Lecture 10

R and the tidyverse // randomization

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AEM 6510

Roadmap

- What is R?
- What is the tidyverse?
- How do we import and manipulate data?

Our goal is to take a hands on approach to learning how we do environmental economics research

A good chunk of this lecture comes from Grant Mcdermott's data science for economists notes, and RStudio education

RStudio Cloud

Getting started

We will be using rstudio.cloud for our coding

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Why?

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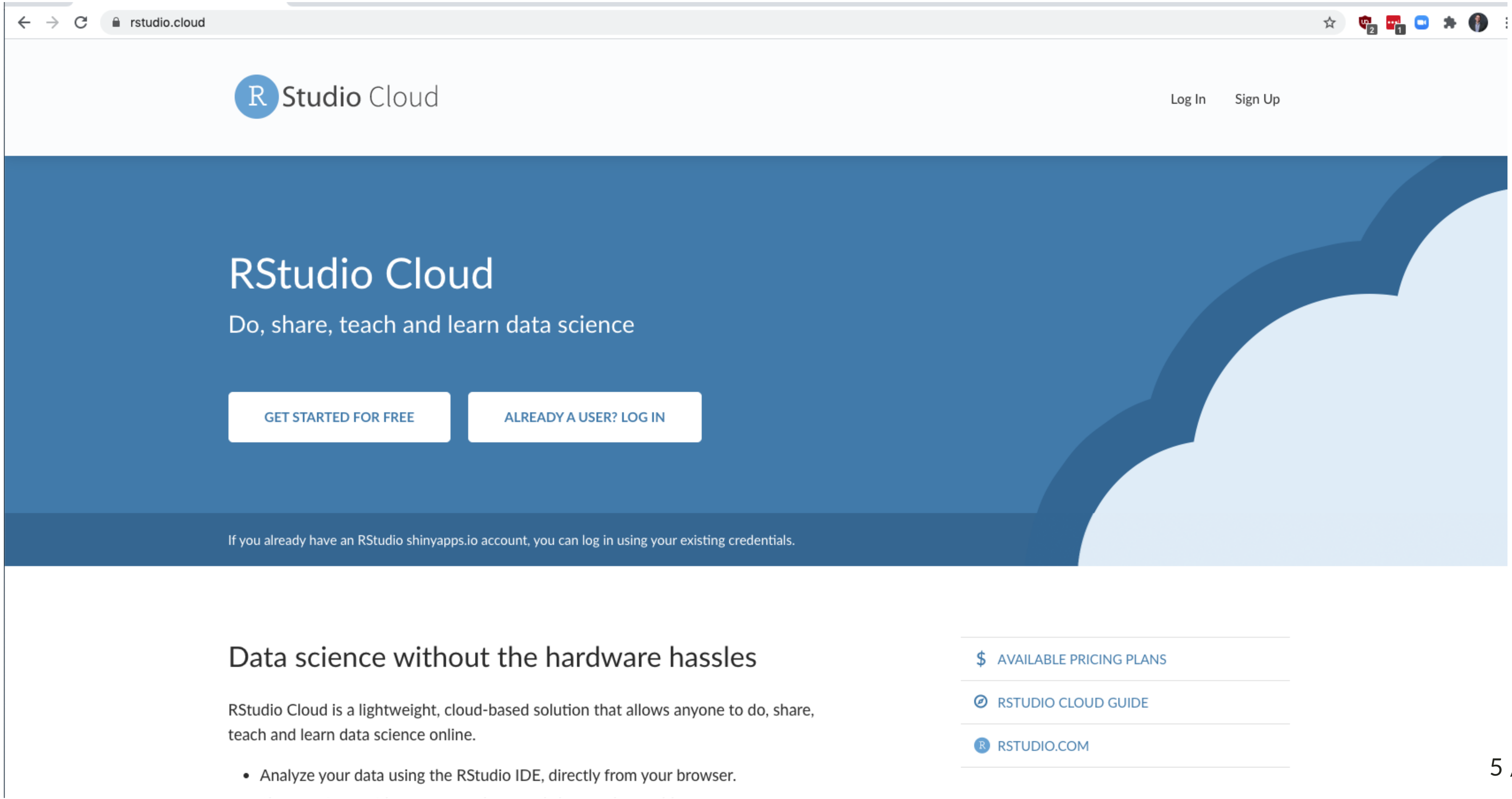
Let's get everything going...

Getting started: login



RStudio Cloud

Do, share, teach and learn data science

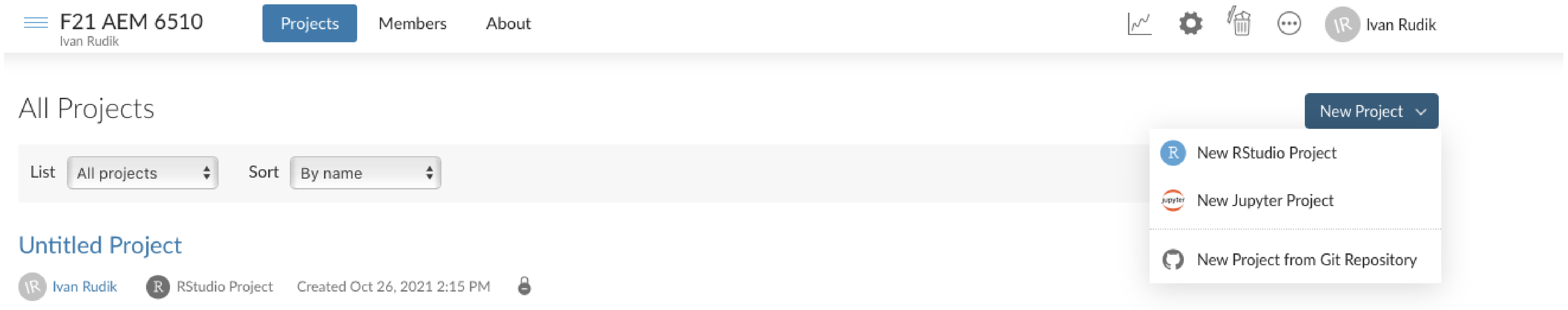
If you already have an RStudio shinyapps.io account, you can log in using your existing credentials.

Data science without the hardware hassles

RStudio Cloud is a lightweight, cloud-based solution that allows anyone to do, share, teach and learn data science online.

- Analyze your data using the RStudio IDE, directly from your browser.

Getting started: new RStudio project



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Projects Members About

Ivan Rudik

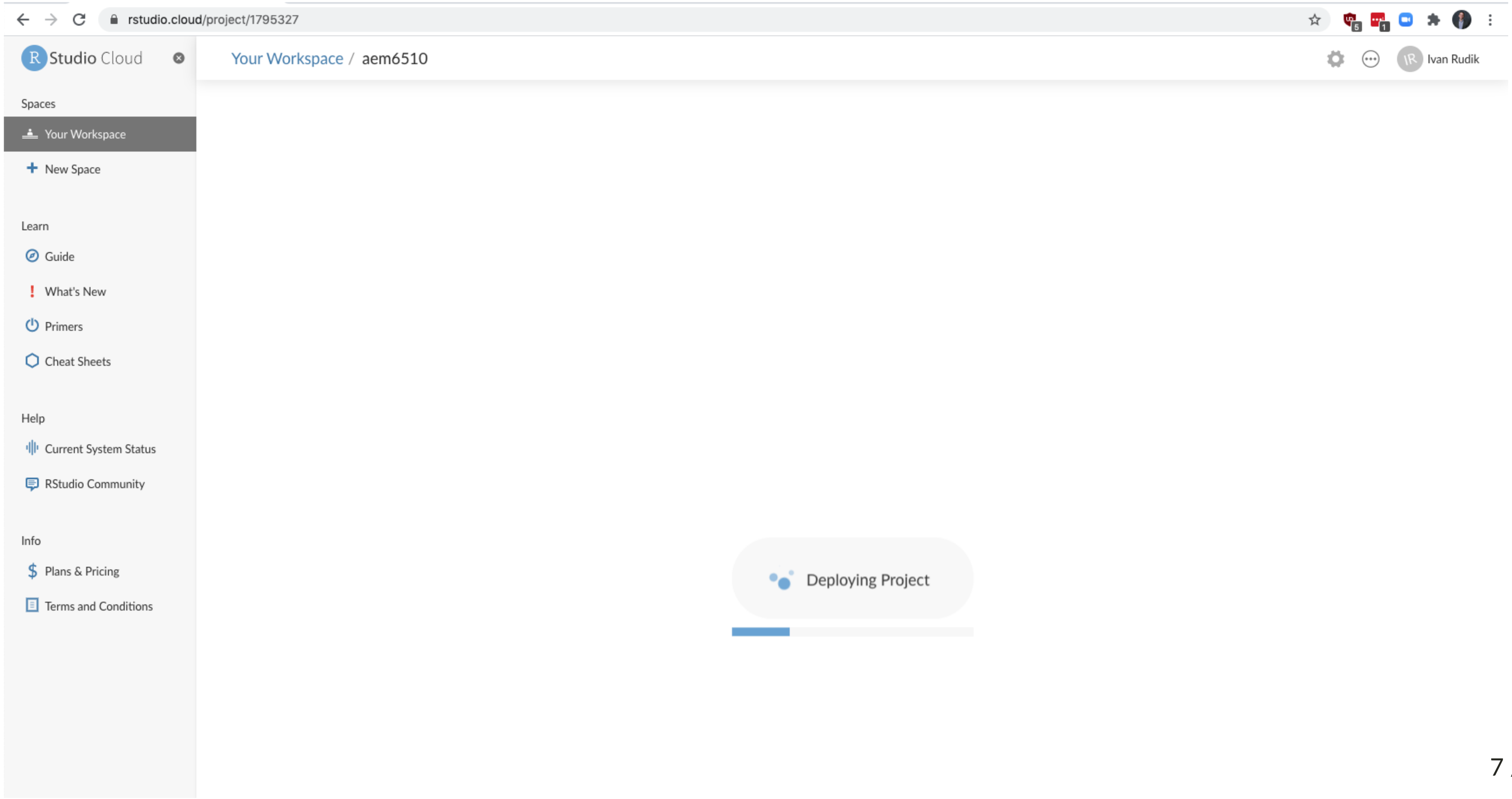
All Projects

List: All projects Sort: By name

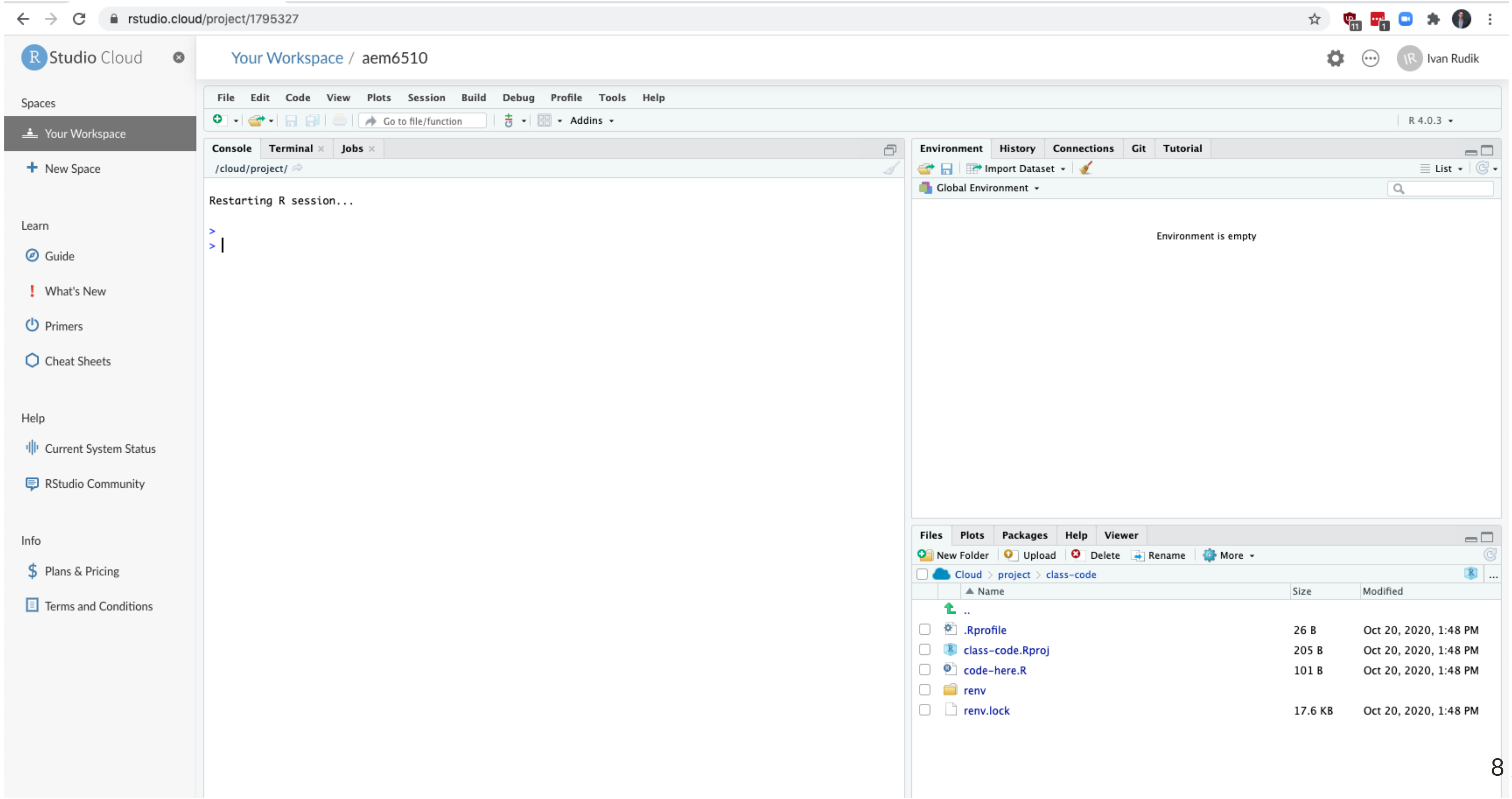
Untitled Project
Ivan Rudik RStudio Project Created Oct 26, 2021 2:15 PM

New Project
- New RStudio Project
- New Jupyter Project
- New Project from Git Repository

Getting started: wait for deployment



Click on class-code.Rproj



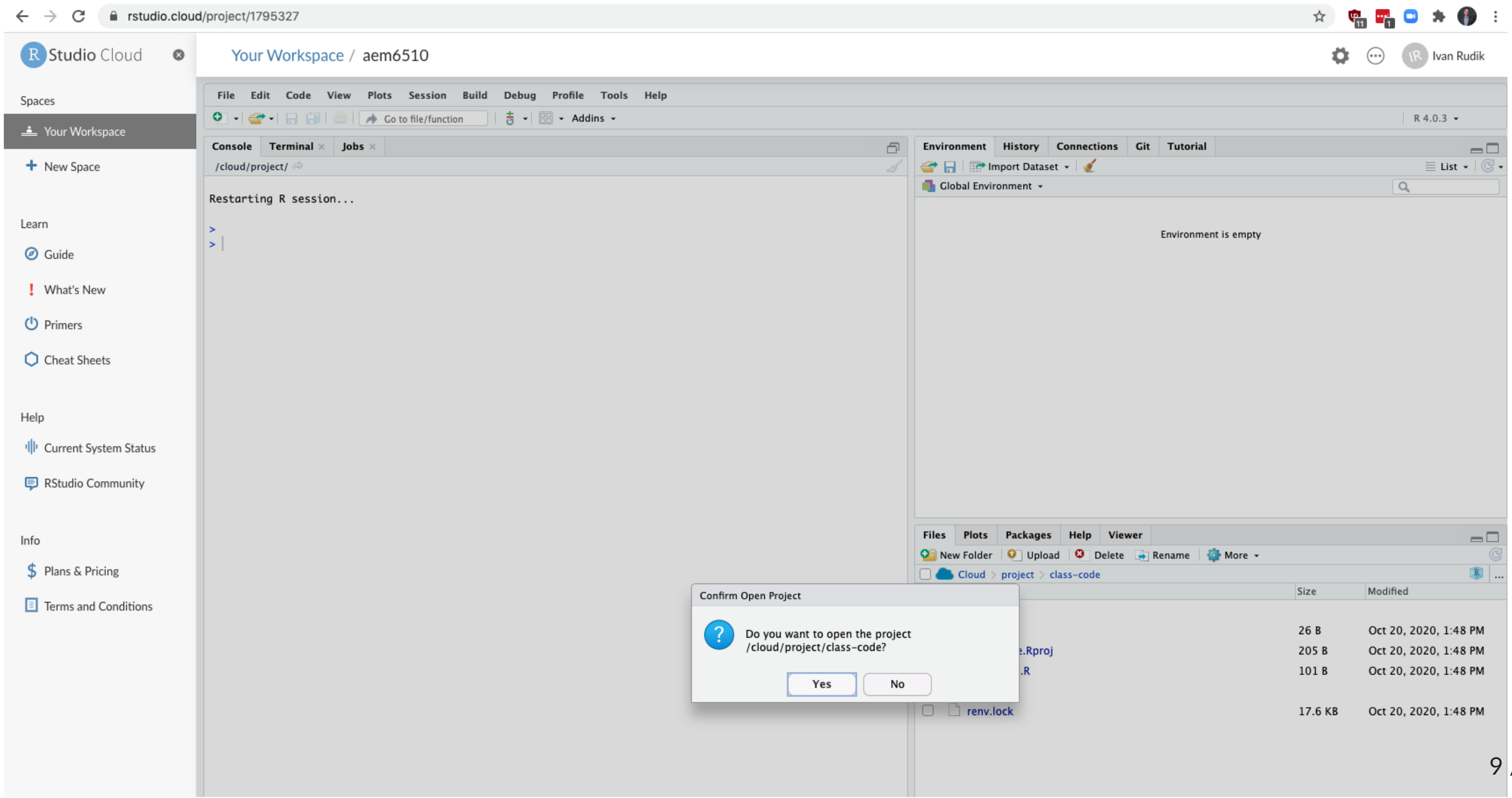
```
/cloud/project/

Restarting R session...

>
> |
```

Name	Size	Modified
..		
.Rprofile	26 B	Oct 20, 2020, 1:48 PM
class-code.Rproj	205 B	Oct 20, 2020, 1:48 PM
code-here.R	101 B	Oct 20, 2020, 1:48 PM
renv		
renv.lock	17.6 KB	Oct 20, 2020, 1:48 PM

Click yes



```
Restarting R session...

>
>
```

Do you want to open the project /cloud/project/class-code?

	Size	Modified
	26 B	Oct 20, 2020, 1:48 PM
.Rproj	205 B	Oct 20, 2020, 1:48 PM
.R	101 B	Oct 20, 2020, 1:48 PM
renv.lock	17.6 KB	Oct 20, 2020, 1:48 PM

Quick intro to R

Arithmetic operations

R can do all the standard arithmetic operations

```
1+2 ## add
```

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

```
6-7 ## subtract
```

```
## [1] -1
```

```
5/2 ## divide
```

```
## [1] 2.5
```

Logical operations

You also have logical operations

```r
1 > 2
```

```
## [1] FALSE
```

```r
(1 > 2) | (1 > 0.5) # | is the or operator
```

```
## [1] TRUE
```

```r
(1 > 2) & (1 > 0.5) # & is the and operator
```

```
## [1] FALSE
```

Logical operations

We can negate expressions with: `!`

This is helpful for filtering data

```
is.na(1:10)
```

```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
!is.na(1:10)
```

```
##  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

Logical operators

For value matching we use: `%in%`

To see whether an object is contained within (i.e. matches one of) a list of items, use `%in%`.

```r
4 %in% 1:10
```

```
## [1] TRUE
```

```r
4 %in% 5:10
```

```
## [1] FALSE
```

This is kind of like an `any` command in other languages

Logical operators

To evaluate whether two expressions are equal, we need to use **two** equal signs

```r
1 = 1 ## This doesn't work
```

```
## Error in 1 = 1: invalid (do_set) left-hand side to assignment
```

```r
1 == 1 ## This does.
```

```
## [1] TRUE
```

```r
1 != 2 ## Note the single equal sign when combined with a negation.
```

```
## [1] TRUE
```

Assignment

In R, we can use either `=` or `←` to handle assignment.[1]

[1] The `←` is really a `<` followed by a `-`. It just looks like an arrow because of the font on the slides.

Assignment

In R, we can use either `=` or `←` to handle assignment.[1]

You can think of it as a (left-facing) arrow saying assign in this direction

[1] The `←` is really a `<` followed by a `-`. It just looks like an arrow because of the font on the slides.

Assignment

```r
a ← 10 + 5
a
```

```
## [1] 15
```

Assignment

You can also use `=` for assignment

```r
b = 10 + 10
b
```

```
## [1] 20
```

Which assignment operator to use?

Most R folks prefer `←` for assignment

In RStudio you can assign `←` to a hotkey to make using it as easy as `=`

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It doesn't really matter though, other languages use `=` for both

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Which assignment operator to use?

Most R folks prefer `<-` for assignment

`=` has a specific role for evaluation *within* functions too

It doesn't really matter though, other languages use `=` for both

Use whatever you prefer, just be consistent

In RStudio you can assign `<-` to a hotkey to make using it as easy as `=`

Help

If you are struggling with a (named) function or object in R, simply type `? commandhere`

```
?Negate
```

Help

Also try `vignette()` for a more detailed introduction to many packages

```r
# Try this:
vignette("dplyr")
```

Help

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Vignettes are a very easy way to learn how and when to use a package

What are objects?

We won't go into OOP details but here are some objects that we'll be working with regularly:

- vectors
- matrices
- data frames
- lists
- functions
- etc.

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- matrices
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- lists
- functions
- etc.

A lot of these are probably familiar if you have coding experience

But there are always language-specific features/subtleties

Global environment

```r
## Create a small data frame called "df".
df ← data.frame(x = 1:2, y = 3:4)
df
```

```
##   x y
## 1 1 3
## 2 2 4
```

Global environment

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```

```
##   x y
## 1 1 3
## 2 2 4
```

Now, let's try to run a regression[1] on these "x" and "y" variables:

[1] Yes, this is a dumb regression with perfectly co-linear variables. Just go with it.

Global environment

```r
lm(y ~ x) ## The "lm" stands for linear model(s)
```

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Error?

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The error message is

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R can't find the variables that we've supplied in our Global Environment

Global environment

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```
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R can't find the variables that we've supplied in our Global Environment

Can you find x or y in the RStudio panel?

Global environment

We have to tell R `x` and `y` are a part of the object `df`

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How?

Global environment

We have to tell R `x` and `y` are a part of the object `df`

How?

There are a various ways to solve this problem. One is to simply specify the datasource:

```
lm(y ~ x, data = df) ## Works when we add "data = df"!
```

```
##
## Call:
## lm(formula = y ~ x, data = df)
##
## Coefficients:
## (Intercept)            x
##           2            1
```

Global environment: why it matters

This matters largely for Stata users

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In Stata, the workspace is basically just a single data frame $\Rightarrow$ all variables are in the global environment

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In Stata, the workspace is basically just a single data frame $\Rightarrow$ all variables are in the global environment

Big problem with this is you can't have multiple data frames / datasets in memory

Working with multiple objects

We can create a second data frame in memory!

```
df2 ← data.frame(x = rnorm(10), y = runif(10))
df
```

```
##   x y
## 1 1 3
## 2 2 4
```

```
df2
```

```
##                x         y
## 1  -0.613382890 0.2259774
## 2   0.130896371 0.2824887
## 3  -0.905843002 0.2304107
## 4  -1.136636840 0.6197059
## 5   1.131662783 0.1040578
## 6  -0.009838234 0.6782971
```

Indexing

How do we index in R?

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We've already seen an example of indexing in the form of R console output:

```
1+2
```

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

The `[1]` above denotes the first (and, in this case, only) element of our output.[1]

Indexing

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We've already seen an example of indexing in the form of R console output:

```
1+2
```

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

The `[1]` above denotes the first (and, in this case, only) element of our output.[1]

In this case, a vector of length one equal to the value "3"

Indexing

Try the following in your console to see a more explicit example of indexed output:

```r
rnorm(n = 100, mean = 0, sd = 1)
```

```
##   [1]  0.30361622 -0.57146408 -0.30867380 -0.40955540  0.04517408  0.10430013
##   [7]  0.17380547 -0.95164107 -0.51172648 -0.22425068  1.33458580  1.15499579
##  [13]  2.05312828  0.17165531 -0.18688468  0.58631875  0.13221947 -0.28582323
##  [19]  0.72600767  0.71954104  0.61187714 -0.59878087 -0.97809484 -1.32639439
##  [25]  0.11650066  0.15587925 -1.57710485  2.50351974 -0.37321754  2.17030535
##  [31]  0.01364178  0.19554214  0.47548680  0.77800681 -1.82338236  0.06250832
##  [37]  1.12761918  0.51172542 -1.13028292  0.66446996  0.19853222  0.53383038
##  [43] -0.62655535 -2.46440515 -0.59379352  1.31853678  1.34202967  0.01819441
##  [49]  0.64271498 -0.71066687  0.87527370 -0.44845575 -1.13081044  0.56774060
##  [55] -0.97787131 -1.03423017 -0.98067760 -0.14674311  0.53411563  0.10658554
##  [61] -0.46979377 -0.46079817 -1.01536509  0.82698389 -1.40094348 -0.67181277
##  [67] -0.08459309  1.15130433  0.03260988 -0.26004754 -1.31336998 -0.42364185
##  [73]  0.85063648 -0.06952117 -0.48511227 -0.77896876 -0.22249120 -0.56392488
##  [79]  0.74349573 -0.99275277 -1.78652358 -0.13506962  0.89185660  0.04830713
```

Indexing: []

We can also use `[]` to index objects that we create in R.

```
a ← 11:20
a
```

```
##  [1] 11 12 13 14 15 16 17 18 19 20
```

```
a[4] ## Get the 4th element of object "a"
```

```
## [1] 14
```

```
a[c(4, 6)] ## Get the 4th and 6th elements
```

```
## [1] 14 16
```

Indexing: []

It also works on larger arrays (vectors, matrices, data frames, and lists). For example:

```r
starwars[1, 1] ## Show the cell corresponding to the 1st row & 1st column of the data frame.
```

```
## # A tibble: 1 x 1
##   name
##   <chr>
## 1 Luke Skywalker
```

Indexing: []

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```

```
## # A tibble: 1 x 1
##   name
##   <chr>
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```

What does `starwars[1:3, 1]` give you?

Indexing: []

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They can contain a random assortment of objects that don't share the same characteristics

- e.g. a list can contain a scalar, a string, and a data frame, or even another list

Indexing: []

The relevance to indexing is that lists require two square brackets `[[]]` to index the parent list item and then the standard `[]` within that parent item:

```
my_list ← list(
  a = "hello",
  b = c(1,2,3),
  c = data.frame(x = 1:5, y = 6:10)
  )
my_list[[1]] ## Return the 1st list object
```

```
## [1] "hello"
```

```
my_list[[2]][3] ## Return the 3rd element of the 2nd list object
```

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

Indexing: $

Lists provide a nice segue to our other indexing operator: `$`

- Let's continue with the `my_list` example from the previous slide.

```
my_list
```

```
## $a
## [1] "hello"
##
## $b
## [1] 1 2 3
##
## $c
##    x  y
## 1 1  6
## 2 2  7
## 3 3  8
## 4 4  9
## 5 5 10
```

Indexing: $

Lists provide a nice segue to our other indexing operator: `$`.

- Let's continue with the `my_list` example

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my_list
```

```
## $a
## [1] "hello"
##
## $b
## [1] 1 2 3
##
## $c
##   x  y
## 1 1  6
## 2 2  7
## 3 3  8
## 4 4  9
```

Indexing: $

We can call these objects directly by name using the dollar sign, e.g.

```
my_list$a ## Return list object "a"
```

```
## [1] "hello"
```

```
my_list$b[3] ## Return the 3rd element of list object "b"
```

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

```
my_list$c$x ## Return column "x" of list object "c"
```

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

Indexing: $

The `$` form of indexing also works for other object types

In some cases, you can also combine the two index options:

```
starwars$name[1] # first element of the name column of the starwars data frame
```

```
## [1] "Luke Skywalker"
```

Indexing: $

However, note some key differences between the output from this example and that of our previous `starwars[1, 1]` example:

```
starwars$name[1]
```

```
## [1] "Luke Skywalker"
```

```
starwars[1, 1]
```

```
## # A tibble: 1 x 1
##   name
##   <chr>
## 1 Luke Skywalker
```

Removing objects

Use `rm()` to remove an object or objects from your working environment.

```
a ← "hello"
b ← "world"
rm(a, b)
```

You can also use `rm(list = ls())` to remove all objects in your working environment (except packages), but this is frowned upon

Removing objects

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Just start a new R session instead

The tidyverse

What is "tidy" data?

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- Vignette (from the **tidyr** package)
- Original paper (Hadley Wickham, 2014 JSS)

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Key points:

1. Each variable forms a column.
2. Each observation forms a row.
3. Each type of observational unit forms a table.

What is "tidy" data?

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- Vignette (from the **tidyr** package)
- Original paper (Hadley Wickham, 2014 JSS)

Key points:

1. Each variable forms a column.
2. Each observation forms a row.
3. Each type of observational unit forms a table.

Basically, tidy data is more likely to be long (i.e. narrow) than wide

Checklist

Install tidyverse: `install.packages('tidyverse')`

Install nycflights13: `install.packages('nycflights13', repos = 'https://cran.rstudio.com')`

Tidyverse vs. base R

Lots of debate over tidyverse vs base R

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The answer is obvious: We should teach the tidyverse first

- Good documentation and support
- Consistent philosophy and syntax
- Nice front-end for big data tools
- For data cleaning, plotting, the tidyverse is elite

Tidyverse vs. base R

Base R is still great

- Base R is extremely flexible and powerful
- The tidyverse can't do everything
- Using base R and the tidyverse together is often a good idea

Tidyverse vs. base R

One point of convenience is that there is often a direct correspondence between a tidyverse command and its base R equivalent:

tidyverse	base
`?readr::read_csv`	`?utils::read.csv`
`?dplyr::if_else`	`?base::ifelse`
`?tibble::tibble`	`?base::data.frame`

Tidyverse functions typically have extra features on top of base R

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`?tibble::tibble`	`?base::data.frame`

Tidyverse functions typically have extra features on top of base R

There are always many ways to achieve a single goal in R

Tidyverse packages

Let's load the tidyverse meta-package and check the output.

```r
library(tidyverse)
```

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library(tidyverse)
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We have actually loaded a number of packages: **ggplot2**, **tibble**, **dplyr**, etc

We can also see information about the package versions and some namespace conflicts

Tidyverse packages

The tidyverse actually comes with a lot more packages than those that are just loaded automatically

```
tidyverse_packages()
```

```
##  [1] "broom"      "cli"        "crayon"     "dbplyr"     "dplyr"
##  [6] "forcats"    "ggplot2"    "haven"      "hms"        "httr"
## [11] "jsonlite"   "lubridate"  "magrittr"   "modelr"     "pillar"
## [16] "purrr"      "readr"      "readxl"     "reprex"     "rlang"
## [21] "rstudioapi" "rvest"      "stringr"    "tibble"     "tidyr"
## [26] "xml2"       "tidyverse"
```

e.g. the **lubridate** package is for working with dates and the **rvest** package is for webscraping

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## [11] "jsonlite"    "lubridate"    "magrittr"    "modelr"      "pillar"
## [16] "purrr"       "readr"        "readxl"      "reprex"      "rlang"
## [21] "rstudioapi"  "rvest"        "stringr"     "tibble"      "tidyr"
## [26] "xml2"        "tidyverse"
```

e.g. the **lubridate** package is for working with dates and the **rvest** package is for webscraping

These packages have to be loaded separately

Tidyverse packages

We're going to focus on two workhorse packages:

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2. **tidyr**

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1. **dplyr**
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These are the packages for cleaning and wrangling data

They are thus the ones that you will likely make the most use of

Data cleaning and wrangling occupies an inordinate amount of time, no matter where you are in your research career

Pipes: %>%

The pipe operator `%>%` lets us perform a sequence of operations in a very nice and tidy way

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Suppose we wanted to figure out the average highway miles per gallon of Audi's in the `mpg` dataset:

```
mpg
```

```
## # A tibble: 234 x 11
##    manufacturer model    displ  year   cyl trans   drv     cty   hwy fl    class
##    <chr>        <chr>    <dbl> <int> <int> <chr>   <chr> <int> <int> <chr> <chr>
##  1 audi         a4         1.8  1999     4 auto(l… f        18    29 p     comp…
##  2 audi         a4         1.8  1999     4 manual… f        21    29 p     comp…
##  3 audi         a4         2     2008     4 manual… f        20    31 p     comp…
##  4 audi         a4         2     2008     4 auto(a… f        21    30 p     comp…
##  5 audi         a4         2.8  1999     6 auto(l… f        16    26 p     comp…
##  6 audi         a4         2.8  1999     6 manual… f        18    26 p     comp…
```

Pipes: %>%

There's two ways you might do this without taking advantage of pipes:

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There's two ways you might do this without taking advantage of pipes:

The first is to do it step-by-step, line-by-line which requires a lot of variable assignment

```r
audis_mpg <- filter(mpg, manufacturer=="audi")
audis_mpg_grouped <- group_by(filter(mpg, manufacturer=="audi"), model)
summarise(audis_mpg_grouped, hwy_mean = mean(hwy))
```

```
## # A tibble: 3 x 2
##   model      hwy_mean
##   <chr>         <dbl>
## 1 a4             28.3
## 2 a4 quattro     25.8
## 3 a6 quattro     24
```

Pipes: %>%

Next you could do it all in one line which is hard to read

```
summarise(group_by(filter(mpg, manufacturer=="audi"), model), hwy_mean = mean(hwy))
```

```
## # A tibble: 3 x 2
##   model      hwy_mean
##   <chr>         <dbl>
## 1 a4             28.3
## 2 a4 quattro     25.8
## 3 a6 quattro     24
```

Pipes: %>%

Or, you could use **pipes** `%>%`:

```
mpg %>% filter(manufacturer=="audi") %>% group_by(model) %>% summarise(hwy_mean = mean(hwy))
```

```
## # A tibble: 3 x 2
##   model      hwy_mean
##   <chr>         <dbl>
## 1 a4             28.3
## 2 a4 quattro     25.8
## 3 a6 quattro     24
```

Pipes: %>%

Or, you could use **pipes** `%>%`:

```
mpg %>% filter(manufacturer=="audi") %>% group_by(model) %>% summarise(hwy_mean = mean(hwy))
```

```
## # A tibble: 3 x 2
##   model      hwy_mean
##   <chr>         <dbl>
## 1 a4             28.3
## 2 a4 quattro     25.8
## 3 a6 quattro     24
```

It performs the operations from left to right, exactly like you'd think of them: take this object (mpg), do this (filter), then do this (group by car model), then do this (take the mean of highway miles)

Use vertical space

Pipes are even more readable if we write it over several lines:

```r
mpg %>%
  filter(manufacturer=="audi") %>%
  group_by(model) %>%
  summarise(hwy_mean = mean(hwy))
```

```
## # A tibble: 3 x 2
##   model      hwy_mean
##   <chr>         <dbl>
## 1 a4             28.3
## 2 a4 quattro     25.8
## 3 a6 quattro     24
```

Using vertical space costs nothing and makes for much more readable code

dplyr

Aside: dplyr 1.0.0 release

Please make sure that you are running at least **dplyr** 1.0.0 before continuing.

```
packageVersion('dplyr')
```

```
## [1] '1.0.5'
```

```
# install.packages('dplyr') ## install updated version if < 1.0.0
```

The five key dplyr verbs

1. `filter`: Subset/filter rows based on their values
2. `arrange`: Reorder/arrange rows based on their values
3. `select`: Select columns/variables
4. `mutate`: Create new columns/variables
5. `summarise`: Collapse multiple rows into a single summary value, potentially by a grouping variable

The five key dplyr verbs

1. `filter`: Subset/filter rows based on their values

2. `arrange`: Reorder/arrange rows based on their values

3. `select`: Select columns/variables

4. `mutate`: Create new columns/variables

5. `summarise`: Collapse multiple rows into a single summary value, potentially by a grouping variable

Let's practice these commands together using the `starwars` data frame that comes pre-packaged with dplyr

Starwars

Here's the `starwars` dataset, it has 87 observations of 14 variables

```
starwars
```

```
## # A tibble: 87 x 14
##    name     height  mass hair_color   skin_color eye_color birth_year sex   gender
##    <chr>     <int> <dbl> <chr>        <chr>      <chr>          <dbl> <chr> <chr>
##  1 Luke S…     172    77 blond        fair       blue            19   male  mascu…
##  2 C-3PO       167    75 <NA>         gold       yellow         112   none  mascu…
##  3 R2-D2        96    32 <NA>         white, bl… red             33   none  mascu…
##  4 Darth …     202   136 none         white      yellow          41.9 male  mascu…
##  5 Leia O…     150    49 brown        light      brown           19   fema… femin…
##  6 Owen L…     178   120 brown, grey light      blue            52   male  mascu…
##  7 Beru W…     165    75 brown        light      blue            47   fema… femin…
##  8 R5-D4        97    32 <NA>         white, red red             NA   none  mascu…
##  9 Biggs …     183    84 black        light      brown           24   male  mascu…
## 10 Obi-Wa…     182    77 auburn, wh… fair       blue-gray       57   male  mascu…
## # … with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

1) dplyr::filter

Here we are subsetting the observations of humans that are at least 190cm

```
starwars %>%
  filter(
    species == "Human",
    height >= 190
    )
```

```
## # A tibble: 4 x 14
##   name      height  mass hair_color skin_color eye_color birth_year sex   gender
##   <chr>      <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr> <chr>
## 1 Darth Va…    202   136 none       white      yellow          41.9 male  mascu…
## 2 Qui-Gon …    193    89 brown      fair       blue            92   male  mascu…
## 3 Dooku        193    80 white      fair       brown          102   male  mascu…
## 4 Bail Pre…    191    NA black      tan        brown           67   male  mascu…
## # … with 5 more variables: homeworld <chr>, species <chr>, films <list>,
## #   vehicles <list>, starships <list>
```

1) dplyr::filter

You can filter using regular expressions with grep-type commands or the `stringr` package

```
starwars %>%
  filter(stringr::str_detect(name, "Skywalker"))
```

```
## # A tibble: 3 x 14
##   name     height  mass hair_color skin_color eye_color birth_year sex    gender
##   <chr>     <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr>  <chr>
## 1 Luke Sk…    172    77 blond      fair       blue            19   male   mascu…
## 2 Anakin …    188    84 blond      fair       blue            41.9 male   mascu…
## 3 Shmi Sk…    163    NA black      fair       brown           72   female femin…
## # … with 5 more variables: homeworld <chr>, species <chr>, films <list>,
## #   vehicles <list>, starships <list>
```

This subsets the observations for individuals whose names contain "Skywalker"

1) dplyr::filter

A very common `filter` use case is identifying/removing missing data cases:

```
starwars %>%
  filter(is.na(height))
```

```
## # A tibble: 6 x 14
##   name     height  mass hair_color skin_color eye_color birth_year sex    gender
##   <chr>     <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr>  <chr>
## 1 Arvel C…     NA    NA brown      fair       brown             NA male   mascu…
## 2 Finn         NA    NA black      dark       dark              NA male   mascu…
## 3 Rey          NA    NA brown      light      hazel             NA female femin…
## 4 Poe Dam…     NA    NA brown      light      brown             NA male   mascu…
## 5 BB8          NA    NA none       none       black             NA none   mascu…
## 6 Captain…     NA    NA unknown    unknown    unknown           NA <NA>   <NA>
## # … with 5 more variables: homeworld <chr>, species <chr>, films <list>,
## #   vehicles <list>, starships <list>
```

1) dplyr::filter

To remove missing observations, use negation:

```
starwars %>%
  filter(!is.na(height))
```

```
## # A tibble: 81 x 14
##    name    height  mass hair_color  skin_color eye_color birth_year sex   gender
##    <chr>    <int> <dbl> <chr>       <chr>      <chr>          <dbl> <chr> <chr>
##  1 Luke S…    172    77 blond       fair       blue            19   male  mascu…
##  2 C-3PO      167    75 <NA>        gold       yellow         112   none  mascu…
##  3 R2-D2       96    32 <NA>        white, bl… red             33   none  mascu…
##  4 Darth …    202   136 none        white      yellow          41.9 male  mascu…
##  5 Leia O…    150    49 brown       light      brown           19   fema… femin…
##  6 Owen L…    178   120 brown, grey light      blue            52   male  mascu…
##  7 Beru W…    165    75 brown       light      blue            47   fema… femin…
##  8 R5-D4       97    32 <NA>        white, red red             NA   none  mascu…
##  9 Biggs …    183    84 black       light      brown           24   male  mascu…
## 10 Obi-Wa…    182    77 auburn, wh… fair       blue-gray       57   male  mascu…
## # … with 71 more rows, and 5 more variables: homeworld <chr>, species <chr>,
```

2) dplyr::arrange

`arrange` sorts the data frame based on the variables you supply:

```r
starwars %>%
  arrange(birth_year)
```

```
## # A tibble: 87 x 14
##    name      height  mass hair_color skin_color eye_color birth_year sex   gender
##    <chr>      <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr> <chr>
##  1 Wicket …      88  20   brown      brown      brown            8   male  mascu…
##  2 IG-88        200 140   none       metal      red             15   none  mascu…
##  3 Luke Sk…     172  77   blond      fair       blue            19   male  mascu…
##  4 Leia Or…     150  49   brown      light      brown           19   fema… femin…
##  5 Wedge A…     170  77   brown      fair       hazel           21   male  mascu…
##  6 Plo Koon     188  80   none       orange     black           22   male  mascu…
##  7 Biggs D…     183  84   black      light      brown           24   male  mascu…
##  8 Han Solo     180  80   brown      fair       brown           29   male  mascu…
##  9 Lando C…     177  79   black      dark       brown           31   male  mascu…
## 10 Boba Fe…     183  78.2 black      fair       brown           31.5 male  mascu…
## # … with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

2) dplyr::arrange

We can also arrange items in descending order using `arrange(desc())`

```
starwars %>%
  arrange(desc(birth_year))
```

```
## # A tibble: 87 x 14
##    name    height  mass hair_color skin_color  eye_color birth_year sex   gender
##    <chr>    <int> <dbl> <chr>      <chr>       <chr>          <dbl> <chr> <chr>
##  1 Yoda        66    17 white      green       brown            896 male  mascu…
##  2 Jabba …    175  1358 <NA>       green-tan,… orange           600 herm… mascu…
##  3 Chewba…    228   112 brown      unknown     blue             200 male  mascu…
##  4 C-3PO      167    75 <NA>       gold        yellow           112 none  mascu…
##  5 Dooku      193    80 white      fair        brown            102 male  mascu…
##  6 Qui-Go…    193    89 brown      fair        blue              92 male  mascu…
##  7 Ki-Adi…    198    82 white      pale        yellow            92 male  mascu…
##  8 Finis …    170    NA blond      fair        blue              91 male  mascu…
##  9 Palpat…    170    75 grey       pale        yellow            82 male  mascu…
## 10 Cliegg…    183    NA brown      fair        blue              82 male  mascu…
## # … with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,
```

3) dplyr::select

Use commas to select multiple columns out of a data frame, deselect a column with "-", select across multiple columns with "first:last":

```
starwars %>%
  select(name:skin_color, species, -height)
```

```
## # A tibble: 87 x 5
##    name                mass hair_color    skin_color  species
##    <chr>              <dbl> <chr>         <chr>       <chr>
##  1 Luke Skywalker        77 blond         fair        Human
##  2 C-3PO                 75 <NA>          gold        Droid
##  3 R2-D2                 32 <NA>          white, blue Droid
##  4 Darth Vader          136 none          white       Human
##  5 Leia Organa           49 brown         light       Human
##  6 Owen Lars            120 brown, grey   light       Human
##  7 Beru Whitesun lars    75 brown         light       Human
##  8 R5-D4                 32 <NA>          white, red  Droid
##  9 Biggs Darklighter     84 black         light       Human
## 10 Obi-Wan Kenobi        77 auburn, white fair        Human
```

3) dplyr::select

You can also rename your selected variables in place

```
starwars %>%
  select(alias = name, crib = homeworld)
```

```
## # A tibble: 87 x 2
##    alias              crib
##    <chr>              <chr>
##  1 Luke Skywalker     Tatooine
##  2 C-3PO              Tatooine
##  3 R2-D2              Naboo
##  4 Darth Vader        Tatooine
##  5 Leia Organa        Alderaan
##  6 Owen Lars          Tatooine
##  7 Beru Whitesun lars Tatooine
##  8 R5-D4              Tatooine
##  9 Biggs Darklighter  Tatooine
## 10 Obi-Wan Kenobi     Stewjon
## # … with 77 more rows
```

3) dplyr::select

If you just want to rename columns without subsetting them, you can use `rename`:

```
starwars %>%
  rename(alias = name, crib = homeworld)
```

```
## # A tibble: 87 x 14
##    alias   height  mass hair_color  skin_color eye_color birth_year sex   gender
##    <chr>    <int> <dbl> <chr>       <chr>      <chr>          <dbl> <chr> <chr>
##  1 Luke S…    172    77 blond       fair       blue            19   male  mascu…
##  2 C-3PO      167    75 <NA>        gold       yellow         112   none  mascu…
##  3 R2-D2       96    32 <NA>        white, bl… red             33   none  mascu…
##  4 Darth …    202   136 none        white      yellow          41.9 male  mascu…
##  5 Leia O…    150    49 brown       light      brown           19   fema… femin…
##  6 Owen L…    178   120 brown, grey light      blue            52   male  mascu…
##  7 Beru W…    165    75 brown       light      blue            47   fema… femin…
##  8 R5-D4       97    32 <NA>        white, red red             NA   none  mascu…
##  9 Biggs …    183    84 black       light      brown           24   male  mascu…
## 10 Obi-Wa     182    77 auburn, wh  fair       blue-gray       57   male  mascu
```

3) dplyr::select *cont.*

The `select(contains(PATTERN))` option provides a nice shortcut in relevant cases.

```
starwars %>%
  select(name, contains("color"))
```

```
## # A tibble: 87 x 4
##    name               hair_color    skin_color  eye_color
##    <chr>              <chr>         <chr>       <chr>
##  1 Luke Skywalker     blond         fair        blue
##  2 C-3PO              <NA>          gold        yellow
##  3 R2-D2              <NA>          white, blue red
##  4 Darth Vader        none          white       yellow
##  5 Leia Organa        brown         light       brown
##  6 Owen Lars          brown, grey   light       blue
##  7 Beru Whitesun lars brown         light       blue
##  8 R5-D4              <NA>          white, red  red
##  9 Biggs Darklighter  black         light       brown
## 10 Obi-Wan Kenobi     auburn, white fair        blue-gray
```

3) dplyr::select

The `select( ... , everything())` option is another useful shortcut if you only want to bring some variable(s) to the "front" of a data frame

```
starwars %>%
  select(species, homeworld, everything()) %>%
  head(5)
```

```
## # A tibble: 5 x 14
##   species homeworld name           height  mass hair_color skin_color  eye_color
##   <chr>   <chr>     <chr>           <int> <dbl> <chr>      <chr>       <chr>
## 1 Human   Tatooine  Luke Skywalker    172    77 blond      fair        blue
## 2 Droid   Tatooine  C-3PO             167    75 <NA>       gold        yellow
## 3 Droid   Naboo     R2-D2              96    32 <NA>       white, blue red
## 4 Human   Tatooine  Darth Vader       202   136 none       white       yellow
## 5 Human   Alderaan  Leia Organa       150    49 brown      light       brown
## # … with 6 more variables: birth_year <dbl>, sex <chr>, gender <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

3) dplyr::select

You can also use `relocate` to do the same thing

```
starwars %>%
  relocate(species, homeworld) %>%
  head(5)
```

```
## # A tibble: 5 x 14
##   species homeworld name           height  mass hair_color skin_color  eye_color
##   <chr>   <chr>     <chr>           <int> <dbl> <chr>      <chr>       <chr>    
## 1 Human   Tatooine  Luke Skywalker    172    77 blond      fair        blue     
## 2 Droid   Tatooine  C-3PO             167    75 <NA>       gold        yellow   
## 3 Droid   Naboo     R2-D2              96    32 <NA>       white, blue red      
## 4 Human   Tatooine  Darth Vader       202   136 none       white       yellow   
## 5 Human   Alderaan  Leia Organa       150    49 brown      light       brown    
## # … with 6 more variables: birth_year <dbl>, sex <chr>, gender <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

4) dplyr::mutate

You can create new columns from scratch as transformations of existing columns:

```r
starwars %>%
  select(name, birth_year) %>%
  mutate(dog_years = birth_year * 7) %>%
  mutate(comment = paste0(name, " is ", dog_years, " in dog years."))
```

```
## # A tibble: 87 x 4
##    name               birth_year dog_years comment
##    <chr>                   <dbl>     <dbl> <chr>
##  1 Luke Skywalker           19         133  Luke Skywalker is 133 in dog years.
##  2 C-3PO                   112         784  C-3PO is 784 in dog years.
##  3 R2-D2                    33         231  R2-D2 is 231 in dog years.
##  4 Darth Vader              41.9       293. Darth Vader is 293.3 in dog years.
##  5 Leia Organa              19         133  Leia Organa is 133 in dog years.
##  6 Owen Lars                52         364  Owen Lars is 364 in dog years.
##  7 Beru Whitesun lars       47         329  Beru Whitesun lars is 329 in dog yea…
##  8 R5-D4                    NA          NA  R5-D4 is NA in dog years
```

4) dplyr::mutate

Note: `mutate` creates variables in order, so you can chain multiple mutates in a single call

```
starwars %>%
  select(name, birth_year) %>%
  mutate(
    dog_years = birth_year * 7, ## Separate with a comma
    comment = paste0(name, " is ", dog_years, " in dog years.")
    )
```

```
## # A tibble: 87 x 4
##    name                  birth_year dog_years comment
##    <chr>                      <dbl>     <dbl> <chr>
##  1 Luke Skywalker              19        133  Luke Skywalker is 133 in dog years.
##  2 C-3PO                      112        784  C-3PO is 784 in dog years.
##  3 R2-D2                       33        231  R2-D2 is 231 in dog years.
##  4 Darth Vader                 41.9      293. Darth Vader is 293.3 in dog years.
##  5 Leia Organa                 19        133  Leia Organa is 133 in dog years.
##  6 Owen Lars                   52        364  Owen Lars is 364 in dog years
```

4) dplyr::mutate

Boolean, logical and conditional operators all work well with `mutate` too:

```
starwars %>%
  select(name, height) %>%
  filter(name %in% c("Luke Skywalker", "Anakin Skywalker")) %>%
  mutate(tall1 = height > 180) %>% # TRUE or FALSE
  mutate(tall2 = ifelse(height > 180, "Tall", "Short")) ## Same effect, but can choose labels
```

```
## # A tibble: 2 x 4
##   name             height tall1 tall2
##   <chr>             <int> <lgl> <chr>
## 1 Luke Skywalker      172 FALSE Short
## 2 Anakin Skywalker    188 TRUE  Tall
```

4) dplyr::mutate

Lastly, combining `mutate` with `across` allows you to easily work on a subset of variables:

```
starwars %>%
  select(name:eye_color) %>%
  mutate(across(where(is.character), toupper)) %>% # Take all character variables, uppercase ther
  head(5)
```

```
## # A tibble: 5 x 6
##   name           height  mass hair_color skin_color  eye_color
##   <chr>           <int> <dbl> <chr>      <chr>       <chr>
## 1 LUKE SKYWALKER    172    77 BLOND      FAIR        BLUE
## 2 C-3PO             167    75 <NA>       GOLD        YELLOW
## 3 R2-D2              96    32 <NA>       WHITE, BLUE RED
## 4 DARTH VADER       202   136 NONE       WHITE       YELLOW
## 5 LEIA ORGANA       150    49 BROWN      LIGHT       BROWN
```

5) dplyr::summarise

Summarising useful in combination with the `group_by` command

```r
starwars %>%
  group_by(species, gender) %>% # for each species-gender combo
  summarise(mean_height = mean(height, na.rm = TRUE)) # calculate the mean height
```

```
## # A tibble: 42 x 3
## # Groups:   species [38]
##    species  gender    mean_height
##    <chr>    <chr>           <dbl>
##  1 Aleena   masculine          79
##  2 Besalisk masculine         198
##  3 Cerean   masculine         198
##  4 Chagrian masculine         196
##  5 Clawdite feminine          168
##  6 Droid    feminine           96
##  7 Droid    masculine         140
##  8 Dug      masculine         112
##  9 Ewok     masculine          88
```

5) dplyr::summarise

Note that including "na.rm = TRUE" is usually a good idea with summarise functions, it keeps NAs from propagating to the end result

```
## Probably not what we want
starwars %>%
  summarise(mean_height = mean(height))
```

```
## # A tibble: 1 x 1
##   mean_height
##         <dbl>
## 1          NA
```

5) dplyr::summarise

We can also use `across` within summarise:

```r
starwars %>%
  group_by(species) %>% # for each species
  summarise(across(where(is.numeric), mean, na.rm = T)) %>% # take the mean of all numeric varia
  head(5)
```

```
## # A tibble: 5 x 4
##   species  height  mass birth_year
##   <chr>     <dbl> <dbl>      <dbl>
## 1 Aleena       79    15        NaN
## 2 Besalisk    198   102        NaN
## 3 Cerean      198    82         92
## 4 Chagrian    196   NaN        NaN
## 5 Clawdite    168    55        NaN
```

Other dplyr goodies

`group_by` and `ungroup`: For (un)grouping

- Particularly useful with the `summarise` and `mutate` commands

Other dplyr goodies

`group_by` and `ungroup`: For (un)grouping

- Particularly useful with the `summarise` and `mutate` commands

`slice`: Subset rows by position rather than filtering by values

- E.g. `starwars %>% slice(c(1, 5))`

Other dplyr goodies

`pull`: Extract a column from as a data frame as a vector or scalar

- E.g. `starwars %>% filter(gender=="female") %>% pull(height)`

Other dplyr goodies

`pull`: Extract a column from as a data frame as a vector or scalar

- E.g. `starwars %>% filter(gender=="female") %>% pull(height)`

`count` and `distinct`: Number and isolate unique observations

- E.g. `starwars %>% count(species)`, or `starwars %>% distinct(species)`
- You could also use a combination of `mutate`, `group_by`, and `n()`, e.g. `starwars %>% group_by(species) %>% mutate(num = n())`.

Other dplyr goodies

There are also a whole class of window functions for getting leads and lags, percentiles, cumulative sums, etc.

- See `vignette("window-functions")`.

dplyr::xxxx_join

The last set of commands we need are the `join` commands

dplyr::xxxx_join

The last set of commands we need are the `join` commands

These are the same as `merge` in stata but with a bit more functionality

dplyr::xxxx_join

We merge data with join operations:

- `inner_join(df1, df2)`
- `left_join(df1, df2)`
- `right_join(df1, df2)`
- `full_join(df1, df2)`
- `semi_join(df1, df2)`
- `anti_join(df1, df2)`

(You can visualize the operations here)

dplyr::xxxx_join

Lets use the data that comes with the the nycflights13 package.

```r
library(nycflights13)
flights
```

```
## # A tibble: 336,776 x 19
##     year month   day dep_time sched_dep_time dep_delay arr_time sched_arr_time
##    <int> <int> <int>    <int>          <int>     <dbl>    <int>          <int>
##  1  2013     1     1      517            515         2      830            819
##  2  2013     1     1      533            529         4      850            830
##  3  2013     1     1      542            540         2      923            850
##  4  2013     1     1      544            545        -1     1004           1022
##  5  2013     1     1      554            600        -6      812            837
##  6  2013     1     1      554            558        -4      740            728
##  7  2013     1     1      555            600        -5      913            854
##  8  2013     1     1      557            600        -3      709            723
##  9  2013     1     1      557            600        -3      838            846
## 10  2013     1     1      558            600        -2      753            745
## # … with 336,766 more rows, and 11 more variables: arr_delay <dbl>,
## #   carrier <chr>, flight <int>, tailnum <chr>, origin <chr>, dest <chr>,
```

dplyr::xxxx_join

```
planes
```

```
## # A tibble: 3,322 x 9
##    tailnum  year type           manufacturer    model   engines seats speed engine
##    <chr>   <int> <chr>          <chr>           <chr>     <int> <int> <int> <chr>
##  1 N10156   2004 Fixed wing m… EMBRAER         EMB-1…        2    55    NA Turbo-…
##  2 N102UW   1998 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  3 N103US   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  4 N104UW   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  5 N10575   2002 Fixed wing m… EMBRAER         EMB-1…        2    55    NA Turbo-…
##  6 N105UW   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  7 N107US   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  8 N108UW   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
##  9 N109UW   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
## 10 N110UW   1999 Fixed wing m… AIRBUS INDUST… A320-…        2   182    NA Turbo-…
## # … with 3,312 more rows
```

Joining operations

Let's perform a left join on the flights and planes datasets

- *Note*: I'm going subset columns after the join, but only to keep text on the slide

Joining operations

Let's perform a left join on the flights and planes datasets

- *Note*: I'm going subset columns after the join, but only to keep text on the slide

```
left_join(flights, planes) %>%
  select(year, month, day, dep_time, arr_time, carrier, flight, tailnum, type, model)
```

```
## Joining, by = c("year", "tailnum")
```

```
## # A tibble: 336,776 x 10
##     year month   day dep_time arr_time carrier flight tailnum type  model
##    <int> <int> <int>    <int>    <int> <chr>    <int> <chr>   <chr> <chr>
##  1  2013     1     1      517      830 UA        1545 N14228  <NA>  <NA>
##  2  2013     1     1      533      850 UA        1714 N24211  <NA>  <NA>
##  3  2013     1     1      542      923 AA        1141 N619AA  <NA>  <NA>
##  4  2013     1     1      544     1004 B6         725 N804JB  <NA>  <NA>
##  5  2013     1     1      554      812 DL         461 N668DN  <NA>  <NA>
```

Joining operations

Note that dplyr made a reasonable guess about which columns to join on (i.e. columns that share the same name), and told us what it chose

```
## Joining, by = c("year", "tailnum")
```

There's an obvious problem here: the variable `year` does not have a consistent meaning across our joining datasets

Joining operations

Note that dplyr made a reasonable guess about which columns to join on (i.e. columns that share the same name), and told us what it chose

```
## Joining, by = c("year", "tailnum")
```

There's an obvious problem here: the variable `year` does not have a consistent meaning across our joining datasets

In one it refers to the *year of flight*, in the other it refers to *year of construction*

Luckily, there's an easy way to avoid this problem: try `?dplyr::join`

Joining operations

You just need to be more explicit in your join call by using the `by =` argument

```
left_join(
  flights,
  planes %>% rename(year_built = year), ## Not necessary w/ below line, but helpful
  by = "tailnum" ## Be specific about the joining column
  ) %>%
  select(year, month, day, dep_time, arr_time, carrier, flight, tailnum, year_built, type, model
  head(3) ## Just to save vertical space on the slide
```

```
## # A tibble: 3 x 11
##    year month   day dep_time arr_time carrier flight tailnum year_built type
##   <int> <int> <int>    <int>    <int> <chr>    <int> <chr>        <int> <chr>
## 1  2013     1     1      517      830 UA        1545 N14228        1999 Fixed w…
## 2  2013     1     1      533      850 UA        1714 N24211        1998 Fixed w…
## 3  2013     1     1      542      923 AA        1141 N619AA        1990 Fixed w…
## # … with 1 more variable: model <chr>
```

Joining operations

Note what happens if we again specify the join column but don't rename the ambiguous `year`:

```
left_join(flights,
          planes, ## Not renaming "year" to "year_built" this time
          by = "tailnum") %>%
  select(contains("year"), month, day, dep_time, arr_time, carrier, flight, tailnum, type, model
  head(3)
```

```
## # A tibble: 3 x 11
##   year.x year.y month   day dep_time arr_time carrier flight tailnum type  model
##    <int>  <int> <int> <int>    <int>    <int> <chr>    <int> <chr>   <chr> <chr>
## 1   2013   1999     1     1      517      830 UA        1545 N14228  Fixe… 737-…
## 2   2013   1998     1     1      533      850 UA        1714 N24211  Fixe… 737-…
## 3   2013   1990     1     1      542      923 AA        1141 N619AA  Fixe… 757-…
```

Joining operations

Note what happens if we again specify the join column but don't rename the ambiguous `year`:

```
left_join(flights,
          planes, ## Not renaming "year" to "year_built" this time
          by = "tailnum") %>%
  select(contains("year"), month, day, dep_time, arr_time, carrier, flight, tailnum, type, model
  head(3)
```

```
## # A tibble: 3 x 11
##   year.x year.y month   day dep_time arr_time carrier flight tailnum type  model
##    <int>  <int> <int> <int>    <int>    <int> <chr>    <int> <chr>   <chr> <chr>
## 1   2013   1999     1     1      517      830 UA        1545 N14228  Fixe… 737-…
## 2   2013   1998     1     1      533      850 UA        1714 N24211  Fixe… 737-…
## 3   2013   1990     1     1      542      923 AA        1141 N619AA  Fixe… 757-…
```

Make sure you know what "year.x" and "year.y" are

tidyr

Key tidyr verbs

1. `pivot_longer`: Pivot wide data into long format (i.e. "melt", "reshape long")

2. `pivot_wider`: Pivot long data into wide format (i.e. "cast", "reshape wide")

3. `separate`: Split one column into multiple columns

4. `unite`: Combine multiple columns into one

Key tidyr verbs

1. `pivot_longer`: Pivot wide data into long format (i.e. "melt", "reshape long")

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3. `separate`: Split one column into multiple columns

4. `unite`: Combine multiple columns into one

Let's practice these verbs together in class

1) tidyr::pivot_longer

```r
stocks <- data.frame(
  time = as.Date('2009-01-01') + 0:1,
  X = rnorm(2, 0, 1),
  Y = rnorm(2, 0, 2),
  Z = rnorm(2, 0, 4)
  )
stocks
```

```
##         time          X        Y         Z
## 1 2009-01-01  0.6163028 1.779204 -1.461802
## 2 2009-01-02 -0.1024888 2.548539 -2.816719
```

We have 4 variables, the date and the stocks

How do we get this in tidy form?

1) tidyr::pivot_longer

```r
stocks %>% pivot_longer(-time, names_to = "stock", values_to = "price")
```

We need to pivot the stock name variables `X, Y, Z` longer

1. Choose non-time variables: `-time`
2. Decide what variable holds the names: `names_to = "stock"`
3. Decide what variable holds the values: `values_to = "price"`

1) tidyr::pivot_longer

```
stocks %>% pivot_longer(-time, names_to = "stock", values_to = "price")
```

```
## # A tibble: 6 x 3
##   time       stock  price
##   <date>     <chr>  <dbl>
## 1 2009-01-01 X      0.616
## 2 2009-01-01 Y      1.78
## 3 2009-01-01 Z     -1.46
## 4 2009-01-02 X     -0.102
## 5 2009-01-02 Y      2.55
## 6 2009-01-02 Z     -2.82
```

1) tidyr::pivot_longer

Let's quickly save the "tidy" (i.e. long) stocks data frame for use on the next slide

```r
tidy_stocks ← stocks %>%
  pivot_longer(-time, names_to = "stock", values_to = "price")
```

2) tidyr::pivot_wider

```
tidy_stocks %>% pivot_wider(names_from = stock, values_from = price)
```

```
## # A tibble: 2 x 4
##   time             X     Y     Z
##   <date>       <dbl> <dbl> <dbl>
## 1 2009-01-01  0.616  1.78 -1.46
## 2 2009-01-02 -0.102  2.55 -2.82
```

```
tidy_stocks %>% pivot_wider(names_from = time, values_from = price)
```

```
## # A tibble: 3 x 3
##   stock `2009-01-01` `2009-01-02`
##   <chr>        <dbl>        <dbl>
## 1 X            0.616       -0.102
## 2 Y            1.78         2.55
## 3 Z           -1.46        -2.82
```

2) tidyr::pivot_wider

```
tidy_stocks %>% pivot_wider(names_from = stock, values_from = price)
```

```
## # A tibble: 2 x 4
##   time              X      Y      Z
##   <date>        <dbl> <dbl> <dbl>
## 1 2009-01-01  0.616  1.78 -1.46
## 2 2009-01-02 -0.102  2.55 -2.82
```

```
tidy_stocks %>% pivot_wider(names_from = time, values_from = price)
```

```
## # A tibble: 3 x 3
##   stock `2009-01-01` `2009-01-02`
##   <chr>         <dbl>        <dbl>
## 1 X             0.616       -0.102
## 2 Y             1.78         2.55
## 3 Z            -1.46        -2.82
```

Note that the second example has effectively transposed the data

3) tidyr::separate

```r
economists <- data.frame(name = c("Adam.Smith", "Paul.Samuelson", "Milton.Friedman"))
economists
```

```
##              name
## 1      Adam.Smith
## 2  Paul.Samuelson
## 3 Milton.Friedman
```

```r
economists %>% separate(name, c("first_name", "last_name"))
```

```
##   first_name last_name
## 1       Adam     Smith
## 2       Paul Samuelson
## 3     Milton  Friedman
```

3) tidyr::separate

```
economists <- data.frame(name = c("Adam.Smith", "Paul.Samuelson", "Milton.Friedman"))
economists
```

```
##              name
## 1      Adam.Smith
## 2  Paul.Samuelson
## 3 Milton.Friedman
```

```
economists %>% separate(name, c("first_name", "last_name"))
```

```
##   first_name last_name
## 1       Adam     Smith
## 2       Paul Samuelson
## 3     Milton  Friedman
```

This command is pretty smart. But to avoid ambiguity, you can also specify the separation character with `separate( ... , sep=".")`

3) tidyr::separate

A related function is `separate_rows`, for splitting up cells that contain multiple fields or observations (a frustratingly common occurence with survey data)

```
jobs <- data.frame(
  name = c("Jack", "Jill"),
  occupation = c("Homemaker", "Philosopher, Philanthropist, Troublemaker")
  )
jobs
```

```
##   name                                occupation
## 1 Jack                                 Homemaker
## 2 Jill Philosopher, Philanthropist, Troublemaker
```

3) tidyr::separate

A related function is `separate_rows`, for splitting up cells that contain multiple fields or observations (a frustratingly common occurence with survey data)

```r
## Now split out Jill's various occupations into different rows
jobs %>% separate_rows(occupation)
```

```
## # A tibble: 4 x 2
##   name  occupation
##   <chr> <chr>
## 1 Jack  Homemaker
## 2 Jill  Philosopher
## 3 Jill  Philanthropist
## 4 Jill  Troublemaker
```

4) tidyr::unite

```r
gdp ← data.frame(
  yr = rep(2016, times = 4),
  mnth = rep(1, times = 4),
  dy = 1:4,
  gdp = rnorm(4, mean = 100, sd = 2)
  )
gdp
```

```
##     yr mnth dy       gdp
## 1 2016    1  1 104.73167
## 2 2016    1  2 102.67609
## 3 2016    1  3  97.35823
## 4 2016    1  4  97.84164
```

4) tidyr::unite

```
## Combine "yr", "mnth", and "dy" into one "date" column
gdp %>% unite(date, c("yr", "mnth", "dy"), sep = "-")
```

```
##        date       gdp
## 1 2016-1-1 104.73167
## 2 2016-1-2 102.67609
## 3 2016-1-3  97.35823
## 4 2016-1-4  97.84164
```

4) tidyr::unite

Note that `unite` will automatically create a character variable:

```r
gdp_u <- gdp %>% unite(date, c("yr", "mnth", "dy"), sep = "-") %>% as_tibble()
gdp_u
```

```
## # A tibble: 4 x 2
##   date        gdp
##   <chr>     <dbl>
## 1 2016-1-1 105.
## 2 2016-1-2 103.
## 3 2016-1-3  97.4
## 4 2016-1-4  97.8
```

4) tidyr::unite

Note that `unite` will automatically create a character variable:

```r
gdp_u ← gdp %>% unite(date, c("yr", "mnth", "dy"), sep = "-") %>% as_tibble()
gdp_u
```

```
## # A tibble: 4 x 2
##   date        gdp
##   <chr>     <dbl>
## 1 2016-1-1 105. 
## 2 2016-1-2 103. 
## 3 2016-1-3  97.4
## 4 2016-1-4  97.8
```

If you want to convert it to something else (e.g. date or numeric) then you will need to modify it using `mutate`

4) tidyr::unite

```r
library(lubridate)
gdp_u %>% mutate(date = ymd(date))
```

```
## # A tibble: 4 x 2
##   date          gdp
##   <date>      <dbl>
## 1 2016-01-01 105. 
## 2 2016-01-02 103. 
## 3 2016-01-03  97.4
## 4 2016-01-04  97.8
```

Other tidyr goodies

Use `crossing` to get the full combination of a group of variables

```
crossing(side=c("left", "right"), height=c("top", "bottom"))
```

```
## # A tibble: 4 x 2
##   side  height
##   <chr> <chr>
## 1 left  bottom
## 2 left  top
## 3 right bottom
## 4 right top
```

Other tidyr goodies

Use `crossing` to get the full combination of a group of variables

```
crossing(side=c("left", "right"), height=c("top", "bottom"))
```

```
## # A tibble: 4 x 2
##   side  height
##   <chr> <chr>
## 1 left  bottom
## 2 left  top
## 3 right bottom
## 4 right top
```

See `?expand` and `?complete` for more specialized functions that allow you to fill in (implicit) missing data or variable combinations in existing data frames

Randomization and inference

The Rubin causal model

What is a causal effect?

The Rubin causal model

What is a causal effect?

A starting point is that a causal effect is a comparison between two potential outcomes

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What the difference in some outcome in the presence vs the absence of a given treatment?

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What the difference in some outcome in the presence vs the absence of a given treatment?

e.g. what is the difference in health between high and low levels of air pollution?

The Rubin causal model

What is a causal effect?

A starting point is that a causal effect is a comparison between two potential outcomes

What the difference in some outcome in the presence vs the absence of a given treatment?

e.g. what is the difference in health between high and low levels of air pollution?

Let's begin formalizing this idea

The Rubin causal model: potential outcomes

Suppose we have a set of **observational units**

- These can be people, states, animals, air quality monitors, etc

Each unit has two potential outcomes, but only one is observed

The Rubin causal model: potential outcomes

Suppose we have a set of **observational units**

- These can be people, states, animals, air quality monitors, etc

Each unit has two potential outcomes, but only one is observed

The potential outcome is Y_i^1 if unit i received some treatment, and Y_i^0 if the unit did not

The Rubin causal model: potential outcomes

Suppose we have a set of **observational units**

- These can be people, states, animals, air quality monitors, etc

Each unit has two potential outcomes, but only one is observed

The potential outcome is Y_i^1 if unit i received some treatment, and Y_i^0 if the unit did not

Y_i^0 corresponds to the control state of the world for i

The Rubin causal model: observable outcomes

Note that these potential outcomes are not the same as observable outcomes

The Rubin causal model: observable outcomes

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Observable outcomes are outcomes that actually show up in the data (i.e. the *factual* outcome)[1]

[1]The potential outcome that did not happen is called the *counterfactual outcome*.

The Rubin causal model: observable outcomes

Note that these potential outcomes are not the same as observable outcomes

Observable outcomes are outcomes that actually show up in the data (i.e. the *factual* outcome)[1]

We can write the observable outcome Y_i as a simple equation:

$$Y_i = D_i Y_i^1 + (1 - D_i) Y_i^0$$

where $D_i = 1$ if i received treatment and 0 otherwise

[1]The potential outcome that did not happen is called the *counterfactual outcome*.

The Rubin causal model: treatment effects

$$Y_i = D_i Y_i^1 + (1 - D_i) Y_i^0$$

This is the basis of the *Rubin causal model*

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This is the basis of the *Rubin causal model*

Rubin defines a treatment/causal effect δ_i as the difference between the two potential outcomes:

$$\delta_i = Y_i^1 - Y_i^0$$

The Rubin causal model: treatment effects

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This is the basis of the *Rubin causal model*

Rubin defines a treatment/causal effect δ_i as the difference between the two potential outcomes:

$$\delta_i = Y_i^1 - Y_i^0$$

This leads to an obvious problem: we only observe one of these two states for each unit i but we need to know both to recover δ_i

The Rubin causal model: average treatment effect

We can derive three parameters of interest from the definition of a treatment effect:

Average treatment effect (ATE):

$$E[\delta_i] = E[Y_i^1 - Y_i^0] = E[Y_i^1] - E[Y_i^0]$$

The Rubin causal model: average treatment effect

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Average treatment effect (ATE):

$$E[\delta_i] = E[Y_i^1 - Y_i^0] = E[Y_i^1] - E[Y_i^0]$$

This is the average of the individual treatment effects

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We can derive three parameters of interest from the definition of a treatment effect:

Average treatment effect (ATE):

$$E[\delta_i] = E[Y_i^1 - Y_i^0] = E[Y_i^1] - E[Y_i^0]$$

This is the average of the individual treatment effects

It is also unknowable

Rubin: average treatment on the treated

Average treatment on the treated (ATT):

$$E[\delta_i | D_i = 1] = E[Y_i^1 - Y_i^0 | D_i = 1] = E[Y_i^1 | D_i = 1] - E[Y_i^0 | D_i = 1]$$

Rubin: average treatment on the treated

Average treatment on the treated (ATT):

$$E[\delta_i|D_i=1] = E[Y_i^1 - Y_i^0|D_i=1] = E[Y_i^1|D_i=1] - E[Y_i^0|D_i=1]$$

This is the average of the individual treatment effects only for the i in the treated group

Rubin: average treatment on the treated

Average treatment on the treated (ATT):

$$E[\delta_i|D_i = 1] = E[Y_i^1 - Y_i^0|D_i = 1] = E[Y_i^1|D_i = 1] - E[Y_i^0|D_i = 1]$$

This is the average of the individual treatment effects only for the i in the treated group

It is also unknowable since we never observe $E[Y_i^0|D_i = 1]$

Rubin: average treatment on the treated

Average treatment on the treated (ATT):

$$E[\delta_i|D_i = 1] = E[Y_i^1 - Y_i^0|D_i = 1] = E[Y_i^1|D_i = 1] - E[Y_i^0|D_i = 1]$$

This is the average of the individual treatment effects only for the i in the treated group

It is also unknowable since we never observe $E[Y_i^0|D_i = 1]$

If the treatment effect differs across i then $ATE \neq ATT$

Rubin: average treatment on the untreated

Average treatment on the untreated (ATU):

$$E[\delta_i|D_i = 0] = E[Y_i^1 - Y_i^0|D_i = 0] = E[Y_i^1|D_i = 0] - E[Y_i^0|D_i = 0]$$

Rubin: average treatment on the untreated

Average treatment on the untreated (ATU):

$$E[\delta_i|D_i=0]=E[Y_i^1-Y_i^0|D_i=0]=E[Y_i^1|D_i=0]-E[Y_i^0|D_i=0]$$

This is the average of the individual treatment effects only for the i in the untreated group

Rubin: average treatment on the untreated

Average treatment on the untreated (ATU):

$$E[\delta_i|D_i = 0] = E[Y_i^1 - Y_i^0|D_i = 0] = E[Y_i^1|D_i = 0] - E[Y_i^0|D_i = 0]$$

This is the average of the individual treatment effects only for the i in the untreated group

It is also unknowable since we never observe $E[Y_i^1|D_i = 0]$

Rubin: average treatment on the untreated

Average treatment on the untreated (ATU):

$$E[\delta_i|D_i=0] = E[Y_i^1 - Y_i^0|D_i=0] = E[Y_i^1|D_i=0] - E[Y_i^0|D_i=0]$$

This is the average of the individual treatment effects only for the i in the untreated group

It is also unknowable since we never observe $E[Y_i^1|D_i=0]$

If the treatment effect differs across i then $ATE \neq ATU$

Hands on: understanding treatment effects

We've got our definitions, now lets be a bit more clear as to what we are doing with some empirical examples putting our new R tools to work

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Suppose treatment D is whether a state has a conservation policy

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Suppose treatment D is whether a state has a conservation policy

The outcome Y is the number of bird species in that state

Hands on: understanding treatment effects

We've got our definitions, now lets be a bit more clear as to what we are doing with some empirical examples putting our new R tools to work

Suppose treatment D is whether a state has a conservation policy

The outcome Y is the number of bird species in that state

We want to understand the causal effect of conservation policy on the number of species

Hands on: understanding treatment effects

Here's our dataset of both potential outcomes:

```
cons_df # data frame of conservation treatment, outcomes
```

```
## # A tibble: 8 x 4
##   state    Y1    Y0 delta
##   <int> <dbl> <dbl> <dbl>
## 1     1     4     7    -3
## 2     2     7     9    -2
## 3     3     7     0     7
## 4     4    10     1     9
## 5     5     7     7     0
## 6     6     6     0     6
## 7     7     9     3     6
## 8     8    13     4     9
```

Calculate the average treatment effect

Hands on: understanding treatment effects

ATE = $E[\delta_i]$ which we can compute with `dplyr::summarise`:

```
cons_df %>%
  dplyr::summarise(mean(delta))
```

```
## # A tibble: 1 x 1
##   `mean(delta)`
##           <dbl>
## 1             4
```

The average treatment effect is 4: a conservation policy increases the number of bird species in a state by 4

Hands on: understanding treatment effects

Notice that not all states benefit from conservation policies, and it even backfires in one state

The ATE is just the average over all the different treatment effects

```
cons_df
```

```
## # A tibble: 8 x 4
##   state    Y1    Y0 delta
##   <int> <dbl> <dbl> <dbl>
## 1     1     4     7    -3
## 2     2     7     9    -2
## 3     3     7     0     7
## 4     4    10     1     9
## 5     5     7     7     0
## 6     6     6     0     6
## 7     7     9     3     6
## 8     8    13     4     9
```

Hands on: understanding treatment effects

Suppose we have a perfect policymaker who knows each state's potential outcomes and can perfectly decide whether each state should have a conservation policy

Hands on: understanding treatment effects

Suppose we have a perfect policymaker who knows each state's potential outcomes and can perfectly decide whether each state should have a conservation policy

The policymaker assigns treatment and then observes the actual outcome according to $Y_i = D_i Y_i^1 + (1 - D_i) Y_i^0$

Hands on: understanding treatment effects

Suppose we have a perfect policymaker who knows each state's potential outcomes and can perfectly decide whether each state should have a conservation policy

The policymaker assigns treatment and then observes the actual outcome according to $Y_i = D_i Y_i^1 + (1 - D_i) Y_i^0$

What does the dataset look like for the observed outcomes?

Hands on: understanding treatment effects

```
observed_df ← cons_df %>%
  mutate(
    Y = ifelse(delta > 0, Y1, Y0),
    D = as.numeric(delta > 0)
    ) %>%
  select(state, Y, D)
observed_df
```

```
## # A tibble: 8 x 3
##   state     Y     D
##   <int> <dbl> <dbl>
## 1     1     7     0
## 2     2     9     0
## 3     3     7     1
## 4     4    10     1
## 5     5     7     0
## 6     6     6     1
## 7     7     9     1
## 8     8    13     1
```

Hands on: estimating ATEs

Given the **observed** data, what if we tried to *estimate* the ATE by comparing mean outcomes of treated $(D_i = 1)$ vs untreated units $(D_i = 0)$

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This is the simple difference in mean outcomes (SDO):

$$
\begin{aligned}
SDO &= E[Y^1|D=1] - E[Y^0|D=0] \\
&= \frac{1}{N_T}\sum_{i=1}^{N_T}(y_i|d_i=1) - \frac{1}{N_U}\sum_{i=1}^{N_U}(y_i|d_i=0)
\end{aligned}
$$

where N_T is the number of treated units and N_U is the number of untreated units

Hands on: estimating ATEs

We can compute the SDO using `dplyr::summarise` in conjunction with `dplyr::group_by` on treatment status D:

```
observed_df %>%
  dplyr::group_by(D) %>%
  dplyr::summarise(meanY = mean(Y))
```

```
## # A tibble: 2 x 2
##       D meanY
##   <dbl> <dbl>
## 1     0  7.67
## 2     1  9
```

The SDO is 9 - 7.67 = 1.33 < 4!

Hands on: estimating ATEs

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Because the SDO is actually composed of three pieces, only one of which is the ATE:[1]

$$\text{SDO} = \text{ATE} +$$

See Mixtape pages 89-91 for the derivation.

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What are these mathematically and intuitively?

[1] See Mixtape pages 89-91 for the derivation.

Hands on: decomposing the SDO

$$
\begin{aligned}
\underbrace{E[Y^1|D=1] - E[Y^0|D=0]}_{\text{SDO}} =& \underbrace{\frac{1}{N_T}\sum_{i=1}^{N_T}(y_i|d_i=1) + \frac{1}{N_U}\sum_{i=1}^{N_U}(y_i|d_i=0)}_{\text{SDO}} \\
=& \underbrace{E[Y^1] - E[Y^0]}_{\text{ATE}} \\
&+ \underbrace{E[Y^0|D=1] - E[Y^0|D=0]}_{\text{Selection bias}} \\
&+ \underbrace{(1-\pi)(ATT - ATU)}_{\text{Het. Treat. Eff. Bias}}
\end{aligned}
$$

where π is the share of treated units

Hands on: decomposing the SDO

The LHS we know sums to 1.33 so the RHS must as well

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The first term is the ATE, what we actually want to estimate

We **know** ATE = 4 so the last two terms are why SDO < ATE

Let's work through these two in more detail

Hands on: Selection bias

The second term is **selection bias:**

$$E[Y^0|D=1] - E[Y^0|D=0]$$

It is the inherent differences between the two groups if they did not *actually* get the conservation policy

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Calculate this with the `cons_df` data frame with both potential outcomes

Hands on: Selection bias

```r
cons_df %>%
  mutate(
    D = as.numeric(delta > 0)
    ) %>%
  group_by(D) %>%
  summarise(mean(Y0)) # Difference in potential control outcomes across the two groups
```

```
## # A tibble: 2 x 2
##       D `mean(Y0)`
##   <dbl>      <dbl>
## 1     0       7.67
## 2     1       1.6
```

Selection bias is thus 1.6 - 7.67 = -6.07

Hands on: het. treat. effect bias

The third term is the bias from heterogeneous treatment effects across groups:

$$\underbrace{(1-\pi)}_{\text{Share w/o policy}} \times \underbrace{(ATT - ATU)}_{\text{Diff. in treat. effect}}$$

It is the difference in the effect of the conservation policy across the two groups multiplied by the share that did not get a conservation policy

Hands on: het. treat. effect bias

$$\underbrace{(1-\pi)}_{\text{Share w/o policy}} \times \underbrace{(ATT - ATU)}_{\text{Diff. in treat. effect}}$$

What's the intuition for this?

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What's the intuition for this?

- How much more of an effect did the policy have on the units that *happened* to get treatment versus the effect the policy would have had on the units that *happened* to be in the control group

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- How much more of an effect did the policy have on the units that *happened* to get treatment versus the effect the policy would have had on the units that *happened* to be in the control group
- Scale the size of this difference by fraction of control units

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- Scale the size of this difference by fraction of control units

Calculate this with the `cons_df` data frame with both potential outcomes

Hands on: het. treat. effect bias

```
cons_df %>%
  mutate(
    D = as.numeric(delta > 0)
    ) %>%
  group_by(D) %>%
  summarise(mean(delta), n()) # Difference in potential control and treatment outcomes across th
```

```
## # A tibble: 2 x 3
##       D `mean(delta)` `n()`
##   <dbl>         <dbl> <int>
## 1     0         -1.67     3
## 2     1          7.4      5
```

Heterogeneous treatment effect bias is thus: (1 - 5/(5+3))*(7.4 - (-1.67)) = 3.40

Hands on: het. treat. effect bias

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cons_df %>%
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Heterogeneous treatment effect bias is thus: (1 - 5/(5+3))*(7.4 - (-1.67)) = 3.40

In total we have: SDO (1.33) = ATE (4) + SB (-6.07) + HTEB (3.40)

Recap: treatment effect estimates

Taking a simple difference in means of outcomes between treatment and control groups does contain what we want

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1. **Selection bias:** The units in the treatment group different from the control group in the absence of treatment

Recap: treatment effect estimates

Taking a simple difference in means of outcomes between treatment and control groups does contain what we want

Unfortunately it is **confounded** by two forms of bias:

1. **Selection bias:** The units in the treatment group different from the control group in the absence of treatment
2. **Heterogeneous treatment effect bias**: The units in the treatment group respond to treatment differently than units in the control group

Bias examples

What are some examples of these forms of bias?

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Selection bias: If we select certain groups into treatment, for example, if we pass conservation policy in states with little biodiversity

- This may lead to a negative bias on conservation policy impacts, even with a positive ATE

HTEB: If we select units into treatment based on expected response, for example, if we pass policy in states where birds are **very** sensitive to conservation

- This may lead to an overestimate of the size of the treatment effect

Empirical economics

A huge chunk of economics is trying circumvent these forms of bias[1]

[1]We're more heavily concerned with selection bias than HTEB. There are also other biases to worry about that we will get to later.

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1. Understanding what tools we have to correctly estimate the ATE

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This should be a less-technical complement to Brian's class

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Recovering the ATE

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We will cover some subset of:

1. Randomized control trials
2. Regression discontinuity
3. Difference-in-differences
4. Cross-sectional regressions
5. Two way fixed effects

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We will cover some subset of:

1. Randomized control trials
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3. Difference-in-differences
4. Cross-sectional regressions
5. Two way fixed effects

All of these approaches have pluses and minuses

Understanding the source of bias

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What is the fundamental problem leading to selection bias and HTEB?

Both stem from treatment being correlated with characteristics of the observational units

Selection bias is because treatment is correlated with unit characteristics in the absence of treatment

HTEB is because treatment is correlated with the size of units' responses to treatment

A potential solution

What's a simple way to deal with this?

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RANDOMIZATION

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If we randomize treatment across observational units then SDO = ATE

Randomization drives selection bias and HTEB to zero

Let's see why

Randomization

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In our example we know independence is violated because we assigned the conservation policy to states that had $Y^1 > Y^0$

What if we randomized conservation policy?

Randomization

Randomization of treatment / policy means that:

$$E[Y^1|D=1] - E[Y^1|D=0] = 0 \qquad E[Y^0|D=1] - E[Y^0|D=0] = 0$$

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Randomization of treatment / policy means that:

$$E[Y^1|D=1] - E[Y^1|D=0] = 0 \qquad E[Y^0|D=1] - E[Y^0|D=0] = 0$$

If we randomized treatment across units, then on average, the difference in potential outcomes across groups should be zero

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This means that:

$$E[Y^1|D=1] = E[Y^1|D=0] \qquad E[Y^0|D=1] = E[Y^0|D=0]$$

The second equation $E[Y^0|D=1] - E[Y^0|D=0] = 0$ directly gives us that selection bias is zero with the SDO

Randomization

What does randomization do to HTEB?

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$$
\begin{aligned}
&ATT - ATU \\
&= (E[Y^1|D=1] - E[Y^0|D=1]) - (E[Y^1|D=0] - E[Y^0|D=0]) \\
&= (E[Y^1|D=1] - E[Y^1|D=0]) - (E[Y^0|D=1] - E[Y^0|D=0]) \\
&= (0) - (0) = 0
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&= (0) - (0) = 0
\end{aligned}$$

HTEB goes to zero!

Randomization and SDO

Randomization means that SDO = ATE:

$$\underbrace{\frac{1}{N_T}\sum_{i=1}^{N_T}(y_i|d_i=1)-\frac{1}{N_C}\sum_{i=1}^{N_C}(y_i|d_i=0)}_{\text{SDO}}=\underbrace{E[Y^1]-E[Y^0]}_{\text{ATE}}$$

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1. Data on treatment assignment

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2. Data on observable outcomes

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All we need to estimate the average treatment effect of a policy is:

1. Data on treatment assignment
2. Data on observable outcomes
3. The independence assumption: $Y^1, Y^0 \perp D$

Hands on: randomization and SDO

Let's see how this works in practice by re-constructing our dataset and then randomizing treatment

Hands on: randomization and SDO

Let's see how this works in practice by re-constructing our dataset and then randomizing treatment

```
set.seed(12345)
ate ← 4 # average treatment effect
n_obs ← 100 # number of observations
cons_rand_df ← tibble(
  state = seq(1, n_obs), # state identifier
  Y0 = floor(runif(n_obs)*10)) %>%  # control/untreated potential outcome
  mutate(
    D = as.numeric(runif(n()) > 0.5), # randomized treatment
    Y1 = Y0 + ate + round(rnorm(n())), # generate treatment potential outcome
    Y = D*Y1 + (1-D)*Y0 # generate observed outcome
  ) %>%
  select(
    state, D, Y # keep only observable variables
  )
```

Hands on: randomization and SDO

```r
cons_rand_df # data frame of randomized treatment, observable outcome
```

```
## # A tibble: 100 x 3
##    state     D     Y
##    <int> <dbl> <dbl>
##  1     1     0     7
##  2     2     1    11
##  3     3     1    11
##  4     4     1    11
##  5     5     1     8
##  6     6     1     4
##  7     7     1     7
##  8     8     1    11
##  9     9     0     7
## 10    10     0     9
## # … with 90 more rows
```

Hands on: randomization and SDO

Now take the SDO:

```
cons_rand_df %>%
  dplyr::group_by(D) %>%
  dplyr::summarise(meanY = mean(Y))
```

```
## # A tibble: 2 x 2
##       D meanY
##   <dbl> <dbl>
## 1     0  4.42
## 2     1  8.82
```

The SDO is 8.82 - 4.42 = 4.40, a very close estimate of the ATE!

Hands on: randomization and SDO

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The SDO is 8.82 - 4.42 = 4.40, a very close estimate of the ATE!

As `n_obs` $\rightarrow \infty$, we will have that $SDO \rightarrow ATE$

Randomization: what it does and doesn't do

What does independence imply?

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$$E[Y^1|D=1] - E[Y^1|D=0] = 0 \qquad E[Y^0|D=1] - E[Y^0|D=0] = 0$$

The two groups have the same potential outcomes, ***on average***

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The two groups have the same potential outcomes, ***on average***

What does independence **not** imply? That:

$$E[Y^1|D=1] - E[Y^0|D=0] = 0 \qquad E[Y^1|D=1] - E[Y^0|D=1] = 0$$

It does not imply that the observed outcomes are the same across the two groups, nor does it imply that the two potential outcomes of a single group are the same

Independence

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Observational data are just data that we collect from the real world

- e.g. observed state policy choices and outcomes, observed pollution levels and outcomes

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So what can we do?

Conditional independence

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$$(Y^1, Y^0 \perp D) | X$$

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This is much weaker than (unconditional) independence: we only need independence to hold for units that share the same X values, not for all units

Many of the estimation tools used in economics rely on (variants of) the conditional independence assumption