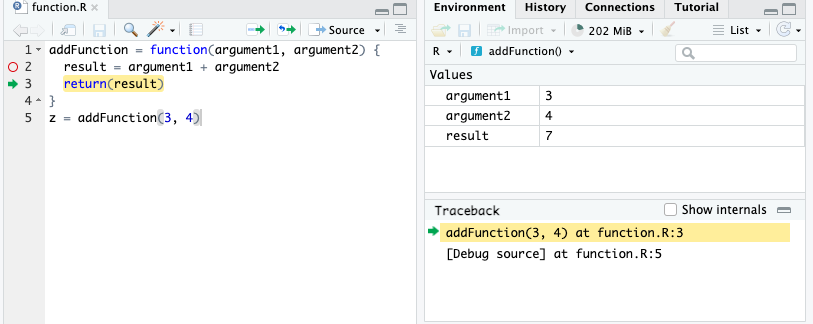


Figure : We run the first line of code in the function body. The new variable “result” is stored in the local environment because it is within { }.

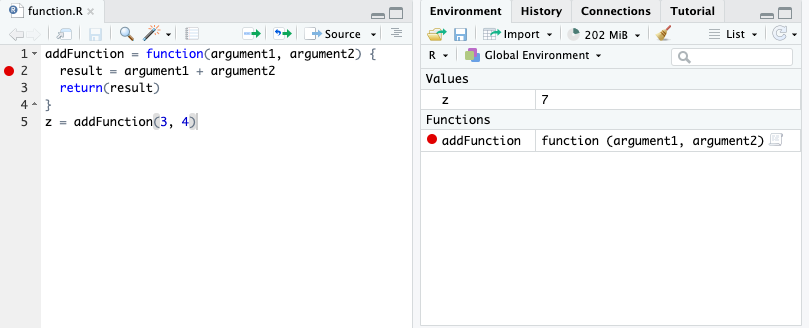


Figure : We run the second line of code in the function body to return a value. The return value from the function is assigned to the variable z in the global environment. All local variables for the function are erased now that the function call is over.

### 8.0.4 Function arguments create modularity

First time writers of functions might ask: why are variables we use for the arguments of a function *reassigned* for function arguments in the local environment? Here is an example when that process is skipped - what are the consequences?

x = 3  
y = 4  
addFunction = function(argument1, argument2) {  
 result = x + y   
 return(result)  
}  
z = addFunction(x, y)  
w = addFunction(10, -5)

What do you expect the value of z to be? How about w?

Here is the execution for w:

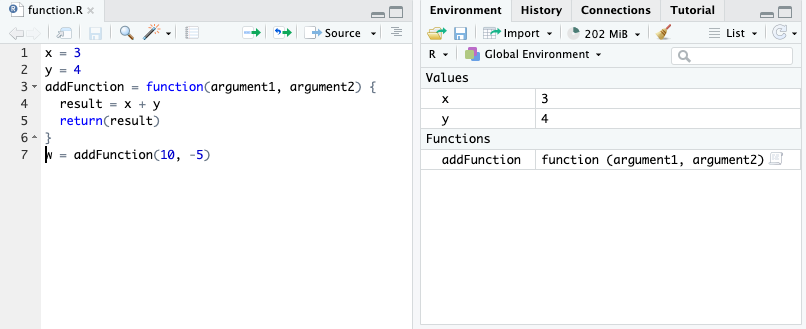


Figure : We define the variables and function in the global environment.

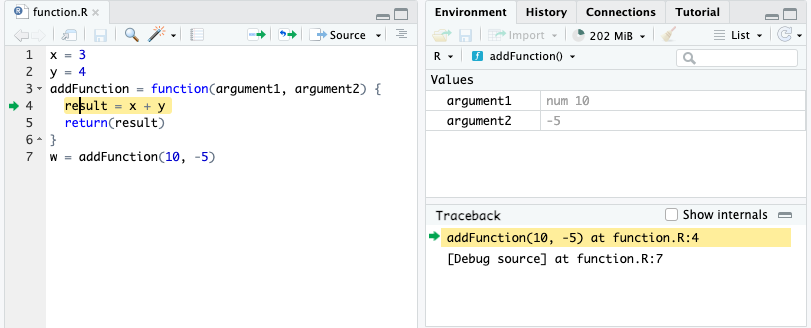


Figure : We call the function, and the function arguments 10, -5 are assigned to argument1 and argument2, respectively in the function’s local environment.

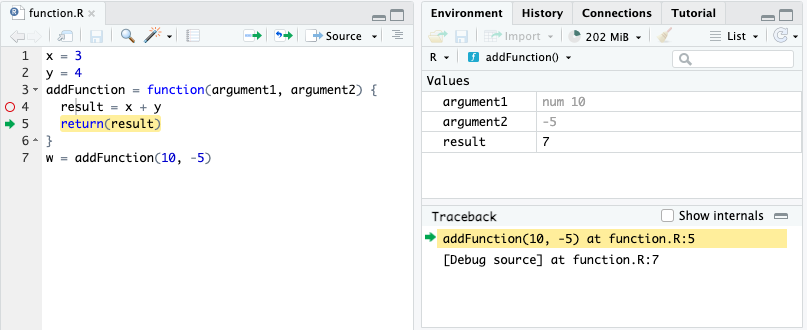


Figure : We run the first line of code in the function body. The new variable “result” is stored in the local environment because it is within { }.

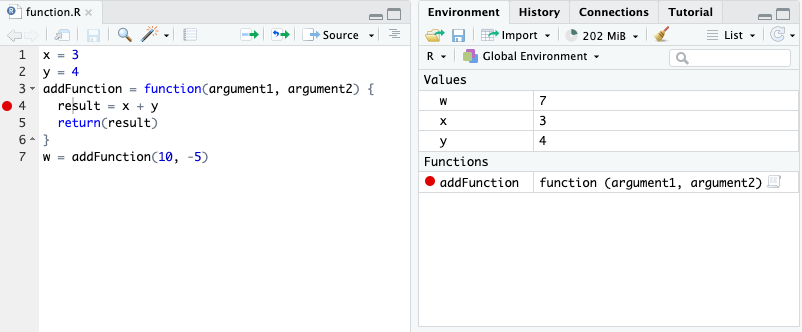


Figure : We run the second line of code in the function body to return a value. The return value from the function is assigned to the variable w in the global environment. All local variables for the function are erased now that the function call is over.

The function did not work as expected because we used hard-coded variables from the global environment and not function argument variables unique to the function use!

### 8.0.5 Exercises

* Create a function, called add\_and\_raise\_power in which the function takes in 3 numeric arguments. The function computes the following: the first two arguments are added together and raised to a power determined by the 3rd argument. The function returns the resulting value. Here is a use case: add\_and\_raise\_power(1, 2, 3) = 27 because the function will return this expression: (1 + 2) ^ 3. Another use case: add\_and\_raise\_power(3, 1, 2) = 16 because of the expression (3 + 1) ^ 2. Confirm with that these use cases work. Can this function used for numeric vectors?
* add\_and\_raise\_power = function(x, y, z) {  
   result = (x + y)^z  
   return(result)  
  }  
  add\_and\_raise\_power(1, 2, 3)
* ## [1] 27
* Create a function, called my\_dim in which the function takes in one argument: a dataframe. The function returns the following: a length-2 numeric vector in which the first element is the number of rows in the dataframe, and the second element is the number of columns in the dataframe. Your result should be identical as the dim function. How can you leverage existing functions such as nrow and ncol? Use case: my\_dim(penguins) = c(344, 8)
* library(palmerpenguins)  
  my\_dim = function(df) {  
   result = c(nrow(df), ncol(df))  
   return(result)  
  }  
  my\_dim(penguins)
* ## [1] 344 8
* Create a function, called medicaid\_eligible in which the function takes in one argument: a numeric vector called age. The function returns a numeric vector with the same length as age, in which elements are 0 for indicies that are less than 65 in age, and 1 for indicies 65 or higher in age. Use cases: medicaid\_eligible(c(30, 70)) = c(0, 1)
* medicaid\_eligible = function(age) {  
   result = age  
   result[age < 65] = 0  
   result[age >= 65] = 1  
   return(result)  
  }  
  medicaid\_eligible(c(30, 70))
* ## [1] 0 1

# 9 Functions Exercises

# 10 Repeating tasks

Suppose that you want to repeat a chunk of code many times, but changing one variable’s value each time you do it. This could be modifying each element of a vector with the same operation, or analyzing a dataframe with different parameters.

There are three common strategies to go about this:

1. Copy and paste the code chunk, and change that variable’s value. Repeat. *This can be a starting point in your analysis, but will lead to errors easily.*
2. Use a for loop to repeat the chunk of code, and let it loop over the changing variable’s value. *This is popular for many programming languages, but the R programming culture encourages a functional way instead*.
3. **Functionals** allow you to take a function that solves the problem for a single input and generalize it to handle any number of inputs. *This is very popular in R programming culture.*

## 10.1 For loops

A for loop repeats a chunk of code many times, once for each element of an input vector.

for (my\_element in my\_vector) {  
 chunk of code  
}

Most often, the “chunk of code” will make use of my\_element.

#### 10.1.0.1 We can loop through elements of a vector and print it out.

my\_vector = c(1, 3, 5, 7)  
for(my\_element in my\_vector) {  
 print(my\_element)  
}

## [1] 1  
## [1] 3  
## [1] 5  
## [1] 7

#### 10.1.0.2 Alternatively, we can loop through the indicies of a vector and print it out.

The function seq\_along() creates the indicies of a vector.

for(i in seq\_along(my\_vector)) {  
 print(my\_vector[i])  
}

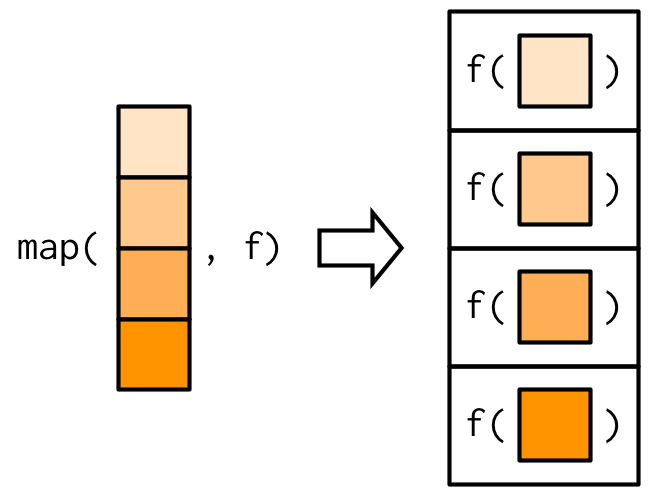
## [1] 1  
## [1] 3  
## [1] 5  
## [1] 7

## 10.2 Functionals

A **functional** is a function that takes in a data structure and function as inputs and applies the function on the data structure, element by element. It *maps* your input data structure to an output data structure based on the function. It encourages the usage of modular functions in your code.

![](data:text/html; charset=utf-8;base64,)

Or,



We will use the purrr package in tidyverse to use functionals.

map() takes in a vector or a list, and then applies the function on each element of it. The output is *always* a list. (You see the output twice, because it prints out element by element, and then returns a list.)

map(my\_vector, print)

## [1] 1  
## [1] 3  
## [1] 5  
## [1] 7

## [[1]]  
## [1] 1  
##   
## [[2]]  
## [1] 3  
##   
## [[3]]  
## [1] 5  
##   
## [[4]]  
## [1] 7

Lists are useful if what you are using it on requires a flexible data structure.

To be more specific about the output type, you can do this via the map\_\* function, where \* specifies the output type: map\_lgl(), map\_chr(), and map\_dbl() functions return vectors of logical values, strings, or numbers respectively.

For example, to make sure your output is a double (numeric):

map\_dbl(my\_vector, log)

## [1] 0.000000 1.098612 1.609438 1.945910

All of these are toy examples that gets us familiar with the syntax, but we already have built-in functions to solve these problems. Let’s see some real-life case studies.

## 10.3 Case studies

### 10.3.1 1. Loading in multiple dataframes from files for analysis

Suppose that we want to load in a few dataframes, and store them in a list of dataframes for analysis downstream.

We start with the filepaths we want to load in as dataframes.

paths = c("classroom\_data/students.csv", "classroom\_data/CCLE\_metadata.csv")

The function we want to use to load the data in will be read\_csv().

Let’s practice writing out one iteration:

result = read\_csv(paths[1])

#### 10.3.1.1 To do this functionally, we think about:

* What variable we need to loop through: paths
* The repeated task as a function: read\_csv()
* The looping mechanism, and its output: map() outputs lists.

loaded\_dfs = map(paths, read\_csv)

#### 10.3.1.2 To do this with a for loop, we think about:

* What variable we need to loop through: paths.
* Do we need to store the outcome of this loop in a data structure? Yes, a list.
* At each iteration, what are we doing? Use read\_csv() on the current element, and store it in the output list.

paths = c("classroom\_data/students.csv", "classroom\_data/CCLE\_metadata.csv")  
loaded\_dfs = vector(mode = "list", length = length(paths))  
for(i in seq\_along(paths)) {  
 df = read\_csv(paths[i])  
 loaded\_dfs[[i]] = df  
}

### 10.3.2 2. Analyze a dataframe differently with different parameters.

Suppose you are working with the penguins dataframe:

library(palmerpenguins)  
head(penguins)

## # A tibble: 6 × 8  
## species island bill\_length\_mm bill\_depth\_mm flipper\_length\_mm body\_mass\_g  
## <fct> <fct> <dbl> <dbl> <int> <int>  
## 1 Adelie Torgersen 39.1 18.7 181 3750  
## 2 Adelie Torgersen 39.5 17.4 186 3800  
## 3 Adelie Torgersen 40.3 18 195 3250  
## 4 Adelie Torgersen NA NA NA NA  
## 5 Adelie Torgersen 36.7 19.3 193 3450  
## 6 Adelie Torgersen 39.3 20.6 190 3650  
## # ℹ 2 more variables: sex <fct>, year <int>

and you want to look at the mean bill\_length\_mm for each of the three species (Adelie, Chinstrap, Gentoo).

Let’s practice writing out one iteration:

species\_to\_analyze = c("Adelie", "Chinstrap", "Gentoo")  
penguins\_subset = filter(penguins, species == species\_to\_analyze[1])  
mean(penguins\_subset$bill\_length\_mm, na.rm = TRUE)

## [1] 38.79139

#### 10.3.2.1 To do this functionally, we think about:

* What variable we need to loop through: c("Adelie", "Chinstrap", "Gentoo")
* The repeated task as a function: a custom function that takes in a specie of interest. The function filters the rows of penguins to the species of interest, and compute the mean of bill\_length\_mm.
* The looping mechanism, and its output: map\_dbl() outputs (double) numeric vectors.

analysis = function(current\_species) {  
 penguins\_subset = dplyr::filter(penguins, species == current\_species)  
 return(mean(penguins\_subset$bill\_length\_mm, na.rm=TRUE))  
}  
  
map\_dbl(c("Adelie", "Chinstrap", "Gentoo"), analysis)

## [1] 38.79139 48.83382 47.50488

#### 10.3.2.2 To do this with a for loop, we think about:

* What variable we need to loop through: c("Adelie", "Chinstrap", "Gentoo").
* Do we need to store the outcome of this loop in a data structure? Yes, a numeric vector.
* At each iteration, what are we doing? Filter the rows of penguins to the species of interest, and compute the mean of bill\_length\_mm.

outcome = rep(NA, length(species\_to\_analyze))  
for(i in seq\_along(species\_to\_analyze)) {  
 penguins\_subset = filter(penguins, species == species\_to\_analyze[i])  
 outcome[i] = mean(penguins\_subset$bill\_length\_mm, na.rm=TRUE)  
}  
outcome

## [1] 38.79139 48.83382 47.50488

### 10.3.3 3. Calculate summary statistics on columns of a dataframe.

Suppose that you are interested in the numeric columns of the penguins dataframe.

penguins\_numeric = penguins %>% select(bill\_length\_mm, bill\_depth\_mm, flipper\_length\_mm, body\_mass\_g)

and you are interested to look at the mean of each column. It is very helpful to interpret the dataframe penguins\_numeric as a *list*, iterating through each column as an element of a list.

Let’s practice writing out one iteration:

mean(penguins\_numeric[[1]], na.rm = TRUE)

## [1] 43.92193

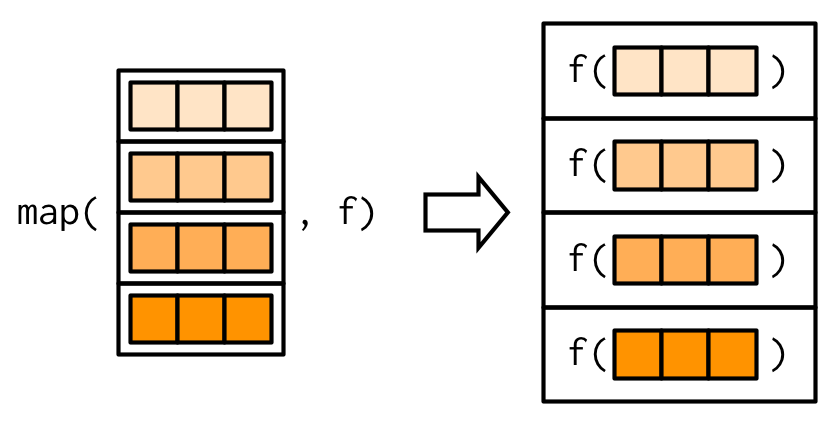
#### 10.3.3.1 To do this functionally, we think about:

* What variable we need to loop through: the list penguins\_numeric
* The repeated task as a function: mean() with the argument na.rm = TRUE.
* The looping mechanism, and its output: map\_dbl() outputs (double) numeric vectors.

map\_dbl(penguins\_numeric, mean, na.rm = TRUE)

## bill\_length\_mm bill\_depth\_mm flipper\_length\_mm body\_mass\_g   
## 43.92193 17.15117 200.91520 4201.75439

Here, R is interpreting the dataframe penguins\_numeric as a *list*, iterating through each column as an element of a list:



#### 10.3.3.2 To do this with a for loop, we think about:

* What variable we need to loop through: the elements of penguins\_numeric as a list.
* Do we need to store the outcome of this loop in a data structure? Yes, a numeric vector.
* At each iteration, what are we doing? Compute the mean of an element of penguins\_numeric.

result = rep(NA, ncol(penguins\_numeric))  
for(i in seq\_along(penguins\_numeric)) {  
 result[i] = mean(penguins\_numeric[[i]], na.rm = TRUE)  
}  
result

## [1] 43.92193 17.15117 200.91520 4201.75439

# 11 Repetition Exercises

# About the Authors

These credits are based on our [course contributors table guidelines](https://www.ottrproject.org/more_features.html#giving-credits-to-contributors).

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| --- | --- |
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## ─ Session info ───────────────────────────────────────────────────────────────  
## setting value   
## version R version 4.0.2 (2020-06-22)  
## os Ubuntu 20.04.5 LTS   
## system x86\_64, linux-gnu   
## ui X11   
## language (EN)   
## collate en\_US.UTF-8   
## ctype en\_US.UTF-8   
## tz Etc/UTC   
## date 2024-03-28   
##   
## ─ Packages ───────────────────────────────────────────────────────────────────  
## package \* version date lib source   
## assertthat 0.2.1 2019-03-21 [1] RSPM (R 4.0.5)   
## bookdown 0.24 2024-03-13 [1] Github (rstudio/bookdown@88bc4ea)   
## cachem 1.0.8 2023-05-01 [1] CRAN (R 4.0.2)   
## callr 3.5.0 2020-10-08 [1] RSPM (R 4.0.2)   
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## crayon 1.3.4 2017-09-16 [1] RSPM (R 4.0.0)   
## desc 1.2.0 2018-05-01 [1] RSPM (R 4.0.3)   
## devtools 2.3.2 2020-09-18 [1] RSPM (R 4.0.3)   
## digest 0.6.25 2020-02-23 [1] RSPM (R 4.0.0)   
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## pkgload 1.1.0 2020-05-29 [1] RSPM (R 4.0.3)   
## prettyunits 1.1.1 2020-01-24 [1] RSPM (R 4.0.3)   
## processx 3.4.4 2020-09-03 [1] RSPM (R 4.0.2)   
## ps 1.4.0 2020-10-07 [1] RSPM (R 4.0.2)   
## R6 2.4.1 2019-11-12 [1] RSPM (R 4.0.0)   
## remotes 2.2.0 2020-07-21 [1] RSPM (R 4.0.3)   
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## rmarkdown 2.10 2024-03-13 [1] Github (rstudio/rmarkdown@02d3c25)  
## rprojroot 2.0.4 2023-11-05 [1] CRAN (R 4.0.2)   
## sessioninfo 1.1.1 2018-11-05 [1] RSPM (R 4.0.3)   
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## stringr 1.4.0 2019-02-10 [1] RSPM (R 4.0.3)   
## testthat 3.0.1 2024-03-13 [1] Github (R-lib/testthat@e99155a)   
## usethis 1.6.3 2020-09-17 [1] RSPM (R 4.0.2)   
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## xfun 0.26 2024-03-13 [1] Github (yihui/xfun@74c2a66)   
## yaml 2.2.1 2020-02-01 [1] RSPM (R 4.0.3)   
##   
## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library

# 12 References