Introduction to R and R data structures

EDUC 260A: Introduction to Programming and Data Management

Ozan Jaquette

What is R? Why R?

What is R?

For detailed info visit R-project.org

The Inter-University Consortium for Political and Social Research (ICPSR) says:

> *R is "an alternative to traditional statistical packages such as SPSS, SAS, and Stata such that it is an extensible, open-source language and computing environment for Windows, Macintosh, UNIX, and Linux platforms. Such software allows for the user to freely distribute, study, change, and improve the software under the Free Software Foundation's GNU General Public License."*

I don't find this definition particularly helpful. I think of *R* as:

- An "open source" programming language and software that provide collections of interrelated "functions"
- "open source" means that *R* is free and created by the user community. The user community can modify basic things about *R* and add new capabilities to what R can do the user community can modify R and
- a "function" is usually something that takes in some "input," processes this input in some way, and creates some "output"
  - e.g., the `max()` function takes as input a collection of numbers (e.g., 3,5,6) and returns as output the number with the maximum value
  - e.g., the `lm()` function takes in as inputs a dataset and a statistical model you specify within the function, and returns as output the results of the regression model

Base R vs. R packages

Base R

- When you install R, you automatically install the "Base R" set of functions
- Example of a few of the functions in in Base R:
  - `as.character()` function
  - `print()` function
  - `setwd()` function

R packages

- an R "package" (or "library") is a collection of (related) functions developed by the R community
- Examples of R packages:
  - `tidyverse` package for manipulating and visualizing data
  - `igraph` package for network analyses
  - `leaflet` package for mapping
  - `rvest` package for webscraping
  - `rtweet` package for streaming and downloading data from Twitter
- **All** R packages are free! More about R packages in later weeks...

Installing and Loading R packages

You only need to install a package once. To install an R package use `install.package()` function.

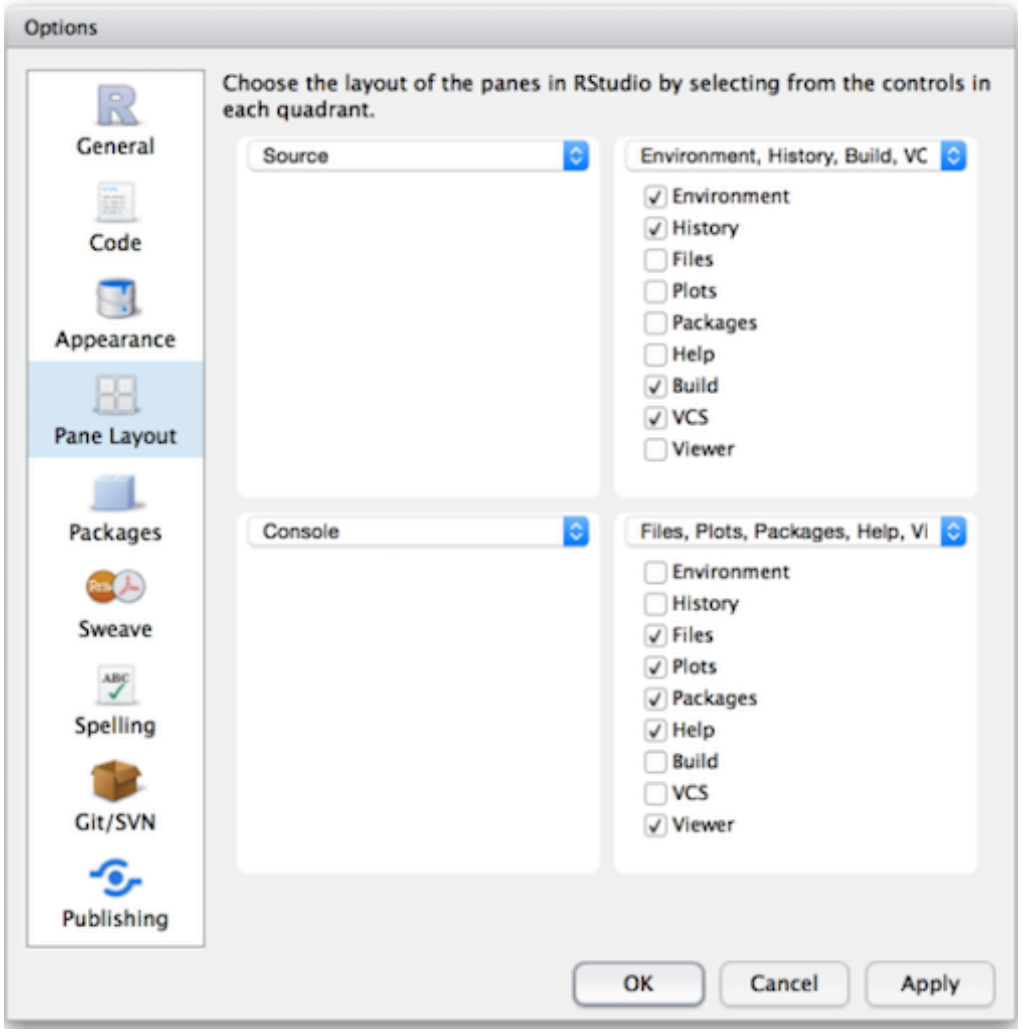
```
#install.packages("tidyverse")
```

You need to load a package everytime you plan to use it. To load a package use the `library()` function.

```
library(tidyverse)
#> -- Attaching packages --------------------------------------- tidyverse 1.3.1
#> v ggplot2 3.3.5     v purrr   0.3.4
#> v tibble  3.1.3     v dplyr   1.0.7
#> v tidyr   1.1.3     v stringr 1.4.0
#> v readr   2.0.0     v forcats 0.5.1
#> -- Conflicts ------------------------------------------ tidyverse_conflicts()
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag()    masks stats::lag()
```

RStudio

"RStudio is an integrated development environment (IDE) for R. It includes a console, syntax-highlighting editor that supports direct code execution, as well as tools for plotting, history, debugging and workspace management."



R Markdown

R Markdown

- R Markdown is a file format – R Markdown files have the extension **.Rmd** – that can create many kinds of static and dynamic documents
- From RStudio
  - "R Markdown is a file format for making dynamic documents with R. An R Markdown document is written in markdown (an easy-to-write plain text format) and contains chunks of embedded R code"
- Examples of static documents
  - PDF documents, PDF presentations, MS word documents
- Examples of dynamic documents
  - html presentations, interactive dashboards, etc.

How we will be using R Markdown in this class

- All lectures created using R Markdown
- You will use R Markdown to complete homework assignments

After this class you might:

- never use Microsoft Word again!
- Use R Markdown to create: papers for class; presentations; journal manuscripts; your dissertation; etc.

Why learn R? R can do a lot of stuff!

How we have used R+RStudio+RMarkdown in our research team

- Stuff traditional statistical software (e.g., SPSS, Stata) can do
  - Data manipulation, creating analysis datasets
  - Descriptive statistics and statistical models
  - Graphs
- Stuff traditional statistical software cannot do
  - Static policy reports
  - Static presentations
    - All lectures for this class written in RMarkdown
  - Interactive presentations
  - Interactive maps
  - Interactive dashboards
  - Interactive graphs

Some of the other stuff R can create/do:

- Websites; journals; books; web-scraping; network analysis; machine learning/artificial intelligence

Executing R commands

R as a calculator

```
5
#> [1] 5
5+2
#> [1] 7
10*3
#> [1] 30
```

Executing commands in R

```
5
#> [1] 5
5+2
#> [1] 7
10*3
#> [1] 30
```

Three ways to execute commands in R

1. Type/copy commands directly into the "console"
2. 'code chunks' in RMarkdown (.Rmd files)
   - Can execute one command at a time, one chunk at a time, or "knit" the entire document
3. R scripts (.R files)
   - This is just a text file full of R commands
   - Can execute one command at a time, several commands at a time, or the entire script

Shortcuts you should learn for executing commands

```
5+2
#> [1] 7
10*3
#> [1] 30
```

Three ways to execute commands in R

1. Type/copy commands directly into the "console"
2. 'code chunks' in RMarkdown (.Rmd files)
   - **Cmd/Ctrl** + **Enter**: execute highlighted line(s) within chunk
   - **Cmd/Ctrl** + **Shift** + **k**: "knit" entire document
3. R scripts (.R files)
   - **Cmd/Ctrl** + **Enter**: execute highlighted line(s)
   - **Cmd/Ctrl** + **Shift** + **Enter** (without highlighting any lines): run entire script

R objects and data structures

Preview of lecture on objects

- This section of the lecture provides a conceptual and practical introduction to "objects" in R
- **Important**: goal is to begin to develop familiarity with concepts that we will introduce in more detail in later weeks
  - I don't expect you to understand or retain all this information perfectly
  - So just focus on understanding as much as you can and ask any questions that come to mind

Assignment

Assignment refers to creating an "object" and assigning values to it

- The object may be a variable, a dataset, a bit of text that reads "la la la"
- `<-` is the assignment operator
  - in other languages `=` is the assignment operator
- general syntax:
  - `object_name <- object_values`
  - good practice to put a space before and after assignment operator

```
# Create an object and assign value
a <- 5
a
#> [1] 5

b <- "yay!"
b
#> [1] "yay!"
```

Objects

R is an "object-oriented" programming language (like Python, JavaScript). So, what is an "object"?

- formal computer science definitions are confusing because they require knowledge of concepts we haven't introduced yet
- More intuitively, I think objects as anything I assign values to
  - For example, below, `a` and `b` are objects I assigned values to

```
a <- 5
a
#> [1] 5
b <- "yay!"
b
#> [1] "yay!"
```

- Ben Skinner (my R maven) says "Objects are like boxes in which we can put things: data, functions, and even other objects."

Most commercial statistical software packages (e.g., SPSS, Stata) operate on datasets, which consist of rows of observations and columns of variables

- Usually, these packages can open only one dataset at a time
- By contrast, in R everything is an object and there is no limit to the number of objects R can hold (except memory)

Vectors

The fundamental data structure in R is the "vector"

- A vector is a collection of values
- The individual values within a vector are called "elements"
- Values in a vector can be numeric, character (e.g., "Apple"), or some other *type*

Below we use the combine function `c()` to create a numeric vector that contains three elements

- Help file says that `c()` "combines values into a vector or list"

```
#?c # to see help file for the c() "combine" function
x <- c(4, 7, 9) # create object called x, which is a vector with three elements
# (each an integer)
x # print object x
#> [1] 4 7 9
```

Vector where the elements are characters

```
animals <- c("lions", "tigers", "bears", "oh my") # create object called animals
animals
#> [1] "lions"  "tigers" "bears"  "oh my"
```

Student task

Either in the R console or within the R markdown file, do the following:

1. Create a vector called `v1` with three elements, where all the elements are numbers. Then print the values.
2. Create a vector called `v2` with four elements, where all the elements are characters (i.e., enclosed in single ' ' or double " " quotes). Then print the values.
3. Create a vector called `v3` with five elements, where some elements are numeric and some elements are characters. Then print the values.

Solution to student task

```r
v1 <- c(1, 2, 3)
# create a vector called v1 with three elements
# all the elements are numbers
v1 # print value
#> [1] 1 2 3
```

```r
v2 <- c("a", "b", "c", "d")
# create a vector called v2 with four elements
# all the elements are characters
v2 # print value
#> [1] "a" "b" "c" "d"
```

```r
v3 <- c(1, 2, 3, "a", "b")
# create a vector called v3 with five element
# some elements are numeric and some elements are characters
v3 # print value
#> [1] "1" "2" "3" "a" "b"
```

Formal classification of vectors in R

Here, I introduce the classification of vectors by Grolemund and Wickham

There are two broad types of vectors

1. **Atomic vectors**. An object that contains elements. Six "types" of atomic vectors:
   - **logical**, **integer**, **double**, **character**, **complex**, and **raw**.
     - **Integer** and **double** vectors are collectively known as **numeric** vectors.
2. **Lists**. Like atomic vectors, lists are objects that contain elements
   - elements within a list may be atomic vectors
   - elements within a list may also be other lists; that is lists can contain other lists

One difference between atomic vectors and lists: **homogeneous** vs. **heterogeneous** elements

- atomic vectors are **homogeneous**: all elements within atomic vector must be of the same type
- lists can be **heterogeneous**: e.g., one element can be an integer and another element can be character

Formal classification of vectors in R

Visual representation of the Grolemund and Wickham classification

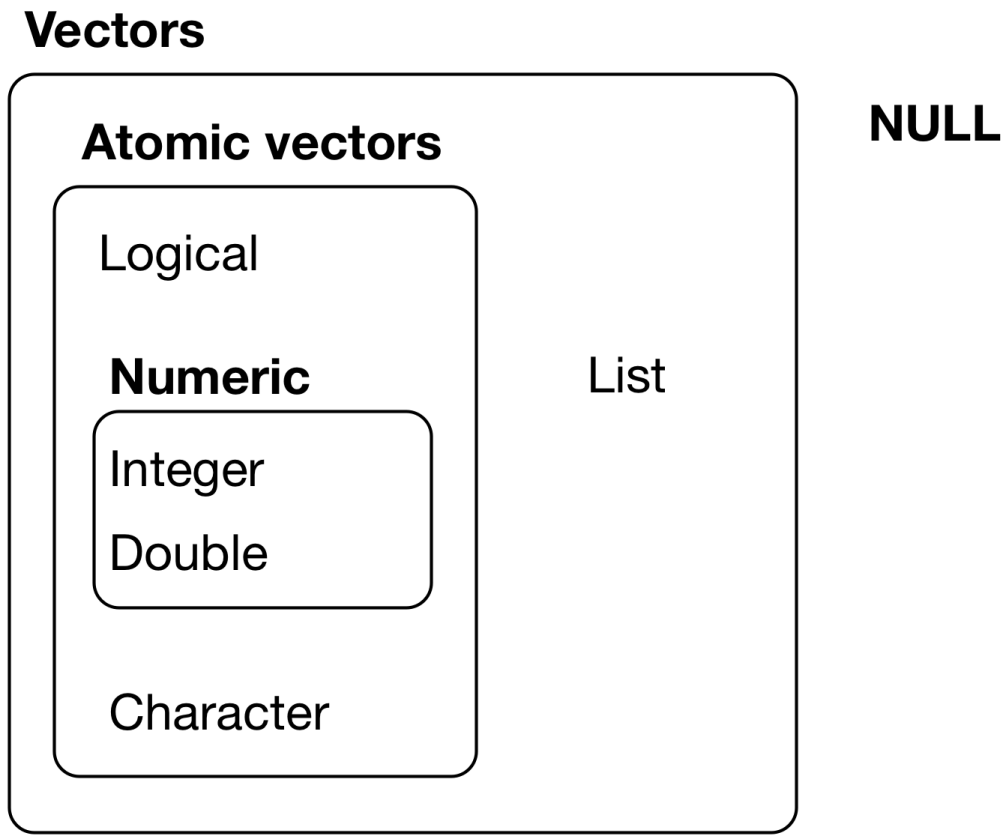


Figure 1: Overview of data structures (Grolemund and Wickham, 2018, chapter 20)

Developing an intuitive understanding of vector types

Grolemund and Wickham classification:

1. **Atomic vectors**. six "types": logical, integer, double, character, complex, raw.
2. **Lists**

Problem with this classification:

- Not conceptually intutive
- Technically, lists are a type of vector, but people often think of atomic vectors and lists as fundamentally different things

Classification used by my R maven Ben Skinner:

- data **type**: logical, numeric (integer and double), character, etc.
- data **structure**: vector, list, matrix, etc.

I find Skinner's classification more intuitive conceptually. However, it isn't completely consistent with how R and R functions think about objects

Atomic vectors

"Length" of an atomic vector is the number of elements

For remainder of lecture, I'll use the term **vector** to refer to atomic vectors

Use `length()` function to examine vector length

```
x <- c(4, 7, 9)
x
#> [1] 4 7 9
length(x)
#> [1] 3

animals <- c("lions", "tigers", "bears", "oh my")
animals
#> [1] "lions"  "tigers" "bears"  "oh my"
length(animals)
#> [1] 4
```

A single number (or a single string/character) is a vector with `length==1`

```
z <- 5
length(z)
#> [1] 1
length("Tommy")
#> [1] 1
```

Data type of a vector

The "type" of an atomic vector refers to the elements within the vector.

While there are six "types" of atomic vectors, we'll focus on the following types:

- numeric:
  - "integer" (e.g., 5)
  - "double" (e.g., 5.5)
- character (e.g., "ozan")
- logical (e.g., `TRUE`, `FALSE`)

Use `typeof()` function to examine vector type

```
x
#> [1] 4 7 9
typeof(x)
#> [1] "double"

p <- c(1.5, 1.6)
p
#> [1] 1.5 1.6
typeof(p)
#> [1] "double"

animals
#> [1] "lions"  "tigers" "bears"  "oh my"
typeof(animals)
#> [1] "character"
```

Data type of a vector, numeric

Numeric vectors can be "integer" (e.g., 5) or "double" (e.g., 5.5)

```
typeof(1.5)
#> [1] "double"
```

R stores numbers as doubles by default.

```
x
#> [1] 4 7 9
typeof(x)
#> [1] "double"
```

To make an integer, place an `L` after the number:

```
typeof(5)
#> [1] "double"
typeof(5L)
#> [1] "integer"
```

Data type of a vector, character

In contrast to "numeric" data types which are used to store numbers, the "character" data type is used to store **strings** of text.

- Strings may contain any combination of numbers, letters, symbols, etc.
- Character vectors are sometimes referred to as string vectors

When creating a vector where elements have `type==character` (or when referring to the value of a string), place single ' or double "" quotes around text

- the text within quotes is the "string"

```
c1 <- c("cat",'cash','candy cane')
c1
#> [1] "cat"         "cash"        "candy cane"
typeof(c1)
#> [1] "character"
length(c1)
#> [1] 3
```

Numeric values can also be stored as strings

```
c2 <- c("1","2","3")
c2
#> [1] "1" "2" "3"
typeof(c2)
#> [1] "character"
```

Data type of a vector, logical

Logical vectors can take three possible values: `TRUE`, `FALSE`, `NA`

- `TRUE`, `FALSE`, `NA` are special keywords; they are different from the character strings `"TRUE"`, `"FALSE"`, `"NA"`
- Don't worry about `"NA"` for now

```
typeof(TRUE)
#> [1] "logical"
typeof("TRUE")
#> [1] "character"

typeof(c(TRUE,FALSE,NA))
#> [1] "logical"
typeof(c(TRUE,FALSE,NA,"FALSE"))
#> [1] "character"

log <- c(TRUE,TRUE,FALSE,NA,FALSE)
typeof(log)
#> [1] "logical"
length(log)
#> [1] 5
```

We'll learn more about logical vectors later

All elements in (atomic) vector must have same data type.

Atomic vectors are **homogenous**;

- An atomic vector has one data type
- all elements within an atomic vector must have the same data "type"

If a vector contains elements of different type, the vector type will be type of the most "complex" element

Atomic vector types from simplest to most complex:

- logical $<$ integer $<$ double $<$ character

```
typeof(c(TRUE,TRUE,NA))
#> [1] "logical"

# recall L after an integer forces type to be integer
# rather than double
typeof(c(TRUE,TRUE,NA,1L))
#> [1] "integer"
typeof(c(TRUE,TRUE,NA,1.5))
#> [1] "double"
typeof(c(TRUE,TRUE,NA,1.5,"howdy!"))
#> [1] "character"
```

Named vectors

All vectors can be "named" (i.e., name individual elements within vector)

Example of creating an unnamed vector

- the `str()` function "compactly display[s] the internal structure of an R object" [from help file]; very useful for describing objects

```
#?str
x <- c(1,2,3,"hi!")
x
#> [1] "1"   "2"   "3"   "hi!"
str(x)
#>  chr [1:4] "1" "2" "3" "hi!"
```

Example of creating a named vector

```
y <- c(a=1,b=2,3,c="hi!")
y
#>     a     b           c
#>   "1"   "2"   "3" "hi!"
str(y)
#>  Named chr [1:4] "1" "2" "3" "hi!"
#>  - attr(*, "names")= chr [1:4] "a" "b" "" "c"
```

Sequences

(Loose) definition: a sequence is a set of numbers in ascending or descending order

A vector containing a "sequence" of numbers (e.g., 1, 2, 3) can be created using the colon operator `:` with the notation `start:end`

```
-5:5
#>  [1] -5 -4 -3 -2 -1  0  1  2  3  4  5
5:-5
#>  [1]  5  4  3  2  1  0 -1 -2 -3 -4 -5
s<- 1:10 #same as this: s<- c(1:10)
s
#>  [1]  1  2  3  4  5  6  7  8  9 10
length(s)
#> [1] 10
```

Creating sequences using `seq()` function - basic syntax [with default values]:

```
seq(from = 1, to = 1, by = 1)
```

```
seq(10,15)
#> [1] 10 11 12 13 14 15
seq(from=10,to=15,by=1)
#> [1] 10 11 12 13 14 15
seq(from=100,to=150,by=10)
#> [1] 100 110 120 130 140 150
```

Vectorized math

Most mathematical operations operate on each element of the vector

- e.g., add a single value to a vector and that value will be added to each element of the vector

```
1:3
#> [1] 1 2 3
1:3+.5
#> [1] 1.5 2.5 3.5
(1:3)*2
#> [1] 2 4 6
```

Mathematical operations involving two vectors with the same length behave differently

- e.g., for addition: add element 1 of vector 1 to element 1 of vector 2, add element 2 of vector 1 to element 2 of vector 2, etc.

```
c(1,1,1)+c(1,0,2)
#> [1] 2 1 3
c(1,1,1)*c(1,0,2)
#> [1] 1 0 2
```

Lists

Lists

What is a **list**?

- Like (atomic) vectors, a list is an object that contains **elements**
- Unlike vectors, data types can differ across elements within a list
- An element within a list can be another list
  - this characteristic makes lists more complicated than vectors
  - suitable for representing hierarchical data

Lists are more complicated than vectors; today we'll just provide a basic introduction

Create lists using `list()` function

Create a vector (for comparison purposes)

```
a <- c(1,2,3)
typeof(a)
#> [1] "double"
length(a)
#> [1] 3
```

Create a list

```
b <- list(1,2,3)
typeof(b)
#> [1] "list"
length(b)
#> [1] 3
b # print list is awkward
#> [[1]]
#> [1] 1
#>
#> [[2]]
#> [1] 2
#>
#> [[3]]
#> [1] 3
```

Investigate structure of lists using `str()` function

When investigating lists, `str()` is better than printing the list

```
b <- list(1,2,3)
typeof(b)
#> [1] "list"
length(b)
#> [1] 3
str(b) # 3 elements, each element is a numeric vector w/ length=1
#> List of 3
#>  $ : num 1
#>  $ : num 2
#>  $ : num 3
```

Each element of a list can be a vector of different length (i.e., different number of elements)

```
c <- list(c(3,4),c(-5,1,3))
typeof(c)
#> [1] "list"
length(c)
#> [1] 2
str(c) # 2 elements; element 1=vector w/ length=2; element 2=vector w/length=3
#> List of 2
#>  $ : num [1:2] 3 4
#>  $ : num [1:3] -5 1 3
```

Elements within lists can have different data types

Lists are **heterogeneous**

- data types can differ across elements within a list

```
b <- list(1,2,"apple")
typeof(b)
#> [1] "list"
length(b)
#> [1] 3
str(b)
#> List of 3
#>  $ : num 1
#>  $ : num 2
#>  $ : chr "apple"
```

Vectors are **homogeneous**

```
a <- c(1,2,"apple")
typeof(a)
#> [1] "character"
str(a)
#>  chr [1:3] "1" "2" "apple"
```

Lists can contain other lists

```
x1 <- list(c(1,2), list("apple", "orange"), list(1, 2, 3))
str(x1)
#> List of 3
#>  $ : num [1:2] 1 2
#>  $ :List of 2
#>   ..$ : chr "apple"
#>   ..$ : chr "orange"
#>  $ :List of 3
#>   ..$ : num 1
#>   ..$ : num 2
#>   ..$ : num 3
```

- first element of list is a numeric vector with length=2
- second element is a list with length=2
  - first element is character vector with length=1
  - second element is character vector with length=1
- third element is a list with length=3
  - first element is numeric vector with length=1
  - second element is numeric vector with length=1
  - third element is numeric vector with length=1

You can name each element in the list

```
x2 <- list(a=c(1,2), b=list("apple", "orange"), c=list(1, 2, 3))
str(x2)
#> List of 3
#>  $ a: num [1:2] 1 2
#>  $ b:List of 2
#>   ..$ : chr "apple"
#>   ..$ : chr "orange"
#>  $ c:List of 3
#>   ..$ : num 1
#>   ..$ : num 2
#>   ..$ : num 3
```

`names()` function shows names of elements in the list

```
names(x2) # has names
#> [1] "a" "b" "c"
names(x1) # no names
#> NULL
```

Access individual elements in a "named" list

Syntax: `list_name$element_name`

```
x2 <- list(a=1, b=list("apple", "orange"), c=list(1, 2, 3))
x2$a
#> [1] 1
typeof(x2$a)
#> [1] "double"
length(x2$a)
#> [1] 1

typeof(x2$b)
#> [1] "list"
length(x2$b)
#> [1] 2

typeof(x2$c)
#> [1] "list"
length(x2$c)
#> [1] 3
```

Note: We'll spend more time practicing "accessing elements of a list" in upcoming weeks

Compare structure of list to structure of element within a list

```
str(x2)
#> List of 3
#>  $ a: num 1
#>  $ b:List of 2
#>   ..$ : chr "apple"
#>   ..$ : chr "orange"
#>  $ c:List of 3
#>   ..$ : num 1
#>   ..$ : num 2
#>   ..$ : num 3

str(x2$c)
#> List of 3
#>  $ : num 1
#>  $ : num 2
#>  $ : num 3
```

A DATASET IS JUST A LIST!!!!!

A data frame is a list with the following characteristics:

- Data type can differ across elements (like all lists)
- Each element (column) is a variable
- Each element in a data frame must have the same length
  - The length of an element is the number of observations (rows)
  - Thus, each variable in a data frame has same number of observations
- Each element is named
  - these element names are the variable names
- Typically, each **element**(variable) in a data frame is a **vector**
  - Elements can also be lists. Happens when the variable has a complicated data structure
    - e.g., a variable that identifies the "@" mentions in a tweet

```
names(df)
#> [1] "mpg" "cyl" "hp"
head(df, n=4) # print first few rows
#> # A tibble: 4 x 3
#>     mpg   cyl    hp
#>   <dbl> <dbl> <dbl>
#> 1  21       6   110
#> 2  21       6   110
#> 3  22.8     4    93
#> 4  21.4     6   110
```

Additionally, data frames have "attributes"; we'll discuss those in upcoming weeks

A data frame is a named list

```
head(df, n= 5)
#> # A tibble: 5 x 3
#>     mpg   cyl    hp
#>   <dbl> <dbl> <dbl>
#> 1  21       6   110
#> 2  21       6   110
#> 3  22.8     4    93
#> 4  21.4     6   110
#> 5  18.7     8   175
typeof(df)
#> [1] "list"
names(df)
#> [1] "mpg" "cyl" "hp"
length(df) # length=number of variables
#> [1] 3
str(df)
#> 'data.frame':    32 obs. of  3 variables:
#>  $ mpg: num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
#>  $ cyl: num  6 6 4 6 8 6 8 4 4 6 ...
#>  $ hp : num  110 110 93 110 175 105 245 62 95 123 ...
```

Like any named list, we can examine the elements

- Individual elements of a data frame are the variables
- these variables are vectors with length equal to the number of rows/observations

```
typeof(df$mpg)
```

Main takeaways about atomic vectors and lists

Basic data stuctures

1. **(Atomic) vectors**: **logical**, **integer**, **double**, **character**.
   - each element in vector must have same data type
2. **Lists**:
   - Data type can differ across elements

Takeaways

- These concepts are difficult; ok to feel confused
- I will reinforce these concepts throughout the course
- Good practice: run simple diagnostics on any new object
  - `length()` : how many **elements** in the object
  - `typeof()` : what **type** of data is the object
  - `str()` : hierarchical structure of the object

Main takeaways about atomic vectors and lists

Basic data stuctures

1. **(Atomic) vectors**: **logical**, **integer**, **double**, **character**.
   - each element in vector must have same data type
2. **Lists**:
   - Data type can differ across elements

Takeaways, continued

- These data structures (vectors, lists) and data types (e.g., character, numeric, logical) are the basic building blocks of all object oriented programming languages
- Application to statistical analysis
  - Datasets are just lists
  - The individual elements – columns/variables – within a dataset are just vectors
- These structures and data types are foundational for all "data science" applications
  - e.g., mapping, webscraping, network analysis, etc.

Matrices

Matrices

A **matrix** is a collection of elements arranged in a two-dimensional rectangular layout

- A matrix is another "data structure," in addition to vectors and lists
- Create a matrix named `m` with 2 rows and 3 columns

```
m <- matrix(
  c(2, 4, 3, 1, 5, 7), # the data elements
  nrow=2,              # number of rows
  ncol=3,              # number of columns
  byrow = TRUE         # fill matrix by rows
)

m # print matrix m
#>      [,1] [,2] [,3]
#> [1,]    2    4    3
#> [2,]    1    5    7
```

Investigate matrix `m`

```
typeof(m) # type = "double"
#> [1] "double"
str(m) # type = numeric; has two rows and three columns
#>  num [1:2, 1:3] 2 1 4 5 3 7
class(m) # class = matrix; more on class later
#> [1] "matrix" "array"
```

Matrices

Like atomic vectors, matrices are homogenous data structures

```
m2 <- matrix(
  c(2, 4, 3, "a", "b", "c"), # the data elements
  nrow=2,                    # number of rows
  ncol=3,                    # number of columns
  byrow = TRUE               # fill matrix by rows
)

m2
#>      [,1] [,2] [,3]
#> [1,] "2"  "4"  "3"
#> [2,] "a"  "b"  "c"
```

Investigate matrix `m`

```
typeof(m2) # type = "character"
#> [1] "character"
str(m2) # type = character; has two rows and three columns
#>  chr [1:2, 1:3] "2" "a" "4" "b" "3" "c"
```

Why are data frames based on lists rather than matrices?

- a matrix is a homogenous data structure, so you couldn't have both a numeric variable and a character variable
- a list is a heterogeneous data structure, allowing for variables of different underlying data types

Matrices

How are matrices used in R

- the underlying code for statistical models uses matrices (e.g., covariance matrix, matrix of regression coefficients)
- For most data manipulation tasks, matrices used much less frequently than vectors and lists
  - In this course, we won't use matrices much at all
- Particular applications (e.g., social network analysis) make frequent use of matrices

Matrices

How are matrices used in R

- Create an "adjacency matrix," which defines whether actors are connected to one another in a social network

```
a <- matrix(
  c(NA,NA,NA,NA,
    1,NA,NA,NA,
    1,0,NA,NA,
    0,1,0,NA), # the data elements
  nrow=4,              # number of rows
  ncol=4,              # number of columns
  byrow = TRUE         # fill matrix by rows
)
a_names <- c("a","b","c","d") # create vector of actor names
rownames(a) <- a_names # assign names to rows
colnames(a) <- a_names # assign names to columns
a
#>    a  b  c  d
#> a NA NA NA NA
#> b  1 NA NA NA
#> c  1  0 NA NA
#> d  0  1  0 NA
```

Practical example

Network data of recruiting visits from colleges to high schools

For this example, don't worry about understanding the code

- We will explain this code over coming weeks

Object `g_2mode_privu` contains:

- off-campus recruiting visits from private colleges/universities to private high schools
- load `g_2mode_privu`

```
# load igraph object of visits by private colleges/universities to private high
load(url("https://github.com/cyouh95/recruiting-chapter/raw/master/data/g_2mode
```

Investigate object `g_2mode_privu`

```
typeof(g_2mode_privu) # igraph package stores network data as type = list
#> [1] "list"
class(g_2mode_privu) # class = igraph
#> [1] "igraph"
```

The "vertices" consist of colleges and high schools

```
vcount(g_2mode_privu) # 1356 "nodes" or "vertices"
#> [1] 1356
table(V(g_2mode_privu)$type) # 1330 private high schools; 26 private colleges/u
#>
#> FALSE  TRUE
#>  1330    26
```

Network data of recruiting visits from colleges to high schools

An igraph object (type = list; class = igraph) can be decomposed into:

- a dataframe that contains characteristics (referred to as "attributes" in network literature) of the vertices
- a matrix that identifies whether two vertices are connected by an edge

Create a data frame of vertex attributes

```
df_attr <- as_data_frame(x = g_2mode_privu, what = "vertices")

typeof(df_attr) # type = list
length(df_attr) # length = number of variables
class(df_attr) # data.frame
str(df_attr)
```

Network data of recruiting visits from colleges to high schools

Examine data frame of vertex attributes

```
#df_attr %>% glimpse()
# vertices = universities
df_attr %>% filter(type == TRUE) %>% select(unitid,univ_name_ipeds,state_code_i

# vertices = high schools
df_attr %>% filter(type == FALSE) %>% select(ppin,name_pss,city_pss, state_code
```

Examine individual variables within data frame

- takeaway: invidividual variables within data frame are vectors!

```
typeof(df_attr$name_pss) # vector of type = character
str(df_attr$name_pss) # length of vector is number of obs

typeof(df_attr$total_enrolled_pss) # vector of type = integer
str(df_attr$total_enrolled_pss)
```

Network data of recruiting visits from colleges to high schools

Create adjacency matrix of which colleges visited which high schools

```
adj_mat <- as_adjacency_matrix(graph = g_2mode_privu, type = "both",
                               sparse = FALSE)
```

Investigate adjacency matrix

```
typeof(adj_mat) # a numeric "double" object
#> [1] "double"
class(adj_mat) # matrix class
#> [1] "matrix" "array"
#str(adj_mat) # 1,356 rows by 1,356 columns
```

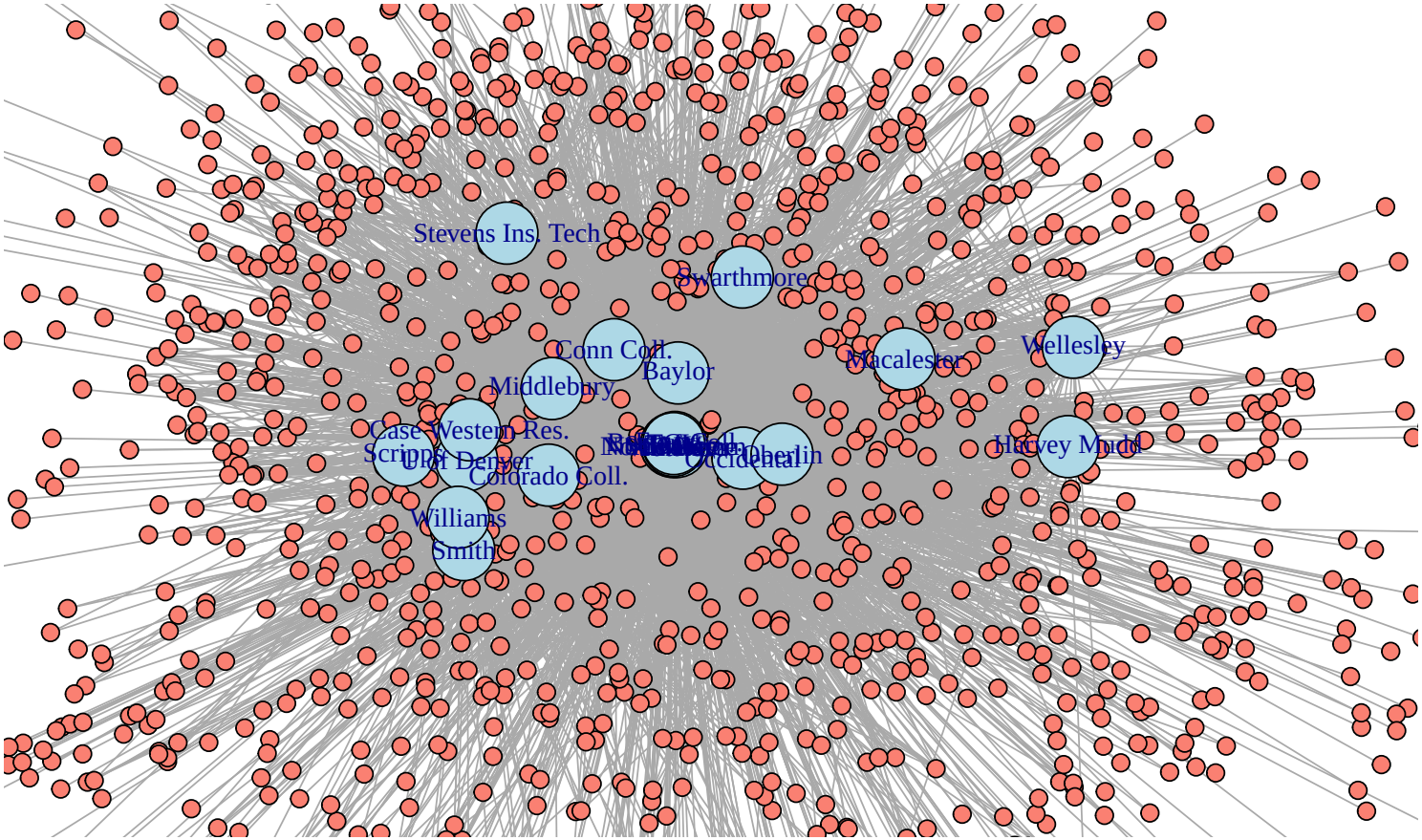
Print a few cells, visits by colleges (columns) to high schools (rows)

- colleges: " `139658` " = Emory University; " `147767` " = Northwestern University; " `152080` " = University of Notre Dame

```
#syntax: object_name[<rows to print>,<columns to print>]
adj_mat[c("00000226","00000237","00000714"),c("139658","147767","152080")]
#>          139658 147767 152080
#> 00000226      1      0      0
#> 00000237      0      0      1
#> 00000714      0      1      1
```

Network data of recruiting visits from colleges to high schools

Plot the 2-mode network



Using R functions

What are functions

Functions are pre-written bits of code that accomplish some task.

Functions generally follow three sequential steps:

1. take in an **input** object(s)
2. **process** the input.
3. **return** (A) a new object or (B) a visualizatoin (e.g., plot)

For example, `sum()` function calculates sum of elements in a vector

1. **input**. takes in a vector of elements (numeric or logical)
2. **processing**. Calculates the sum of elements
3. **return**. Returns numeric vector of length=1; value is sum of input vector

```
sum(c(1,2,3))
#> [1] 6
typeof(sum(c(1,2,3))) # type of object created by sum()
#> [1] "double"
length(sum(c(1,2,3))) # length of object created by sum()
#> [1] 1

#sum(c(TRUE,TRUE,FALSE))
#typeof(sum(c(TRUE,TRUE,FALSE))); length(sum(c(TRUE,TRUE,FALSE)))
```

Function syntax

Components of a function

- function name (e.g., `sum()`, `length()`, `seq()`)
- function arguments
  - Inputs that the function takes, which determine what function does
    - can be vectors, data frames, logical statements, etc.
  - In "function call" you specify values to assign to these function arguments
    - e.g., `sum(c(1,2,3))`
  - Separate arguments with a comma `,`
    - e.g., `seq(10,15)` Example: the sequence function, `seq()`

```
seq(10,15)
#> [1] 10 11 12 13 14 15
```

Function syntax: More on function arguments

Usually, function arguments have names

- e.g., the `seq()` function includes the arguments `from`, `to`, `by`
- when you call the function, you need to assign values to these arguments; but you usually don't have to specify the name of the argument

```
seq(from=10, to=20, by=2)
#> [1] 10 12 14 16 18 20
seq(10,20,2)
#> [1] 10 12 14 16 18 20
```

Many function arguments have "default values", set by whoever wrote the function

- if you don't specify a value for that argument, the default value is inserted
- e.g., partial list of default values for `seq()`: `seq(from=1, to=1, by=1)`

```
seq()
#> [1] 1
seq(to=10)
#>  [1]  1  2  3  4  5  6  7  8  9 10
seq(10) # R assigned value of 10 to "to" rather than "from" or "by"
#>  [1]  1  2  3  4  5  6  7  8  9 10
```

Function arguments, the `na.rm` argument

When R performs a calculation and an input has value `NA`, output value is `NA`

```
5+4+NA
#> [1] NA
```

R functions that perform calculations often have argument named `na.rm`

- `na.rm` argument asks whether to remove `NA` values prior to calculation
- For most functions, default value is `na.rm = FALSE`
  - This means "do not remove `NAs`" prior to calculation
  - e.g., default values for `sum()` function: `sum(..., na.rm = FALSE)`

```
sum(c(1,2,3,NA), na.rm = FALSE) # default value
#> [1] NA
sum(c(1,2,3,NA))
#> [1] NA
```

- if you specify, `na.rm = TRUE`, `NA` values removed prior to calculation

```
sum(c(1,2,3,NA), na.rm = TRUE)
#> [1] 6
```

Help files for functions

To see help file on a function, type `?function_name` without parentheses

```
?sum
?seq
```

Contents of help files

- **Description**. What the function does
- **Usage**. Syntax, including default values for arguments
- **Arguments**. Description of function arguments
- **Details**. Details and idiosyncracies of about how the function works.
- **Value**. What (object) the function "returns"
  - e.g., `sum()` returns vector of length 1 whose value is sum of input vector
- **References**. Additional reading
- **See Also**. Related functions
- **Examples**. Examples of function in action
- Bottom of help file identifies the package the function comes from

Practice!

- when you encounter a new function, spend two minutes reading the help file
- over time, help files will feel less cryptic and will start to feel helpful

Function arguments, the dot-dot-dot (`...`) argument

On help file for many functions, you will see an argument called `...`, referred to as the "dot-dot-dot" argument

```
?sum
?seq
```

"Dot-dot-dot" arguments have several uses. What you should know for now:

- `...` refers to arguments that are "un-named"; but user can specify values
  - e.g., default syntax for `sum()` : `sum(..., na.rm = FALSE)`
    - argument `na.rm` is "named" (name is `na.rm`); argument `...` un-named
- `...` used to allow a function to take an arbitrary number of arguments:

```
#Here, sum function takes 1 un-named argument, specifically c(10,5,NA)
sum(c(10,5,NA),na.rm=TRUE)
#> [1] 15

#Here the sum function takes 3 un-named arguments
sum(10,5,NA,na.rm=TRUE)
#> [1] 15

#Here the sum function takes 5 un-named arguments
sum(10,5,10,20,NA,na.rm=TRUE)
#> [1] 45
```

Appendix

Directories and filepaths

Directories and filepaths

- Give you a very brief overview of "directories" (i.e., folders) and "filepaths" (tells you where folder is located) in R
- Why? After this overview we will ask you to create the directory structure you will use for all files related to this class
- Your problem set due before class next Friday will give you more practice with filepaths and we have created a short document that may be helpful in working through this problem set LINK

Working directory

(Current) Working directory

- The folder/directory in which you are currently working
- This is where R looks for files
- Files located in your current working directory can be accessed without specifying a filepath because R automatically looks in this folder

Function `getwd()` shows current working directory

```
getwd()
#> [1] "C:/Users/ozanj/Documents/rclass1/lectures/intro_to_r"
```

Command `list.files()` lists all files located in working directory

```
getwd()
#> [1] "C:/Users/ozanj/Documents/rclass1/lectures/intro_to_r"
list.files()
#> [1] "data-structures-overview.png" "fp1.JPG"
#> [3] "fp2.JPG"                      "intro_to_r.pdf"
#> [5] "intro_to_r.Rmd"               "intro_to_r.tex"
#> [7] "intro_to_r_files"             "pane_layout.png"
#> [9] "test.txt"
```

Working directory, "Code chunks" vs. "console" and "R scripts"

When you run **code chunks** in RMarkdown files (.Rmd), the working directory is set to the filepath where the .Rmd file is stored

```
getwd()
#> [1] "C:/Users/ozanj/Documents/rclass1/lectures/intro_to_r"
list.files()
#> [1] "data-structures-overview.png" "fp1.JPG"
#> [3] "fp2.JPG"                      "intro_to_r.pdf"
#> [5] "intro_to_r.Rmd"               "intro_to_r.tex"
#> [7] "intro_to_r_files"             "pane_layout.png"
#> [9] "test.txt"
```

When you run code from the **R Console** or an **R Script**, the working directory is your R Project directory (we'll cover this in the next section).

Command `getwd()` shows current working directory

```
getwd()
#> [1] "C:/Users/ozanj/Documents/rclass1/lectures/intro_to_r"
```

Absolute vs. relative filepath

Absolute file path: The absolute file path is the complete list of directories needed to locate a file or folder.

```
setwd("/Users/pm/Desktop/rclass1/lectures/intro_to_r")
```

Relative file path: The relative file path is the path relative to your current location/directory. Assuming your current working directory is in the "intro_to_r" folder and you want to change your directory to the data folder, your relative file path would look something like this:

```
setwd("../../data")
```

`File path shortcuts (Mac)`

Key	Description
~	tilde is a shortcut for user's home directory (mine is my name pm)
../	moves up a level
../../	moves up two level

Exercise

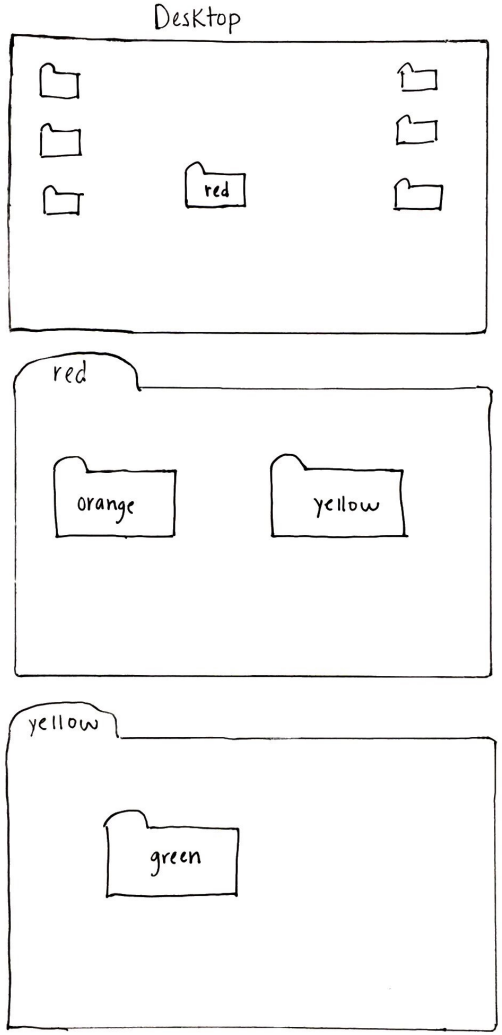
1. Let's create a folder on our desktop and name it red
2. Inside the red folder, create two subfolders named orange and yellow
3. Inside the yellow folder create another subfolder named green

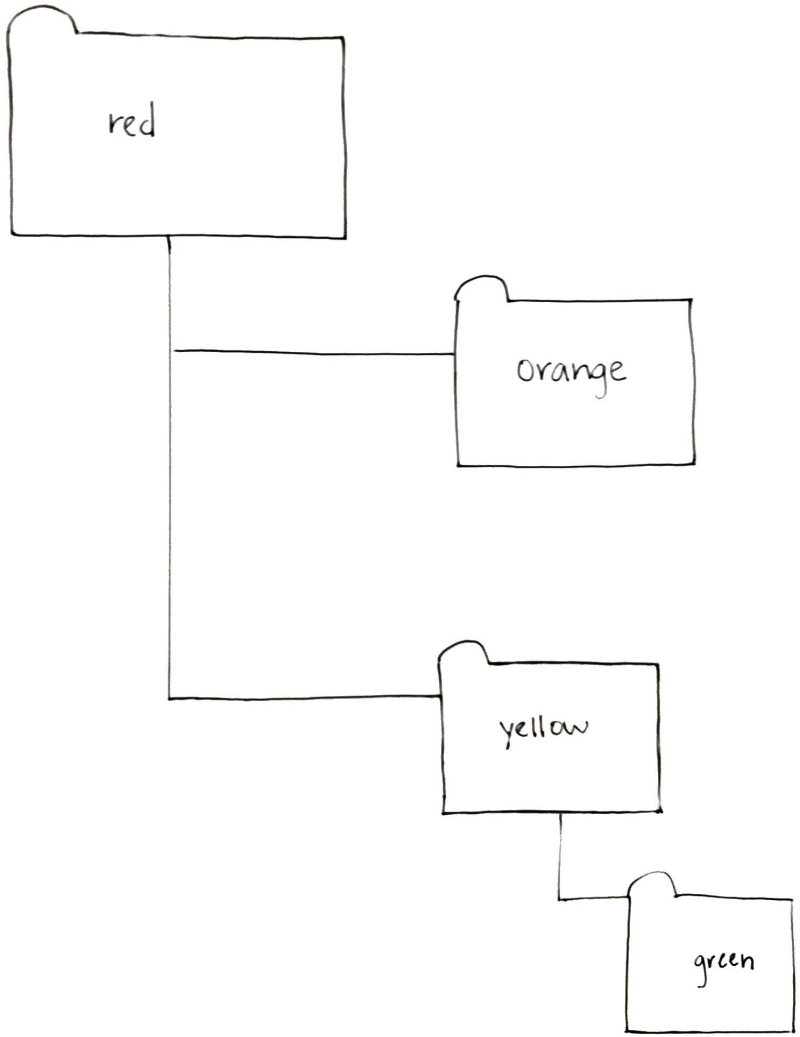
Make sure to name these folders in lowercase.

You should have 1 folder on your desktop called red. Inside the red folder you have two folders called orange and yellow. Inside the yellow folder you have a folder called green.

Here is a visual of how it should look...

File path visual





Exercise continued

Let's say we want to get to the green folder using the absolute file path.

1. View your current working directory `getwd()`
2. Set your working directory to the green folder using the absolute file path
3. Now set your working directory to the orange folder using the relative file path (hint: use `../`)

Solution

```
getwd()
setwd("~/Desktop/red/yellow/green")
getwd()
setwd("../../orange")
getwd()
```

Create “R project” and directory structure

What is an R project? Why are you doing this?

What is an "R project"?

- Helps you keep all files for a project in one place
- When you open an R project, the file-path of your current working directory is automatically set to the file-path of your R-project

Why are we asking you to create R project and download a specific directory structure?

- We want you to be able to run the .Rmd files for each lecture on your own computer
- Sometimes these .Rmd files point to certain sub-folders
- If you create R project and create directory structure we recommend, you will be able to run .Rmd files from your own computer without making any changes to file-paths!

Follow these steps to create "R project" and directory structure

1. Download this zip folder: LINK HERE
   - This zip file contains the shell file directory you should use for this class
   - Unzip the folder
     - Contains folder named "rclass1"; this is the folder that will contain all materials for this course
     - "rclass1" contains two folders: "data" and "lectures"
   - Move "rclass1" folder to your preferred location (e.g, documents, desktop, dropbox, etc)
2. In RStudio, click on "File" » "New Project" » "Existing Directory" » "New Project"
   - "Browse" to find "rclass1" folder you just saved
   - Then click on Create Project
3. Save the following files in "rclass1/lectures/intro_to_r"
   - intro_to_r.Rmd
   - intro_to_r.pdf

Next, you follow these steps

- You can add any additional sub-folders you want to the "rclass1" folder
  - e.g., "syllabus", "resources"
- You can add any additional files you want to the sub-directory folders you unzipped
  - e.g., in "rclass1/lectures/intro_to_r" you might add an additional document of notes you took

R Markdown

What is R Markdown

- R Markdown documents embed R code, output associated with R code, and text into one document
- An R Markdown document is a " 'Living' document that updates every time you compile ["knit"] it"
- R Markdown documents have the extension .Rmd
  - Can think of them as text files with the extension .Rmd rather than .txt
- At top of .Rmd file you specify the "output" style, which dictates what kind of formatted document will be created
  - e.g., `html_document` or `pdf_document`
- When you compile ["knit"] a .Rmd file, the resulting formatted document can be an HTML document, a PDF document, an MS Word document, or many other types

This slide borrows from Darin Christensen

How people use R Markdown

R Markdown creates many types of static and dynamic/interactive documents

- Example of static policy report
- Example of dynamic/interactive presentation

How I use R Markdown

- Journal manuscripts; reports; presentations; for taking notes when I am learning new methods or reading an empirical paper

How we will be using R Markdown files in this class:

- Homework you submit will be .Rmd files, where "output" style will be `html_document` or `pdf_document`
- Lectures we write are .Rmd files, where the output style will be `beamer_presentation` or `html_document`
  - `beamer_presentation` is essentially a PDF document, where each page is a slide

Creating R Markdown documents

Do this with a partner

Approach for creating a RMarkdown document.

1. Point-and-click from within RStudio
   - Click on *File* » *New File* » *R Markdown* » *Document* » choose *HTML* » click *OK*
     - Optional: add title (this is not the file name, just what appears at the top of document)
     - Optional: add author name
   - Save the .Rmd file; *File* » *Save As*
     - Any file name
     - Recommend you save it in same folder you saved this lecture
   - "Knit" the entire .Rmd file
     - Point-and-click OR shortcut: **Cmd/Ctrl + Shift + k**

Components of a .Rmd file

An R Markdown (.Rmd) file consists of several parts

1. **YAML header**
   - YAML stands for "yet another markup language"
   - Controls settings that apply to the whole document (e.g., "output" should be `html_document` or `pdf_document`, whether to include table of contents, etc.)
   - YAML header goes at the very top of the document
   - Starts with a line of three horizontal dashes `---`; ends with a line of three horizontal dashes `---`
2. **Text** in body of .Rmd file
   - e.g., headings; description of results, etc.
3. **R code chunks** in body of .Rmd file

```
a <- c(2,4,6)
a
a-1
```

4. **R output** associated with code chunks

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

Comment: Running R code chunks vs. "knit" entire .Rmd file

Two ways to execute R commands in .Rmd file:

1. "Knit" entire .Rmd file
   - shortcut: **Cmd/Ctrl + Shift + k**
2. "Run" code chunk or selected lines within code chunk
   - Run selected line(s): **Cmd/Ctrl + Enter**
   - Run current chunk: **Cmd/Ctrl + Shift + Enter**

Comment on default settings for RStudio:

- When you knit entire .Rmd file, "objects" created within .Rmd file will not be available after file compiles
- When you run code chunk (or selected lines in chunk), objects created by lines you run will be in your "environment" until you remove them or quit R session

Output types of .Rmd file

Common/important output types:

- **html_document**: R Markdown originally designed to create HTML documents
  - Most features/code in .Rmd files were written for html_document
  - Many of these features are available in other output types
  - When learning R Markdown, best to start by learning html_document
- **pdf_document**: Requires installation of `tinytex` R package or LaTeX (MiKTeX/MacTeX)
  - How it works:
    - You write .Rmd code
    - When you compile, this .Rmd code is transformed into LaTeX code
    - LaTeX "engine" creates the formatted .pdf file
  - Can include some of the same features available for *html_document*
  - Can insert LaTeX commands in .Rmd file with *pdf_document* output
- **beamer_presentation**: Requires installation of LaTeX
  - "beamer" is the name for presentations written in LaTeX
  - Essentially creates PDF of presentation slides
  - Lectures for this class created with *beamer_presentation* output
  - Note: YAML header includes `beamer_header.tex` file, which creates some formatting rules and additional commands

Learning more about R Markdown

Resources

- Cheat sheets and quick reference:
  - Cheat Sheet
  - Quick Reference [I prefer the quick reference]
- Chapters/books
  - Chapter 27 of "R for Data Science" book
  - R Markdown: The Definative Guide book [I prefer this book]

How you will learn R Markdown

- Lectures written as .Rmd file
  - During class run "code chunks" and try to "knit" entire .Rmd file
- I'll assign **small** amount of reading on R Markdown
  - Prior to next week:
    - Spend 15 minutes familiarizing yourself with Quick Reference
    - Read section 3.1 of R Markdown: The Definative Guide, about creating html_document
- Homework must be written in .Rmd file
  - You will submit .Rmd file AND output of compiled file
  - For next week, you will submit homework as html_document output

Directory structure for this class

In order to be able to "knit" entire lectures [rather than just run specific code chunks] make sure that you have the following directory structure:

- rclass1
  - lectures
    - intro_to_r/
    - ...
    - join_data/
    - beamer_header.tex

What is beamer_header.tex?

- A text file that contains LaTeXcode
- This code creates formatting rules that are applied to all lecture slides
- If you go YAML header you will see:

```
includes:
  in_header: ../beamer_header.tex
```

- This runs beamer_header.tex; assumes that beamer_header.tex is located one level up from your current directory
- If you don't have beamer_header.tex saved to appropriate place, you can download it here LINK
- Note: we may revise beamer_header.tex as we work out formatting bugs