

# **Graduate Student Lunch & Learn**

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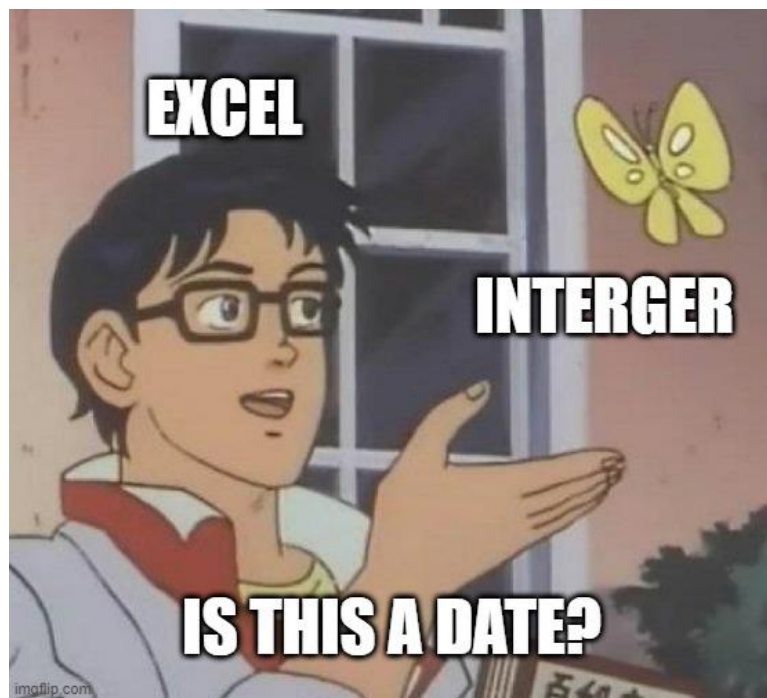
**What I wish I knew when started grad school...**

(with memes)

1 Excel sucks

# If statistics programs/languages were cars...



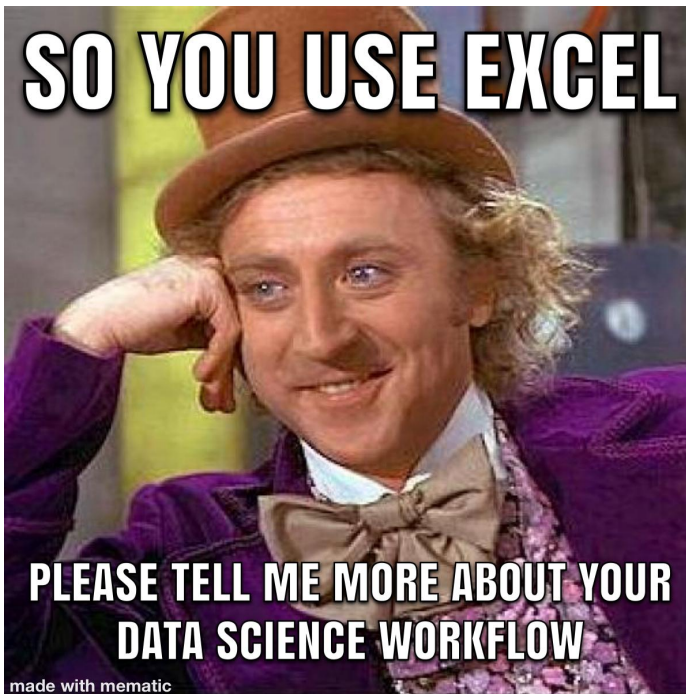


**EXCEL**

**INTERGER**

**IS THIS A DATE?**

imgflip.com



**SO YOU USE EXCEL**

**PLEASE TELL ME MORE ABOUT YOUR  
DATA SCIENCE WORKFLOW**

made with mematic

2 Learning to code is hard, but worth it



**Matt Dancho (Business Scie...** · 9/27/21 · ...

Even seasoned useRs get smacked sometimes. Never give up. [#rstats](#)





3 Programming is 90% googling



**Bonnie** @The\_GreatBonnie · 1/23/22



Are you a developer or you can't relate.



4 Best code is working code



Dorsa Amir  
@DorsaAmir



When your code is a mess but it somehow still works.





**R basics: syntax, data structures, loops, etc.**

(no memes)



≠



File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins R 4.1.2

basics.R

```
1 # using your first function
2 hello <- "yet another hello world"
3 print(hello)
4
5 # modifying variables
6 genes_A <- 100
7 genes_B <- 50
8 total_genes <- genes_A + genes_B
9 print(total_genes)
10
```

10:1 (Top Level) R Script

Environment History Connections Tutorial

Import Dataset 162 MiB

R Global Environment

Values

genes_A	100
genes_B	50
hello	"yet another hello world"
total_genes	150

Files Plots Packages Help Viewer

New Folder Upload Delete Rename More

Cloud > project > scripts

Name	Size	Modified
..		
basics.R	180 B	Feb 10, 2022, 4:28 PM

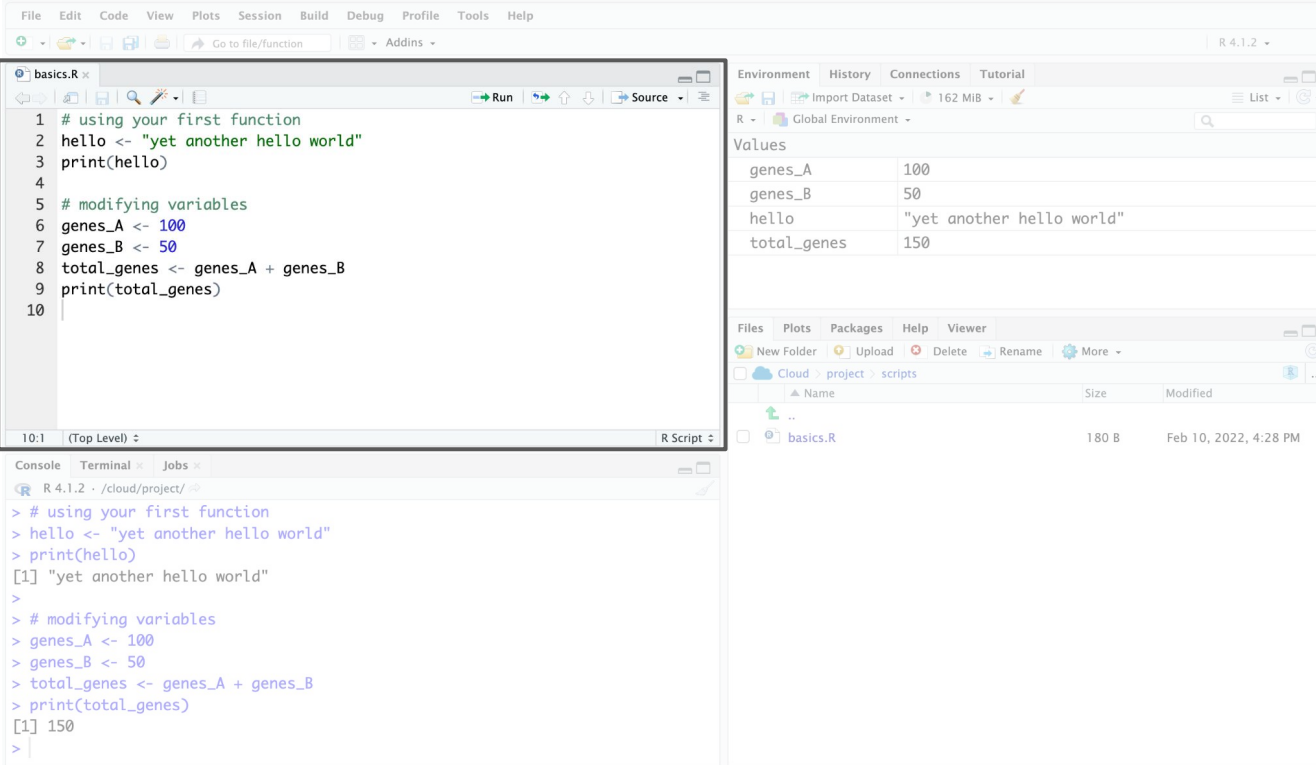
Console Terminal Jobs

R 4.1.2 · /cloud/project/

```
> # using your first function
> hello <- "yet another hello world"
> print(hello)
[1] "yet another hello world"
>
> # modifying variables
> genes_A <- 100
> genes_B <- 50
> total_genes <- genes_A + genes_B
> print(total_genes)
[1] 150
>
```



Write your code here



The screenshot displays the RStudio interface with the following components:

- Script Editor:** Contains the following R code:

```
1 # using your first function
2 hello <- "yet another hello world"
3 print(hello)
4
5 # modifying variables
6 genes_A <- 100
7 genes_B <- 50
8 total_genes <- genes_A + genes_B
9 print(total_genes)
10
```
- Console:** Shows the execution output:

```
> # using your first function
> hello <- "yet another hello world"
> print(hello)
[1] "yet another hello world"
>
> # modifying variables
> genes_A <- 100
> genes_B <- 50
> total_genes <- genes_A + genes_B
> print(total_genes)
[1] 150
>
```
- Environment Pane:** Displays the current values of variables in the Global Environment:

Values	
genes_A	100
genes_B	50
hello	"yet another hello world"
total_genes	150
- Files Pane:** Shows a file named `basics.R` in the `project/scripts` directory, with a size of 180 B and a modification date of Feb 10, 2022, 4:28 PM.

The screenshot displays the RStudio interface with three main panels. The top-left panel shows a script file named 'basics.R' with the following R code:

```
1 # using your first function
2 hello <- "yet another hello world"
3 print(hello)
4
5 # modifying variables
6 genes_A <- 100
7 genes_B <- 50
8 total_genes <- genes_A + genes_B
9 print(total_genes)
10
```

The top-right panel shows the 'Environment' tab, indicating the 'Global Environment' with 162 MIB of memory. It lists the following variables:

Variable	Value
genes_A	100
genes_B	50
hello	"yet another hello world"
total_genes	150

The bottom panel shows the 'Console' tab, which displays the output of the R script:

```
> # using your first function
> hello <- "yet another hello world"
> print(hello)
[1] "yet another hello world"
>
> # modifying variables
> genes_A <- 100
> genes_B <- 50
> total_genes <- genes_A + genes_B
> print(total_genes)
[1] 150
>
```

An arrow points from the text 'R does its things here' to the console output.

R does its things here

Keep track of all your objects here

The screenshot displays the RStudio interface with the following components:

- Source Editor:** Contains R code for a function and variable manipulation.
- Environment Pane:** Shows the current environment with the following objects:

Object	Value
genes_A	100
genes_B	50
hello	"yet another hello world"
total_genes	150
- Console:** Shows the execution output of the code in the source editor.
- Files Pane:** Displays the project structure, including a file named 'basics.R'.

The R code in the source editor is as follows:

```
1 # using your first function
2 hello <- "yet another hello world"
3 print(hello)
4
5 # modifying variables
6 genes_A <- 100
7 genes_B <- 50
8 total_genes <- genes_A + genes_B
9 print(total_genes)
10
```

The console output is as follows:

```
> # using your first function
> hello <- "yet another hello world"
> print(hello)
[1] "yet another hello world"
>
> # modifying variables
> genes_A <- 100
> genes_B <- 50
> total_genes <- genes_A + genes_B
> print(total_genes)
[1] 150
>
```

The image shows the RStudio IDE interface. The main editor window displays a script named 'basics.R' with the following code:

```
1 # using your first function
2 hello <- "yet another hello world"
3 print(hello)
4
5 # modifying variables
6 genes_A <- 100
7 genes_B <- 50
8 total_genes <- genes_A + genes_B
9 print(total_genes)
10
```

The Environment pane on the right shows the current state of the workspace:

Values	
genes_A	100
genes_B	50
hello	"yet another hello world"
total_genes	150

The Files pane at the bottom right shows the project structure:

Name	Size	Modified
..		
basics.R	180 B	Feb 10, 2022, 4:28 PM

The Console pane at the bottom left shows the output of the script:

```
> # using your first function
> hello <- "yet another hello world"
> print(hello)
[1] "yet another hello world"
>
> # modifying variables
> genes_A <- 100
> genes_B <- 50
> total_genes <- genes_A + genes_B
> print(total_genes)
[1] 150
>
```

An arrow points from the text 'See where your files are' to the Files pane.

See where your files are

# Basic syntax

```
# using your first function  
hello <- "yet another hello world"  
print(hello)
```

# Basic syntax

Comment (aka your best friend)



```
# using your first function  
hello <- "yet another hello world"  
print(hello)
```

# Basic syntax

Assignment operator

Object / Variable

```
# using your first function  
hello <- "yet another hello world"  
print(hello)
```

Some data:

- **Character / string** → "hello world!"
- **Integer** → 30
- **Numeric** → 2.5
- **Logical** → TRUE or FALSE

# Basic syntax

```
# using your first function  
hello <- "yet another hello world"  
print(hello)
```

Function





# Style guide

<https://style.tidyverse.org/>

Best practices on how to name variables and write clean code!

Variable and function names should use only lowercase letters, numbers, and `_`. Use underscores (`_`) (so called snake case) to separate words within a name.

```
# Good
day_one
day_1
```

```
# Bad
DayOne
dayone
```

Generally, variable names should be nouns and function names should be verbs. Strive for names that are concise and meaningful (this is not easy!).

```
# Good
day_one
```

```
# Bad
first_day_of_the_month
djm1
```

# Operators

## Arithmetic

**+** addition

**-** subtraction

**\*** multiplication

**/** division

**^** or **\*\*** exponentiation

**x %% y** integer-divide x by y and  
return the remainder

**x %/ y** integer division

# Operators

## Logical

<

less than

<=

less than or equal to

>

greater than

>=

greater than or equal to

**==**

**exactly equal to**

**!=**

not equal to

**!x**

not x

x **|** y

x or y

x **&** y

x and y

# Operations

# Operations

Be careful! Certain operations are **specific** to certain data types



# Operations

`class( 10 ) → numeric`

`class( 10 ) → character`

`as.numeric( 10 ) → 10`

# Operations

$$\boxed{10} == \boxed{10} \rightarrow \boxed{\text{TRUE}}$$

$$\boxed{B} != \boxed{B} \rightarrow \boxed{\text{FALSE}}$$

$$\boxed{\text{TRUE}} + \boxed{\text{TRUE}} \rightarrow \boxed{2}$$

$$\boxed{\text{FALSE}} + \boxed{\text{FALSE}} \rightarrow \boxed{0}$$

# Functions



# Functions

`print(my_variable)`



num

`?round`



Rounds the values in its first argument to the specified number of decimal places (default 0)

`round(my_variable)`



num

# Functions

```
my_data <- read.file(file = "filename.txt", sep = "\t")
```

Function name



Arguments

\*type **?read.file** for more arguments and their default values

# Data structures

# Data structures

```
my_vector <- c(1, 55, 2.5, 333)
```



```
my_vector <- c("C", "O", "R", "N")
```



# Data structures

```
my_matrix <- matrix(
```

1	55	2.5	333
0.2	0	11	2
0	9.9	2.5	758
1	5	2	90


)


# Data structures

```
my_dataframe <- data.frame(
```

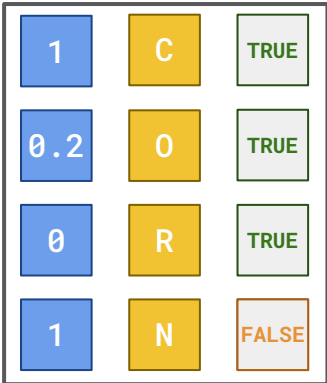
1	C	TRUE	333
0.2	0	TRUE	2
0	R	TRUE	758
1	N	FALSE	90

# Data structures

numbers = 

best\_plant = 

my\_list <- **list**(

data =  )

# Subsetting

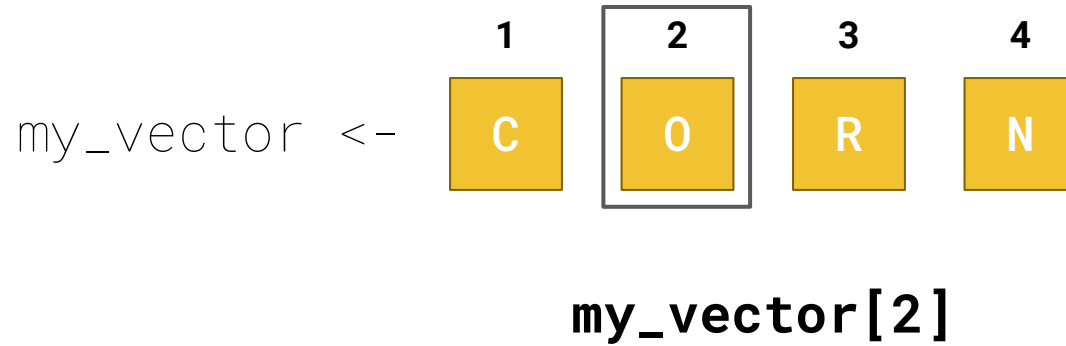


# Subsetting

my\_vector <-

1	2	3	4
C	O	R	N

# Subsetting



# Subsetting

`my_vector <-`

1	2	3	4
C	O	R	N

**`my_vector[1:3]`**

# Subsetting

`my_vector <-`

1	2	3	4
C	O	R	N

`my_vector[c(1,4)]`

# Subsetting

`my_df <-`

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

# Subsetting

`my_df <-`

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

`my_df[ , ]`

# Subsetting

`my_df <-`

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

`my_df[2,3]`

# Subsetting

`my_df <-`

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

`my_df[4, ]`



# Subsetting

`my_df <-`

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

`my_df[, c(1, 3)]`

# Subsetting

my\_df <-

	1	2	3	4
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

```
my_df[my_df[, 1] < 0.5, c(1,3)]
```

\*also check **subset()** and **grep()** functions

# Subsetting

```
df_with_header <-
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	0	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

# Subsetting

```
df_with_header <-
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

**df\_with\_header\$plant**

# Subsetting

```
df_with_header <-
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

```
df_with_header[,2]
```

# Subsetting

```
df_with_header <-
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

```
df_with_header[3:4, c("maf", "n")]
```

# if / else statements

```
if (condition) {  
    ...do something...  
} else {  
    ...do other thing...  
}
```

# if / else statements

```
big_number <- 1.000
```

```
if (big_number > 100) {  
  print("this is a big number")  
} else {  
  print("not that big")  
}
```



# if / else statements

```
big_number <- 1.000
```

```
if (big_number > 100) {  
  print("this is a big number")  
} else {  
  print("not that big")  
}
```



**“not that big”**

# if / else statements

```
plant <- "corn"
```

```
if (plant == "corn") {  
  plant <- paste(plant, "is the best")  
} else {  
  plant <- "not corn"  
}
```

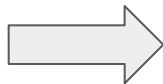
```
print(plant)
```

# if / else statements

```
plant <- "corn"
```

```
if (plant == "corn") {  
  plant <- paste(plant, "is the best")  
} else {  
  plant <- "not corn"  
}
```

```
print(plant)
```



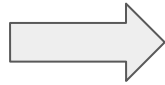
**"corn is the best"**

# for loop

```
for (variable in vector) {  
    ...do something...  
}
```

I want to create a vector containing **only vowels** from the plant column

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90



**df\$plant**

C O R N



**new\_vector**

O

Need to tell R some important things first...

```
# vowels I know  
vowels <- c("A", "E", "I", "O", "U")  
# create an empty vector to store values  
vowels_in_plant <- c()
```

Need to tell R some important things first...

```
# vowels I know  
vowels <- c("A", "E", "I", "O", "U")  
# create an empty vector to store values  
vowels_in_plant <- c()
```

... and then do what you gotta do

```
# get letter from first row of column "plant"  
letter <- df[1, "plant"]
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90

Need to tell R some important things first...

```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()
```

... and then do what you gotta do

```
# get letter from first row of column "plant"
letter <- df[1, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90





Need to tell R some important things first...

```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()
```

... and then do what you gotta do

```
# get letter from first row of column "plant"
letter <- df[2, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90



Need to tell R some important things first...

```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()
```

... and then do what you gotta do

```
# get letter from first row of column "plant"
letter <- df[3, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90



Need to tell R some important things first...

```
# vowels I know  
vowels <- c("A", "E", "I", "O", "U")  
# create an empty vector to store values  
vowels_in_plant <- c()
```

... and then do what you gotta do

```
# get letter from first row of column "plant"  
letter <- df[4, "plant"]  
# if letter is a vowel  
if (letter %in% vowels) {  
  # append letter to vector  
  vowels_in_plant <- append(vowels_in_plant, letter)  
}
```

	maf	plant	treat	n
1	1	C	TRUE	333
2	0.2	O	TRUE	2
3	0	R	TRUE	758
4	1	N	FALSE	90



```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()

# get letter from first row of column "plant"
letter <- df[1, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[2, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[3, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[4, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()
```

```
# get letter from first row of column "plant"
letter <- df[1, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

```
# get letter from first row of column "plant"
letter <- df[2, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

```
# get letter from first row of column "plant"
letter <- df[3, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```

```
# get letter from first row of column "plant"
letter <- df[4, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}
```



```
# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()
```

```
for (row in 1:4) {
  # get letter from column "plant"
  letter <- df[row, "plant"]
  # if letter is a vowel
  if (letter %in% vowels) {
    # append letter to vector
    vowels_in_plant <- append(vowels_in_plant, letter)
  }
}
```

```

# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()

# get letter from first row of column "plant"
letter <- df[1, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[2, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[3, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

# get letter from first row of column "plant"
letter <- df[4, "plant"]
# if letter is a vowel
if (letter %in% vowels) {
  # append letter to vector
  vowels_in_plant <- append(vowels_in_plant, letter)
}

```

```

# vowels I know
vowels <- c("A", "E", "I", "O", "U")
# create an empty vector to store values
vowels_in_plant <- c()

for (row in 1:4) {
  # get letter from column "plant"
  letter <- df[row, "plant"]
  # if letter is a vowel
  if (letter %in% vowels) {
    # append letter to vector
    vowels_in_plant <- append(vowels_in_plant, letter)
  }
}

```

# while loop

```
while (condition) {  
    ...do something...  
}
```

```
# initial number of seeds
total_seeds <- 0
# initial number of surprise packages opened
surprise_packages <- 0

while(total_seeds < 1000) {

  # open surprise packages and add to total number of seeds
  total_seeds <- total_seeds + sample(x = 1:100, size = 1)
  # increase number of surprise packages opened
  surprise_packages <- surprise_packages + 1

}

# let me know how many packages I opened
print(surprise_packages)
```



```
# initial number of seeds
total_seeds <- 0
# initial number of surprise packages opened
surprise_packages <- 0
```

```
while(total_seeds < 1000) {

  # open surprise packages and add to total number of seeds
  total_seeds <- total_seeds + sample(x = 1:100, size = 1)
  # increase number of surprise packages opened
  surprise_packages <- surprise_packages + 1

}
```

```
# let me know how many packages I opened
print(surprise_packages)
```

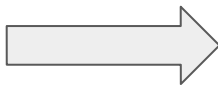
```
# initial number of seeds
total_seeds <- 0
# initial number of surprise packages opened
surprise_packages <- 0

while(total_seeds < 1000) {

  # open surprise packages and add to total number of seeds
  total_seeds <- total_seeds + sample(x = 1:100, size = 1)
  # increase number of surprise packages opened
  surprise_packages <- surprise_packages + 1

}

# let me know how many packages I opened
print(surprise_packages)
```



First time → **19**

Second time → **17**

Third time → **21**

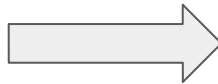
```
# initial number of seeds
total_seeds <- 0
# initial number of surprise packages opened
surprise_packages <- 0

while(total_seeds < 1000) {

  # open surprise packages and add to total number of seeds
  total_seeds <- total_seeds + sample(x = 1:100, size = 1)
  # increase number of surprise packages opened
  surprise_packages <- surprise_packages + 1

}

# let me know how many packages I opened
print(surprise_packages)
```



## Infinite loop

(will never finished running)



## **Getting help: a matter of asking the right questions**

(google == “best friend”)

## **Read the docs**

1

Use `?function` in R, go to package website, look for tutorials/examples online

## **Google error/question**

2

Spend some time reading through the comments in StackOverflow or other forum post, and know that you may need to try slightly different things

## **Learn how to ask the right question**

3

This is a skill that you get better as you go, but usually involves being precise on what you ask and use certain terminology of your programming language



## Learn how to ask the right question

3

“how to get lines of my table according to a number in R”

vs

“how to **subset** my **data frame** in R”

4

## **Ask your friend :)**

They don't need to be experts, but they might have had similar problems before or they can help you debug

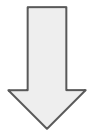


**Pseudocoding: write your code in a human language**

(then translate to computer language)

Break down a complex task into a  
series of **smaller and simpler** tasks

Calculate allele frequencies for each marker in this file



```
load the file
```

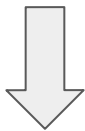
```
for each marker in that data frame
```

```
    count total number of alleles
```

```
    count how many times each allele shows up
```

```
    divide the allele count by total
```

Calculate allele frequencies for each marker in this file



```
load the file
```

```
create empty vector to store values
```

```
for each marker in that data frame
```

```
  count total number of alleles
```

```
  count how many times each allele shows up
```

```
  divide the allele count by total
```

```
append frequencies to vector
```

```
write file with allele frequencies
```

**This is a skill and takes time to develop!**

Writing you pseudocode as comments in your script, helps you visualize what you need to do and make your translation to R language easier





**Your turn!**

Hands-on exercises



1

If you want to practice some R basics:

**simple\_marker\_analysis.R**

2

If you know the basics and want some challenge:

**need4speed.R**

# Extra

More advanced stuff...



# apply() function

Do something at each iteration

```
apply(x, MARGIN, FUN)
```

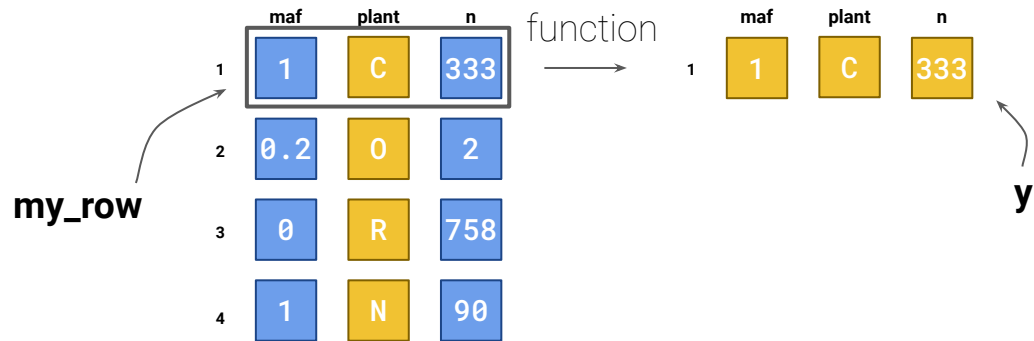
Iterate through data frame by:

**Row** → MARGIN = 1

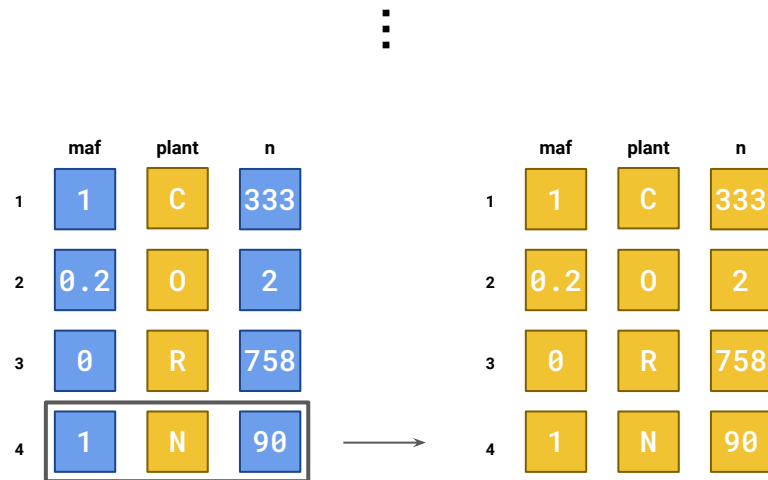
**Column** → MARGIN = 2

**Element** → MARGIN = c(1, 2)

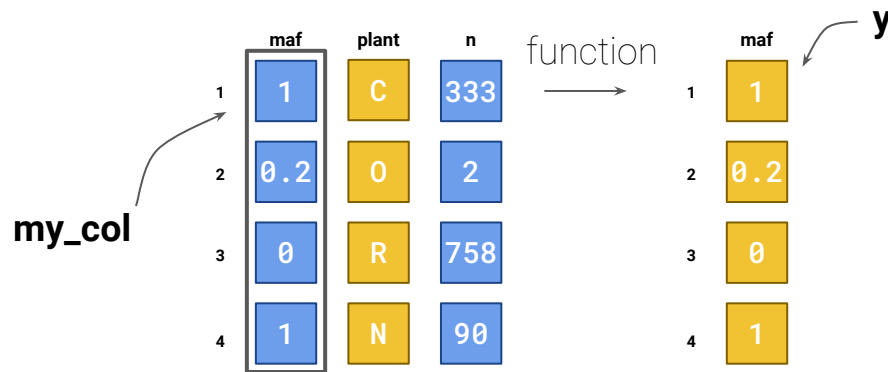
# apply() function



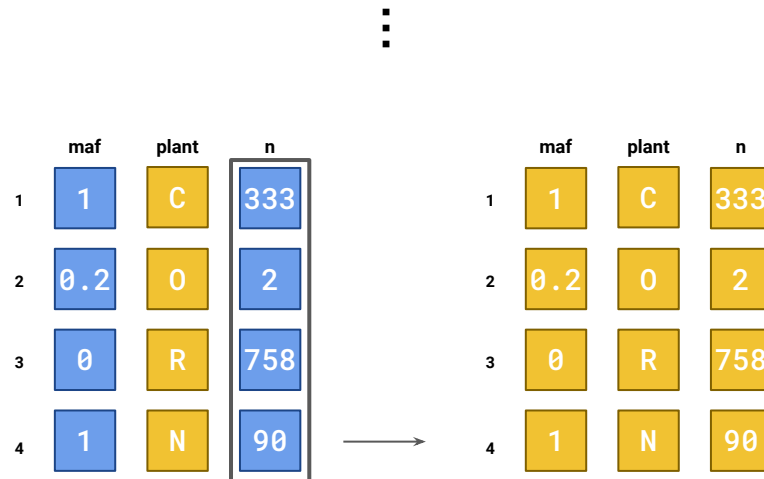
```
apply(my_df,  
      MARGIN = 1,  
      function(my_row) {  
        y <- as.character(my_row)  
        return(y)  
      })
```



# apply() function



```
apply(my_df,  
      MARGIN = 2,  
      function(my_col) {  
        y <- as.character(my_col)  
        return(y)  
      })
```



# Plotting with ggplot2

<https://datacarpentry.org/R-ecology-lesson/04-visualization-ggplot2.html>



# Working directory

Know where you are:

**getwd()**

Change where you are:

**setwd()**

```
getwd()
```

```
[1] "/rcloud/project/"
```

```
read.file("file.txt")
```

```
[1] error
```

```
read.file("data/file.txt")
```

```
getwd()
```

```
[1] "/rcloud/project/"
```

```
read.file("file.txt")
```

```
[1] error
```

```
setwd("data")
```

```
getwd()
```

```
[1] "/rcloud/project/data"
```

```
read.file("data/file.txt")
```

```
[1] error
```

```
read.file("file.txt")
```

**Keep learning!**

Online courses:

**[www.datacamp.com](http://www.datacamp.com)**

**[www.edx.org](http://www.edx.org)**

**[www.coursera.org](http://www.coursera.org)**

Data carpentry:

**[datacarpentry.org/](http://datacarpentry.org/)**

Style guide:

**[style.tidyverse.org/](http://style.tidyverse.org/)**