# Lecture 2: R Basics

## Peng Chap 4-6

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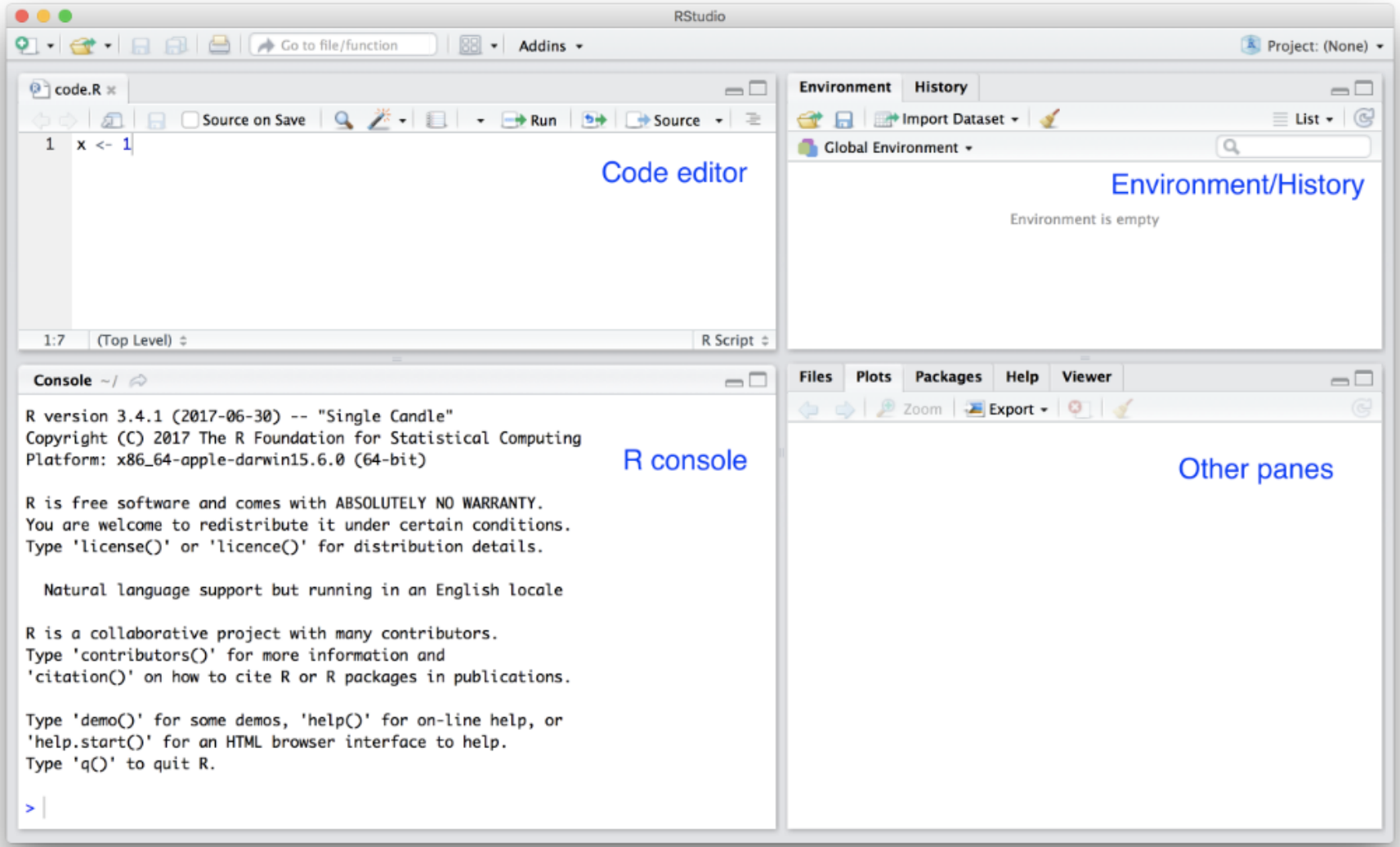
2022-09-19

# Agenda

- R Studio
- Basic Operations and Data Type
- Input/ Output

Quick Survey: Have you installed RStudio?

# RStudio Interface



# RStudio Basics

- Key binding: to start a new script, Ctrl+Shift+N on Windows and command+shift+N on the Mac
- RStudio IDE cheatsheet: Help-> Cheatsheets -> RStudio IDE cheatsheet
- Load Libraries: library()
- Install packages:
  Type in the console: install.packages("name of the package")

```
install.packages("tidyverse")
# install more than one package
install.packages(c("tidyverse", "ggplot2"))
# check all installed packages
installed.packages()
```

# Basics: value assignment

We use assignment operator: `<-`

```
x <- 1    # Input
x = 1
msg <- "hello"
```

Question: Can we use `<-` and `=` interchangeably?

```
# Equal sign specifying parameters in function
mean(a, na.rm=FALSE)
# Creating a function
sqroot <- function(n) sqrt(1:n)
```

Now, to check your understanding, what will happen to following lines?

```
system.time(result <- sqroot(1000))
system.time(result = sqroot(1000))
```

# Printing

```
x <- 5  ## nothing printed
x       ## auto-printing occurs
```

```
## [1] 5
```

```
print(x)  ## explicit printing
```

```
## [1] 5
```

- Auto-print: easier for interactive work.
- Explicit-print: more convenient when writing scripts, functions, or longer programs.

# R Objects

R has five basic objects (Everything you see in R!):

- character
- numeric (real numbers)
  - `L` suffix to specify integer: `1L`
  - `Inf` represents infinity, 1 / Inf is 0.
  - `NaN`: undefined value ("not a number") or missing value.
- integer
- complex
- logical (True/False)

The most basic type of R object is a vector.

- A vector can **only contain objects of the same class.**
- Empty vectors can be created with the `vector()` function.

```
x <- vector("numeric", length = 10)
```

# Vector

The `c()` function can be used to create vectors of objects by concatenating things together.

```
x <- c(0.5, 0.6)        ## numeric
x <- c(TRUE, FALSE)     ## logical
x <- c(T, F)            ## logical
x <- c("a", "b", "c")   ## character
x <- 9:29               ## integer
x <- c(1+0i, 2+4i)      ## complex
```

Question: what happens to the following code?

```
y <- c(1.7, "a")
```

```
y
```

```
## [1] "1.7" "a"
```

# Coercion

When different objects are mixed in a vector, **coercion** occurs so that every element in the vector is of the same class.

In the example above, we see the effect of implicit coercion. What R tries to do is find a way to represent all of the objects in the vector in a reasonable fashion.

Sometimes, it could violate your expectation.

Objects can be explicitly coerced from one class to another using the `as.*` functions, if available.

```
as.numeric(x)
```

```
## Warning: imaginary parts discarded in coercion
```

```
## [1] 1 2
```

```
as.logical(x)
```

# Attribute

- Attributes are metadata for the object (to describe the object). Some examples of R object attributes are
  - names, dimnames
  - dimensions (e.g. matrices, arrays)
  - class (e.g. integer, numeric)
  - length
  - other user-defined attributes/metadata
- Attributes of an object (if any) can be accessed using the `attributes()` function.
- Not all R objects contain attributes: attributes() function returns NULL.

# Matrices

There are several options to create a matrix

```
m <- matrix(nrow = 2, ncol = 3)
m
```

```
##      [,1] [,2] [,3]
## [1,]   NA   NA   NA
## [2,]   NA   NA   NA
```

```
dim(m)
```

```
## [1] 2 3
```

```
attributes(m)
```

```
## $dim
## [1] 2 3
```

# Matrices

Constructed from vector: start from upper left corner, column-wise.

```
m <- matrix(1:6, nrow = 2, ncol = 3)
m
```

```
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

Or create directly from vectors by adding a dimension attribute.

```
m <- 1:10
dim(m) <- c(2, 5)
m
```

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

# Matrices

Column-binding or row-binding with the `cbind()` and `rbind()` functions.

```
x <- 1:3
y <- 10:12
cbind(x, y)
```

```
##      x  y
## [1,] 1 10
## [2,] 2 11
## [3,] 3 12
```

```
rbind(x, y)
```

```
##   [,1] [,2] [,3]
## x    1    2    3
## y   10   11   12
```

# Missing Values

- Missing values are denoted by `NA` or `NaN`.
- `is.na()` is used to test objects if they are NA
- `is.nan()` is used to test for NaN
- NA values have a class also, so there are integer NA, character NA, etc. (More general)
- A NaN value is also NA but the converse is not true

Question: What is the output of following code?

```
x <- c(1, 2, NA, 10, 3)
is.na(x)
is.nan(x)
```

# Search for documentation

If you ever want to use a new function and would like to check its documentation

- ?pattern
- ??pattern
- help.search(pattern)

# Reading Data

There are a few principal functions reading data into R.

- `read.table`, `read.csv`, for reading tabular data
- `readLines`, for reading lines of a text file source, for reading in R code files
- `dget`, for reading in R code files
- `load`, for reading in saved workspaces.
- `unserialize`, for reading single R objects in binary form

For small to moderately sized datasets, you can usually call `read.table` without specifying any other arguments.

```
data <- read.table("foo.txt")
```

- R automatically figures out how many rows there are (and how much memory needs to be allocated)
- figure what type of variable is in each column of the table.

# Example

```
data <- read.table("baby.csv", sep=",", header=TRUE)
head(data,n=3L)
```

```
##   Birth.Weight Gestational.Days Maternal.Age Maternal.Heigh
## 1          120              284           27              6
## 2          113              282           33              6
## 3          128              279           28              6
##   Maternal.Pregnancy.Weight Maternal.Smoker
## 1                       100           False
## 2                       135           False
## 3                       115            True
```

Question:

What if the dataset is too large?

# Reading in Larger Datasets

Several Suggestions:

- Compare your RAM with memory required to store your dataset.
- Use the `colClasses` argument.

```
initial <- read.table("bigdata.txt", nrows = 100)
classes <- sapply(initial, class)
tabAll <- read.table("bigdata.txt", colClasses = classes)
```

- Set `nrows`. This doesn't make R run faster but it helps with memory usage.

# Exercise

1. Write your R code to read the first 100 rows from "baby.csv", skip the headers, and assign it to variable 'data'.
2. Check the class type of variable 'data', and print the total number of rows and columns for 'data'. (Hint: nrow(), ncol())
3. Convert variable 'data' to matrix type and assign it to 'dataM'. (Hint: data.matrix())

```
data <- read.table("baby.csv", sep=",", skip=1, nrows=100)
nrow(data)
```

```
## [1] 100
```

```
ncol(data)
```

```
## [1] 6
```

```
dataM <- data.matrix(data)
dataM
```

# Reading Data Summary

There are of course, many R packages that have been developed to read in all kinds of other datasets, and you may need to resort to one of these packages if you are working in a specific area.

For large dataset:

- How much memory is available on your system?
- What other applications are in use? Can you close any of them?
- Are there other users logged into the same system?
- Operating systems, some limit the amount of memory a single process can access

# Writing Data

There are analogous functions for writing data to files

- `write.table`, `write.csv`, for writing tabular data to text files (i.e. CSV)
- `writeLines`, for writing character data line-by-line to a file or connection
- `dump`, for dumping a textual representation of multiple R objects
- `dput`, for outputting a textual representation of an R object
- `save`, for saving an arbitrary number of R objects in binary format (possibly compressed) to a file.
- `serialize`, for converting an R object into a binary format.

# Writing Data

```
m <- matrix(seq(1,100,5),4,5)
m
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1   21   41   61   81
## [2,]    6   26   46   66   86
## [3,]   11   31   51   71   91
## [4,]   16   36   56   76   96
```

```
write.table(m,sep=' ',file="output.R")
m1 <- read.table("output.R",sep =' ')
m1
```

```
##   V1 V2 V3 V4 V5
## 1  1 21 41 61 81
## 2  6 26 46 66 86
## 3 11 31 51 71 91
## 4 16 36 56 76 96
```

# Using the readr Package

The `readr` package is recently developed by Hadley Wickham to deal with reading in large flat files quickly.

```
library(readr)
read_csv(mtcars_path)
write_csv(mtcars, mtcars_path)
```

# Interfaces to the Outside World

Data are read in using connection interfaces. Connections can be made to files (most common) or to other more exotic things.

- file, opens a connection to a file
- gzfile, opens a connection to a file compressed with gzip
- bzfile, opens a connection to a file compressed with bzip2
- url, opens a connection to a webpage

# Connect to text files

Connections to text files can be created with the file() function.

```
str(file)
```

```
## function (description = "", open = "", blocking = TRUE, enc
##     raw = FALSE, method = getOption("url.method", "default"
```

The open argument allows for the following options:

- "r" open file in read only mode
- "w" open a file for writing (and initializing a new file)
- "a" open a file for appending
- "rb", "wb", "ab" reading, writing, or appending in binary mode

# Example - 1

```
## Create a connection to 'foo.txt'
con <- file("foo.txt")

## Open connection to 'foo.txt' in read-only mode
open(con, "r")

## Read from the connection
data <- read.csv(con)

close(con)
```

# Example - 2

Open connection to gz-compressed text file

```
con <- gzfile("words.gz")
x <- readLines(con, 10)
```

The above example used the gzfile() function which is used to create a connection to files compressed using the gzip algorithm. There is a complementary function writeLines() that takes a character vector and writes each element of the vector one line at a time to a text file.

# Example - 3

Open connection to url

```
con <- url("http://www.sjtu.edu.cn", "r")
## Read the web page
x <- readLines(con)
## Print out the first few lines
head(x)
```

Using URL connections can be useful:

1. producing a reproducible analysis
2. Opening a web browser and downloading a dataset by hand.

Of course, the code you write with connections may not be executable at a later date if things on the server side are changed or reorganized.

# Your turn!

Please read chapter 3 of Introduction to Data Science (2020) by Rafael Irizarry. (https://rafalab.github.io/dsbook)

We will ask you to write r code for homework 1 (coming tonight!)