- **L3 MIASHS**
- **Université Paris Cité**
- Année 2023-2024
- Course Homepage
- Moodle

> ⚠ This lab intends to walk you through basic aspects of the R language and programming environment.
> Readers who really want to learn R should spend time on
> - R for Data Science by Wickham, Çetinkaya-Rundel, and Grolemund.
> - Advanced R 2nd Edition by Wickham
> - Advanced R Solutions by Grosser and Bumann
> - Hands-On Programming with R by Grolemund
>
> Don't go without Base R cheatsheet

Packages

Base R can do a lot. But the full power of R comes from a fast growing collection of `packages`.

Packages are first *installed* (that is downloaded from `cran` and copied somewhere on the hard drive), and if needed, *loaded* during a session.

- Installation can usually be performed using command `install.packages()`. In some circumstances, ad hoc installation commands (often from packages `devtools`) are needed
- Once a package has been installed/downloaded on your drive
  - if you want all objects exported by the package to be available in your session, you should *load* the package, using `library()` or `require()` (what's the difference?). Technically, this loads the `NameSpace` defined by the package.
  - if you just want to pick some objects exported from the package, you can use *qualified names* like `package_name::object_name` to access the object (function, dataset, …).

For example. when we write

```r
gapminder <- gapminder::gapminder
```

we assign dataframe `gapminder` from package `gapminder` to identifier `"gapminder"` in global environment 🙄.

Function `p_load()` from `pacman` (package manager) blends installation and loading: if the package named in the argument of `p_load()` is not installed (not among the `installed.packages()`), `p_load()` attempts to install the package. If installation is successful, the package is loaded.

```r
to_be_loaded <- c("devtools",
                  "tidyverse",
                  "lobstr",
                  "ggforce",
                  "nycflights13",
                  "patchwork",
                  "glue",
                  "DT",
                  "kableExtra",
                    "viridis")

for (pck in to_be_loaded) {
  if (!require(pck, character.only = T)) {
    install.packages(pck, repos="http://cran.rstudio.com/")
    stopifnot(require(pck, character.only = T))
  }
}
```

A very nice feature of `R` is that functions from base `R` as well as from packages have *optional* arguments with sensible *default* values. Look for example at documentation of `require()` using expression `?require`.

Optional settings may concern individual functions or the collection of functions exported by some packages. In the next chunk, we reset the default color scales used by graphical functions from `ggplot2`.

```
opts <- options()  # save old options

options(ggplot2.discrete.colour="viridis")
options(ggplot2.continuous.colour="viridis")
```

Numerical (atomic) vectors

Numerical (atomic) vectors form the most primitive type of `R`.

Vector creation and assignment

The next three lines create three numerical atomic vectors.

In IDE `Rstudio`, have a look at the `environment` pane on the right before running the chunk, and after.

Use `ls()` to investigate the *environment* before and after the execution of the three assignments.

```
ls()
## [1] "has_annotations" "opts"            "params"          "pck"            
## [5] "to_be_loaded"
x <- c(1, 2, 12)
y <- 5:7
z <- 10:1
x ; y ; z
## [1]  1  2 12
## [1] 5 6 7
##  [1] 10  9  8  7  6  5  4  3  2  1
ls()
## [1] "has_annotations" "opts"            "params"          "pck"            
## [5] "to_be_loaded"    "x"               "y"               "z"
```

Solution

The chunks adds three identifiers `x,y,z` to the global environment. Identifiers are bound to R objects which turn out to be numerical vectors.

What does the next chunk?

```
ls()
## [1] "has_annotations" "opts"            "params"          "pck"
## [5] "to_be_loaded"    "x"               "y"               "z"
w <- y
ls()
## [1] "has_annotations" "opts"            "params"          "pck"
## [5] "to_be_loaded"    "w"               "x"               "y"
## [9] "z"
```

Solution

The chunk inserts a new identifier w in the global environment.

- Is the content of object denoted by y copied to a new object bound to w?
- Interpret the result of w == y.
- Interpret the result of identical(w,y) (use help("identical") if needed).

```
w == y
## [1] TRUE TRUE TRUE
identical(w,y)
## [1] TRUE
```

Solution

Package lobstr lets us explore low-level aspects of R (and much more). Function lobstr::obj_addr() returns the address of the object denoted by the argument.

```
lobstr::obj_addr(w)
## [1] "0x5589a809d8d0"
lobstr::obj_addr(y)
## [1] "0x5589a809d8d0"
```

Now, if we modify either y or w

```
y <- y + 1
identical(y, w)
## [1] FALSE
c(lobstr::obj_addr(w), lobstr::obj_addr(y))
## [1] "0x5589a809d8d0" "0x5589aad83ac8"
```

The adress associated with y has changed!

⚠ The meaning of assignment in R differs from its countrepart in Python

Indexation, slicing, modification

Slicing a vector can be done in two ways:

- providing a vector of indices to be selected. Indices need not be consecutive

- providing a Boolean mask, that is a logical vector to select a set of positions

```
x <- c(1, 2, 12) ; y <- 5:7 ; z <- 10:1
```

- Explain the next lines

```
z[1]    # slice of length 1
## [1] 10
z[0]    # What did you expect?
## integer(0)
z[x]    # slice of length ??? index error ?
## [1] 10  9 NA
z[y]
## [1] 6 5 4
z[x %% 2]    # what happens with x[0] ?
## [1] 10
z[0 == (x %% 2)] # masking
## [1] 9 8 6 5 3 2
z[c(2, 1, 1)]
## [1]  9 10 10
```

Solution

- Indices start at `1` (not like in `C`, `Java`, or `Python`)
- `z[0]` does not return an Error message. It returns an empty vector with the same basetype as `x`
- `z[x]` returns a vector made of `z[x[1]]`, `z[x[2]]` and `z[x[3]]==z[12]`. Note again that `z[12]` does not raise an exception. It is simply not available (`NA`).
- `x %% 2` returns `1 0 0` as `%%` stands for `mod`. `z[x %% 2]` returns the same thing as `z[1]`

`c( )` stands for combine, or concatenate.

- If the length of mask and and the length of the sliced vector do not coincide, what happens?

Solution

No error is signalled, the returned sequence is as long as the number of truthies in the mask.
Out of bound truthies show up as `NA`

```
z[rep(c(TRUE, FALSE), 6)]
## [1] 10  8  6  4  2 NA
```

A scalar is just a vector of length 1!

```
class(z)
## [1] "integer"
class(z[1])
## [1] "integer"
class(z[c(2,1)])
## [1] "integer"
```

- Explain the next lines

```
y[2:3] <- z[2:3]
y == z[-10]
```

```
[1] FALSE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
z[-11]
```

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

Solution

We can assign a slice of a vector to a slice of identical size of another vector.
What is the result of `z[-11]`, `z[-c(11:7)]`?

- Explain the next line

```
z[-(1:5)]
## [1] 5 4 3 2 1
```

Solution

We pick all positions in `z` but the ones in `1:5`, that is `{r} setdiff(seq_along(z), 1:5)`

- How would you select the last element from a vector (say `z`)?

Solution

```
z[length(z)]
## [1] 1
```

`R` is not `Python` (reminder)!

- Reverse the entries of a vector. Find two ways to do that.

Solution

```
z[seq(length(z), 1, by=-1)]
##  [1]  1  2  3  4  5  6  7  8  9 10
z[length(z):1]
##  [1]  1  2  3  4  5  6  7  8  9 10
rev(z)   # the simplest way, once you know rev()
##  [1]  1  2  3  4  5  6  7  8  9 10
```

In statistics, machine learning, we are often faced with the task of building grid of regularly spaced elements (these elements can be numeric or not). `R` offers a collection of tools to perform this. The most basic tool is `rep()`.

- Repeat a vector 2 times
- Repeat each element of a vector twice

Solution

```
w <- c(1, 7, 9)
rep(w, 2)
## [1] 1 7 9 1 7 9
rep(w, rep(2, length(w)))
## [1] 1 1 7 7 9 9
```

Now, we can try something more fancy.

```
rep(w, 1:3)
## [1] 1 7 7 9 9 9
```

What are the requirements on the second (`times`) argument?

Let us remove objects from the global environment.

```
rm(w, x, y ,z)
```

Numbers

So far, we told about numeric vectors. Numeric vectors are vectors of floating point numbers. `R` distinguishes several kinds of numbers.

- Integers
- Floating point numbers (`double`)

To check whether a vector is made of `numeric` or of `integer`, use `is.numeric()` or `is.integer()`. Use `as.integer`, `as.numeric()` to enforce type conversion.

Explain the outcome of the next chunk

```
class(113L) ; class(113) ; class(113L + 113) ; class(2 * 113L) ; class(pi) ; as.integer(
## [1] "integer"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] 3
```

```
class(as.integer(113))
## [1] "integer"
```

```
pi ; class(pi)
## [1] 3.141593
## [1] "numeric"
```

```
floor(pi) ; class(floor(pi)) # mind the floor
## [1] 3
## [1] "numeric"
```

Integer arithmetic

```
29L * 31L ; 899L %/% 32L ; 899L %% 30L
## [1] 899
## [1] 28
## [1] 29
```

🔥 R integers are not the natural numbers from Mathematics
R numerics are not the real numbers from Mathematics

```
.Machine$double.eps
## [1] 2.220446e-16
.Machine$double.xmax
## [1] 1.797693e+308
.Machine$sizeof.longlong
## [1] 8

u <- double(19L)
v <- numeric(5L)
w <- integer(7L)
lapply(list(u, v, w), typeof)
## [[1]]
## [1] "double"
##
## [[2]]
## [1] "double"
##
## [[3]]
## [1] "integer"
length(c(u, v, w))
## [1] 31
typeof(c(u, v, w))
## [1] "double"
```

R is (sometimes) able to make sensible use of Infinite.

```
log(0)
## [1] -Inf
log(Inf)
## [1] Inf
1/0
## [1] Inf
0/0
## [1] NaN
max(c( 0/0,1,10))
## [1] NaN
max(c(NA,1,10))
## [1] NA
max(c(-Inf,1,10))
## [1] 10
is.finite(c(-Inf,1,10))
## [1] FALSE  TRUE  TRUE
is.na(c(NA,1,10))
## [1]  TRUE FALSE FALSE
is.nan(c(NaN,1,10))
## [1]  TRUE FALSE FALSE
```

Computing with vectors

Summing, scalar multiplication

```
x <- 1:3
y <- 9:7

sum(x) ; prod(x)
## [1] 6
## [1] 6

z <- cumsum(1:3)
w <- cumprod(3:5)

x + y
## [1] 10 10 10
x + z
## [1] 2 5 9
2 * w
## [1]   6  24 120
2 + w
## [1]  5 14 62
w / 2
## [1]  1.5  6.0 30.0
```

- How would you compute a factorial?

Solution

```
n <- 10
cumprod(1:n)
##  [1]       1       2       6      24     120     720    5040   40320  362880
## [10] 3628800
```

- Approximate $\sum_{n=1}^{\infty} 1/n^2$ within 10^{-3}?

Solution

$$\sum_{n>N} \frac{1}{n^2} < \sum_{n>N} \frac{1}{n(n-1)} = \sum_{n>N} \left(\frac{1}{n-1} - \frac{1}{n}\right) = \frac{1}{N}$$

So we may pick $N = 1000$.

```
sum(x*y) # inner product
## [1] 46
prod(1:5) # factorial(n) as prod(1:n)
## [1] 120
N <- 1000L
sum(1/((1:N)^2)) ; pi^2/6 # grand truth
## [1] 1.643935
## [1] 1.644934
(pi^2/6 - sum(1/((1:N)^2))) < 1e-3
## [1] TRUE
# N <- 999L
# (pi^2/6 - sum(1/((1:N)^2))) < 1e-3
```

- How would you compute the inner product between two (atomic numeric) vectors?

Solution

Inner product between two vectors can be computed as a matrix product between a row vector and a column vector using `%*%`. Is this a good idea.

```
matrix(w, ncol=3) %*% matrix(y, nrow=3) == sum(w * y)
##      [,1]
## [1,] TRUE
```

What we have called `vectors` so far are indeed `atomic vectors`.

- Read Chapter on Vectors in `R advanced Programming`
- Keep an eye on package `vctrs` for getting insights into the `R` vectors.

Numerical matrices

`R` offers a `matrix` class.

```
A <- matrix(1:50, nrow=5)
A
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]    1    6   11   16   21   26   31   36   41    46
## [2,]    2    7   12   17   22   27   32   37   42    47
## [3,]    3    8   13   18   23   28   33   38   43    48
## [4,]    4    9   14   19   24   29   34   39   44    49
## [5,]    5   10   15   20   25   30   35   40   45    50
class(A)
## [1] "matrix" "array"
```

- From the evaluation of the preceding chunk, can you guess whether it is easier the traverse a matrix in row first order or in column first order?

Solution

Default traversal seems to proceed columnwise.

Creation, transposition and reshaping

A vector can be turned into a column matrix.

```
v <- as.matrix(1:5)
v
##      [,1]
## [1,]    1
## [2,]    2
## [3,]    3
## [4,]    4
## [5,]    5
```

```
t(v)  # transpose
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    2    3    4    5
cat(dim(v), ' ', dim(t(v)), '\n')
## 5 1   1 5
```

```
A <- matrix(1, nrow=5, ncol=2) ; A
##      [,1] [,2]
## [1,]    1    1
## [2,]    1    1
## [3,]    1    1
## [4,]    1    1
## [5,]    1    1
```

- Is there a difference between the next two assignments?
- How would you assign value to all entries of a matrix?

```
A[] <- 0 ; A
##      [,1] [,2]
## [1,]    0    0
## [2,]    0    0
## [3,]    0    0
## [4,]    0    0
## [5,]    0    0
A   <- 0 ; A
## [1] 0
```

Solution

There is!
The first assignment assigns `0` to every entry in `A`.
The second assignment binds `0` to name `A`

```
A <- matrix(1, nrow=5, ncol=2) ; A
##      [,1] [,2]
## [1,]    1    1
## [2,]    1    1
## [3,]    1    1
## [4,]    1    1
## [5,]    1    1
A[] <- 1:15 ; A
##      [,1] [,2]
## [1,]    1    6
## [2,]    2    7
## [3,]    3    8
## [4,]    4    9
## [5,]    5   10
```

```
diag(1, 3)  # building identity matrix
##      [,1] [,2] [,3]
## [1,]    1    0    0
## [2,]    0    1    0
## [3,]    0    0    1

matrix(0, 3, 3) # building null matrix
##      [,1] [,2] [,3]
## [1,]    0    0    0
## [2,]    0    0    0
## [3,]    0    0    0
```

Is there any difference between the next two assignments?

```
B <- A[]
B ; A
##      [,1] [,2]
## [1,]    1    6
## [2,]    2    7
## [3,]    3    8
## [4,]    4    9
## [5,]    5   10
##      [,1] [,2]
## [1,]    1    6
## [2,]    2    7
## [3,]    3    8
## [4,]    4    9
## [5,]    5   10
lobstr::obj_addr(B) ; lobstr::obj_addr(A)
## [1] "0x5589ac37dab8"
## [1] "0x5589ac83ab38"
B <- A
```

Indexation, slicing, modification

Indexation consists in getting one item from a vector/list/matrix/array/dataframe.

Slicing and subsetting consists in picking a substructure:

- subsetting a vector returns a vector
- subsetting a list returns a list
- subsetting a matrix/array returns a matrix/array (beware of implicit simplifications and dimension dropping)
- subsetting a dataframe returns a dataframe or a vector (again, beware of implicit simplifications).
- Explain the next results

```
A <- matrix(1, nrow=5, ncol=2)

dim(A[sample(5, 3), -1])
## NULL
dim(A[sample(5, 3), 1])
## NULL
length(A[sample(5, 3), 1])
## [1] 3
is.vector(A[sample(5, 3), 1])
## [1] TRUE
A[10:15]
## [1]  1 NA NA NA NA NA
A[60]
## [1] NA
dim(A[])
## [1] 5 2
```

- How would you create a fresh copy of a matrix?

Computing with matrices

`*` versus `%*%` `%*%` stands for matrix multiplication. In order to use it, the two matrices should have conformant dimensions.

```
t(v) %*% A
##      [,1] [,2]
## [1,]   15   15
```

There are a variety of reasonable products around. Some of them are available in `R`.

- How would you compute the Hilbert-Schmidt inner product between two matrices?

$$\langle A, B\rangle_{\text{HS}} = \text{Trace}(A \times B^T)$$

Solution

In `R`, `trace()` does not return the trace of a matrix! Function is used for debugging. Just remember that the trace of a matrix is the sum of its diagonal elements.

```r
A <- matrix(runif(6), 2, 3)
B <- matrix(runif(6), 2, 3)
foo <- sum(diag(A %*% t(B)))
bar <- sum(A * B)
foo ; bar
## [1] 1.696852
## [1] 1.696852
```

Are you surprised?

- How can you invert a square (invertible) matrix?

Use `solve(A)` which is a shorthand for `solve(A, diag(1, nrow(3)))`.

Logicals

- `R` has constants `TRUE` and `FALSE`.
- Numbers can be coerced to `logicals`.
- Which numbers are truthies? falsies?
- What is the value (if any) of `! pi & TRUE` ?
- What is the meaning of `all( )` ?
- What is the meaning of `any( )` ?
- Recall De Morgan's laws. Check them with `R`.
- Is `|` denoting an inclusive or an exclusive OR?

```r
w <- c(TRUE, FALSE, FALSE)

sum(w)
## [1] 1
any(w)
## [1] TRUE
all(w)
## [1] FALSE

!w
## [1] FALSE  TRUE  TRUE

TRUE  & FALSE
## [1] FALSE
TRUE | FALSE
## [1] TRUE
```

```
TRUE | TRUE
## [1] TRUE
```

Solution

Handling three-valued logic

Read and understand the next expressions

```
TRUE &  (1> (0/0))
## [1] NA
(1> (0/0)) | TRUE
## [1] TRUE
(1> (0/0)) | FALSE
## [1] NA
TRUE || (1> (0/0))
## [1] TRUE
TRUE |  (1> (0/0))
## [1] TRUE
TRUE || stopifnot(4<3)
## [1] TRUE
# TRUE |  stopifnot(4<3)  # uncomment to see outcome
FALSE && stopifnot(4<3)
## [1] FALSE
# FALSE & stopifnot(4<3)
```

- What is the difference between logical operators `||` and `|` ?

Solution

`||` is *lazy*. It does not evaluate its second argument if the first one evaluates to `TRUE`. `&&` is also lazy.

Remark: favor `&, |` over `&&, ||`.

`all` and `any`

Look at the definition of `all` and `any`.

How would you check that a square matrix is symmetric?

Solution

A square matrix is symmteric iff it is equal to its transpose. Recall that `t(A)` denotes the transpose of matrix `A`.

```r
A <- matrix(rnorm(9), nrow=3, ncol=3) # a.s. non-symmetric
all(A == t(A))
## [1] FALSE

A <- A %*% t(A)  # build a symmetric matrix, A + t(A) would work also
all(A == t(A))
## [1] TRUE
```

`A == t(A)` returns a matrix a logical matrix, whose entries are all `TRUE` iff `A` is symmetric.
`all()` works for matrices as well as for vectors. This is sensible as matrices can be considered as vectors with some additional structure.

Lists

While an instance of an atomic `vector` contains objects of the same type/class, an instance of `list` may contain objects of widely different types.

- Check the output of the next chunk

```r
p <- c(2, 7, 8)
q <- c("A", "B", "C")
x <- list(p, q)
x[2]
## [[1]]
## [1] "A" "B" "C"
x
## [[1]]
## [1] 2 7 8
##
## [[2]]
## [1] "A" "B" "C"
length(x)
## [1] 2
rlang::is_vector(x)
## [1] TRUE
rlang::is_atomic(x)
## [1] FALSE
y <- c(p, q)
y
## [1] "2" "7" "8" "A" "B" "C"
length(y)
## [1] 6
rlang::is_atomic(y)
## [1] TRUE
rlang::is_list(y)
## [1] FALSE
```

- How would you build a list made of `p`, `q`, and `x`?
- What is `x[2]` made of?
- How does it compare with `x[[2]]`?

Solution

```
nl <- list(p=p, q=q, x=x)
nl
## $p
## [1] 2 7 8
##
## $q
## [1] "A" "B" "C"
##
## $x
## $x[[1]]
## [1] 2 7 8
##
## $x[[2]]
## [1] "A" "B" "C"
```

Note that we have defined a *named* list. Each `=` expression, binds the string on the left-hand side to the object on the right-hand side. List elements can be extracted in defferent ways.

```
names(nl)
## [1] "p" "q" "x"

nl$q
## [1] "A" "B" "C"

nl[["q"]]
## [1] "A" "B" "C"

nl[[2]]
## [1] "A" "B" "C"
```

Read and understand the next expressions.

```
is_atomic(p);  is_atomic(p[2]) ; is_atomic(p[[2]])
## [1] TRUE
## [1] TRUE
## [1] TRUE

is_list(q); is_atomic(q)
## [1] FALSE
## [1] TRUE

is_list(x); is_atomic(x) ; class(x)
## [1] TRUE
## [1] FALSE
## [1] "list"

class(x[2]) ; class(x[[2]])
## [1] "list"
## [1] "character"
length(x[2]) ; length(x[[2]])
## [1] 1
## [1] 3

identical(q, x[[2]]) ; identical(q, x[2])
## [1] TRUE
## [1] FALSE

obj_addr(q) ; obj_addr(x[[2]]) ; obj_addr(x[2])
## [1] "0x5589aca924d8"
## [1] "0x5589aca924d8"
## [1] "0x5589acd90b68"
ref(x)
##   [1:0x5589aa43f6d8] <list>
##  [2:0x5589acaa5b08] <dbl>
##  [3:0x5589aca924d8] <chr>
obj_addrs(x)
## [1] "0x5589acaa5b08" "0x5589aca924d8"
identical(x[2],x[[2]])
## [1] FALSE
```

Functions `is_atomic()`, `is_list()`, `...`, `obj_addr()` are from packages `rlang` and `lobstr`. See https://rlang.r-lib.org and https://lobstr.r-lib.org

Solution

`p` and `a` are atomic vectors with different base types. They are not lists. A list like `x` is not an atomic vector.
Inspection of object addresses shows that when building `x` from objects `p` and `q`, objects bound to `"p"` and `"q"` are not copied.
Note that `x[[2]]` and `x[2]` are different objects, the former is one element list, the second is an atomic vector.

```
ref(x[2])
##   [1:0x5589ad357f48] <list>
##  [2:0x5589aca924d8] <chr>
obj_addr(x[[2]])
## [1] "0x5589aca924d8"
```

- How would you replace `"A"` in `x` with `"K"`?

Solution

```
w <- c(2, 7, 8)
v <- c("A", "B", "C")
x <- list(w, v)
```

Lookup tables (aka dictionaries) using named vectors

A lookup table maps strings to values. It can be implemented using named vectors. If we want to map: `"seine"` to `"75"`, `"loire"` to `"42"`, `"rhone"` to `"69"`, `"savoie"` to `"73"` we can proceed in the following way:

```r
codes <- c(75L, 42L, 69L, 73L)
names(codes) <- c("seine", "loire", "rhone", "savoie")

codes["rhone"];  codes["aube"]
## rhone
##    69
## <NA>
##   NA
```

- what is the class of `codes` ?

Solution

```r
names(codes)
## [1] "seine"  "loire"  "rhone"  "savoie"
class(codes); class(names(codes))
## [1] "integer"
## [1] "character"
is_atomic(codes); is_character(codes) ; is_integer(codes)
## [1] TRUE
## [1] FALSE
## [1] TRUE
```

- Capitalize the `names` used by `codes`

Package `stringr` offers a function `str_to_title()` that could be of interest.

Solution

```r
names(codes) <- stringr::str_to_title(names(codes))
codes
##  Seine  Loire  Rhone Savoie
##     75     42     69     73
```

Read Chapter on Lists in `R advanced Programming`

Factors

Factors exist in Base `R`. They play a very important role. Qualitative/Categorical variables are implemented as Factors.

Meta-package `tidyverse` offers a package dedicated to `factor` engineering: `forcats`.

```
yraw <- c("g1","g1","g2","g2","g2","g3")
print(yraw)
## [1] "g1" "g1" "g2" "g2" "g2" "g3"
summary(yraw)
##    Length     Class      Mode 
##         6 character character 
is.vector(yraw) ; is.atomic(yraw)
## [1] TRUE
## [1] TRUE
```

`yraw` takes few values. It makes sense to make it a `factor`. How does it change the behavior of *generic* function `summary` ?

```
fyraw <- as.factor(yraw)
levels(fyraw)
## [1] "g1" "g2" "g3"

summary(fyraw)
## g1 g2 g3 
##  2  3  1
```

Load the (celebrated) `iris` dataset, and inspect variable `Species`

```
data(iris)

species <- iris$Species

levels(species)
```

```
[1] "setosa"     "versicolor" "virginica" 
```

```
summary(species)
```

```
    setosa versicolor  virginica 
        50         50         50 
```

We may want to collapse `virginica` and `versicolor` into a single level called `versinica`

`forcats` offer a function `fct_collapse`.

Solution

```
col_species <- forcats::fct_collapse(species,
                          versinica = c("versicolor", "virginica"))

summary(col_species)
```

```
   setosa versinica 
       50       100 
```

Factors are used to represent *categorical* variables.

Load the `whiteside` data from package `MASS`.

Have a glimpse.

Assign column `Insul` to `y`

Solution

```
whiteside <- MASS::whiteside  # importing the whiteside data
# ?whiteside                  # what are the whiteside data about?

tibble::glimpse(whiteside)
```

```
Rows: 56
Columns: 3
$ Insul <fct> Before, Before, Before, Before, Before, Before, Before, Before, ~
$ Temp  <dbl> -0.8, -0.7, 0.4, 2.5, 2.9, 3.2, 3.6, 3.9, 4.2, 4.3, 5.4, 6.0, 6.~
$ Gas   <dbl> 7.2, 6.9, 6.4, 6.0, 5.8, 5.8, 5.6, 4.7, 5.8, 5.2, 4.9, 4.9, 4.3,~
```

```
y <- whiteside$Insul          # picking a factor column
```

- What is the `class` of `y`?
- Is `y` a `vector`
- Is `y` *ordered*? What does *ordered* mean here?
- What are the `levels` of `y` ? How many levels has `y`?
- Can you slice `y` ?
- What are the binary representations of the different levels of `y`?

Solution

```
is.factor(y) ; is.vector(y) ; is.ordered(y)
```

```
[1] TRUE
[1] FALSE
[1] FALSE
```

```
class(y)
```

```
[1] "factor"
```

```
levels(y)
```

```
[1] "Before" "After"
```

```
nlevels(y)
```

```
[1] 2
```

```
y[1:10] # yes we can
```

```
 [1] Before Before Before Before Before Before Before Before Before Before
Levels: Before After
```

```
pryr::bits(y[31]) # looks like the two levels are represented by integers
```

```
[1] "00000000 00000000 00000000 00000010"
```

Summarize factor y

Solution

```
summary(y)   # counts
```

```
Before  After 
    26     30 
```

```
table(y)     # one-way contingency table
```

```
y
Before  After 
    26     30 
```

```
table(y)/sum(table(y))*100   # one-way contingency table as percentages
```

```
y
  Before    After 
46.42857 53.57143 
```

```
table(y) %>%
  knitr::kable(col.names = c("Insulation", "Frequency"),
               caption = "Whiteside data")  # Pb encoding sur machine windows
```

```
forcats::fct_count(y) %>%
  knitr::kable(col.names = c("Insulation", "Frequency"),
               caption = "Whiteside data")
```

Factors nuts and bolts

When coercing a vector (integer, character, …) to a factor, use `forcats::as_factor()` rather than base R `as.factor()`.

Useful function to make nice `barplots` when constructing `barplots`.

Recall that when you want to display counts for a univariate *categorical* sample, you use a `barplot`. It is often desirable to rank the levels according to the displayed statistics (usually a count).

This can be done in a seamless way using functions like `forcats::fct_infreq()`.

```
forcats::fct_count(y, prop = TRUE)
```

```
# A tibble: 2 x 3
  f          n     p
  <fct>  <int> <dbl>
1 Before    26 0.464
```

```
2 After     30 0.536
```

```
z <- sample(y, length(y), replace = TRUE)  # permutation of whiteside$Insul

sort(forcats::fct_infreq(z))       # first level is most frequent one
```

```
 [1] After  After  After  After  After  After  After  After  After  After 
[11] After  After  After  After  After  After  After  After  After  After 
[21] After  After  After  After  After  After  After  After  After  Before
[31] Before Before Before Before Before Before Before Before Before Before
[41] Before Before Before Before Before Before Before Before Before Before
[51] Before Before Before Before Before Before
Levels: After Before
```

```
forcats::fct_count(z)
```

```
# A tibble: 2 x 2
  f          n
  <fct>  <int>
1 Before    27
2 After     29
```

Make `z` ordered with level `After` preceding `Before`. Does ordering impact the behavior of `forcats::fct_count()`?

Solution

```
forcats::fct_count(z)
```

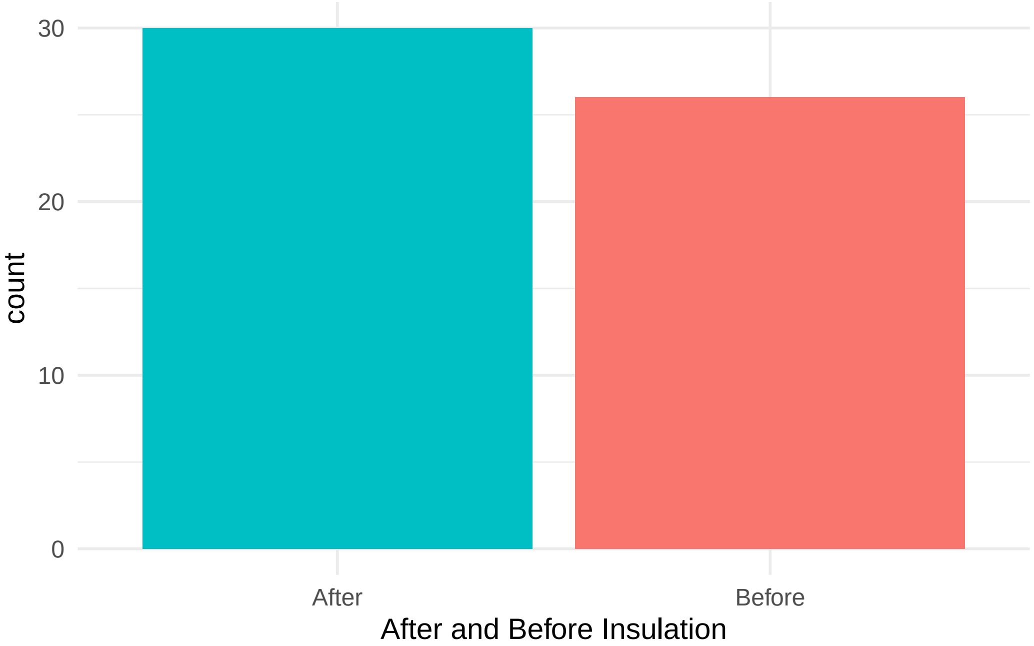
```
# A tibble: 2 x 2
  f          n
  <fct>  <int>
1 Before    27
2 After     29
```

```
forcats::fct_count(factor(z, ordered=TRUE, levels=c("After", "Before")))
```

```
# A tibble: 2 x 2
  f          n
  <ord>  <int>
1 After     29
2 Before    27
```

Solution

```
whiteside %>%
  ggplot2::ggplot() +
  ggplot2::aes(x=forcats::fct_infreq(Insul), fill=Insul) +
  ggplot2::geom_bar() +
  ggplot2::xlab("After and Before Insulation") +
  ggplot2::theme_minimal() +
  ggplot2::theme(legend.position="None")
```



! Read Chapter on Factors in `R for Data Science`

Dataframes, `tibbles` and `data.tables`

A dataframe is a list of vectors with equal lengths. This is the way `R` represents and manipulates multivariate samples.

Any software geared at data science supports some kind of dataframe

- `Python Pandas`
- `Python Dask`
- `Spark`
- …

The `iris` dataset is the "Hello world!" of dataframes.

```
data(iris)

iris %>%
  glimpse()
## Rows: 150
## Columns: 5
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9, 5.4, 4.~
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, 3.7, 3.~
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5, 1.5, 1.~
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, 0.2, 0.~
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, setosa, s~
```

A `matrix` can be transformed into a `data.frame`

```
A <- matrix(rnorm(10), ncol=2)
data.frame(A)
##           X1         X2
## 1 -0.3093333 -0.1512694
## 2 -0.3848313 -0.1213958
## 3  0.7473324 -0.5827866
## 4  0.4772969  0.7070918
## 5  1.5486242 -0.7784089
```

There are several flavors of dataframes in `R`: `tibble` and `data.table` are modern variants of `data.frame`.

```
t <- tibble::tibble(x=1:3, a=letters[11:13], d=Sys.Date() + 1:3)

head(t)
## # A tibble: 3 x 3
##       x a     d
##   <int> <chr> <date>
## 1     1 k     2024-01-25
## 2     2 l     2024-01-26
## 3     3 m     2024-01-27
```

```
glimpse(t)
## Rows: 3
## Columns: 3
## $ x <int> 1, 2, 3
## $ a <chr> "k", "l", "m"
## $ d <date> 2024-01-25, 2024-01-26, 2024-01-27
ref(t)
##  [1:0x5589add0bbe8] <tibble[,3]>
##  x = [2:0x5589a5cd5510] <int>
##  a = [3:0x5589adcbd428] <chr>
##  d = [4:0x5589adcd04d8] <date>
```

Read Chapter on data frames and tibbles in Advanced R

Perform a random permutation of the columns of a data.frame/tibble.

Function `sample()` from base `R` is very convenient

Solution

```
t[sample(names(t))]
## # A tibble: 3 x 3
##   d              x a
##   <date>     <int> <chr>
## 1 2024-01-25     1 k
## 2 2024-01-26     2 l
## 3 2024-01-27     3 m
# or
t[sample(ncol(t))]
## # A tibble: 3 x 3
##       x a     d
##   <int> <chr> <date>
## 1     1 k     2024-01-25
## 2     2 l     2024-01-26
## 3     3 m     2024-01-27
```

`nycflights` data

Wrestling with tables is part of the data scientist job. Out of the box data are often messy. In order to perform useful data analysis, we need *tidy* data. The notion of tidy data was elaborated during the last decade by experienced data scientists.

You may benefit from looking at the following online documents.

Tidy data in R for Data Science

Introduction to Table manipulation in R for Data Science in `R`.

More data of that kind is available following guidelines from https://github.com/hadley/nycflights13

In this exercise, you are advised to use functions from dplyr.

> `dplyr` is a grammar of data manipulation, providing a consistent set of verbs that help you solve the most common data manipulation challenges.

```
data <- nycflights13::flights
```

- Have a glimpse at the data.
- What is the `class` of object `data`?
- What kind of object is `data`?

Hint: use `class(), is.data.frame() tibble::is_tibble()`

Solution

```
#| label: flight_glimpse
#| eval: true
data %>% glimpse()
```

```
Rows: 336,776
Columns: 19
$ year           <int> 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2~
$ month          <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1~
$ day            <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1~
$ dep_time       <int> 517, 533, 542, 544, 554, 554, 555, 557, 557, 558, 558, ~
$ sched_dep_time <int> 515, 529, 540, 545, 600, 558, 600, 600, 600, 600, 600, ~
$ dep_delay      <dbl> 2, 4, 2, -1, -6, -4, -5, -3, -3, -2, -2, -2, -2, -2, -1~
$ arr_time       <int> 830, 850, 923, 1004, 812, 740, 913, 709, 838, 753, 849,~
$ sched_arr_time <int> 819, 830, 850, 1022, 837, 728, 854, 723, 846, 745, 851,~
$ arr_delay      <dbl> 11, 20, 33, -18, -25, 12, 19, -14, -8, 8, -2, -3, 7, -1~
$ carrier        <chr> "UA", "UA", "AA", "B6", "DL", "UA", "B6", "EV", "B6", "~
$ flight         <int> 1545, 1714, 1141, 725, 461, 1696, 507, 5708, 79, 301, 4~
$ tailnum        <chr> "N14228", "N24211", "N619AA", "N804JB", "N668DN", "N394~
$ origin         <chr> "EWR", "LGA", "JFK", "JFK", "LGA", "EWR", "EWR", "LGA",~
$ dest           <chr> "IAH", "IAH", "MIA", "BQN", "ATL", "ORD", "FLL", "IAD",~
$ air_time       <dbl> 227, 227, 160, 183, 116, 150, 158, 53, 140, 138, 149, 1~
$ distance       <dbl> 1400, 1416, 1089, 1576, 762, 719, 1065, 229, 944, 733, ~
$ hour           <dbl> 5, 5, 5, 5, 6, 5, 6, 6, 6, 6, 6, 6, 6, 6, 6, 5, 6, 6, 6~
$ minute         <dbl> 15, 29, 40, 45, 0, 58, 0, 0, 0, 0, 0, 0, 0, 0, 0, 59, 0~
$ time_hour      <dttm> 2013-01-01 05:00:00, 2013-01-01 05:00:00, 2013-01-01 0~
```

```
class(data)
```

```
[1] "tbl_df"     "tbl"        "data.frame"
```

```
is.data.frame(data)
```

```
[1] TRUE
```

```
is_tibble(data)
```

```
[1] TRUE
```

- Extract the name and the type of each column.

Solution

Compute the mean of the numerical columns

Base R has plenty of functions that perform statistical computations on univariate samples. Look at the documentation of mean (just type ?mean). For a while, leave aside the optional arguments.

In database parlance, we are performing *aggregation*

```
mean(data$dep_delay)
```

```
[1] NA
```

```
# mean(data[["dep_delay"]])
```

- If we want the mean of all numerical columns, we need to project the data frame on numerical columns.

A verb of the summarize family can be useful.

> Have a look at across in latest versions of dplyr()
> Use across() from dplyr 1.x. See Documentation

Solution

```
data %>%
  dplyr::select(where(is.numeric)) %>%  # projecting on numerical columns
  purrr::map(mean)                      # applying the treatment to each column
## $year
## [1] 2013
##
## $month
## [1] 6.54851
##
## $day
## [1] 15.71079
##
## $dep_time
## [1] NA
##
## $sched_dep_time
## [1] 1344.255
##
## $dep_delay
## [1] NA
##
## $arr_time
## [1] NA
##
## $sched_arr_time
## [1] 1536.38
##
## $arr_delay
## [1] NA
##
## $flight
## [1] 1971.924
##
## $air_time
## [1] NA
##
## $distance
## [1] 1039.913
##
## $hour
## [1] 13.18025
##
## $minute
## [1] 26.2301

data %>%
  dplyr::select(where(is.numeric)) %>%  # projecting on numerical columns
  dplyr::summarise(across(everything(), mean, na.rm=T))
## # A tibble: 1 x 14
##     year month   day dep_time sched_dep_time dep_delay arr_time sched_arr_time
##    <dbl> <dbl> <dbl>    <dbl>          <dbl>     <dbl>    <dbl>          <dbl>
## 1  2013  6.55  15.7    1349.          1344.      12.6     1502.          1536.
## # i 6 more variables: arr_delay <dbl>, flight <dbl>, air_time <dbl>,
## #   distance <dbl>, hour <dbl>, minute <dbl>
```

```
data %>%
  dplyr::summarise(across(where(is.numeric), mean))
```

If applied to a data.frame, `summary()`, produces a summary of each column. The summary depends on the column type. The output of `summary` is a shortened version the list of outputs obtained from applying `summary` to each column (`lapply(data, summary)`).

```
data %>%
  summary()
```

```
     year          month             day           dep_time    sched_dep_time
Min.   :2013   Min.   : 1.000   Min.   : 1.00   Min.   :   1   Min.   : 106  
1st Qu.:2013   1st Qu.: 4.000   1st Qu.: 8.00   1st Qu.: 907   1st Qu.: 906  
Median :2013   Median : 7.000   Median :16.00   Median :1401   Median :1359  
Mean   :2013   Mean   : 6.549   Mean   :15.71   Mean   :1349   Mean   :1344  
3rd Qu.:2013   3rd Qu.:10.000   3rd Qu.:23.00   3rd Qu.:1744   3rd Qu.:1729  
Max.   :2013   Max.   :12.000   Max.   :31.00   Max.   :2400   Max.   :2359  
                                                NA's   :8255                 
  dep_delay          arr_time    sched_arr_time   arr_delay      
Min.   : -43.00   Min.   :   1   Min.   :   1   Min.   : -86.000  
1st Qu.:  -5.00   1st Qu.:1104   1st Qu.:1124   1st Qu.: -17.000  
Median :  -2.00   Median :1535   Median :1556   Median :  -5.000  
Mean   :  12.64   Mean   :1502   Mean   :1536   Mean   :   6.895  
3rd Qu.:  11.00   3rd Qu.:1940   3rd Qu.:1945   3rd Qu.:  14.000  
Max.   :1301.00   Max.   :2400   Max.   :2359   Max.   :1272.000  
NA's   :8255      NA's   :8713                  NA's   :9430      
  carrier              flight       tailnum             origin         
Length:336776      Min.   :   1   Length:336776      Length:336776     
Class :character   1st Qu.: 553   Class :character   Class :character  
Mode  :character   Median :1496   Mode  :character   Mode  :character  
                   Mean   :1972                                        
                   3rd Qu.:3465                                        
                   Max.   :8500                                        
                                                                       
    dest              air_time        distance         hour      
Length:336776      Min.   : 20.0   Min.   :  17   Min.   : 1.00  
Class :character   1st Qu.: 82.0   1st Qu.: 502   1st Qu.: 9.00  
Mode  :character   Median :129.0   Median : 872   Median :13.00  
                   Mean   :150.7   Mean   :1040   Mean   :13.18  
                   3rd Qu.:192.0   3rd Qu.:1389   3rd Qu.:17.00  
                   Max.   :695.0   Max.   :4983   Max.   :23.00  
                   NA's   :9430                                  
    minute        time_hour                  
Min.   : 0.00   Min.   :2013-01-01 05:00:00  
1st Qu.: 8.00   1st Qu.:2013-04-04 13:00:00  
Median :29.00   Median :2013-07-03 10:00:00  
Mean   :26.23   Mean   :2013-07-03 05:22:54  
3rd Qu.:44.00   3rd Qu.:2013-10-01 07:00:00  
Max.   :59.00   Max.   :2013-12-31 23:00:00  
```

Handling NAs

We add now a few `NA`s to the data….

```
data2 <- data
data2$arr_time[1:10] <- NA
```

Houston, we have a problem!

How should we compute the column means now?

Solution

```
data2 %>%
  dplyr::summarise(across(is.numeric, mean))
## # A tibble: 1 x 14
##    year month   day dep_time sched_dep_time dep_delay arr_time sched_arr_time
##   <dbl> <dbl> <dbl>    <dbl>          <dbl>     <dbl>    <dbl>          <dbl>
## 1  2013  6.55  15.7       NA          1344.        NA       NA          1536.
## # i 6 more variables: arr_delay <dbl>, flight <dbl>, air_time <dbl>,
## #   distance <dbl>, hour <dbl>, minute <dbl>
```

It is time to look at optional arguments of function `mean`.

- Decide to ignore `NA` and to compute the mean with the available data

Solution

```
data2 %>%
  dplyr::summarise(across(is.numeric, mean, na.rm=TRUE))
## # A tibble: 1 x 14
##    year month   day dep_time sched_dep_time dep_delay arr_time sched_arr_time
##   <dbl> <dbl> <dbl>    <dbl>          <dbl>     <dbl>    <dbl>          <dbl>
## 1  2013  6.55  15.7    1349.          1344.      12.6    1502.          1536.
## # i 6 more variables: arr_delay <dbl>, flight <dbl>, air_time <dbl>,
## #   distance <dbl>, hour <dbl>, minute <dbl>
```

Note: it is possible to remove all rows that contain at least one `NA`.

- Show this leads to a different result.

Solution

```
data2 %>%
  drop_na() %>%
  dplyr::summarise(across(is.numeric, mean, na.rm=FALSE))
```

```
# A tibble: 1 x 14
   year month   day dep_time sched_dep_time dep_delay arr_time sched_arr_time
  <dbl> <dbl> <dbl>    <dbl>          <dbl>     <dbl>    <dbl>          <dbl>
1  2013  6.56  15.7    1349.          1340.      12.6    1502.          1533.
# i 6 more variables: arr_delay <dbl>, flight <dbl>, air_time <dbl>,
#   distance <dbl>, hour <dbl>, minute <dbl>
```

- Compute the minimum, the median, the mean and the maximum of numerical columns

Solution

```
data2 %>%
  dplyr::select_if(is.numeric) %>%
  lapply(function(x) c(med=median(x, na.rm=TRUE),
                       avg=mean(x, na.rm=TRUE),
                       max=max(x, na.rm=TRUE))
         )
## $year
##  med  avg  max
## 2013 2013 2013
##
## $month
##      med      avg      max
##  7.00000  6.54851 12.00000
##
## $day
##      med      avg      max
## 16.00000 15.71079 31.00000
##
## $dep_time
##     med     avg     max
## 1401.00 1349.11 2400.00
##
## $sched_dep_time
##      med      avg      max
## 1359.000 1344.255 2359.000
##
## $dep_delay
##        med        avg        max
##   -2.00000   12.63907 1301.00000
##
## $arr_time
##      med      avg      max
## 1536.000 1502.075 2400.000
##
## $sched_arr_time
##     med     avg     max
## 1556.00 1536.38 2359.00
##
## $arr_delay
##         med         avg         max
##   -5.000000    6.895377 1272.000000
##
## $flight
##      med      avg      max
## 1496.000 1971.924 8500.000
##
## $air_time
##      med      avg      max
## 129.0000 150.6865 695.0000
##
## $distance
##      med      avg      max
##  872.000 1039.913 4983.000
##
## $hour
##      med      avg      max
## 13.00000 13.18025 23.00000
```

- Obtain a *nicer* output!

Check with https://dplyr.tidyverse.org/reference/scoped.html?q=funs#arguments

Solution

```
data2 %>%
  dplyr::summarise(across(is.numeric,
                          list(median=median,
                               mean=mean,
                               max=max) ,
                          na.rm=TRUE))
```

```
# A tibble: 1 x 42
  year_median year_mean year_max month_median month_mean month_max day_median
        <dbl>     <dbl>    <int>        <dbl>      <dbl>     <int>      <dbl>
1        2013      2013     2013            7       6.55        12         16
# i 35 more variables: day_mean <dbl>, day_max <int>, dep_time_median <int>,
#   dep_time_mean <dbl>, dep_time_max <int>, sched_dep_time_median <dbl>,
#   sched_dep_time_mean <dbl>, sched_dep_time_max <int>,
#   dep_delay_median <dbl>, dep_delay_mean <dbl>, dep_delay_max <dbl>,
#   arr_time_median <int>, arr_time_mean <dbl>, arr_time_max <int>,
#   sched_arr_time_median <dbl>, sched_arr_time_mean <dbl>,
#   sched_arr_time_max <int>, arr_delay_median <dbl>, arr_delay_mean <dbl>, ...
```

- Mimic `summary` on numeric columns

Solution

```
mysum <- data2 %>%
  dplyr::summarise(across(is.numeric,
                          list(median=median,
                               mean=mean,
                               max=max,
                               min=min,
                               sd=sd,
                               IQR=IQR) ,
                      na.rm=TRUE))
mysum
## # A tibble: 1 x 84
##   year_median year_mean year_max year_min year_sd year_IQR month_median
##         <dbl>     <dbl>    <int>    <int>   <dbl>    <dbl>        <dbl>
## 1        2013      2013     2013     2013       0        0            7
## # i 77 more variables: month_mean <dbl>, month_max <int>, month_min <int>,
## #   month_sd <dbl>, month_IQR <dbl>, day_median <dbl>, day_mean <dbl>,
## #   day_max <int>, day_min <int>, day_sd <dbl>, day_IQR <dbl>,
## #   dep_time_median <int>, dep_time_mean <dbl>, dep_time_max <int>,
## #   dep_time_min <int>, dep_time_sd <dbl>, dep_time_IQR <dbl>,
## #   sched_dep_time_median <dbl>, sched_dep_time_mean <dbl>,
## #   sched_dep_time_max <int>, sched_dep_time_min <int>, ...
```

- Compute a new `itinerary` column concatenating the `origin` and `dest` one.

Have a look at Section Operate on a selection of variables

Solution

```
data %>%
  dplyr::mutate(itinerary=paste(dest, origin, sep="-")) %>%
  dplyr::select(itinerary, dest, origin, everything())
## # A tibble: 336,776 x 20
##    itinerary dest  origin  year month   day dep_time sched_dep_time dep_delay
##    <chr>     <chr> <chr>  <int> <int> <int>    <int>          <int>     <dbl>
##  1 IAH-EWR   IAH   EWR     2013     1     1      517            515         2
##  2 IAH-LGA   IAH   LGA     2013     1     1      533            529         4
##  3 MIA-JFK   MIA   JFK     2013     1     1      542            540         2
##  4 BQN-JFK   BQN   JFK     2013     1     1      544            545        -1
##  5 ATL-LGA   ATL   LGA     2013     1     1      554            600        -6
##  6 ORD-EWR   ORD   EWR     2013     1     1      554            558        -4
##  7 FLL-EWR   FLL   EWR     2013     1     1      555            600        -5
##  8 IAD-LGA   IAD   LGA     2013     1     1      557            600        -3
##  9 MCO-JFK   MCO   JFK     2013     1     1      557            600        -3
## 10 ORD-LGA   ORD   LGA     2013     1     1      558            600        -2
## # i 336,766 more rows
## # i 11 more variables: arr_time <int>, sched_arr_time <int>, arr_delay <dbl>,
## #   carrier <chr>, flight <int>, tailnum <chr>, air_time <dbl>, distance <dbl>,
## #   hour <dbl>, minute <dbl>, time_hour <dttm>
```

- Compute the coefficient of variation (ratio between the standard deviation and the mean) for each itinerary. Can you find several ways?

Solution

```
data %>%
  dplyr::mutate(itinerary=paste(dest, origin, sep="-")) %>%
  dplyr::select(itinerary, dest, origin, everything()) %>%
  dplyr::group_by(itinerary) %>%
  dplyr::summarise(coef_var=sd(air_time, na.rm=T)/mean(air_time, na.rm=T), .groups = "
  slice_sample(n=10)
## # A tibble: 10 x 2
##    itinerary coef_var
##    <chr>        <dbl>
##  1 CLT-JFK     0.102
##  2 BTV-JFK     0.0738
##  3 LAS-EWR     0.0573
##  4 SAT-EWR     0.0828
##  5 FLL-LGA     0.0807
##  6 DFW-LGA     0.0852
##  7 EYW-LGA     0.0662
##  8 MHT-EWR     0.0757
##  9 RDU-EWR     0.0844
## 10 MDW-LGA     0.0821
```

- Compute for each flight the ratio between the `distance` and the `air_time` in different ways and compare the execution time (use `Sys.time()`).

Solution

```
before <- Sys.time()

data %>%
  dplyr::mutate(itinerary=paste(dest, origin, sep="-")) %>%
  dplyr::group_by(itinerary) %>%
  dplyr::summarize(ratio=mean(air_time)/max(distance)) %>%
  dplyr::arrange(desc(ratio))
## # A tibble: 224 x 2
##    itinerary ratio
##    <chr>     <dbl>
##  1 BWI-LGA   0.219
##  2 MEM-JFK   0.172
##  3 MYR-LGA   0.166
##  4 CAE-LGA   0.164
##  5 AVL-LGA   0.154
##  6 LEX-LGA   0.149
##  7 SBN-LGA   0.149
##  8 SBN-EWR   0.147
##  9 JAC-JFK   0.145
## 10 STL-JFK   0.145
## # i 214 more rows

required_time <- Sys.time() - before
required_time
## Time difference of 0.1587234 secs
```

- Which carrier suffers the most delay?

Solution

```
data %>%
  dplyr::select(carrier, arr_delay) %>%
  dplyr::filter(arr_delay > 0) %>%
  dplyr::group_by(carrier) %>%
  dplyr::summarise(ndelays= n()) %>%
#   dplyr::arrange(desc(ndelays)) %>%
#   head(3)
  dplyr::top_n(3, ndelays)
## # A tibble: 3 x 2
##   carrier ndelays
##   <chr>     <int>
## 1 B6        23609
## 2 EV        24484
## 3 UA        22222
```

Puzzle

```
year <- 2012L

data %>%
  dplyr::select(year, dest, origin) %>%
  head()
## # A tibble: 6 x 3
##    year dest  origin
##   <int> <chr> <chr>
## 1  2013 IAH   EWR
## 2  2013 IAH   LGA
## 3  2013 MIA   JFK
## 4  2013 BQN   JFK
## 5  2013 ATL   LGA
## 6  2013 ORD   EWR

data %>%
  dplyr::filter(year==year) %>%
  dplyr::summarize(n())
## # A tibble: 1 x 1
##    `n()`
##    <int>
## 1 336776

data %>%
  dplyr::filter(year==2012L) %>%
  dplyr::summarize(n())
## # A tibble: 1 x 1
##   `n()`
##   <int>
## 1     0

data %>%
  dplyr::filter(year==.env$year) %>%
  dplyr::summarize(n())
## # A tibble: 1 x 1
##   `n()`
##   <int>
## 1     0

data %>%
  dplyr::filter(year==.data$year) %>%
  dplyr::summarize(n())
## # A tibble: 1 x 1
##    `n()`
##    <int>
## 1 336776
```

- Can you explain what happens?

Solution

When `dplyr::filter(year==year)` does `year` refer to the column of `data` or to the variable in the global environment?

Flow control

`R` offers the usual flow control constructs:

- branching/alternative `if (...) {...} else {...}`
- iterations (while/for) `while (...) {...} for (it in iterable) {...}`
- function calling `callable(...)` (how do we pass arguments? how do we rely on defaults?)

If () then {} else

There exists a selection function `ifelse(test, yes_expr, no_expr)`.

```
ifelse(test, yes, no)
```

If expressions `yes_expr` and `no_expr` are complicated it makes sense to use the `if (...) {...} else {...}` construct

Note that `ifelse(...)` is vectorized.

```
x <-  1L:6L
y <-  rep("odd", 6)
z <- rep("even", 6)

ifelse(x %% 2L, y, z)
## [1] "odd"  "even" "odd"  "even" "odd"  "even"
```

There is also a conditional statement with an optional `else {}`

```
if (condition) {

} else {

}
```

Is there an `elif` construct in `R`?

Nope!

`R` also offers a `switch`

```
switch (object,
  case1 = {action1},
  case2 = {action2},
  ...
)
```

Iterations `for (it in iterable) {...}`

Have a look at Iteration section in R for Data Science

- Create a lower triangular matrix which represents the 5 first lines of the Pascal triangle.

Recall

$$\binom{n}{k} = \binom{n-1}{k-1} + \binom{n-1}{k}$$

Solution

```
T <- matrix(0L, nrow=6, ncol=6)
T[1,1] <- 1L

for (i in 2:ncol(T))
  T[i, 1:i] <- c(0L, T[i-1, 2:i-1]) + T[i-1, 1:i]

colnames(T) <- 0L:5L
rownames(T) <- 0L:5L

T
##   0 1  2  3 4 5
## 0 1 0  0  0 0 0
## 1 1 1  0  0 0 0
## 2 1 2  1  0 0 0
## 3 1 3  3  1 0 0
## 4 1 4  6  4 1 0
## 5 1 5 10 10 5 1
```

- Locate the smallest element in a numerical vector

Solution

```
v <- sample(1:100, 100)
v[1:10]
##  [1] 52 28  7 55 53 33 12 21 16 54

pmin <- 1

for (i in seq_along(v)) {
  if (v[i]<v[pmin]) {
    pmin <- i
  }
}

print(stringr::str_c('minimum is at ', pmin, ', it is equal to ', v[pmin]))
## [1] "minimum is at 64, it is equal to 1"
```

There are some redundant braces `{}`

While (condition) {...}

- Find the location of the minimum in a vector v

Solution

```
v <- sample(100, 100)

pmin <- 1   # Minimum in v[1:1]
i <- 2

while (i <= length(v)) {
  # loop invariant: v[pmin] == min(v[1:i])
  if (v[i]<v[pmin]) {
    pmin <- i
  }
  i <- i + 1
}

print(stringr::str_c('minimum is at ', pmin, ', it is equal to ', v[pmin]))
## [1] "minimum is at 10, it is equal to 1"

which.min(v); v[which.min(v)]
## [1] 10
## [1] 1
```

- Write a loop that checks whether vector `v` is non-decreasing.

Solution

```
result <- TRUE

for (i in 2:length(v))
  if (v[i] < v[i-1]) {
    result <- FALSE
    break
  }

if (result) {
  print("non-decreasing")
} else {
  print("not non-decreasing")
}
## [1] "not non-decreasing"
```

- Write a loop that perform binary search in a non-decreasing vector.

Solution

```
u <-  100 * sort(rnorm(10))

v <- pi
# should return position i such that u[i] <=  v < u[i+1]
# with conventions
#   u[0] == - Inf
#   u[length(u)+1] = Inf

n <- length(u)
low <- 1 ; high <- n

if (v < u[low]) {
  position <- 0
} else if (u[high]<= v) {
  position <- high
} else while (low < high) {
# loop invariant: the u[low] <= v < u[high]
    middle <-  floor((low + high)/2)
    if (v < u[middle]) {

    }

}
```

Functions

To define a function, whether named or not, you can use the `function` constructor.

```
foo <- function() {
  # body
  1
}
```

- Write a function that checks whether vector `v` is non-decreasing.

Solution

```
is_non_decreasing <- function(v) {
  for (i in 2:length(v))
    if (v[i] < v[i-1]) {
      return(FALSE)
    }
  return(TRUE)
}

is_non_decreasing(v)
## [1] FALSE
is_non_decreasing(1:10)
## [1] TRUE
```

A function is an object like any other

```
is_non_decreasing
## function(v) {
##   for (i in 2:length(v))
##     if (v[i] < v[i-1]) {
##       return(FALSE)
##     }
##   return(TRUE)
## }
## <bytecode: 0x5589b76f67e8>
```

```
body(is_non_decreasing)
## {
##     for (i in 2:length(v)) if (v[i] < v[i - 1]) {
##         return(FALSE)
##     }
##     return(TRUE)
## }

args(is_non_decreasing)
## function (v)
## NULL
```

- Write a function with integer parameter n, that returns the Pascal Triangle with $n+1$ rows.

Solution

```
triangle_pascal <- function(n) {
  m <- n+1
  T <- matrix(c(rep(1, m), rep(0, m*(m-1))), nrow=m, ncol=m)

  for (i in 2:m)
    T[i, 2:i] <- T[i-1, 1:i-1] + T[i-1, 2:i]

  for (i in 1:(m-1))
    T[i, (i+1):m] <- NA

  colnames(T) <- 0:n
  rownames(T) <- 0:n

  T
}

print(triangle_pascal(10), na.print=" " )
```

```
   0  1  2   3   4   5   6   7  8  9 10
0  1
1  1  1
```

```
2  1  2  1
3  1  3  3   1
4  1  4  6   4   1
5  1  5 10  10   5   1
6  1  6 15  20  15   6   1
7  1  7 21  35  35  21   7   1
8  1  8 28  56  70  56  28   8  1
9  1  9 36  84 126 126  84  36  9  1
10 1 10 45 120 210 252 210 120 45 10  1
```

Sanity check: `R` provides us with function `choose`

```
n <- 5
map(0:n, ~ choose(., 0:.))
## [[1]]
## [1] 1
##
## [[2]]
## [1] 1 1
##
## [[3]]
## [1] 1 2 1
##
## [[4]]
## [1] 1 3 3 1
##
## [[5]]
## [1] 1 4 6 4 1
##
## [[6]]
## [1]  1  5 10 10  5  1
t10 <- triangle_pascal(10)

for (n in 0:10)
  for (p in 0:n)
    stopifnot(t10[as.character(n), as.character(p)] == choose(n, p))
```

- How would you generate a Fibonacci sequence of length n ?

Recall the Fibonacci sequence is defined by

$$F_{n+2} = F_{n+1} + F_n \qquad F_1 = F_2 = 1$$

Solution

```r
fibo <- function(n) {
  res <- integer(n)
  res[1:2] <- 1
  for (k in 3:n) {
    res[k] <- res[k-1] + res[k-2]
  }
  return(res)
}

fibo(5)
```

```
[1] 1 1 2 3 5
```

! Read Chapter on functions in Advanced R

Functional programming

In `R`, functions are first class entities, they can be defined at run-time, they can be used as function arguments. You can define list of functions, and iterate over them.

Try to use https://purrr.tidyverse.org.

Package `purrr::map_`

- Write truth tables for `&`, `|`, `&&`, `||`, `!` and `xor`

Solution

```r
vals <- c(TRUE, FALSE, NA)
ops <- c(`&`, `|`, `xor`)

truth <- purrr::map(ops, ~ outer(vals,vals, .))

names(truth) <- (ops)
truth
## $`.Primitive("&")`
##       [,1]  [,2]  [,3]
## [1,]  TRUE FALSE    NA
## [2,] FALSE FALSE FALSE
## [3,]    NA FALSE    NA
##
## $`.Primitive("|")`
##      [,1]  [,2] [,3]
## [1,] TRUE  TRUE TRUE
## [2,] TRUE FALSE   NA
## [3,] TRUE    NA   NA
##
## $`function (x, y) \n{\n    (x | y) & !(x & y)\n}`
##       [,1]  [,2] [,3]
## [1,] FALSE  TRUE   NA
## [2,]  TRUE FALSE   NA
## [3,]    NA    NA   NA
```

- Write a function that takes as input a square matrix and returns `TRUE` if it is lower triangular.

Solution

```r
lt <- function(A){
  n <- nrow(A)
  all(purrr::map_lgl(1:(n-1), ~ all(0== A[., (.+1):n])))
}
```

- Use `map` , `choose` and proper use of pronouns to deliver the `n` first lines of the Pascal triangle using one line of code.
- As far as the total number of operations is concerned, would you recommend this way of computing the Pascal triangle?

Solution

```r
n <- 5

tp5 <- matrix(unlist(map(0:n,
            ~ c(choose(., 0:.), rep(0L, n-.)))),
       nrow=n+1,
       byrow=T)

rownames(tp5) <- 0:n

colnames(tp5) <- 0:n

tp5
##   0 1  2  3 4 5
## 0 1 0  0  0 0 0
## 1 1 1  0  0 0 0
## 2 1 2  1  0 0 0
## 3 1 3  3  1 0 0
## 4 1 4  6  4 1 0
## 5 1 5 10 10 5 1
```

No. Using `map` and `choose`, we do not reuse previous computations. The total number of arithmetic operations is $\Omega(n^3)$, it should be $O(n^2)$.

! Read Chapter on Functional Programming in Advanced R

Further exploration

This notebook walked you through some aspects of `R` and its packages. We just saw the tip of the iceberg.

We barely mentioned:

- (Non-standard) Lazy evaluation
- Different flavors of object oriented programming
- Connection with `C++`: `RCpp`
- Connection with databases: `dbplyr`
- Building modeling pipelines: `tidymodels`
- Concurrency
- Building packages
- Building interactive Apps: `Shiny`
- Attributes (metadata)
- Formulae `formula`
- Strings `stringi`, `stringr`
- Dates `lubridate`
- and plenty other things ….
-

References

- https://www.statmethods.net/index.html
- https://www.datacamp.com/courses/free-introduction-to-r

- dplyr videos
- ggplot2 video tutorial
- cheatsheets