

R intro: super-crash course

Learn (base) R in hours

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Agenda

- Data types
- Variables & Assignment
- Data structures
- Naming
- Slicing
- Working directory, reading files, saving objects
- Functions & libraries
- Apply family
- Useful functions
- Good R coding practices

Here: base R

- base R = core R functions and utilities
- Doesn't require any library
- Pretty low-level
- Can (and will) get difficult to read
- Later we will see R on steroid: ***The Tidyverse***

Pre-requisites

- R installation
=> <https://ftp.belnet.be/mirror/CRAN/> (🇧🇪 mirror)
- RStudio
=> <https://www.rstudio.com/products/rstudio/download/>

Data types

Basic Data types

- **numeric** (including **double**)

24.3, 5, -12

- **integer** (L is old notation)

1L, 20L, 32L

- **character** (n=1), and **string** (n>1)

'John', "John", “FALSE”

- **logical**, aka **boolean** (always capital letters)

TRUE, FALSE, T, F

- **factors**: ordered strings (more on that later)

Unsure?

=> Use the functions **type()** and **class()**

RStudio Syntax highlight (Cobalt theme)

```
1  'John' "John"
2  24.3
3  5
4  5L
5  T TRUE F FALSE
6  variable
7  + - / *
8  # this is a comment
9  this_is_a_function()
```

Variables & assignment

Variables & Assignment

No need to declare a variable first:
it gets created when you assign a value.

- Python uses the equal sign: =

ex:

a=3

- R uses an arrow: “<-“

This better reflects the information flow and its direction

ex:

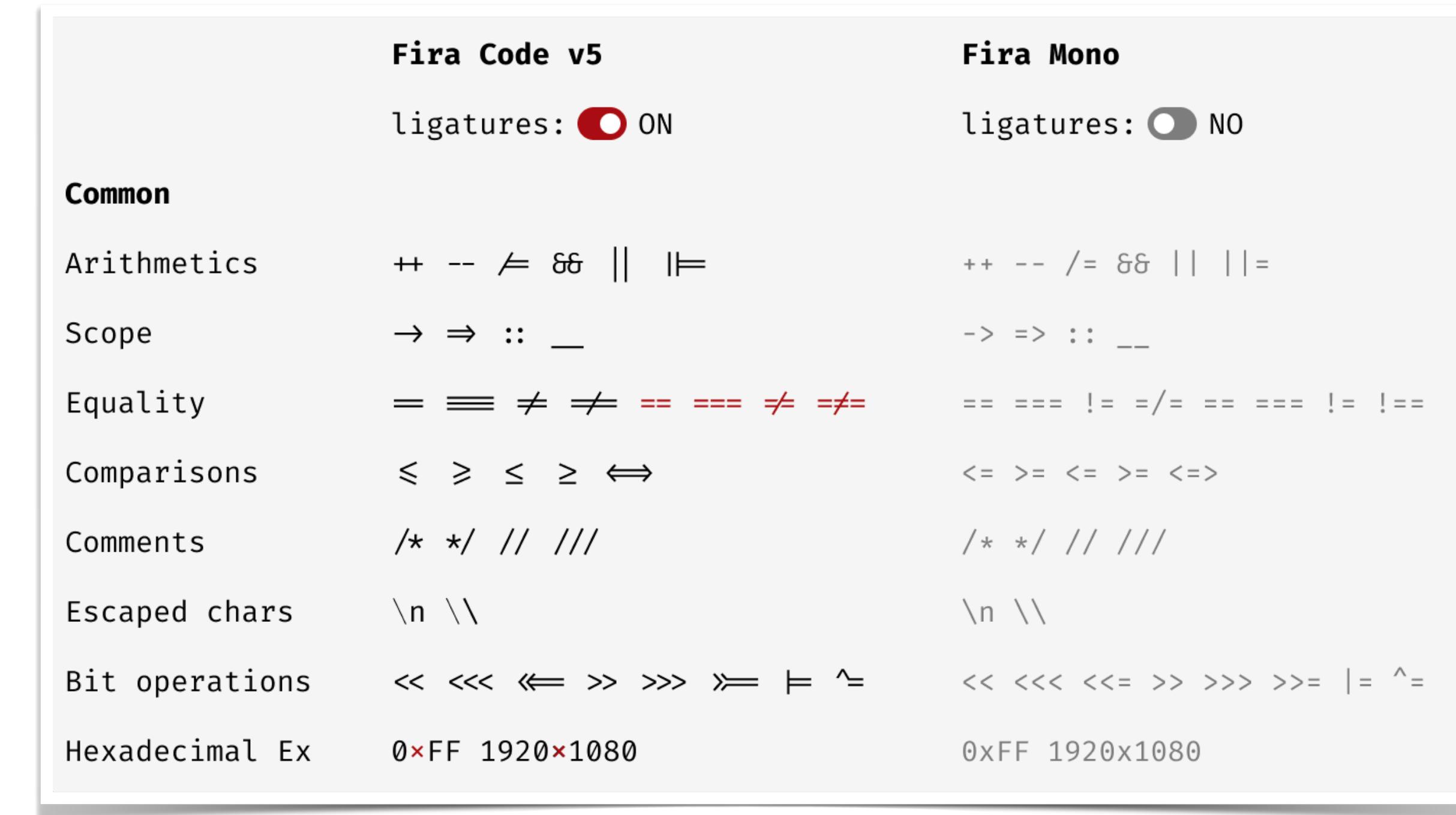
a <- 3

- **Note:** a=3 will also work in R, but is bad practice!

We keep = and == signs to assign names (more on that later) or test equality

PRO-tip: change font & get a theme!

- Let's install **FiraCode**: github.com/tomsky/FiraCode



- Get a nice theme: **RStudio > Preferences > Appearance > Editor theme**
My favourite is 'Cobalt

Variables & Assignment

No need to declare a variable first:
it gets created when you assign a value.

- Python uses the equal sign: `=`

ex:

`a=3`

Previous slide with
FiraCode On! 💪

- R uses an arrow: “`←`”

This better reflects the information flow and its direction

ex:

`a ← 3`

- Note: `a=3` will also work in R, but is bad practice!

We keep `=` and `==` signs to assign names (more on that later) or test equality

Variables

As usual....

- Use meaningful and non-cryptic variable names
- Choose a variable style (and stick to it!)

ex:

- camelcase: MyDataFrame
- underscores: my_data_frame
- dots: my.data.frame

Probably the best for biology

- Don't use special characters, no spaces, don't start with a number, no - (will be interpreted as the mathematical operator 'minus')

Data structures

(atomic) Vector

- One-dimension
- Homogeneous: One data type
- Most often created by concatenation: `c()`
`c(1, 5, 12)`
`c("ORF42", 'ORF43', "noORF")`
- Always flat:
`c(1, 2, c(32, -4))`
is the same as
`c(1, 2, 32, -4)`

Coercion

- To ***coerce*** = fancy word for “trying to change the type”
- All elements of an atomic vector must be the same. So if you combine different types, they will be *coerced* to the **most flexible type**.
- Types from least to most flexible: logical, integer, (numeric), double, character

```
> class( c(1, 2) )
[1] "numeric"
> class( c(1L, 2L) )
[1] "integer"
> class( c(1L, 2L, 3) )
[1] "numeric"
> class( c(1, '2') )
[1] "character"
```

Coercion

- Some functions will try to coerce the data if they are fed with inadequate types.
- This can be very useful when working with logicals:

```
x <- c(F, F, T)  
as.numeric(x)  
#> [1] 0 0 1
```

FALSE will be 0
TRUE will be 1

```
sum(x)  
#> [1] 1
```

```
mean(x)  
#> [1] 0.3333333
```

Calculate proportions
super fast!

Quickly create a vector of integers

- Sadly, this doesn't work for letters...

D:F

won't give you [1] "D" "E" "F"

- But! Try:

letters

LETTERS

```
> 1:5  
[1] 1 2 3 4 5  
> 5:1  
[1] 5 4 3 2 1  
> -4:-1  
[1] -4 -3 -2 -1  
> -1:-4  
[1] -1 -2 -3 -4  
> -2:2  
[1] -2 -1 0 1 2  
> 1.5:2.7  
[1] 1.5 2.5  
> 1.3:2.7  
[1] 1.3 2.3
```

List

- Different from atomic vectors: can **mix data types**
- Create a list using `list()`

```
x <- list(1:3, "a", c(TRUE, FALSE, TRUE), c(2.3, 5.9))
str(x)
#> List of 4
#> $ : int [1:3] 1 2 3
#> $ : chr "a"
#> $ : logi [1:3] TRUE FALSE TRUE
#> $ : num [1:2] 2.3 5.9
```

List

- Lists are sometimes called “***recursive vectors***” because they can contain other lists.
- **c()** will combine several lists into one
- Ways to ingress and egress from lists:

as.list(x)

unlist(mylist)

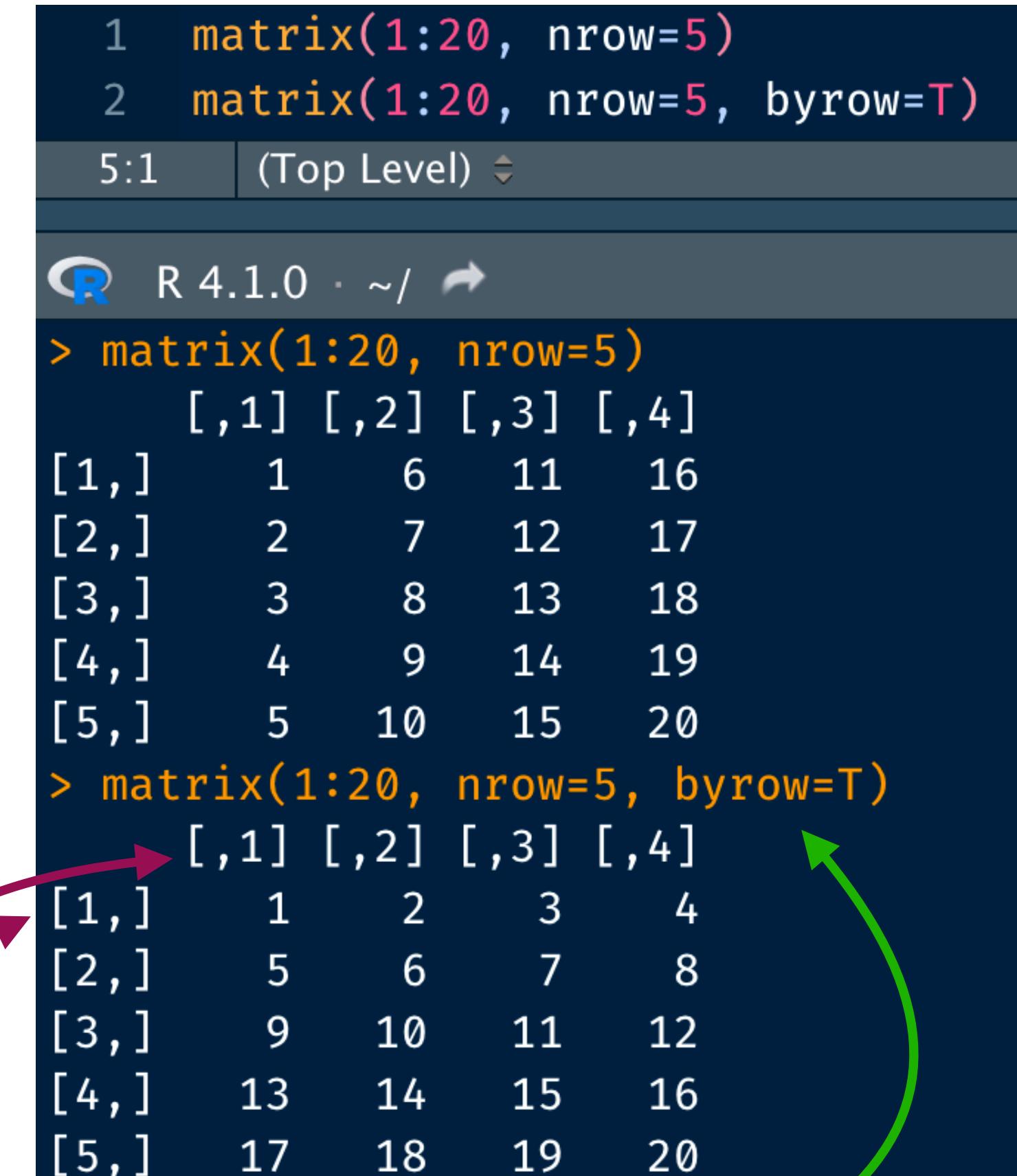
```
x <- list(list(list(list())))
str(x)
#> List of 1
#> $ :List of 1
#>   ..$ :List of 1
#>     ...$ : list()
is.recursive(x)
#> [1] TRUE
```

Matrix

- 2-D object with homogeneous data type
- Create a matrix with `matrix()`
- Coerce to a matrix with `as.matrix()`
- Can be created from **vectors** when specifying the structure of the matrix
- Note: create a *diagonal* matrix with `diag()`

```
1 d ← diag(nrow=3, ncol=3)
2 names(d) ← letters[1:9]
3 colnames(d) ← letters[1:3]
4 rownames(d) ← LETTERS[1:3]
```

Try me !



The screenshot shows the R console interface. At the top, there are two code snippets:

```
1 matrix(1:20, nrow=5)
2 matrix(1:20, nrow=5, byrow=T)
```

Below this, the status bar indicates "5:1 (Top Level)". The main area of the console displays two matrices:

For the first snippet (without `byrow`):

	[,1]	[,2]	[,3]	[,4]
[1,]	1	6	11	16
[2,]	2	7	12	17
[3,]	3	8	13	18
[4,]	4	9	14	19
[5,]	5	10	15	20

For the second snippet (with `byrow=T`):

	[,1]	[,2]	[,3]	[,4]
[1,]	1	2	3	4
[2,]	5	6	7	8
[3,]	9	10	11	12
[4,]	13	14	15	16
[5,]	17	18	19	20

A red arrow points from the text "Notice that indexes in R start at 1 !!" to the index values in the first column of the first matrix. A green arrow points from the text "Notice the 'byrow'" to the index values in the first column of the second matrix.

Notice that indexes in R start at 1 !!

Notice the 'byrow'

Data frame

- 2D object with heterogeneous data types

The diagram illustrates the structure of a data frame. At the top, the word "Columns" is centered above five arrows pointing down to the column headers of a table: "Name", "Team", "Number", "Position", and "Age". To the left of the table, the word "Rows" is written vertically above three orange arrows pointing right to the row indices 1, 2, and 3. A pink rectangular box labeled "Data" encloses the entire table area.

	Name	Team	Number	Position	Age
1	Avery Bradley	Boston Celtics	0.0	PG	25.0
2	John Holland	Boston Celtics	30.0	SG	27.0
3	Jonas Jerebko	Boston Celtics	8.0	PF	29.0
4	Jordan Mickey	Boston Celtics	NaN	PF	21.0
5	Terry Rozier	Boston Celtics	12.0	PG	22.0
6	Jared Sullinger	Boston Celtics	7.0	C	NaN
7	Evan Turner	Boston Celtics	11.0	SG	27.0

Data frame creation & basic methods

- By reading in Excel, text, csv, tsv, files (more on that later)
- Manually with `data.frame()`
- By coercing an object with `as.data.frame()`

```
1 mydf <- data.frame('letters'=c('a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j'),  
2   |   |   |   |   'numbers'=1:10)  
3 rownames(mydf) <- c('A', 'B', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'J')  
4 dim(mydf)  
5 colnames(mydf)  
6 rownames(mydf)  
7 ncol(mydf)  
8 nrow(mydf)
```

Try me !

- Interesting methods with data frames:
 - `dim()`
 - `ncol()`
 - `nrow()`
 - `colnames()`
 - `rownames()`
 - `summary()`

Naming

Naming

- Names can be attributed to the elements of **lists** and **vectors**
- Names can be set with **names()** or **set_names()** or the **=** sign

```
1 wt_counts ← c(5, 12, 3, 0, 14, 13)
2 mut_counts ← c(5, 14, 3, 20, 7, 10)
3 gene_names ← c('P53', 'HSF2', 'CDF4', 'UGA4', 'DAL5', 'FLS2')
4 samples_names ← c('wt', 'mut')
5
6 names(wt_counts) ← names(mut_counts) ← gene_names
7 wt_counts ; mut_counts
8
9 list(wt_counts, mut_counts)
10 setNames(list(wt_counts, mut_counts), samples_names)
11 list('wt'=wt_counts, 'mut'=mut_counts)
```

Reproduce the following commands and explain what happens.

Slicing

Slicing

- *Slicing* is the fancy R word for “subsetting”
- Can be done on vectors, data.frames, and lists
- Use `[]` and `[[]]` if based on position
- Use `$` if based on names

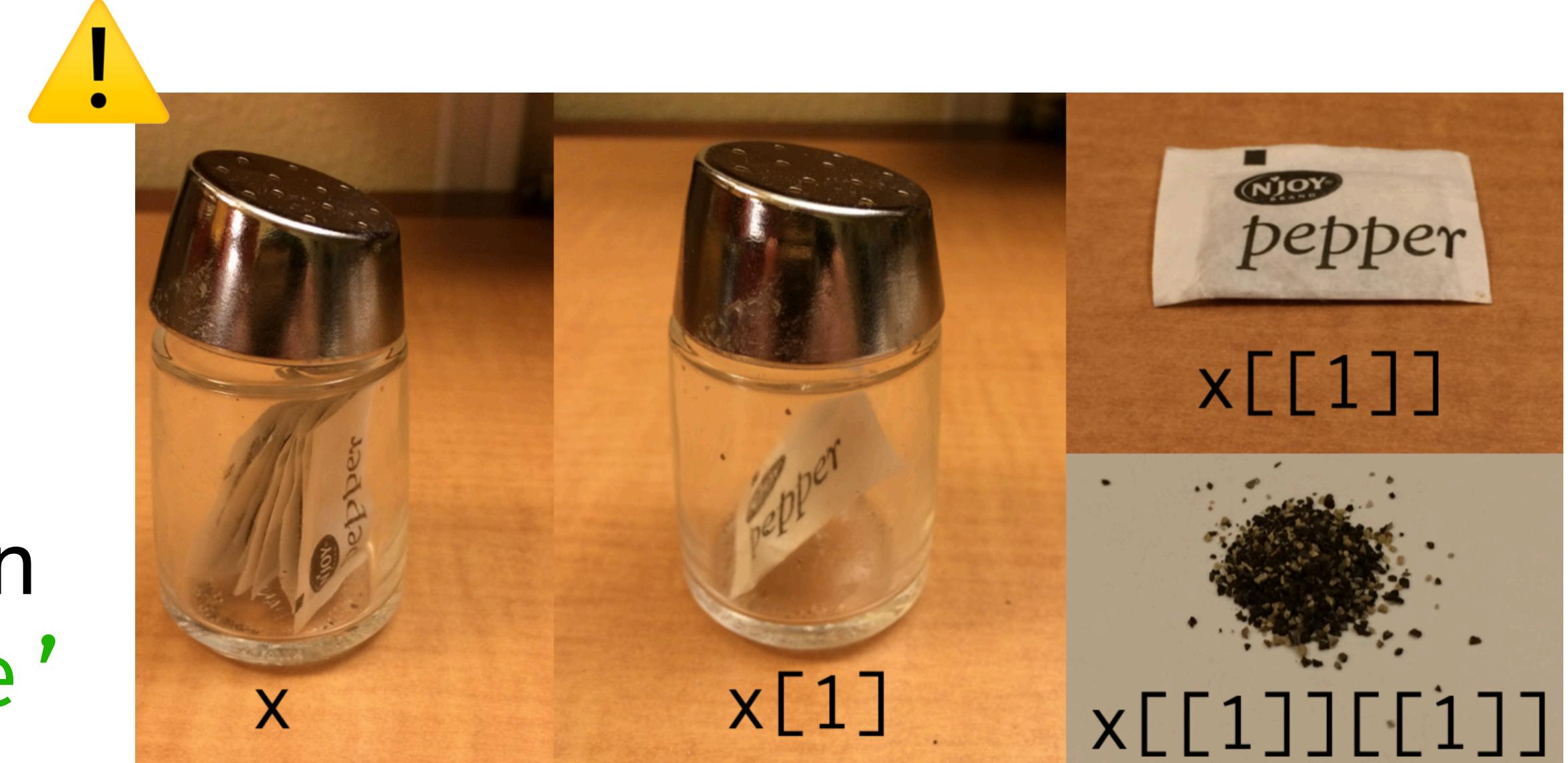
Slicing vectors

```
1 vec ← c(1:10)                                vec ← 1:10 would actually do the trick
2 vec[-1]
3 vec[-1:-3]
4 vec[5]
5
6 named_vec ← c('first'=1, 'second'=2, 'third'=3)
7 named_vec['second']
```

Reproduce the following commands and explain what happens.

Slicing lists

- Using [] and [[]]
- Note that if your list is named you can access items using: myList\$'name'

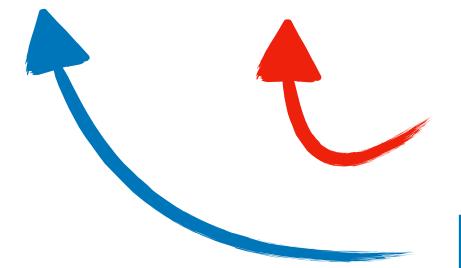


```
1 test <- list(c('a', 'b', 'c'),
2                   1:3,
3                   paste0(1:3, c('a', 'b', 'c')))
4
5 test[3]
6 test[[1]]
7
8 names(test) <- c('letters', 'numbers', 'both')
9 test$numbers
10 test['numbers']
```

Reproduce the following commands and explain what happens.
Can you understand the differences?

Slicing dataframes

- Using `[]`, `[[]]`, and `$`

- `my_data_frame[..., ...]`


For columns
For rows

*Rainbow parenthesis.
Enable them in
RStudio preferences!*

```
1 iris[1, ]  
2 iris[, 1]  
3 iris[[1, 5]]  
4 iris[1:5, 1:5]  
5 iris[1:5, 1:7]  
6 iris$Sepal.Width
```

Let's try by doing.

Slicing using logicals!

```
1 iris[iris$Sepal.Length > 7, ]  
2 subset(iris, Sepal.Length > 7)  
3  
4 iris$Sepal.Length[iris$Sepal.Length <= 7.0] <- 0
```

Reproduce the following commands and explain what happens.

Can you understand the differences?

Recycling

```
1 rec <- 1:20  
2 logicals <- c(T, F)  
3 rec[logicals]
```

What happened here?

Tips: try
length(rec)
length(logicals)

Working directory, files, and saving objects

Working directory

- `getwd()`
tells you the path from which your script is executed
- `setwd("path/to/directory")`
changes the working directory

Listing files

- `list.files()`

Reading files

- `read.table()`
- `read.csv()`
- `readxl :: read_xlsx()`

Writing files

- `write.table()`
- `WriteXLS :: WriteXLS()`

Saving objects

- Sometimes interesting to save R-object(s). For example:
 - i) Output of an intense parsing or analysis, that will be used for many other R analyses.
This is a way to compartmentalise R analyses into smaller, more manageable scripts.
 - ii) Output of a large R analysis that might be needed in many (yet unforeseen) formats
(Export for Excel, export for mySQL, export for the web, etc...)
- **RDS**: one object, can be renamed when imported at a later stage

```
saveRDS(cleaned_data_df, 'cleaned_data_for_R.rds')
uORFs ← readRDS('cleaned_data_for_R.rds')
```
- **RDA** (R data): can be a collection of objects, cannot be renamed when imported

```
saveRDS(list(uORF_list, DEGs_mut_vs_ctrl), 'data_21102021.Rdata')
load('data_21102021.Rdata')
# uORF_list and DEGs_mut_vs_ctrl will now be in your R environment
```

Functions & Libraries

Base R functions

- Typical syntax:

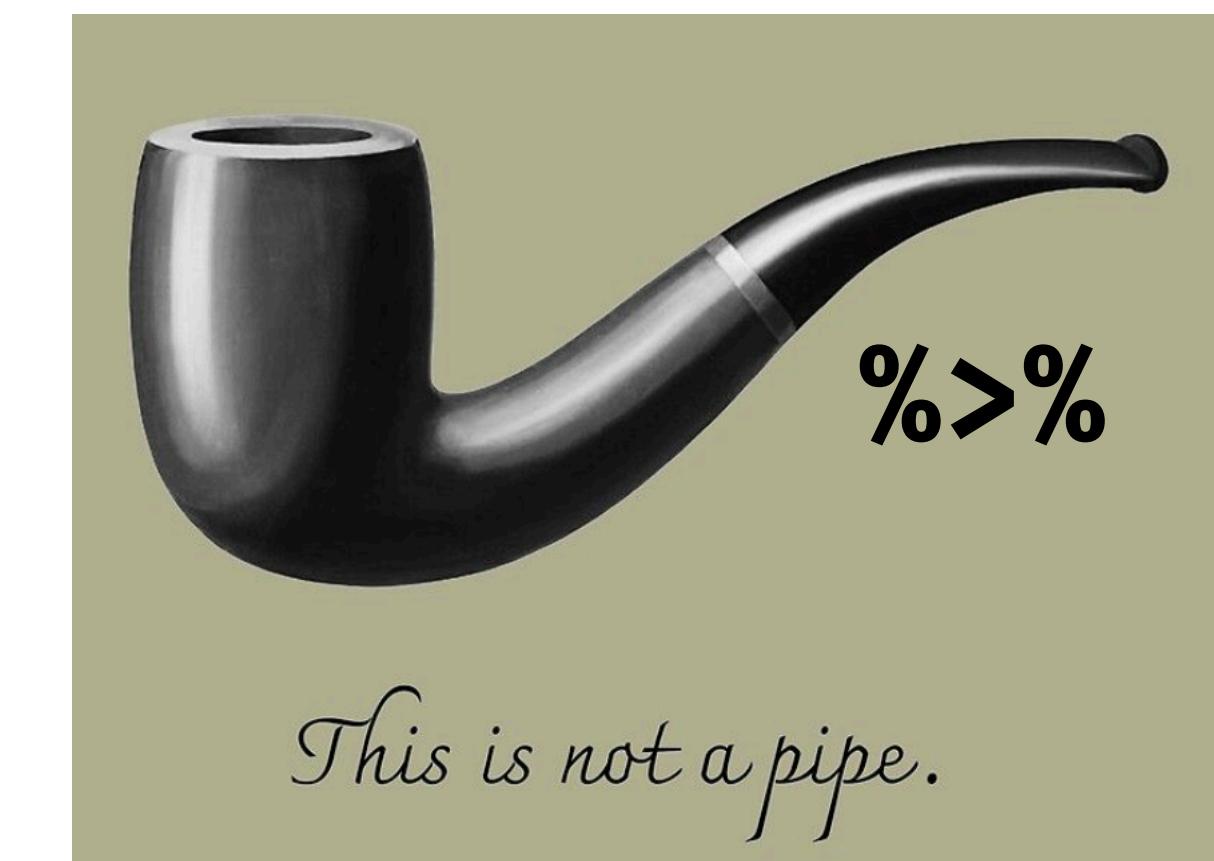
```
function(argument=value, ...)
```

- They can be nested, but reading rapidly becomes difficult

```
length(unique(round(iris$Sepal.Length)))
```

- Later on we will see how to use **pipes** with the **magrittr** package.
This improves readability a lot:

```
iris %>%  
  select(Sepal.Length) %>%  
  round() %>%  
  unique() %>%  
  length()
```



GET-ter and SET-ters

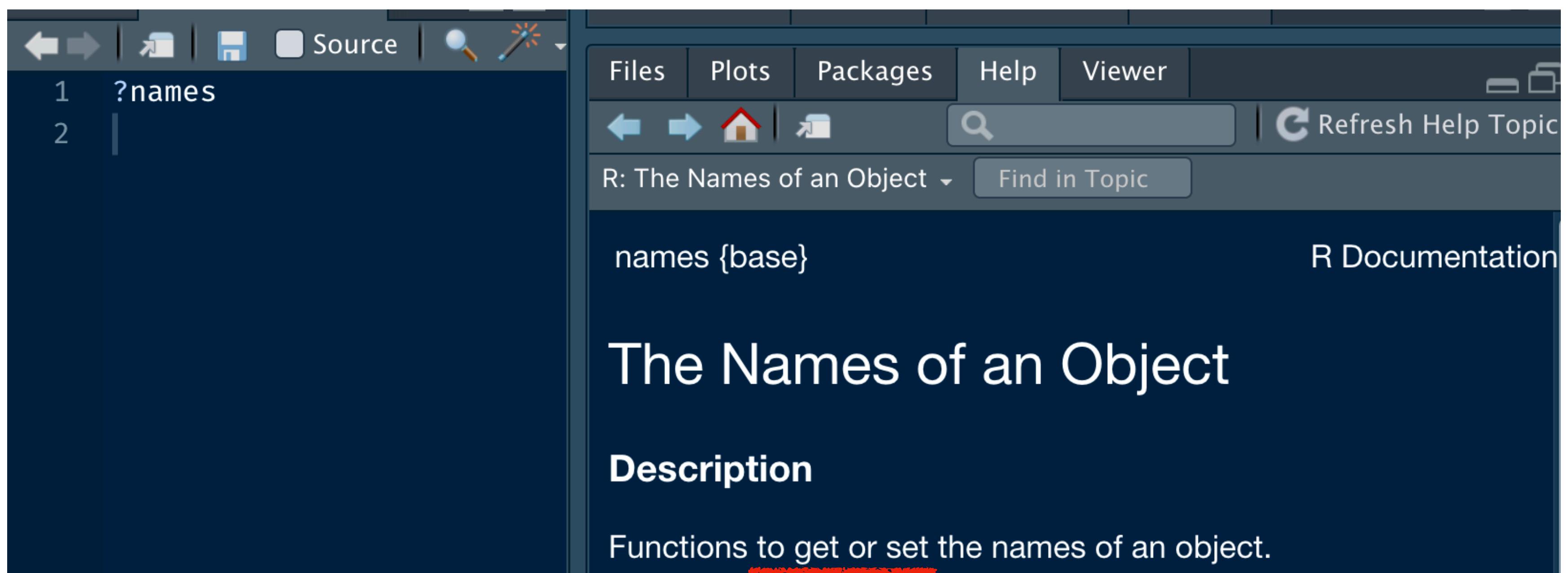
- Some functions can be used both to **GET** info or to **SET** data
- Examples: `names()`, `colnames()`, `rownames()`

```
1 # create vector
2 read_counts ← c(1, 50, 2, 0, 34, 24, 32)
3 # assign names to elements of vector
4 names(read_counts) ← letters[1:length(read_counts)]
5 # get names of vector elements
6 names(read_counts)
```

Try it !

Get help

- type the name of the function preceded by “?”
- **No parenthesis!**
- Ex: ?names



This help page is called the “Vignette”.
Basically the manual for the ‘names’ function.

Custom functions

- Create you own function:

```
my_custom_fun <- function(x, y) {  
  result <- x + y  
  return(result)  
}
```

- Use you own function:

```
my_custom_fun(x=input1, y=input2)
```

- You can set some default values for your input variables
- Sadly, no “docstring” as can be done in Python...

Libraries

- Libraries are a collection of high-level functions
- Installation of a library (only once!) depends on which repository it is hosted:

- **CRAN**:

```
install.packages('library_name')
```

- **Bioconductor**:

```
install.packages('BiocManager')
```

```
BiocManager::install('GenomicRanges')
```

- **GitHub**:

```
install.packages('devtools')
```

```
devtools::install_github('athieffry/TxDb.Athaliana.BioMart.plantsmart51')
```

- Loading a library is accomplished by:

```
library(library_name)
```

See how Bioconductor is a package manager that needs to be installed from CRAN first?

Conflicts & masked functions

```
> library(tidyverse)
— Attaching packages —
✓ ggplot2 3.3.5     ✓ purrr   0.3.4
✓ tibble   3.1.4     ✓ dplyr    1.0.7
✓ tidyr    1.1.3     ✓ stringr 1.4.0
✓ readr    2.0.1     ✓ forcats 0.5.1
— Conflicts —
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()   masks stats::lag()
> library(reshape2)

Attaching package: 'reshape2'

The following object is masked from 'package:tidyverse':

  smiths
```

- If you want to use `smiths()` from the `tidyverse` library rather than from `reshape2`:
`tidyverse::smiths()`

Apply family

**If you use a loop (for or while) in R,
you are doing it wrong in 99% of cases.**

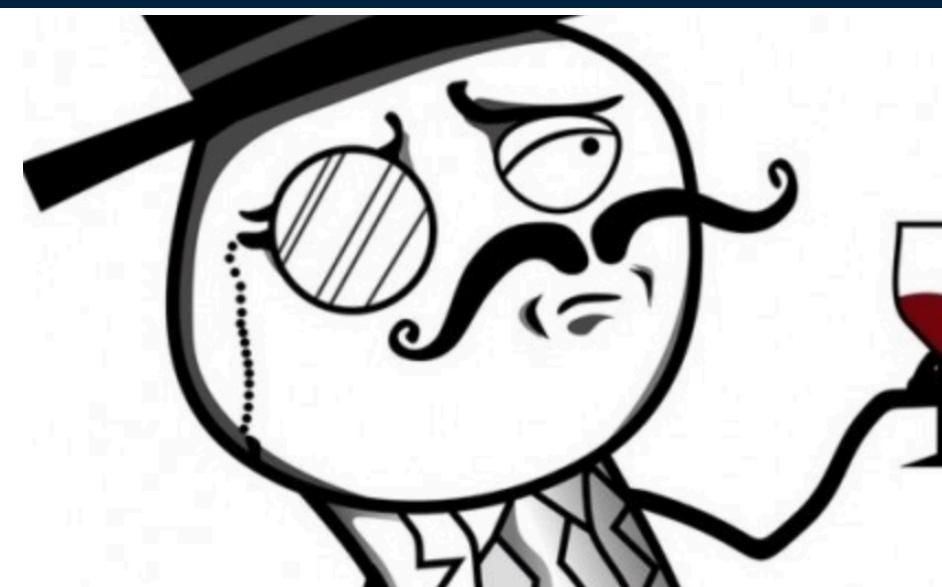
This is because most of R's functions are vectorised:
the function will operate on all elements of a vector without needing to loop
through and act on each element one at a time.

Vectorisation example:

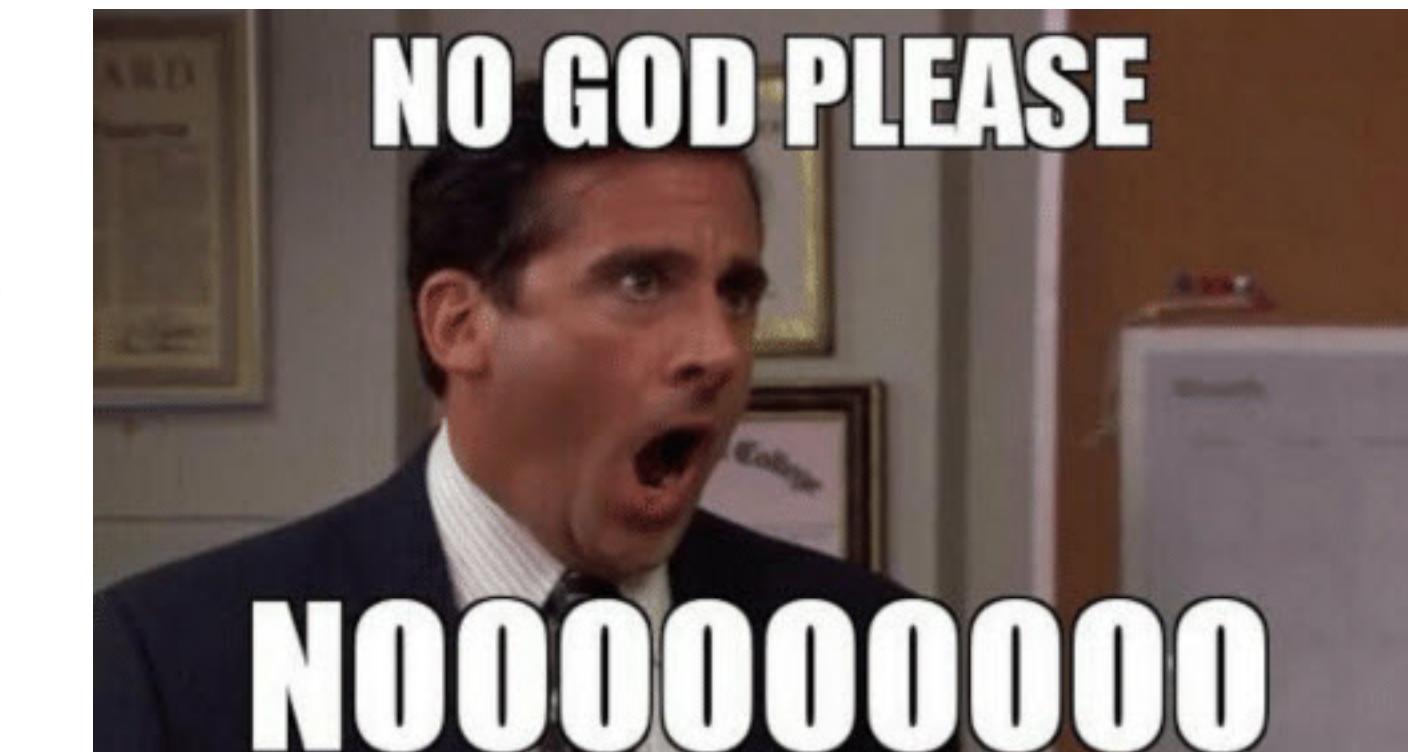
```
> nums ← 1:5  
> nums  
[1] 1 2 3 4 5
```

Multiply each element by 2:

```
nums ← nums * 2
```



```
for (i in 1:length(nums)) {  
  nums[i] ← nums[i] * 2  
}
```



Apply family

- Collection of functions to execute repetitive tasks on data structures
- Intuitively: a R-way of doing for loops
- Many of them, depending on the data structure and what you want out:
`apply()`
`lapply()`
`sapply()`
`mapply()`
and some other exotic ones...

Apply family

`apply(X, MARGIN, FUN, ...)`

- X: a **dataframe**, **matrix**, or **array**
- MARGIN: how the function is applied: 1 = on rows, 2 = on columns
- FUN: the function you want to apply over MARGIN

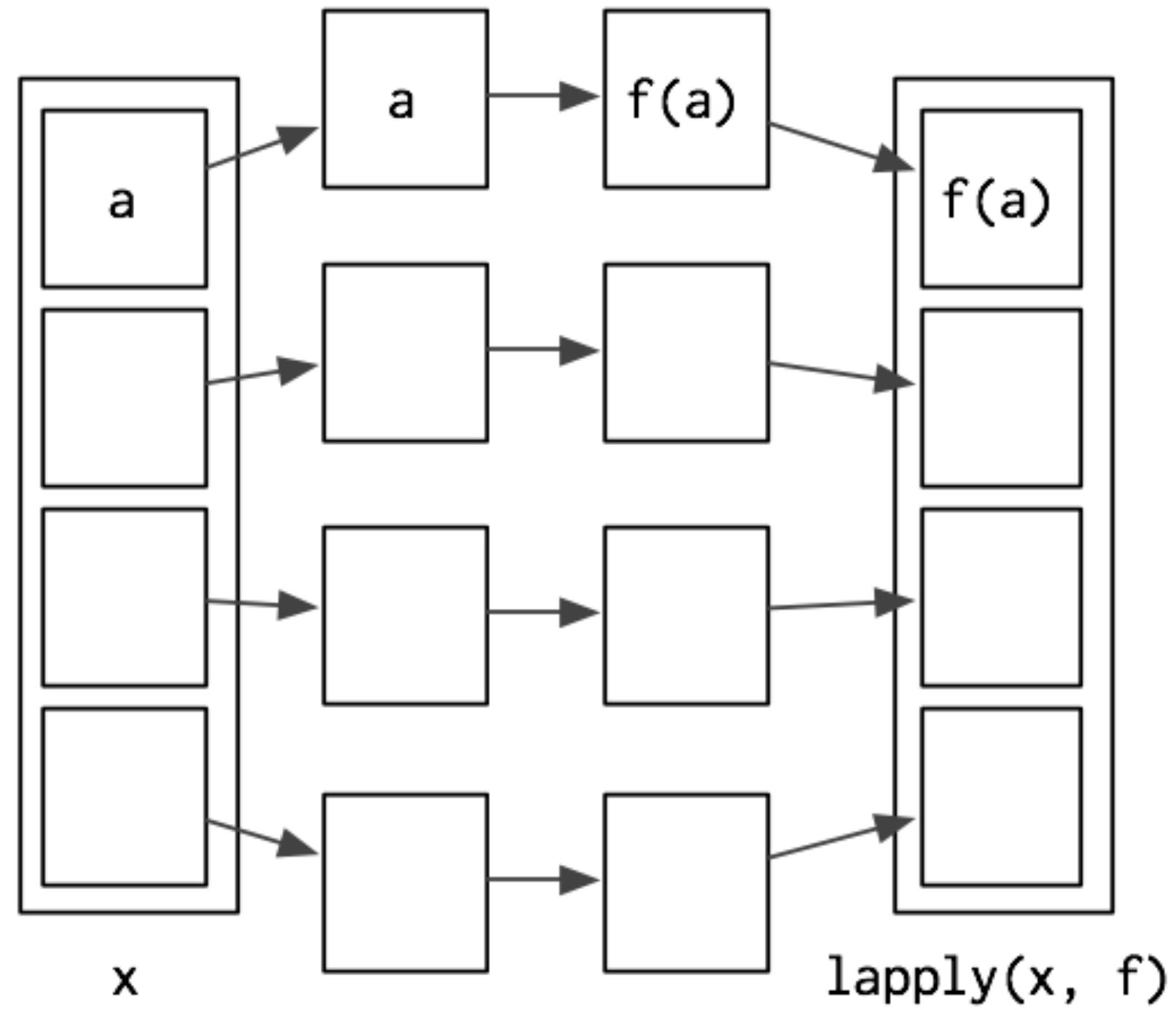
X	apply(X ,2, sum)
	Dimension — 2 →
1	-1.7189391 -1.0863995 -2.2542126 -1.3201873 1.9874737 0.6265486 0.2140376 0.8850445 0.9637687 1.3191502
	1.0996117 -2.0533779 -0.3684977 1.4782993 0.8000988
	-0.55559727 -0.1792310 -0.8088577 1.29055209 0.3264156 0.5412132 1.40028967 -0.7574303 -2.3241569 -1.28177703 -0.5015628 1.1537703 0.09345943 1.4535431 1.0935720
Result	sum
	-0.8078717 0.4241565 0.9561342 0.9469269 0.3417346 -0.3444591

Note: this summing of columns/rows are so often needed that base R functions readily exist:
`rowSums(X)`
`colSums(X)`
`rowMeans(X)`
`colMeans(X)`

Apply family

`lapply(x, FUN, ...)`

- X: a **vector** (atomic or list)
- FUN: function to be applied to each element of X



What if I simply want a vector for result?

Apply family

`sapply(X, FUN, ..., simplify=T, USE.NAMES=T)`

- Same as `lapply()` but with a simplified response: a **vector** is returned instead of a list
- Just meant to save time by not having to coerce the list into an atomic vector
- Note that if X was named, the resulting atomic vector will keep the names

```
1 iris
2 iris_dfl <- split(iris, iris$Species)
3 lapply(iris_dfl, nrow)
4 sapply(iris_dfl, nrow)
5 names(iris_dfl) <- NULL
6 sapply(iris_dfl, nrow)
```

Reproduce the following commands
and explain what happens

Apply family

`mapply(X, Y, FUN, ..., simplify=T, USE.NAMES=T)`

- Multivariate apply
- Vectorize arguments to a function that would otherwise not accept vectors as argument
- Intuitively:
 - a) two vectors are passed to a function
 - b) the function is executed while going through the vectors in a “parallel”, incremented, and ordered way
- Easier with an example:

Reproduce the following commands and explain what happens

```
1 iris_dfl <- split(iris, iris$Species)
2 filenames <- paste0(names(iris_dfl), '.csv')
3
4 mapply(function(df, fn) write.table(df, fn, sep=',', row.names=F), iris_dfl, filenames)
```

Read more:

- More details on the apply family at [Datacamp.com](#)

Tutorial on the R Apply Family

In this tutorial, you'll learn about the use of the apply functions in R, its variants, and a few of its relatives applied to different data structures.



The Apply Functions As Alternatives To Loops

This post will show you how you can use the R `apply()` function, its variants such as `mapply()` and a few of `apply()`'s relatives, applied to different data structures. Of course, not all the variants can be discussed, but when possible, you will be introduced to the use of these functions in cooperation, via a couple of slightly more beefy examples.

Also, you might find it useful to look at this [introduction to R tutorial](#) to better understand lists, vectors, arrays, and dataframes, though you don't necessarily need to have completed the tutorial to follow this post!

Useful functions

A couple of useful functions

- head()
- tail()
- summary()
- length()
- class()
- typeof()
- rowSums()
- colSums()
- rowMeans()
- colMeans()
- all()
- names()
- colnames()
- rownames()
- basename()
- c()
- data.frame()
- list()
- matrix()
- paste()
- paste0()
- rep()
- sample()
- cut()
- rm()
- dim()
- nrow()
- ncols()
- floor()
- ceiling()
- toupper()
- round()
- table()
- list.files()
- read.table()
- write.table()
- unique()
- duplicated()
- etc...

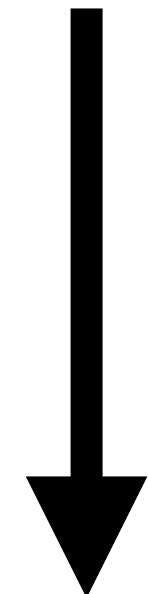
Don't know how to do something?

In 95% of cases there is already a function for what you are trying to accomplish, Google it!

Good R coding practices

1. STRUCTURE YOUR SCRIPT

A widely adopted top-to-bottom structure is:



1. #Script title, brief description, coder, date
2. Load libraries
3. Set working directory (if needed)
4. Code

2. STRUCTURE YOUR CODE

- # Use comments!
- Enumerate bigger & smaller steps (whatever your favourite style)
- Indentation is not interpreted by R, use if for readability!

Ex:

```
1 ##### CAGE TFs 2.0 - uORF analysis
2 ##### Axel Thieffry - December 2020
3 set.seed(42)
4 library(tidyverse)
5 library(tidylog)
6 library(magrittr)
7 library(reshape2)
8 library(CAGEfightR)
9 library(GenomicRanges)
10
11 '%!in%' <- function(x,y)!('%in%'(x,y))
12 'select' <- dplyr::select
13 'rename' <- dplyr::rename
14 'count' <- dplyr::count
15 'l' <- length
16 'h' <- head
17
18 setwd('~/Dropbox/CAGE PTI 2.0/scripts')
19
20
21 # 0. RAD INPUT DATA #####
22 #
23 myseqinfo <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/myseqinfo.rds')
24 universe <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/universe_geneID.rds')$geneID
25 uorf_gr <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/uORFs_GR_7238.rds')
26
27 # 1. POTENTIAL FOR uORF EXCLUSION #####
28 #
29 # 1a. number of genes with an uORF
30 n_distinct(uorf_gr$geneID) # 3,433 genes
31
32 # 1b. length distribution of uORFs
33 uorf_gr %>%
34   as.data.frame() %>%
35   ggplot(aes(x=width)) +
36     geom_density(fill='grey80') +
37     scale_x_log10(expand=c(0, 0)) +
38     cowplot::theme_cowplot() + theme(aspect.ratio=.35) +
39     scale_y_continuous(expand=c(0, 0)) +
40     labs(x='uORF length (bp)', titleuORF length distribution')
```

Ex:

```
1 ##### CAGE TFs 2.0 - uORF analysis
2 ##### Axel Thieffry - December 2020
3 set.seed(42)
4 library(tidyverse)
5 library(tidylog)
6 library(magrittr)
7 library(reshape2)
8 library(CAGEfightR)
9 library(GenomicRanges)
10
11 '%!in%' <- function(x,y)!('%in%')(x,y))
12 'select' <- dplyr::select
13 'rename' <- dplyr::rename
14 'count' <- dplyr::count
15 'l' <- length
16 'h' <- head
17
18 setwd('~/Dropbox/CAGE PTI 2.0/scripts')
19
20
21 # 0. RAD INPUT DATA #####
22 #
23 myseqinfo <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/myseqinfo.rds')
24 universe <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/universe_geneID.rds')$geneID
25 uorf_gr <- readRDS('~/Dropbox/CAGE PTI 2.0/data/RDS files/uORFs_GR_7238.rds')
26
27 # 1. POTENTIAL FOR uORF EXCLUSION #####
28 #
29 # 1a. number of genes with an uORF
30 n_distinct(uorf_gr$geneID) # 3,433 genes
31
32 # 1b. length distribution of uORFs
33 uorf_gr %>%
34   as.data.frame() %>%
35   ggplot(aes(x=width)) +
36     geom_density(fill='grey80') +
37     scale_x_log10(expand=c(0, 0)) +
38     cowplot::theme_cowplot() + theme(aspect.ratio=.35) +
39     scale_y_continuous(expand=c(0, 0)) +
40     labs(x='uORF length (bp)', titleuORF length distribution')
```

Title, description, author, date

Libraries and bits of custom script-wide stuffs

Working directory

Big step **Code**

Big step small step **Code**

small step **Code**

3. BE CONSISTENT

- Use single ‘ or double “ quotes, but stick to one when possible
- Spaces around characters and operators: , = ≠ + ≤
Like them or hate them, but be consistent.
- Widely adopted styles for best readability:

Space after a comma:	c(17, 4, 88)
Spaces around assignment:	foo ← 32
Spaces around operators:	sum(a) / 3.14
No spaces for function arguments:	read.table('data.txt', header=T)

4. TABULATION

- Let R help you, use TAB ➔ !
 - autocomplete **variable names** (known to your Global env.)
 - autocomplete **function names** (known to your Global env.)
 - discover and autocomplete **function parameters**

```
read.table()  
  
◆ file =  
◆ header =  
◆ sep =  
◆ quote =  
◆ dec =  
◆ numerals =  
◆ row.names =  
◆ ...  
  
file  
the name of the file which the data are to be read from. Each row  
of the table appears as one line of the file. If it does not contain an  
absolute path, the file name is relative to the current working  
directory, getwd(). Tilde-expansion is performed where  
supported. This can be a compressed file (see file).  
Alternatively, file can be a readable text-mode connection (which  
will be opened for reading if necessary, and if so closed (and  
Press F1 for additional help
```

Congratulations



You now know more R than 75% of
Scientists.

Let's play with some data

The iris dataset

- # load the data (they are included in base R)
`data(iris)`
- Inspect the iris dataset, try:
`iris, type(), str(), dim(), head(), tail(), summary(), colnames(), rownames(), View()`
- Coerce to a matrix:
`as.matrix(iris)`
- Get the “Petal.Width” column:
 - still in a dataframe
 - as a simple vector

tips: remember the simple and double brackets!
- For “Petal.Width” column, calculate:
`sum(), mean(), max(), and min()`

Datacamp assignment

Introduction to R

- Complete the [Datacamp](#) course “*Introduction to R*” that has been assigned to you
- Deadline: Friday 28th, no later than 18:00
- You can use any resource available to you (slides, Google, etc)
Note: nice [base R cheatsheet available here](#)