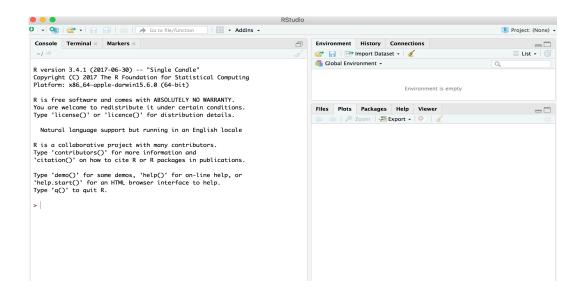
STA130 - Class #2: How R You?

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Today's Class

- · R and RStudio
- · Base R
- · R libraries
- · Main tidyverse libraries: ggplot2 and dplyr

RStudio User Interface



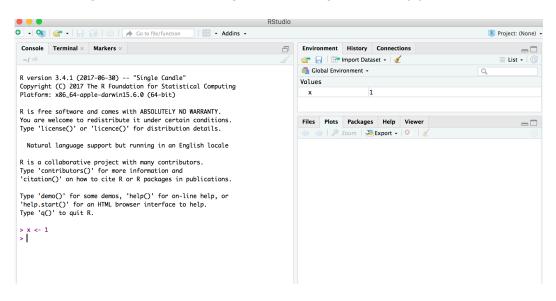
R Objects

- · R lets you save data by storing it inside an R object.
- · What's an object? Just a name that you can use to call up stored data.

```
x <- 1
x
## [1] 1
```

Environment Pane in RStudio

· When you create an object, the object will appear in the environment pane of RStudio.



Functions

- · R comes with many functions that you can use to do sophisticated tasks like random sampling.
- For example, you can round a number with the round function round(), or calculate its absolute value with abs().
- · Write the name of the function and then the data you want the function to operate on in parentheses:

```
round(-2.718282, 2)

## [1] -2.72

abs(-5)

## [1] 5

abs(round(-2.718282, 2))

## [1] 2.72
```

Function Constructor

- Every function in R has three basic parts: a name, a body of code, and a set of arguments.
- To make your own function, you need to replicate these parts and store them in an R object, which you can do with the function function.
- · To do this, call function() and follow it with a pair of braces, {}: my function <- function() {}

Function Constructor

· We can simulate rolling a pair of dice and adding the result with the code:

```
die <- 1:6
dice <- sample(die, size = 2, replace = TRUE)
sum(dice)
## [1] 11</pre>
```

Function Constructor

· We can create our own function with

```
roll <- function() {
   die <- 1:6
   dice <- sample(die, size = 2, replace = TRUE)
   sum(dice)
}

Call the function roll()

roll() # call the function. NB: result will differ with every call

## [1] 10</pre>
```

Function Arguments

Instead of rolling one die consider rolling four or ten dice then adding the results of all the rolls together.

```
roll2 <- function(numrolls) { # x is the argument of the function roll2
  die <- 1:6
  dice <- sample(die, size = numrolls, replace = TRUE) # the size of the sample
  sum(dice) # add up the roll results
}</pre>
```

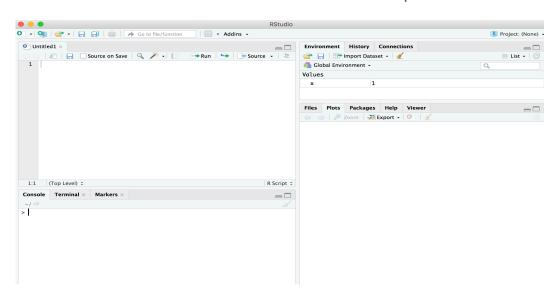
numrolls is called an *argument* of the function roll2().

Let's simulate rolling ten dice and adding the results together.

```
roll2(10)
## [1] 31
```

Scripts

- \cdot If we want to edit the function roll2() then we will want to save it in a script.
- $\cdot\,\,$ To do this in RStudio File > New File > R script in the menu bar.

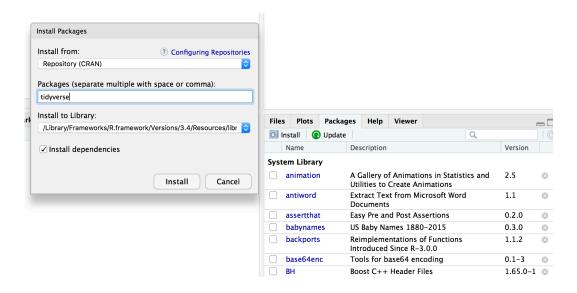


Packages

- · You're not the only person writing your own functions with R.
- · Many professors, programmers, and statisticians use R to design tools that can help people analyze data.
- · They then make these tools free for anyone to use.
- To use these tools, you just have to download them. They come as preassembled collections of functions and objects called packages.
- · We have already used two packages ggplot2 and dplyr.

Packages

To install the package tidyverse in RStudio go to the Packages tab in RStudio and click Install.

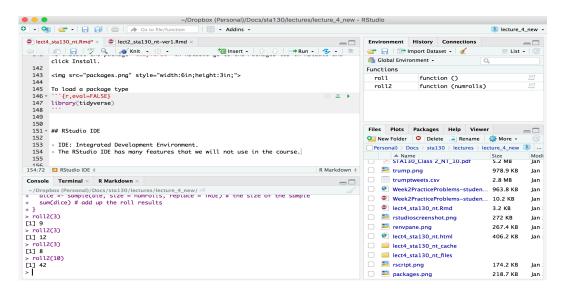


To load a package type

library(tidyverse)

RStudio IDE

- · IDE: Integrated Development Environment.
- · The RStudio IDE has many features that we will not use in the course.



- The **console** is where you can type an R command at the prompt and the result is returned.
- · Write code in an R script, R Markdown document, or R Notebook.
- · Run a script or R chunks from an R Markdown or R Notebook by pushing the run button in the chunk.

R Objects

- · R stores data in objects such as vectors, arrays, and matricies.
- · In most applications we will ususally load data from an external file.

R Objects - Atomic Vectors

You can make an atomic vector by grouping some values of data together with c:

```
die<-c(1,2,3,4,5,6)
die

## [1] 1 2 3 4 5 6

is.vector(die)

## [1] TRUE

length(die)

## [1] 6</pre>
```

You can also make an atomic vector with just one value. R saves single values as an atomic vector of length 1:

```
two <- 2
two
## [1] 2
```

R Objects - Atomic Vectors: Integer and Character

- Each atomic vector can only store one type of data. You can save different types of data in R by using different types of atomic vectors.
- · R recognizes six basic types of atomic vectors: doubles, integers, characters, logicals, complex, and raw.
- We will not be using complex or raw types in STA130.
- Integer vectors included a capital L with input, and character vectors have input surounded by quotation marks.

R Objects - Atomic Vectors: Integer and Character

```
mynums <- c(2L,3L)
courses <- "STA130"
courses <- c("STA130", "MAT137")
sum(mynums)

## [1] 5

sum(courses)

## Error in sum(courses): invalid 'type' (character) of argument

sum(courses == "STA130")

## [1] 1</pre>
```

R Objects - Double Vectors

· A double vector stores real numbers. Doubles are often called numerics.

```
die <- c(1,2,3,4,5,6)
typeof(die)
## [1] "double"</pre>
```

R Objects - Logical Vectors

· Logical vectors store TRUEs and FALSEs, R's form of Boolean data. Logicals are very helpful for doing things like comparisons:

```
3 > 4
## [1] FALSE
```

• TRUE or FALSE in capital letters (without quotation marks) will be treated as logical data. R also assumes that T and F are shorthand for TRUE and FALSE.

```
logic <- c(TRUE, FALSE, TRUE)
logic
## [1] TRUE FALSE TRUE</pre>
```

R Objects - Atomic Vectors: dim()

You can transform an atomic vector into an n-dimensional array by giving it a dimen- sions attribute with dim.

R always fills up each matrix by columns, instead of by rows unless you use matrix() or array().

Factors

- Factors are R's way of storing categorical information, like ethnicity or eye color.
- · A factor as something like sex since it can only have certain values.
- · Factors very useful for recording the treatment levels of a categorical variable.

```
sex <- factor(c("male", "female", "female", "male"))
typeof(sex)

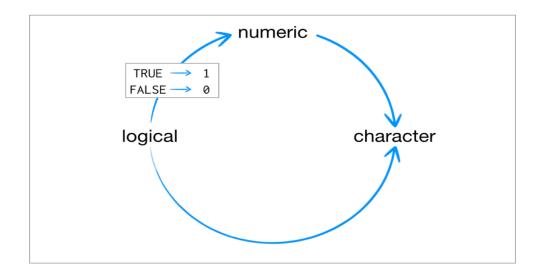
## [1] "integer"

unclass(sex) # shows how R is storing the factor vector

## [1] 2 1 1 2
## attr(,"levels")
## [1] "female" "male"</pre>
```

Coercion

R always follows the same rules when it coerces data types. Once you are familiar with these rules, you can use R's coercion behavior to do surprisingly useful things.



For example sum(c(TRUE, TRUE, FALSE, FALSE)) will become sum(c(1, 1, 0, 0)).

```
sum(c(TRUE, TRUE, FALSE, FALSE))
```

[1] 2

Lists

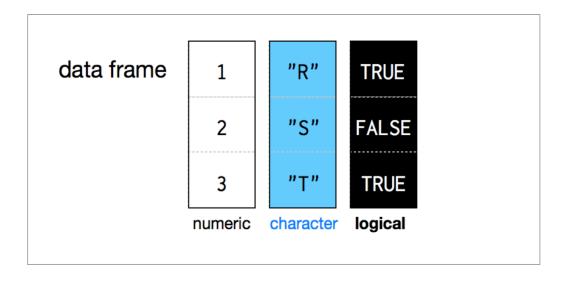
- · Lists are like atomic vectors because they group data into a one-dimensional set.
- · Lists do not group together individual values.
- · Lists group together R objects, such as atomic vectors and other lists.
- For example, you can make a list that contains a numeric vector of length 31 in its first element, a character vector of length 1 in its second element, and a new list of length 2 in its third element.

```
list1 <- list(1:31, "Prof. Taback", list(TRUE, FALSE))
list1

## [[1]]
## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
## [24] 24 25 26 27 28 29 30 31
##
## [[2]]
## [[3]]
## [[3]]
[[1]]
## [[3]][[1]]
## [[3]][[2]]
## [1] FALSE</pre>
```

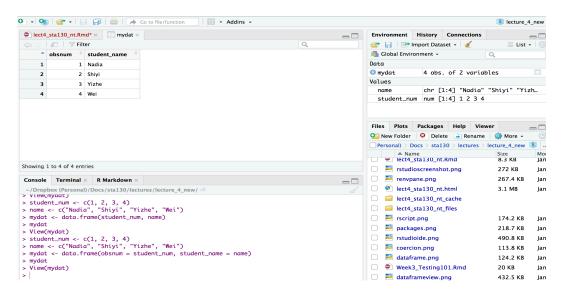
- · Data frames are the two-dimensional version of a list.
- · They are the most useful storage structure for data analysis
- · A data frame is R's equivalent to the Excel spreadsheet because it stores data in a similar format.

- · Data frames group vectors together into a two-dimensional table.
- · Each vector becomes a column in the table.
- · As a result, each column of a data frame can contain a different type of data; but within a column, every cell must be the same type of data.



- · Creating a data frame by hand takes a lot of typing, but you can do it with the data.frame() function.
- · Give data.frame() any number of vectors, each separated with a comma.
- · Each vector should be set equal to a name that describes the vector.
- · data.frame() will turn each vector into a column of the new data frame.

You can view a data frame in RStudio by clicking on the data frame name in the Environment tab



R Notation - [,]

• To extract a value or set of values from a data frame, write the data frame's name followed by a pair of square brackets with a comma [,].

```
mydat[ , ]
```

R Notation - [,]

mydat

[1] Nadia Shiyi

Levels: Nadia Shiyi Wei Yizhe

obsnum student_name
1 1 Nadia
2 2 Shiyi
3 3 Yizhe
4 4 Wei

mydat[1,2] # the value in row 1 and column 2

[1] Nadia
Levels: Nadia Shiyi Wei Yizhe

mydat[c(1,2),2] # all values in rows 1 and 2 in second column

R Notation - \$

The \$ tells R to return all of the values in a column as a vector.

```
mydat$student name
## [1] Nadia Shiyi Yizhe Wei
## Levels: Nadia Shiyi Wei Yizhe
vec <- mydat$student_name # assign it to vec</pre>
attributes(vec) # info associated with object vec
## $levels
## [1] "Nadia" "Shiyi" "Wei" "Yizhe"
##
## $class
## [1] "factor"
vec[2] # get second element of vector
## [1] Shiyi
## Levels: Nadia Shiyi Wei Yizhe
```

R Notation - combine [,] and \$

```
mydat[mydat$obsnum == 1,] # first row of data frame and all columns

## obsnum student_name
## 1 1 Nadia

mydat[mydat$obsnum == 1 | mydat$obsnum == 4 ,] # first and fourth rows of data frame and all columns

## obsnum student_name
## 1 1 Nadia
## 4 4 Wei
```

Missing Data - NA

- · Missing information problems happen frequently in data science.
- For example a value is mising because the measurement was lost, corrupted, or never recorded.
- The NA character is a special symbol in R. It stands for "not available" and can be used as a placeholder for missing information.

1 + NA

[1] NA

Missing Data - na.rm()

· Suppose you collected the ages of five students, but you forgot to record the fifth students age.

```
age <- c(19, 20, 17, 20, NA)
mean(age) # mean will be NA

## [1] NA

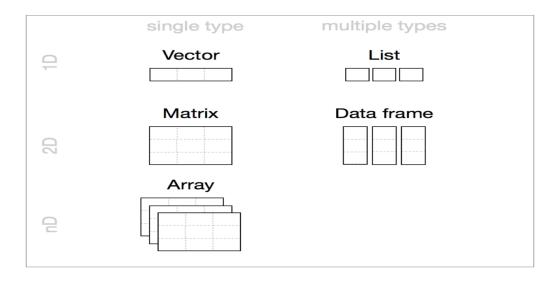
age <- c(19, 20, 17, 20, NA)
mean(age, na.rm = TRUE) # R will ignore missing values
## [1] 19</pre>
```

Identify and Set Missing Data - is.na()

```
age <- c(19, 20, 17, 20, NA)
is.na(age) # check which elements of age are missing
## [1] FALSE FALSE FALSE TRUE

age[1] <- NA # set the first element of age to NA
age
## [1] NA 20 17 20 NA</pre>
```

Summary of R Data Structures



Tidyverse



https://www.tidyverse.org

The provincial rates for the week ending January 6, 2018 are in the file fludat_prov.csv and the the size of the population in each province is in the file population. The code below reads the files into R data frames.

```
library(tidyverse)
fludat_prov <- read_csv("fludat_prov.csv") # import data from file
popdat <- read_csv("popdat.csv") # import data from file</pre>
```

head(fludat_prov) # head shows the first six rows of a data frame

```
## # A tibble: 6 x 3
     prov
                         testpop size fluA
     <chr>
                                <int> <int>
## 1 Newfoundland
                                   96
                                         12
## 2 Prince Edward Island
                                         11
## 3 Nova Scotia
                                  144
                                         23
## 4 New Brunswick
                                  347
                                         80
## 5 Province of Ouébec
                                 6361 1190
## 6 Province of Ontario
                                 2320 344
```

head(popdat)

```
## # A tibble: 6 x 3
                     prov pop size region
     prov
                            <int> <chr>
    <chr>
## 1 Nunavut
                           35944 Territories
## 2 Alberta
                           4067175 <NA>
## 3 Saskatchewan
                          1098352 West
## 4 Yukon
                            35874 Territories
## 5 Manitoba
                           1278365 West
## 6 British Columbia
                           4648055 West
```

How many Provinces/Territories are in the fludat_prov data frame?

```
fludat_prov %>% summarise(numprov = n()) # n() counts the number of rows in the data frame

## # A tibble: 1 x 1

## numprov

## <int>
## 1 13
```

Do any variables in fludat or popdat have missing values?

Recode specific values using R data frame notation [,] and \$.

```
popdat$region[popdat$prov == "Alberta"] <- "West" #recode only the region value for Alberta
popdat$region[popdat$prov == "Quebec"] <- "East" #recode only the region value for Alberta
popdat$region #print region variable in popdat data</pre>
```

```
## [1] "Territories" "West" "West" "Territories" "West" ## [6] "West" "East" "Atlantic" "Atlantic" "Atlantic"
```

Canadian Flu Rates with dplyr - Joining Two Tables with inner_join()

We can join two data frames with $inner_{join(x,y)}$: return all rows from x where there are matching values in y, and all columns from x and y. If there are multiple matches between x and y, all combination of the matches are returned.

1278365 West

4648055 West

35874 Territories

35944 Territories

41786 Territories

```
## # A tibble: 9 x 5
                        testpop size fluA prov pop size region
    prov
                               <int> <int>
   <chr>
                                                 <int> <chr>
                                           519716 Atlantic
## 1 Newfoundland
## 2 Prince Edward Island
                                64
                                      11
                                               142907 Atlantic
## 3 Nova Scotia
                                 144
                                               923598 Atlantic
## 4 New Brunswick
                                 347
                                                747101 Atlantic
```

fludat prov %>% inner join(popdat, by = "prov")

5 Manitoba

7 Yukon

9 Nunavut

6 British Columbia

8 Northwest Territories

Why are there only 9 observations when there are 13 Provinces/Territories?

849

15

18

1078

186

198

10

Canadian Flu Rates with dplyr - Joining Two Tables with inner_join()

fludat prov\$prov

```
"Prince Edward Island"
## [1] "Newfoundland"
## [3] "Nova Scotia"
                                   "New Brunswick"
## [5] "Province of Ouébec"
                                   "Province of Ontario"
## [7] "Manitoba"
                                   "Province of Saskatchewan"
## [9] "Province of Alberta"
                                   "British Columbia"
## [11] "Yukon"
                                   "Northwest Territories"
## [13] "Nunavut"
popdat$prov
## [1] "Nunavut"
                                "Alberta"
                                "Yukon"
## [3] "Saskatchewan"
## [5] "Manitoba"
                                "British Columbia"
                                "Ouebec"
## [7] "Ontario"
## [9] "Prince Edward Island" "Newfoundland"
## [11] "Northwest Territories" "Nova Scotia"
## [13] "New Brunswick"
```

Province needs to be recoded. Exercise on this week's practice problems.

Canadian Flu Rates with dplyr - Joining Two Tables with inner_join()

		X							Y			
Α	₩	В	₩	С	₩		A	₩	В	₩	D	4
а		t		1			a		t		3	
b		u		2			b		u		2	
С		٧		3			d		W		1	
		inner_joi	n(X,	Y)								
А		В		С		D						
a		t		1		3						
b		и		2		2						