

Lecture 10

Base R // Tidyverse // Regression

Ivan Rudik
AEM 4510

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 actually **do** environmental economics

A good chunk of this lecture comes from Grant McDermott's **data science for economists** notes, Ed Rubin's **intro to econometrics**, and **RStudio education**

RStudio Cloud

Getting started

We will be using [rstudio.cloud](#) for our coding

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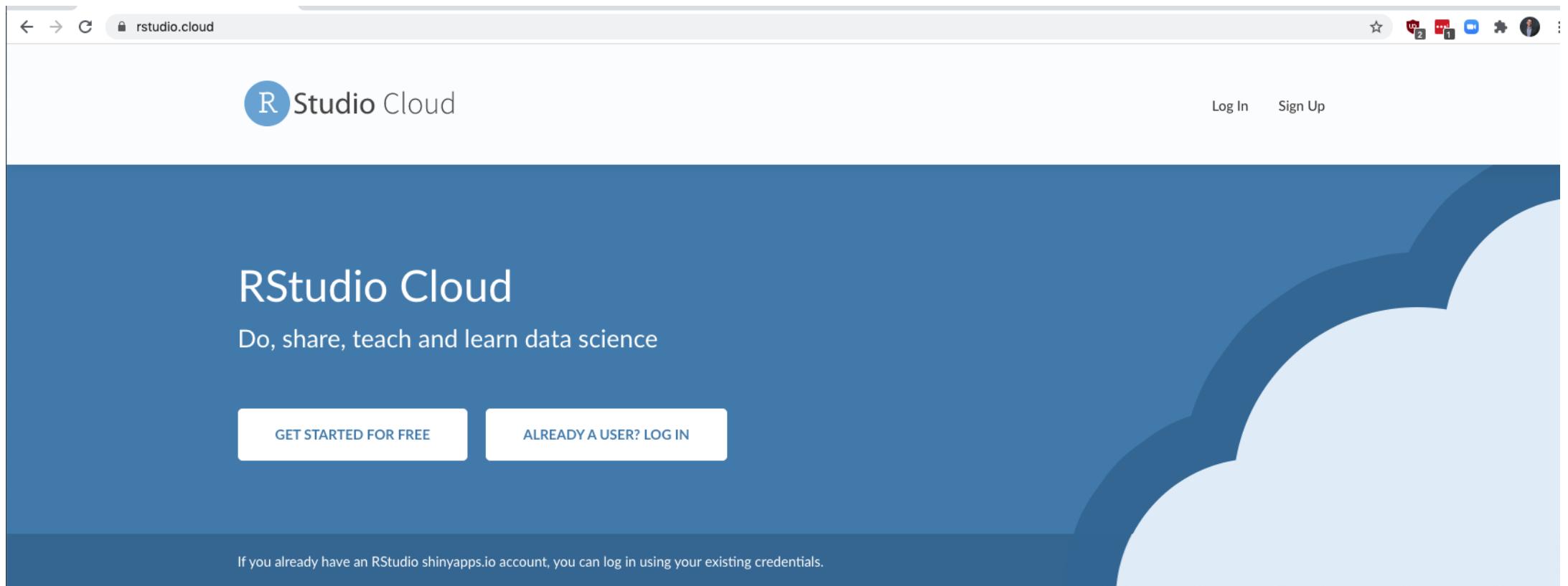
Why?

You don't need to download/install anything

I can prepare the packages and code and make it easy to download

Let's get everything going...

Getting started: login



The screenshot shows the RStudio Cloud homepage. At the top, there's a navigation bar with icons for back, forward, refresh, and search, followed by the URL 'rstudio.cloud'. On the right side of the bar are various browser extension icons. Below the bar, the RStudio Cloud logo is on the left, and 'Log In' and 'Sign Up' buttons are on the right. The main background is a large blue graphic featuring a white cloud shape on the right. The text 'RStudio Cloud' is prominently displayed in white, with the subtitle 'Do, share, teach and learn data science' below it. Two buttons are visible: 'GET STARTED FOR FREE' and 'ALREADY A USER? LOG IN'. A small note at the bottom of the main section says, 'If you already have an RStudio shinyapps.io account, you can log in using your existing credentials.' The overall design is clean and modern.

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.

\$ AVAILABLE PRICING PLANS

🕒 RSTUDIO CLOUD GUIDE

🌐 RSTUDIO.COM

Getting started: new project

The screenshot shows the RStudio Cloud interface for a workspace named 'AEM 4510' created by Ivan Rudik. The left sidebar includes links for 'Your Workspace', 'New Space', 'Learn' (with 'Guide', 'What's New', 'Primers', and 'Cheat Sheets'), and 'Help'. The main content area displays 'All Projects' with a single item, 'In-10', listed. A context menu for this project offers options like 'New Project', 'New Project from Git Repository', 'Delete', 'Move', and 'Export'. The top navigation bar has tabs for 'Projects', 'Members', and 'About', along with user-specific icons.

AEM 4510
Ivan Rudik

Projects Members About

All Projects

List All projects Sort By name

In-10
Ivan Rudik
Created Mar 29, 2021 10:22 AM

New Project

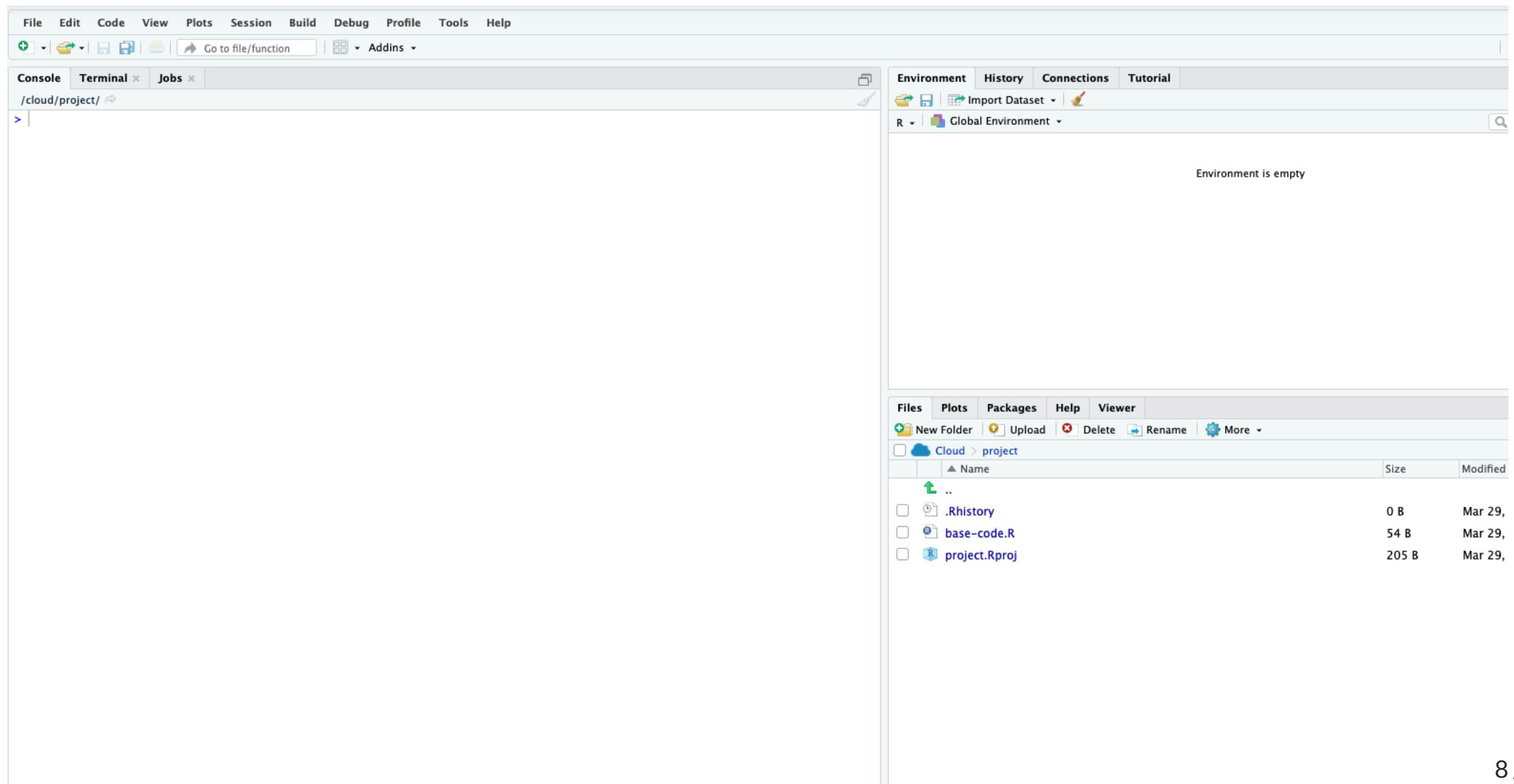
New Project from Git Repository

Delete Move Export

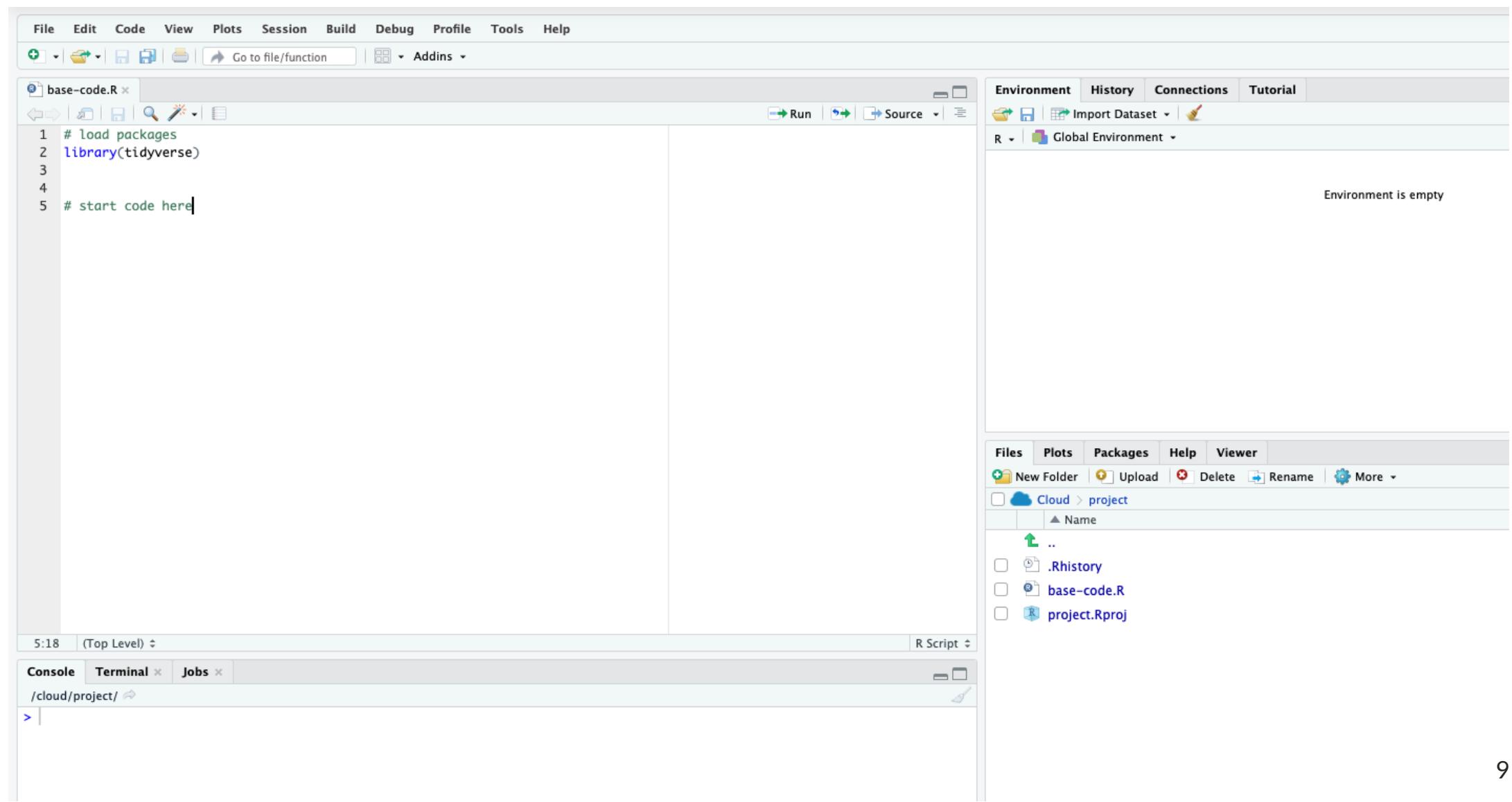
Getting started: wait for deployment

The screenshot shows the RStudio Cloud interface with the URL `rstudio.cloud/project/1795327` in the address bar. The main navigation bar includes links for "Your Workspace / aem6510", "Ivan Rudik", and various system icons. On the left, a sidebar menu is open under "Your Workspace", showing options like "New Space", "Learn" (with "Guide", "What's New", "Primers", and "Cheat Sheets"), "Help" (with "Current System Status" and "RStudio Community"), and "Info" (with "Plans & Pricing" and "Terms and Conditions"). In the center, a large, semi-transparent circular overlay displays the message "Deploying Project" with a blue progress bar at the bottom.

Click on base-code in bottom-right



Code script open!



Now we're set

Now we're all set with our coding environment

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You can write code in the top window and save it as a file

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Highlight code in the top window and press cmd+enter to run those highlighted lines

Quick intro to R

Introduction to base R

Basic arithmetic

R is a powerful calculator and recognizes all of the standard arithmetic operators:

```
1+2 # add / subtraction
```

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

```
5/2 # divide
```

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

```
2^3 # exponentiate
```

```
## [1] 8
```

```
2+4*1^3 # standard order of precedence (`*` before `+`, etc.)
```

Logic

R also comes equipped with a full set of logical operators and Booleans

```
1 > 2
```

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

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

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

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

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

Logic

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
```

NA means **not available** (i.e., missing)

Logic

For value matching we can use: `%in%`

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

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

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

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

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

Logic

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

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

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

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

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

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

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

Logic

Evaluation caveat: What do you think will happen if we evaluate $0.1 + 0.2 == 0.3$?

Logic

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```
0.1 + 0.2 == 0.3
```

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

Uh-oh! What went wrong here?

Logic

Evaluation caveat: What do you think will happen if we evaluate `0.1 + 0.2 == 0.3?`

```
0.1 + 0.2 == 0.3
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## [1] FALSE
```

Uh-oh! What went wrong here?

Problem: Computers represent numbers as binary (i.e., base 2) floating-points. More [here](#)

- Fast and memory efficient, but can lead to unexpected behavior
- Similar to how standard decimals can't precisely capture certain fractions

Logic

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Assignment

In R, we can use either `<-` or `=` to handle assignment

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Assignment with `=`

`<-` is normally read aloud as "gets". You can think of it as a (left-facing) arrow saying *assign in this direction*.

```
a = 10 + 5  
a
```

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

Assignment

Assignment with `=`

You can also use `=` for assignment.

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

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

Which assignment operator should you use?

The proper one to use is <- , which can be inserted using the keyboard shortcut Alt/Option + -

It doesn't really matter for our purposes, other languages use =

I will use =

Bottom line: Use whichever you prefer, just be consistent

Help

For more information on a (named) function or object in R, consult the "help" documentation using ?

For example:

```
?plot
```

Vignettes

For some packages, `vignette()` will provide a detailed intro

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

Vignettes are a great way to learn how and when to use a package

Comments

Comments in R code are demarcated by `#`

Use comments to document your logic in `.R` scripts and within `.Rmd` code chunks

```
# THIS IS A CODE SECTION ----  
# this is a comment  
cornell = "big red"
```

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Comments should be concise and used only when necessary (unlike the comments above)

Comments

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Using at least four trailing dashes (----) creates a code section, which simplifies navigation and code folding

- Also works with trailing equals (=====) or pound signs (#####)

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Keyboard shortcut: use `Ctrl/Cmd+/` or `Ctrl/Cmd+Shift+C` in RStudio to (un)comment whole sections of highlighted code

Object-oriented programming in R

Object-oriented programming

In R:

| "Everything is an object and everything has a name."

"Everything is an object"

What are objects?

There are many different *types* (or *classes*) of objects

Here are some objects that we'll be working with regularly:

- vectors
- matrices
- data frames
- lists
- functions

Data frames

The most important object we will be working with is the **data frame**

You can think of it basically as an Excel spreadsheet

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

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

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d
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##   x y  
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This is essentially just a table with columns named x and y

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d
```

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

This is essentially just a table with columns named `x` and `y`

Each row is an observation telling us the values of both `x` and `y`

Aside: built-in data frames

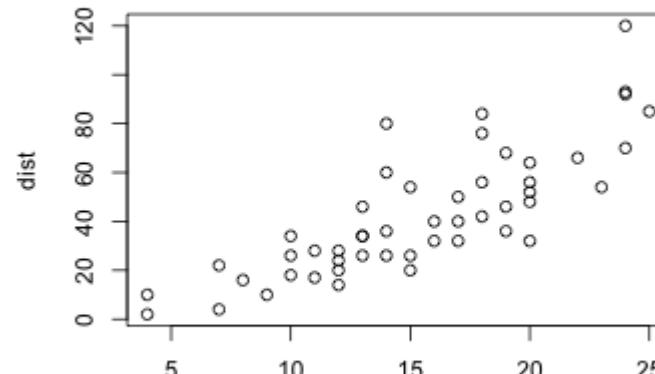
Base R and packages have a bunch of built in data frames with special names you can call on

For example we have `cars`:

```
head(cars)
```

```
##      speed dist
## 1        4    2
## 2        4   10
## 3        7    4
## 4        7   22
## 5        8   16
## 6        9   10
```

```
plot(cars)
```



Back to objects

Each object class has its own set of rules for determining valid operations

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

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

Back to objects

At the same time, you can (usually) convert an object from one type to another

```
# Convert it to (i.e., create) a matrix call "mat"
mat = as.matrix(d)
mat
```

```
##      x y
## [1,] 1 3
## [2,] 2 4
```

Working with multiple objects

In R we can have multiple data frames in memory at once

Even though we just made `mat`, `d` still exists:

```
d
```

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

Ways to learn about objects

Printing an object directly in the console is often handy

- e.g., Type `d` and hit Enter

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`View()` is very helpful, and has the same effect as clicking on the object in your RStudio *Environment* pane

- e.g., Type `View(d)` and hit Enter

Ways to learn about objects

Use the `str` command to learn about an object's **structure**

```
# d = data.frame(x = 1:2, y = 3:4) # Create a small data frame called "d"  
str(d) # Evaluate its structure
```

```
## 'data.frame':    2 obs. of  2 variables:  
##   $ x: int  1 2  
##   $ y: int  3 4
```

Ways to learn about objects

Use the `str` command to learn about an object's **structure**

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# d = data.frame(x = 1:2, y = 3:4) # Create a small data frame called "d"  
str(d) # Evaluate its structure
```

```
## 'data.frame': 2 obs. of 2 variables:  
## $ x: int 1 2  
## $ y: int 3 4
```

You can also use `class` to get an object's class without all the other details

Global environment

Let's go back to the simple data frame that we created a few slides earlier.

```
d
```

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

Global environment

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d
```

```
##   x y  
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## 2 2 4
```

Now, let's try to do a logical comparison of these "x" and "y" variables:

```
x < y
```

```
## Error in eval(expr, envir, enclos): object 'x' not found
```

Global environment

Let's go back to the simple data frame that we created a few slides earlier.

```
d
```

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

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Global environment

The error message provides the answer to our question:

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R looked in our *Global Environment* and couldn't find x

The screenshot shows the RStudio interface with the 'Environment' tab selected. The global environment contains the following objects:

Data	Values
d	2 obs. of 2 variables
mat	int [1:2, 1:2] 1 2 3 4
a	15
b	20
vibe	"immaculate"

Global environment

The error message provides the answer to our question:

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R looked in our *Global Environment* and couldn't find `x`

The screenshot shows the RStudio interface with the 'Environment' tab selected. The global environment contains the following objects:

Data	Values
d	2 obs. of 2 variables
mat	int [1:2, 1:2] 1 2 3 4
a	15
b	20
vibe	"immaculate"

We have to tell R that `x` and `y` belong to the object `d`

"Everything has a name"

Reserved words

R has a bunch of key/reserved words that serve specific functions

- You can't (re)assign these, even if you wanted to

See [here](#) for a full list, including (but not limited to):

```
if  
else  
while # looping  
function  
for # looping  
TRUE  
FALSE  
NULL # null/undefined  
Inf #infinity  
NaN # not a number  
NA # not available / missing
```

Semi-reserved words

There are other words that are sort of reserved, in that they have a particular meaning

- These are named functions or constants (e.g., `pi`) that you can re-assign if you really want to... but that already come with important meanings from base R

The most important example is `c()`, which binds and concatenates objects together

```
my_vector = c(1, 2, 5)  
my_vector
```

Semi-reserved words

What do you think will happen if you type the following?

```
c = 4  
c(1, 2 ,5)
```

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What do you think will happen if you type the following?

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Semi-reserved words

What do you think will happen if you type the following?

```
c = 4  
c(1, 2, 5)
```

```
## [1] 1 2 5
```

In this case, R is "smart" enough to distinguish between the variable `c` and the built-in function `c()`

Semi-reserved words (cont.)

But R won't always be able to distinguish between conflicting definitions! For example:

```
pi
```

```
## [1] 3.141593
```

```
pi = 2  
pi
```

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

Semi-reserved words (cont.)

But R won't always be able to distinguish between conflicting definitions! For example:

```
pi
```

```
## [1] 3.141593
```

```
pi = 2  
pi
```

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

Bottom line: Don't use (semi-)reserved words!

Indexing

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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

Indexing

How do we index in R?

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

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:

```
rnorm(n = 50, mean = 0, sd = 1) # take 50 draws from the standard normal distribution
```

Indexing

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

```
rnorm(n = 50, mean = 0, sd = 1) # take 50 draws from the standard normal distribution

## [1] 1.62295858 -0.55469929 0.46628731 -1.65669765 -0.86058426 0.83158347
## [7] 1.64737544 0.39299903 0.09431285 -1.27440466 1.40794961 0.30169538
## [13] 2.24490962 -0.09224972 2.02745594 2.07531253 -0.23003648 -1.18919684
## [19] -1.34631467 -1.34120251 1.05576193 0.80117986 0.52700501 0.12804045
## [25] -1.32675305 -1.56985114 -0.33249858 1.47752658 -0.56441158 0.73609594
## [31] 1.75009711 0.10072173 0.77832664 -0.73818997 0.15799774 0.29318796
## [37] -0.33782394 -0.58011189 -1.20873018 -0.89561165 1.99983961 0.46884044
## [43] 0.33656194 -0.52128777 0.64874559 0.20858868 -0.01103537 -0.16479979
## [49] 0.04249935 -1.66497370
```

Option 1: []

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

```
a = 1:10  
a[4] ## Get the 4th element of object "a"
```

```
## [1] 4
```

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

```
## [1] 4 6
```

Option 1: []

This also works on larger arrays (vectors, matrices, data frames, and lists)

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

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

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

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

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

Option 1: []

This also works on larger arrays (vectors, matrices, data frames, and lists)

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

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

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

```
## # A tibble: 3 × 1
##   name
##   <chr>
## 1 Luke Skywalker
## 2 C-3PO
## 3 R2-D2
```

Option 1: []

We haven't discusssed them yet, but **lists** are a more complex type of array object in R

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For example, you can have lists containing:

- a scalar, a string, and a data frame
- a list of data frames
- a list of lists

Option 1: []

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. An example might help to illustrate:

```
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
```

Option 2: \$

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 12
```

Option 2: \$

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 12
```

Option 2: \$

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
```

Option 2: \$

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

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

```
starwars$name[1]  
## [1] "Luke Skywalker"
```

Option 2: \$

Finally, `$` provides another way to avoid the "object not found" problem that we ran into earlier

```
x < y # Doesn't work
```

```
## Error in eval(expr, envir, enclos): object 'x' not found
```

```
d$x < d$y # Works!
```

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

Cleaning up

Removing objects

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

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

You can use `rm(list = ls())` to remove all objects in your working environment, though this is **frowned upon**

- Better just to start a new R session

The tidyverse

What is "tidy" data?

What we are going to learn is how to use a set of packages called the **tidyverse**

What is "tidy" data?

What we are going to learn is how to use a set of packages called the **tidyverse**

These sets of packages make working with data **extremely easy** and **intuitive**

What is "tidy" data?

Resources:

- [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?

Resources:

- [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')` (already done on cloud)

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

Tidyverse vs. base R

Lots of debate over tidyverse vs base R

Tidyverse vs. base R

Lots of debate over tidyverse vs base R

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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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.

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library(tidyverse)
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```
library(tidyverse)
```

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"  
## [5] "dplyr"          "dtplyr"         "forcats"        "googledrive"  
## [9] "googlesheets4"  "ggplot2"        "haven"          "hms"  
## [13] "httr"           "jsonlite"       "lubridate"      "magrittr"  
## [17] "modelr"         "pillar"         "purrr"          "readr"  
## [21] "readxl"         "reprex"         "rlang"          "rstudioapi"  
## [25] "rvest"          "stringr"        "tibble"         "tidyverse"  
## [29] "xml2"
```

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

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## [1] "broom"          "cli"            "crayon"         "dbplyr"  
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## [17] "modelr"         "pillar"         "purrr"          "readr"  
## [21] "readxl"         "reprex"         "rlang"          "rstudioapi"  
## [25] "rvest"          "stringr"        "tibble"         "tidyverse"  
## [29] "xml2"
```

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

Tidyverse packages

We're going to focus on two workhorse packages:

1. **dplyr**
2. **tidyr**

These are the packages for cleaning and wrangling data

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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 is important and knowing how to do it well is a good skill for any data-oriented job

Pipes: |>

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

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

Let's consider a fake example to get the idea for why its really beneficial

Pipes: |>

Let's say we wanted to apply a sequence of operations that tells the computer what you did throughout your day:

1. Wake up
2. Get out of bed
3. Comb hair
4. Go downstairs
5. Drink a cup
6. Grab hat
7. Catch bus

Pipes: |>

If you were to code this up in a traditional way it might look one of two ways:

A bunch of lines doing all the different steps

```
me = wake_up(me)
me = get_out_of_bed(me)
me = comb_hair(me)
me = go(me, "downstairs")
me = drink(me, "cup")
me = grab(me, "hat")
me = catch(me, "bus")
```

Pipes: |>

If you were to code this up in a traditional way it might look one of two ways:

Or if you're a little crazy then do it all in one line

```
me = catch(grab(drink(go(comb_hair(get_out_of_bed(wake_up(me)))), where = "downstairs"), what = "cups")))
```

These are kind of tedious or messy and out of the order you'd think

Pipes: |>

With pipes we can do everything at once, but have it be **in order**:

```
me = me |>  
wake_up() |>  
get_out_of_bed() |>  
comb_hair() |>  
go("downstairs") |>  
drink("cup") |>  
grab("hat") |>  
catch("bus")
```

This makes everything **very intuitive** to read and code!

Pipes: |>

Here's a real example: suppose we wanted to figure out the average highway miles per gallon of Audi's in the `mpg` dataset:

```
mpg
```

```
## # A tibble: 234 × 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... f       18    29 p   comp...
## 2 audi         a4          1.8  1999     4 manu... f       21    29 p   comp...
## 3 audi         a4          2    2008     4 manu... f       20    31 p   comp...
## 4 audi         a4          2    2008     4 auto... f       21    30 p   comp...
## 5 audi         a4          2.8  1999     6 auto... f       16    26 p   comp...
## 6 audi         a4          2.8  1999     6 manu... f       18    26 p   comp...
## 7 audi         a4          3.1  2008     6 auto... f       18    27 p   comp...
## 8 audi         a4 quattro  1.8  1999     4 manu... 4      18    26 p   comp...
## 9 audi         a4 quattro  1.8  1999     4 auto... 4      16    25 p   comp...
## 10 audi        a4 quattro 2    2008     4 manu... 4      20    28 p   comp...
## # ... with 224 more rows
```

Pipes: |>

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

Pipes: |>

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

```
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 × 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 × 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 × 2
##   model      hwy_mean
##   <chr>       <dbl>
## 1 a4          28.3
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Pipes: |>

Or, you could use **pipes** |>:

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

```
## # A tibble: 3 × 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:

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

```
## # A tibble: 3 × 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] '1.0.8'
```

```
# 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
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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 × 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   mascul...
## 2 C-3PO         167    75 <NA>       gold        yellow        112 none   mascul...
## 3 R2-D2          96     32 <NA>       white, bl... red           33 none   mascul...
## 4 Darth V...     202    136 none      white        yellow        41.9 male   mascul...
## 5 Leia Or...     150     49 brown      light       brown          19 fema... femin...
## 6 Owen La...     178    120 brown, gr... light       blue           52 male   mascul...
## 7 Beru Wh...     165     75 brown      light       blue           47 fema... femin...
## 8 R5-D4          97     32 <NA>       white, red red           NA none   mascul...
## 9 Biggs D...     183     84 black      light       brown          24 male   mascul...
## 10 Obi-Wan...    182     77 auburn, w... fair        blue-gray       57 male   mascul...
## # ... with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

1) dplyr::filter

Why filter?

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Filtering subsets your data

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This means that you can take out data that meet certain characteristics

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Why filter?

Filtering subsets your data

This means that you can take out data that meet certain characteristics

e.g. if you want to run your analysis only on low income areas, or if you want to focus on years after 2005

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 × 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  masculin...  
## 2 Qui-Gon ...    193     89 brown      fair        blue         92   male  masculin...  
## 3 Dooku        193     80 white      fair        brown        102  male  masculin...  
## 4 Bail Pre...    191     NA black      tan         brown        67   male  masculin...  
## # ... 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 × 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 Skywalker 172     77 blond     fair       blue        19 male   masculin...  
## 2 Anakin Skywalker 188     84 blond     fair       blue        41.9 male   masculin...  
## 3 Shmi Skywalker 163     NA black     fair       brown       72 female feminin...  
## # ... 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 × 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 Cr...     NA     NA brown      fair        brown          NA male  masculin...  
## 2 Finn            NA     NA black      dark        dark          NA male  masculin...  
## 3 Rey             NA     NA brown      light       hazel          NA femal... feminin...  
## 4 Poe Dame...     NA     NA brown      light       brown          NA male  masculin...  
## 5 BB8             NA     NA none       none       black          NA none  masculin...  
## 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 × 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  masculin...  
## 2 C-3PO        167     75 <NA>      gold       yellow         112 none  masculin...  
## 3 R2-D2         96     32 <NA>      white, bl... red            33 none  masculin...  
## 4 Darth V...     202    136 none      white       yellow         41.9 male  masculin...  
## 5 Leia Or...     150     49 brown     light      brown            19 female feminin...  
## 6 Owen La...     178    120 brown, gr... light      blue            52 male  masculin...  
## 7 Beru Wh...     165     75 brown     light      blue            47 female feminin...  
## 8 R5-D4         97     32 <NA>      white, red red            NA none  masculin...  
## 9 Biggs D...     183     84 black     light      brown            24 male  masculin...  
## 10 Obi-Wan...    182     77 auburn, w... fair      blue-gray         57 male  masculin...  
## # ... with 71 more rows, and 5 more variables: homeworld <chr>, species <chr>,  
## #   film_1 <dbl>, film_2 <dbl>, film_3 <dbl>, film_4 <dbl>
```

2) dplyr::arrange

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

```
starwars |>  
  arrange(birth_year)
```

```
## # A tibble: 87 × 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  masculin...  
## 2 IG-88          200   140 none       metal      red            15  none  masculin...  
## 3 Luke Sk...     172    77 blond      fair       blue           19  male  masculin...  
## 4 Leia Or...     150    49 brown      light      brown          19  femal... feminin...  
## 5 Wedge A...     170    77 brown      fair       hazel          21  male  masculin...  
## 6 Plo Koon       188    80 none       orange     black           22  male  masculin...  
## 7 Biggs D...     183    84 black      light      brown          24  male  masculin...  
## 8 Han Solo       180    80 brown      fair       brown          29  male  masculin...  
## 9 Lando C...     177    79 black      dark       brown          31  male  masculin...  
## 10 Boba Fe...    183   78.2 black     fair       brown         31.5 male  masculin...  
## # ... with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,  
## #   film_1 <dbl>, film_2 <dbl>, film_3 <dbl>, film_4 <dbl>
```

1) dplyr::arrange

Why arrange?

1) dplyr::arrange

Why arrange?

Arrange sorts your data

1) dplyr::arrange

Why arrange?

Arrange sorts your data

This makes it easy to check and see patterns in the data

2) dplyr::arrange

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

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

```
## # A tibble: 87 × 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   masculin...  
## 2 Jabba D... 175    1358 <NA>      green-tan... orange        600 herm... masculin...  
## 3 Chewbac... 228    112  brown      unknown     blue          200 male   masculin...  
## 4 C-3PO      167     75 <NA>      gold       yellow        112 none   masculin...  
## 5 Dooku      193     80  white      fair       brown         102 male   masculin...  
## 6 Qui-Gon... 193     89  brown      fair       blue          92 male   masculin...  
## 7 Ki-Adi-... 198     82  white      pale       yellow        92 male   masculin...  
## 8 Finis V... 170     NA  blond      fair       blue          91 male   masculin...  
## 9 Palpati... 170     75  grey       pale       yellow        82 male   masculin...  
## 10 Cliegg ... 183     NA  brown      fair       blue          82 male   masculin...  
## # ... with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,  
## #   film_1_id <dbl>, film_2_id <dbl>, film_3_id <dbl>
```

3) dplyr::select

Why select?

3) dplyr::select

Why select?

Select lets you choose columns to keep or drop

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This means you are essentially getting rid of variables, likely ones you do not need

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Why select?

Select lets you choose columns to keep or drop

This means you are essentially getting rid of variables, likely ones you do not need

e.g. if you used an emissions rate and marginal damage per unit of pollution variable to construct the marginal damage of output, you may not need the first two variables any more

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 × 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 × 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 × 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 Sk...     172     77 blond     fair       blue          19 male   masculin...  
## 2 C-3PO         167     75 <NA>      gold       yellow        112 none   masculin...  
## 3 R2-D2          96     32 <NA>      white, bl... red          33 none   masculin...  
## 4 Darth V...     202    136 none      white       yellow        41.9 male   masculin...  
## 5 Leia Or...     150     49 brown     light      brown          19 female feminin...  
## 6 Owen La...     178    120 brown, gr... light      blue          52 male   masculin...  
## 7 Beru Wh...     165     75 brown     light      blue          47 female feminin...  
## 8 R5-D4          97     32 <NA>      white, red red          NA none   masculin...  
## 9 Biggs D...     183     84 black     light      brown          24 male   masculin...  
## 10 Obi-Wan      182     77 auburn   w. fair      blue-gray       57 male   masculin...
```

3) dplyr::select cont.

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

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

```
## # A tibble: 87 × 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 × 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 × 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

Why mutate?

4) dplyr::mutate

Why mutate?

You may need to create new variables

4) dplyr::mutate

Why mutate?

You may need to create new variables

e.g. if I give you nominal house prices and the rate of house price inflation, you need to combine these two things to make a new **real house price** variable

4) dplyr::mutate

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

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

```
## # A tibble: 87 × 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 × 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 × 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 them
head(5)
```

```
## # A tibble: 5 × 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

Why summarise?

5) dplyr::summarise

Why summarise?

Often we want to get summary statistics or *collapse* our data

5) dplyr::summarise

Why summarise?

Often we want to get summary statistics or *collapse* our data

e.g. if I gave you a data set of each individual's marginal damage in the US, we may want to aggregate up to county-level marginal damages

5) dplyr::summarise

Summarising useful in combination with the `group_by` command

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

```
## `summarise()` has grouped output by 'species'. You can override using the  
## `.`groups` argument.
```

```
## # A tibble: 42 × 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
```

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 × 1
##   mean_height
##       <dbl>
## 1        NA
```

5) dplyr::summarise

We can also use `across` within summarise:

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

```
## # A tibble: 5 × 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)`

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

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

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Why join?

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Why join?

Suppose we want to understand how pollution affects housing prices

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

Why join?

Suppose we want to understand how pollution affects housing prices

You may need to combine data sets: one data sets on house prices in all counties, and another data set on pollution levels in all counties

dplyr::xxxx_join

How does joining work?

dplyr::xxxx_join

How does joining work?

We need two datasets (e.g. housing prices and pollution)

dplyr::xxxx_join

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Each dataset has the same set of **key** variables (e.g. county)

dplyr::xxxx_join

How does joining work?

We need two datasets (e.g. housing prices and pollution)

Each dataset has the same set of **key** variables (e.g. county)

When we join, we match up the two datasets on the key, and combine them into one

dplyr::xxxx_join

How does joining work?

We need two datasets (e.g. housing prices and pollution)

Each dataset has the same set of **key** variables (e.g. county)

When we join, we match up the two datasets on the key, and combine them into one

In our housing example, each row of the joined dataset would now tell us the house price, the county its in, and the county's pollution

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)`

(You can visualize the operations [here](#))

dplyr::xxxx_join

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

```
library(nycflights13)
flights
```

```
## # A tibble: 336,776 × 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>, tailnum <chr>, origin <chr>, dest <chr>, distance <dbl>,
## #   hour <dbl>, minute <dbl>, hour_s <dbl>, minute_s <dbl>, hour_min <dbl>
```

dplyr::xxxx_join

planes

```
## # A tibble: 3,322 × 9
##   tailnum year type          manufacturer model engines seats speed engine
##   <chr>    <int> <chr>        <chr>       <chr>    <int> <int> <int> <chr>
## 1 N10156  2004 Fixed wing multi... EMBRAER   EMB-...     2     55   NA Turbo...
## 2 N102UW   1998 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 3 N103US   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 4 N104UW   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 5 N10575   2002 Fixed wing multi... EMBRAER   EMB-...     2     55   NA Turbo...
## 6 N105UW   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 7 N107US   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 8 N108UW   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 9 N109UW   1999 Fixed wing multi... AIRBUS INDU... A320...     2    182   NA Turbo...
## 10 N110UW  1999 Fixed wing multi... AIRBUS INDU... 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 to 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 to 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 × 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        161  NCC6DN  <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 × 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 × 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 × 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 tidy 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 tidy 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) tidyverse::pivot_longer

```
stocks = data.frame(  
  time = as.Date('2009-01-01') + 0:1,  
  stock_X = rnorm(2, 0, 1),  
  stock_Y = rnorm(2, 0, 2),  
  stock_Z = rnorm(2, 0, 4)  
)  
stocks
```

```
##           time   stock_X   stock_Y   stock_Z  
## 1 2009-01-01 -1.2748637 0.5036504 -7.56014  
## 2 2009-01-02  0.4597851 0.2333985 -2.14677
```

We have 4 variables, the date and the stocks

How do we get this in tidy form?

1) tidyverse::pivot_longer

```
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) tidyverse::pivot_longer

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

```
## # A tibble: 6 × 3
##   time      stock    price
##   <date>    <chr>    <dbl>
## 1 2009-01-01 stock_X -1.27
## 2 2009-01-01 stock_Y  0.504
## 3 2009-01-01 stock_Z -7.56
## 4 2009-01-02 stock_X  0.460
## 5 2009-01-02 stock_Y  0.233
## 6 2009-01-02 stock_Z -2.15
```

1) tidyverse::pivot_longer

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

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

2) tidyverse::pivot_wider

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

```
## # A tibble: 2 × 4
##   time      stock_X stock_Y stock_Z
##   <date>     <dbl>    <dbl>    <dbl>
## 1 2009-01-01 -1.27    0.504   -7.56
## 2 2009-01-02  0.460    0.233   -2.15
```

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

```
## # A tibble: 3 × 3
##   stock   `2009-01-01` `2009-01-02`
##   <chr>     <dbl>      <dbl>
## 1 stock_X    -1.27      0.460
## 2 stock_Y     0.504      0.233
## 3 stock_Z    -7.56     -2.15
```

2) tidyverse::pivot_wider

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

```
## # A tibble: 2 × 4
##   time      stock_X stock_Y stock_Z
##   <date>     <dbl>    <dbl>    <dbl>
## 1 2009-01-01 -1.27    0.504   -7.56
## 2 2009-01-02  0.460    0.233   -2.15
```

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

```
## # A tibble: 3 × 3
##   stock   `2009-01-01` `2009-01-02`
##   <chr>     <dbl>      <dbl>
## 1 stock_X    -1.27      0.460
## 2 stock_Y     0.504      0.233
## 3 stock_Z    -7.56     -2.15
```

Note that the second example has effectively transposed the data

3) tidyverse::separate

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

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

```
conomists |> separate(name, c("first_name", "last_name"))
```

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

3) tidyverse::separate

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

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

```
conomists |> 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=".")`

4) tidyverse

```
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   1 102.16210  
## 2 2016    1   2  98.96899  
## 3 2016    1   3  99.70125  
## 4 2016    1   4 100.25458
```

4) tidyverse

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

```
##           date      gdp
## 1 2016-1-1 102.16210
## 2 2016-1-2  98.96899
## 3 2016-1-3  99.70125
## 4 2016-1-4 100.25458
```

4) tidyverse::unite

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

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

```
## # A tibble: 4 × 2  
##   date      gdp  
##   <chr>     <dbl>  
## 1 2016-1-1 102.  
## 2 2016-1-2  99.0  
## 3 2016-1-3  99.7  
## 4 2016-1-4 100.
```

4) tidyverse::unite

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

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

```
## # A tibble: 4 × 2
##   date      gdp
##   <chr>    <dbl>
## 1 2016-1-1 102.
## 2 2016-1-2  99.0
## 3 2016-1-3  99.7
## 4 2016-1-4  100.
```

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

4) tidyverse

```
library(lubridate)
gdp_u |> mutate(date = ymd(date))
```

```
## # A tibble: 4 × 2
##   date      gdp
##   <date>    <dbl>
## 1 2016-01-01 102.
## 2 2016-01-02  99.0
## 3 2016-01-03  99.7
## 4 2016-01-04 100.
```

Regression and ordinary least squares

Why?

Motivation

Let's start with a few **basic, general questions**

Why?

Motivation

Let's start with a few **basic, general questions**

1. What is the goal of econometrics?
2. Why do economists (or other people) study or use econometrics?

Why?

Motivation

Let's start with a few **basic, general questions**

1. What is the goal of econometrics?
2. Why do economists (or other people) study or use econometrics?

One simple answer: Learn about the world using data

Why? Example

GPA is an output from endowments (ability), and hours studied (inputs), and pollution exposure (externality)

Why? Example

GPA is an output from endowments (ability), and hours studied (inputs), and pollution exposure (externality)

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We can test these hypotheses **using a regression model**

How?

We can write down a linear regression model of the relationship between GPA and (H, P, SAT, PCT):

$$\text{GPA}_i = \beta_0 + \beta_1 I_i + \beta_2 P_i + \beta_3 \text{SAT}_i + \beta_4 H_i + \varepsilon_i$$

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The subscript i means that the variable contains the value for some person i in our dataset where $i = 1, \dots, N$

How?

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β_2 tells us how GPA changes, given a 1 unit increase in pollution!

Our goal will be to estimate β_2 , we denote estimates with hats: $\hat{\beta}_2$

How?

How do we estimate β_2 ?

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First, suppose we have a set of estimates for all of our β s, then we can *estimate* the GPA (\widehat{GPA}_i) for any given person based on just (I, P, SAT, H):

$$\widehat{GPA}_i = \hat{\beta}_0 + \hat{\beta}_1 I_i + \hat{\beta}_2 P_i + \hat{\beta}_3 \text{SAT}_i + \hat{\beta}_4 H_i$$

How?

We estimate the β s with **linear regression**, specifically ordinary least squares

Ordinary least squares: choose all the β s so that the sum of squared errors between the *real* GPAs and model-estimated GPAs are minimized:

$$SSE = \sum_{i=1}^N (GPA_i - \widehat{GPA}_i)^2$$

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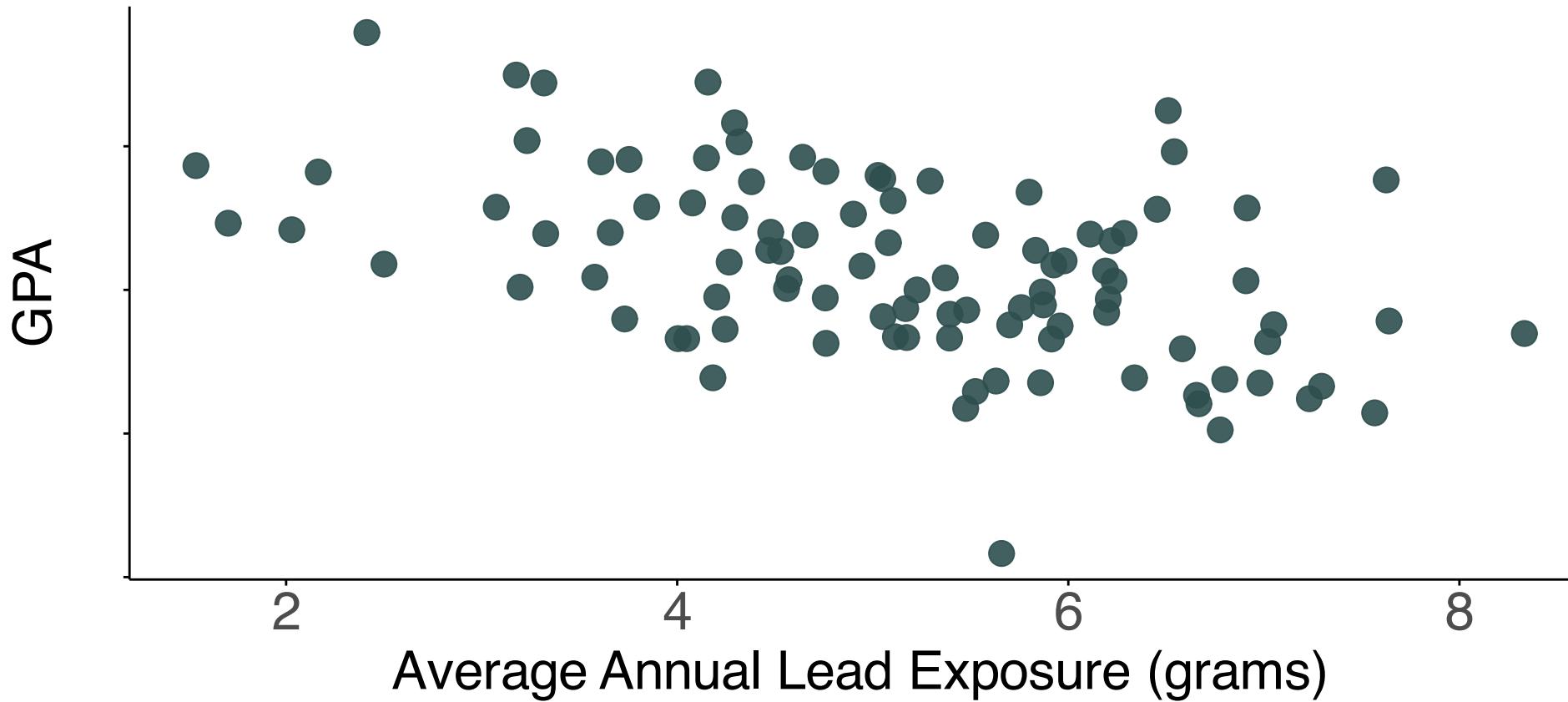
Choosing the β s in this fashion gives us the best-fit line through the data

How?

Simple example

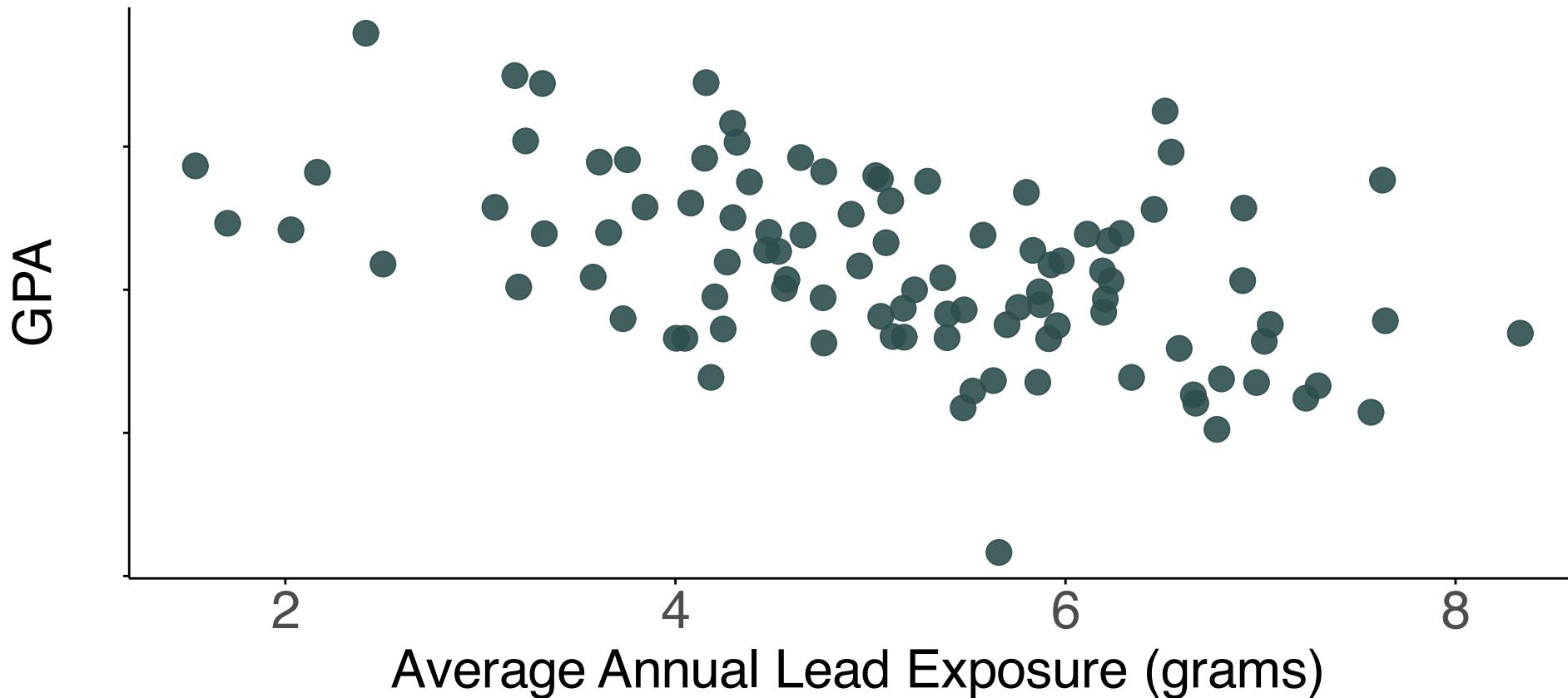
Suppose we were only looking at GPA and pollution (lead/Pb):

$$GPA_i = \beta_0 + \beta_1 P_i + \varepsilon_i$$



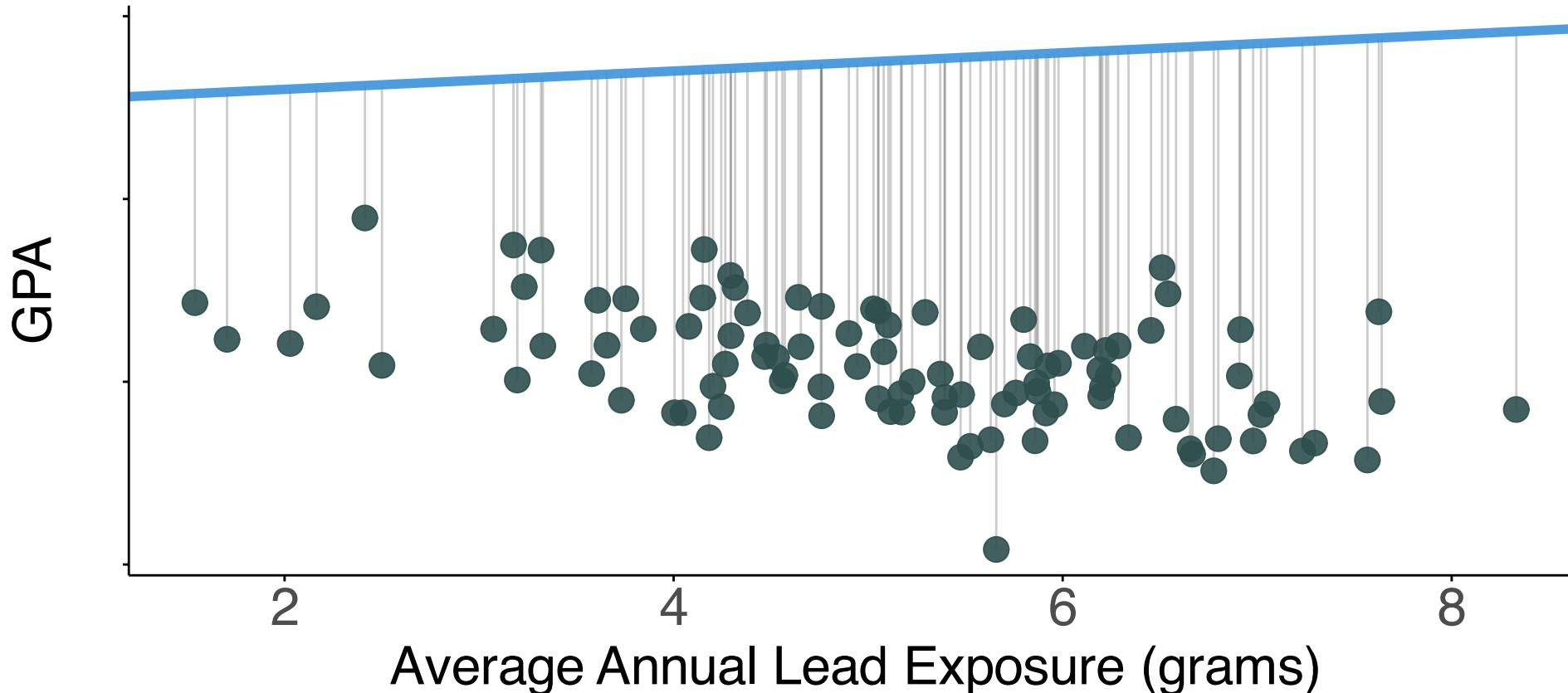
Simple example

For any line $(GPA_i = \hat{\beta}_0 + \hat{\beta}_1 P_i)$



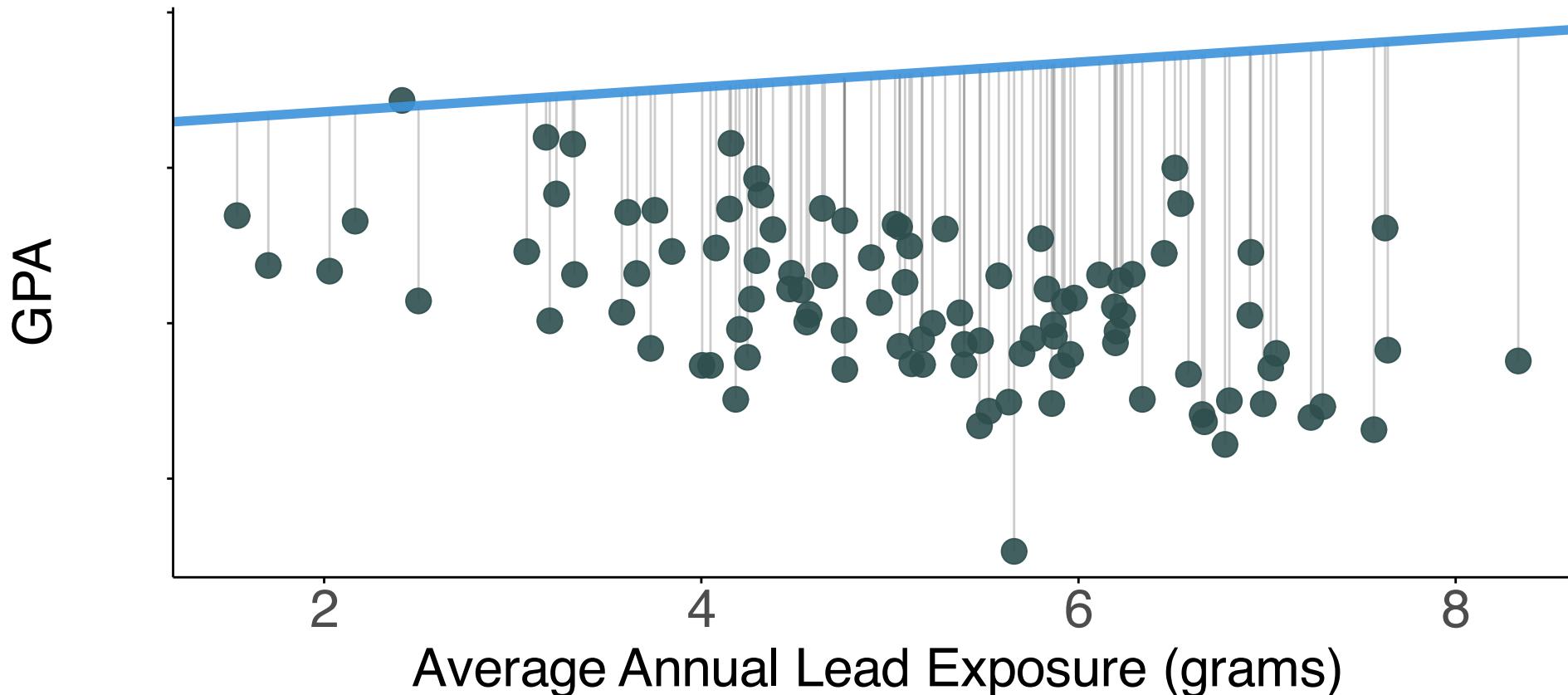
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For any line $(GPA_i = \hat{\beta}_0 + \hat{\beta}_1 P_i)$, we calculate errors: $e_i = GPA_i - \hat{GPA}_i$



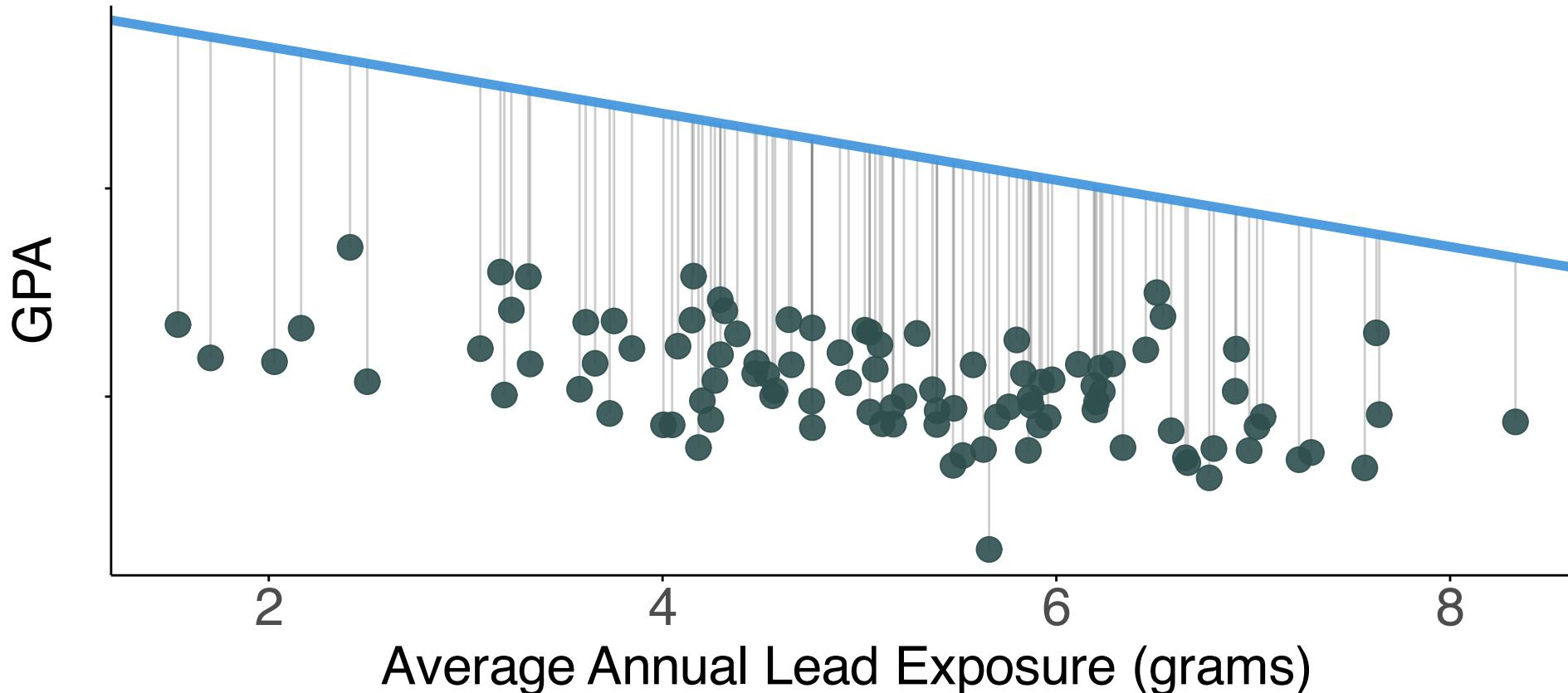
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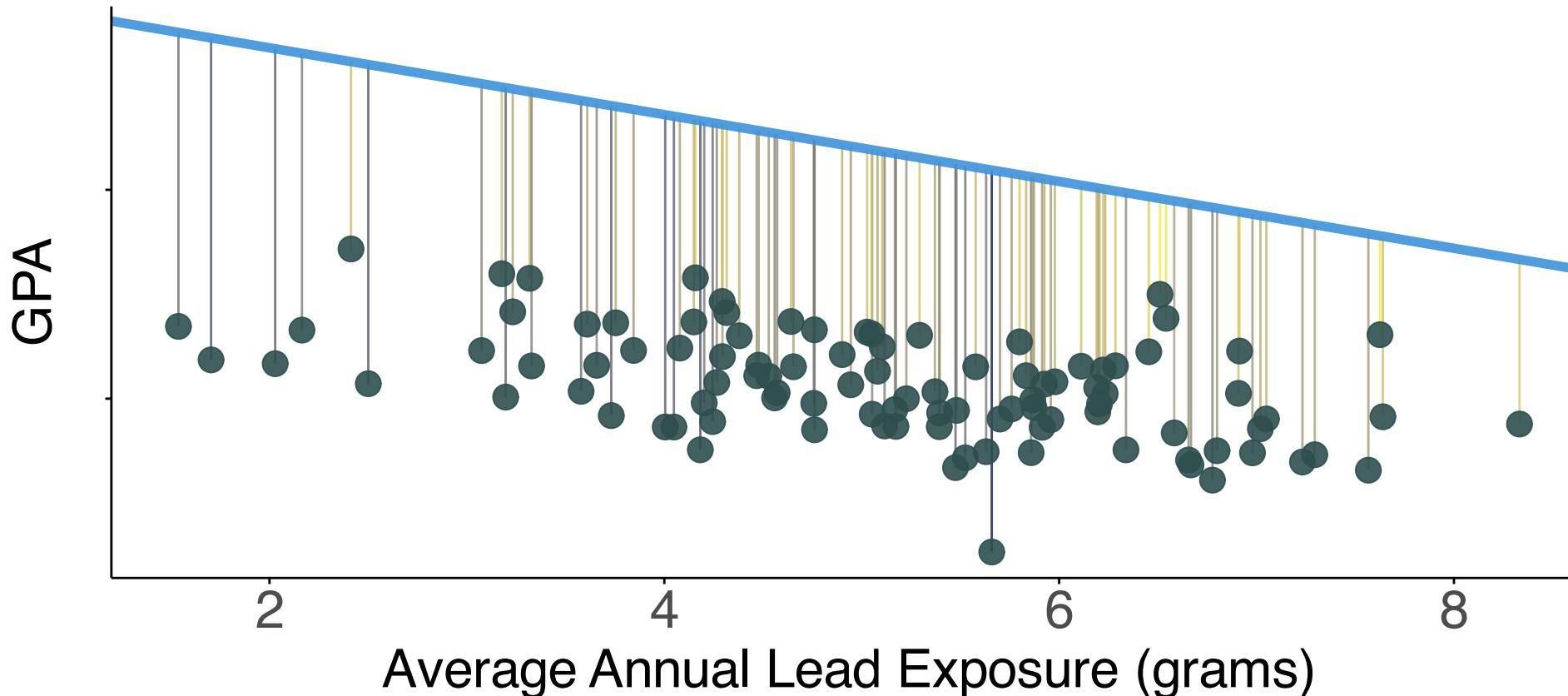
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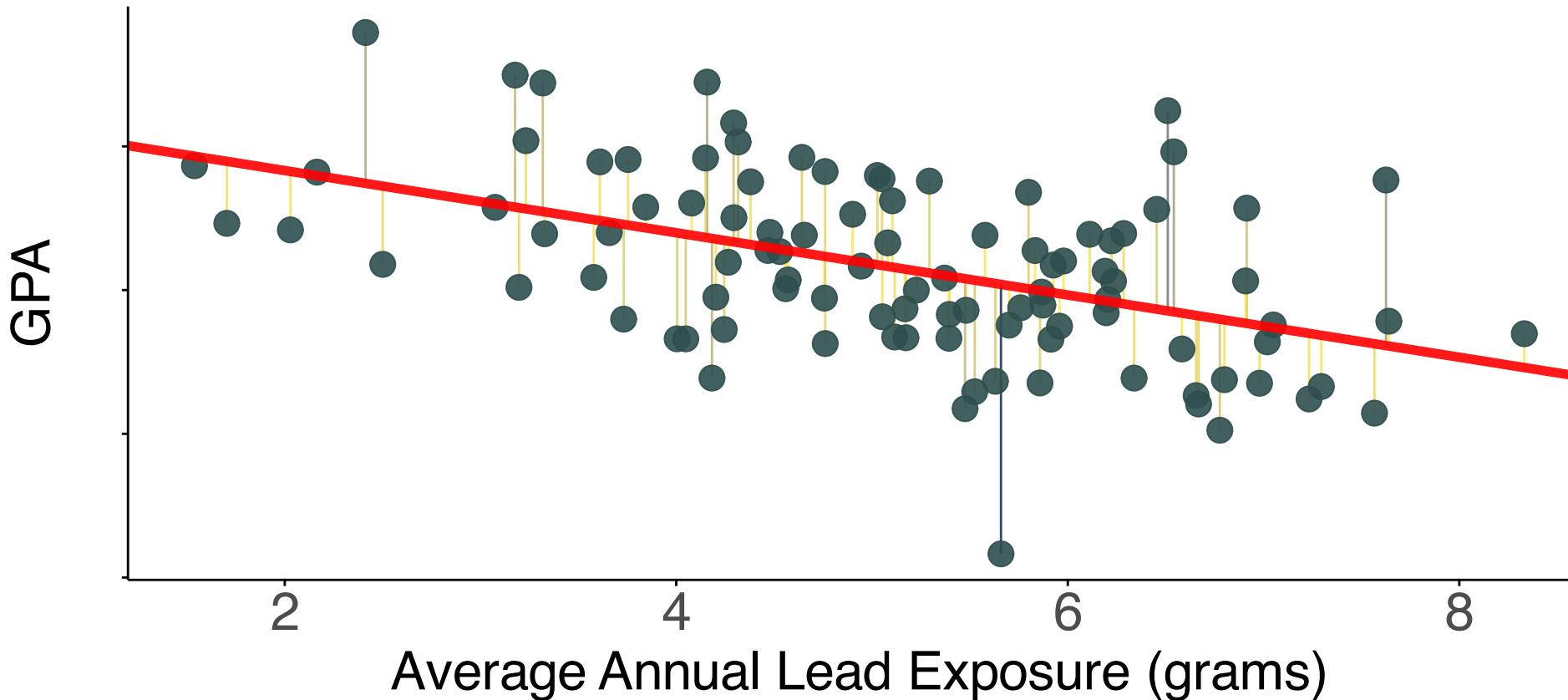
Simple example

SSE squares the errors ($\sum e_i^2$): bigger errors get bigger penalties



Simple example

The OLS estimate is the combination of $\hat{\beta}_0$ and $\hat{\beta}_1$ that minimize SSE



OLS error term

So OLS is just the best-fit line through your data

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Why?

OLS error term

So OLS is just the best-fit line through your data

Why?

Our model isn't perfect, the people in our dataset (i.e. our sample) may not perfectly match up to the entire population of people

OLS error term

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We jam all that stuff into error term ε_i :

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So ε_i contains all the determinants of GPA that we aren't explicitly addressing in our model

OLS properties

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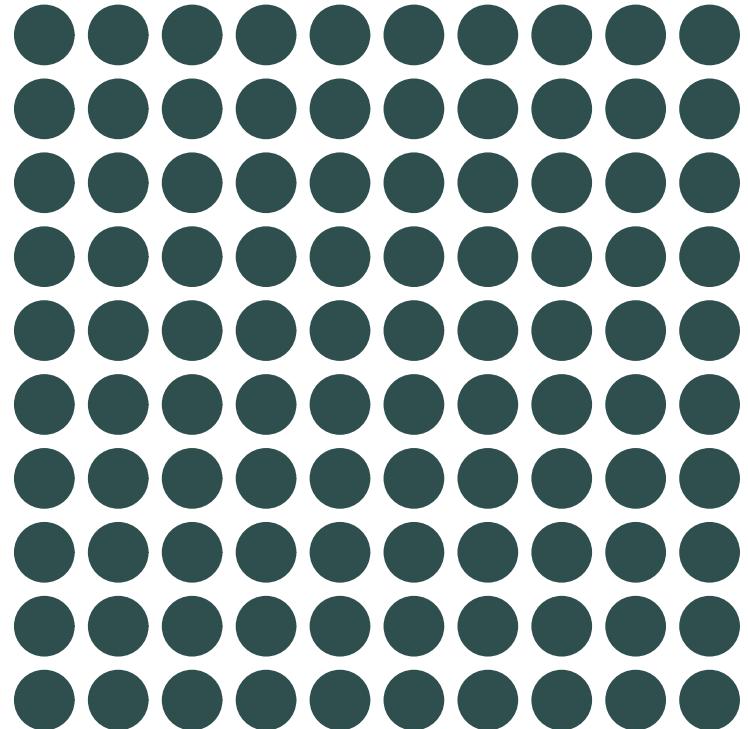
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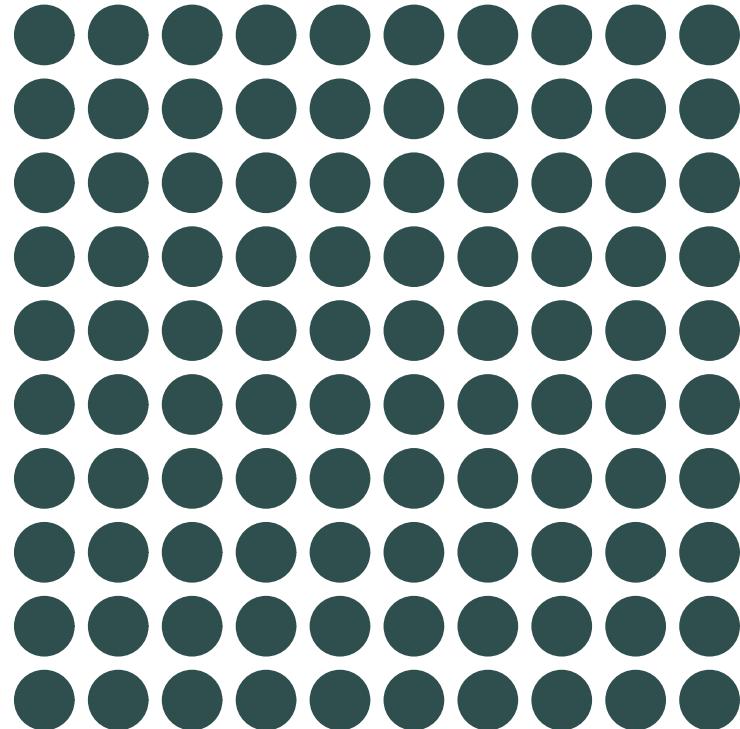
Let's see in an example where we only have a subsample of the full population of data

OLS properties

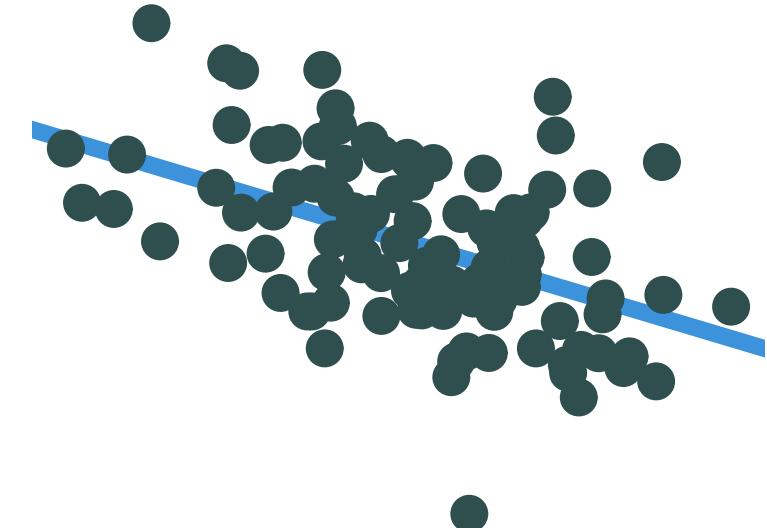


Population

OLS properties



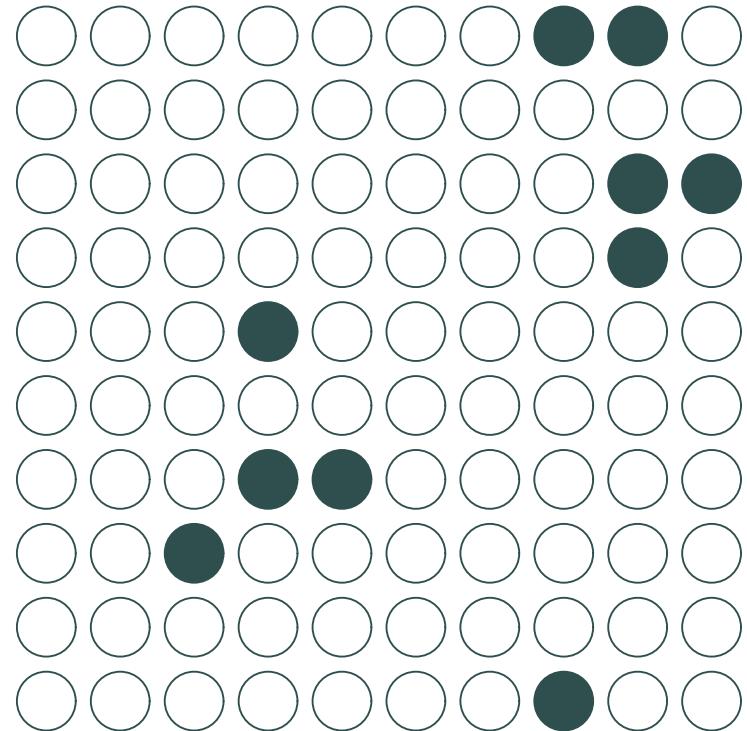
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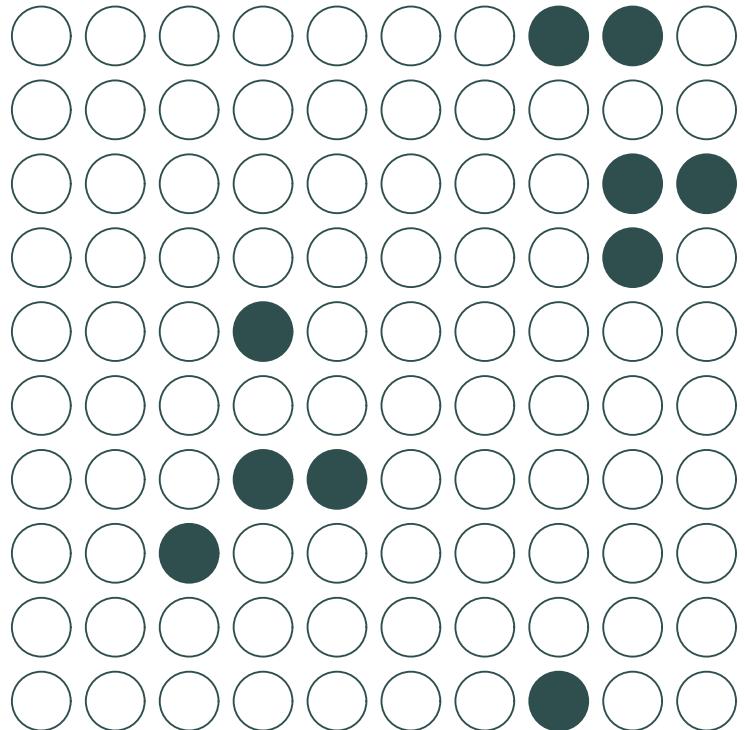
Population relationship

$$y_i = 2.53 + -0.43x_i + u_i$$

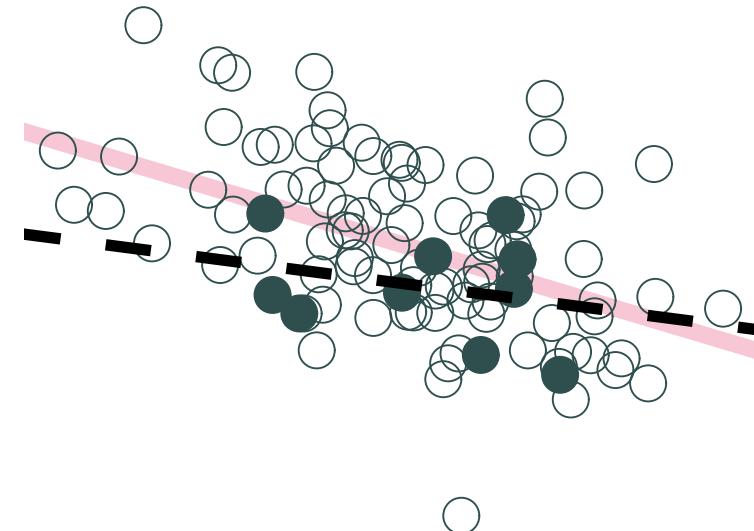
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Sample 1: 10 random individuals



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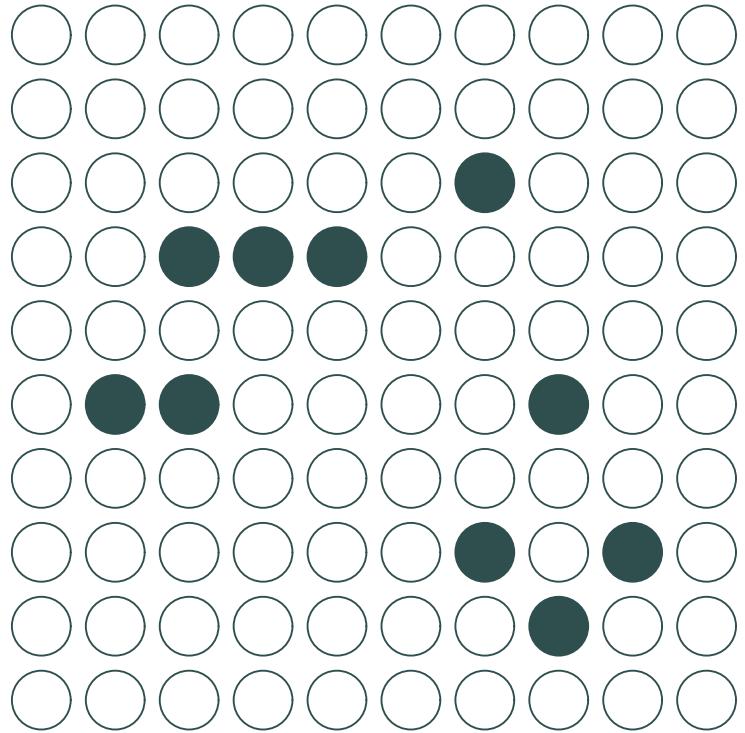


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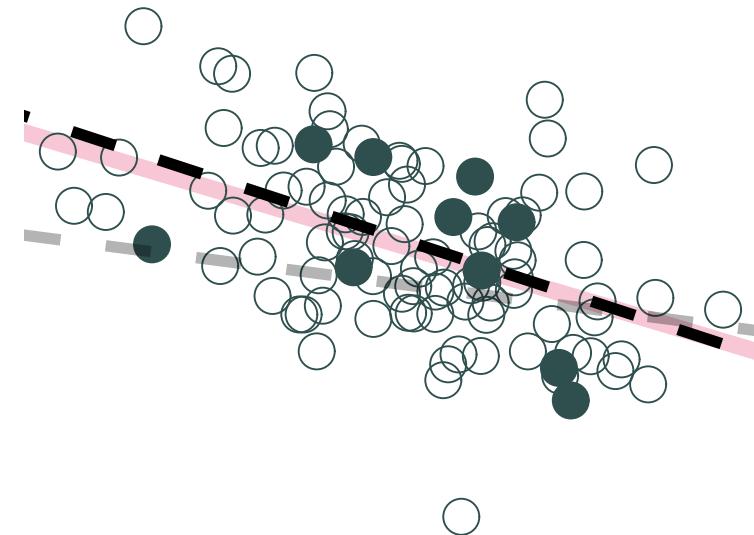
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Sample relationship

$$\hat{y}_i = 0.72 + -0.19x_i$$



Sample 2: 10 random individuals

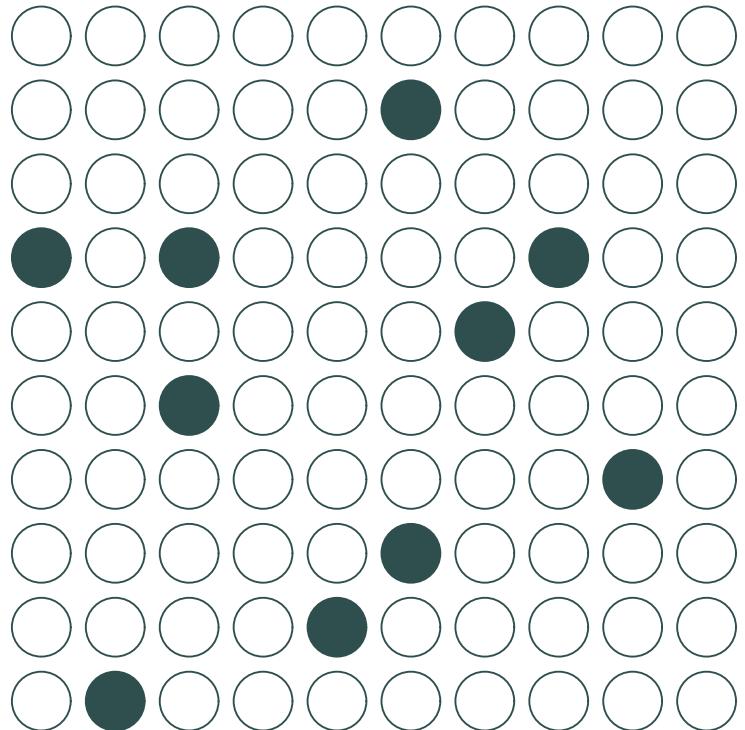


Population relationship

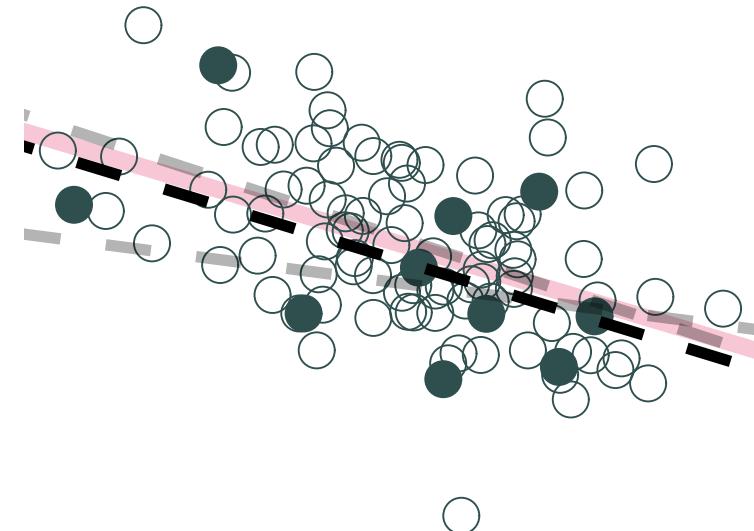
$$y_i = 2.53 + -0.43x_i + u_i$$

Sample relationship

$$\hat{y}_i = 2.82 + -0.47x_i$$



Sample 3: 10 random individuals



Population relationship

$$y_i = 2.53 + -0.43x_i + u_i$$

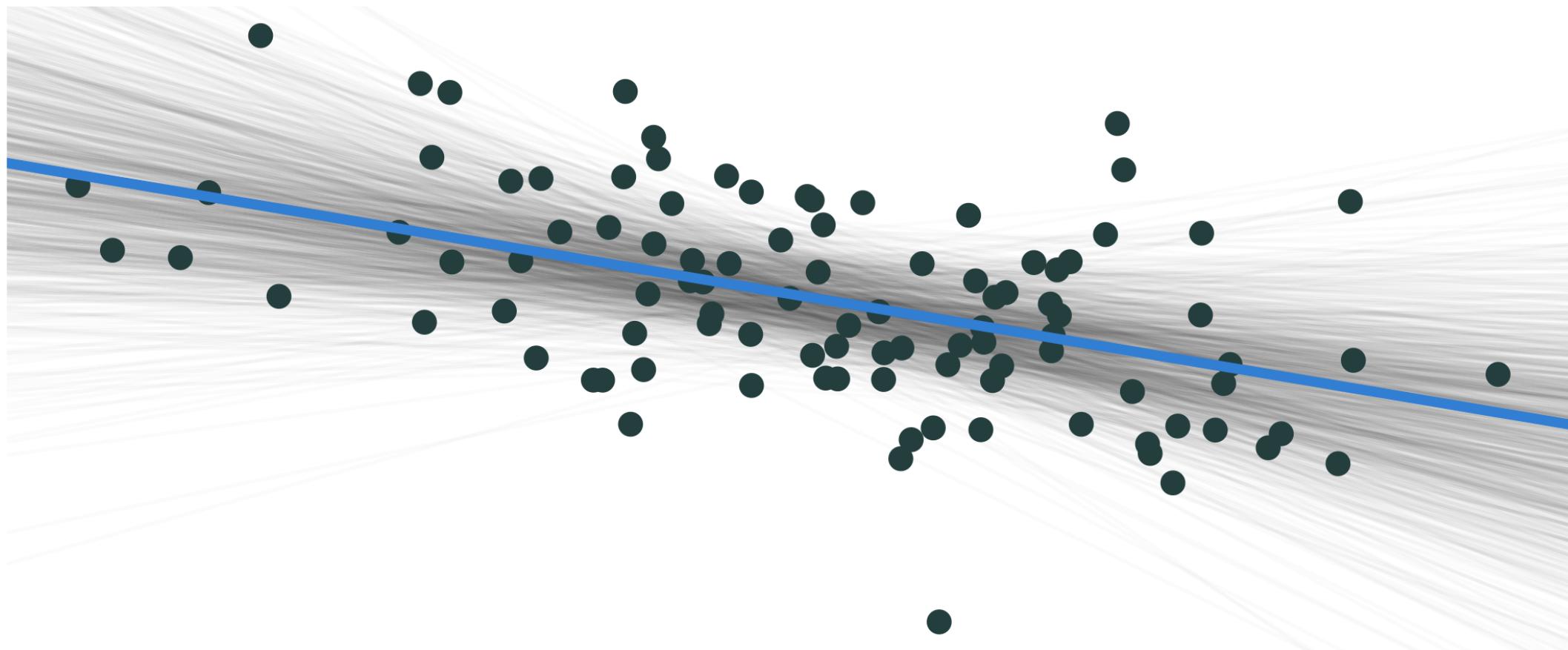
Sample relationship

$$\hat{y}_i = 2.32 + -0.44x_i$$

Let's repeat this 1,000 times.

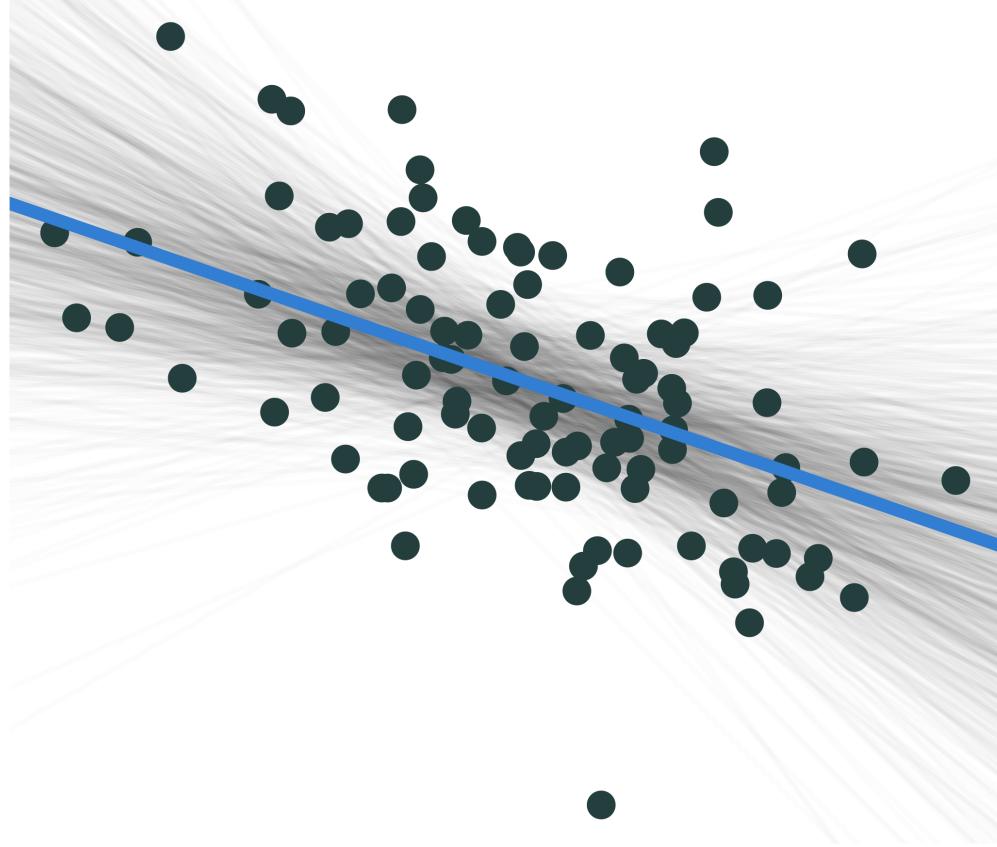
(This exercise is called a (Monte Carlo) simulation.)

Population vs. sample



Population vs. sample

Question: Why do we care about *population* vs. *sample*?



On **average**, our regression lines match the population line very nicely

However, **individual lines** (samples) can really miss the mark

Differences between individual samples and the population lead to **uncertainty** for us in the true effect

Population vs. sample

Answer: Uncertainty matters!

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$\hat{\beta}$ itself is random, it will depend on the sample of data we have

When we take a sample and run a regression, we don't know if it's a 'good' sample ($\hat{\beta}$ is close to β) or a 'bad sample' (our sample differs greatly from the population)

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If x is correlated with any of them, then we will have something called **omitted variable bias**

Omitted variable bias

Here's an intuitive example

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lead harms children's brain development, especially before age 6

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Suppose we wanted to understand the effect of lead exposure P on GPAs

lead harms children's brain development, especially before age 6

We should expect early-life lead exposure to reduce future GPAs

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Our model might look like:

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What would happen if we took a sample of *real world data* and used OLS to estimate $\hat{\beta}_1$?

Omitted variable bias

We would have omitted variable bias

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Why? What are some examples?

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Poorer families likely have more lead exposure, why?

Richer families can move away, pay to replace lead paint, lead pipes, etc

This means lead exposure is correlated with lower income

Omitted variable bias

Why does this correlation cause us problems?

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Children from richer families tend to have higher GPAs

Why?

Access to tutoring, better schools, parental pressure, etc, etc

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So $\hat{\beta}_1$ will pick up the effect of both!

Our estimate $\hat{\beta}_1$ is **biased** and overstates the negative effects of lead

Omitted variable bias

How do we fix this bias?

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Make income not omitted: control for it in our model

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How do we fix this bias?

Make income not omitted: control for it in our model

If we have data on family income I we can instead write our model as:

$$\text{GPA}_i = \beta_0 + \beta_1 P_i + \beta_2 I_i + \varepsilon_i$$

I is no longer omitted

Omitted variable bias

How do we fix this bias?

Make income not omitted: control for it in our model

If we have data on family income I we can instead write our model as:

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Independent variables in our model that we include to address bias are called **controls**

Regression in R

How do we actually run regressions?

Now we are going to learn how to run regressions in R

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There's a lot of regression packages, built-in is `lm`, or you can also use a new one called `fixest`

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They work almost identically

Using regression packages

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You can then store the output by assigning it to a variable: `results =`

```
package_name(formula_here, data = dataframe_here)
```

Using regression packages

Let's start by using the built-in `lm` package along with the `starwars` dataset

```
starwars
```

```
## # A tibble: 87 × 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  mascul...
## 2 C-3PO         167    75 <NA>       gold        yellow        112 none  mascul...
## 3 R2-D2          96    32 <NA>       white, bl... red           33 none  mascul...
## 4 Darth V...     202   136 none       white        yellow        41.9 male  mascul...
## 5 Leia Or...     150    49 brown      light       brown          19 fema... femin...
## 6 Owen La...     178   120 brown, gr... light       blue           52 male  mascul...
## 7 Beru Wh...     165    75 brown      light       blue           47 fema... femin...
## 8 R5-D4          97    32 <NA>       white, red red           NA none  mascul...
## 9 Biggs D...     183    84 black      light       brown          24 male  mascul...
## 10 Obi-Wan...    182    77 auburn, w... fair        blue-gray       57 male  mascul...
## # ... with 77 more rows, and 5 more variables: homeworld <chr>, species <chr>,
## #   films <list>, vehicles <list>, starships <list>
```

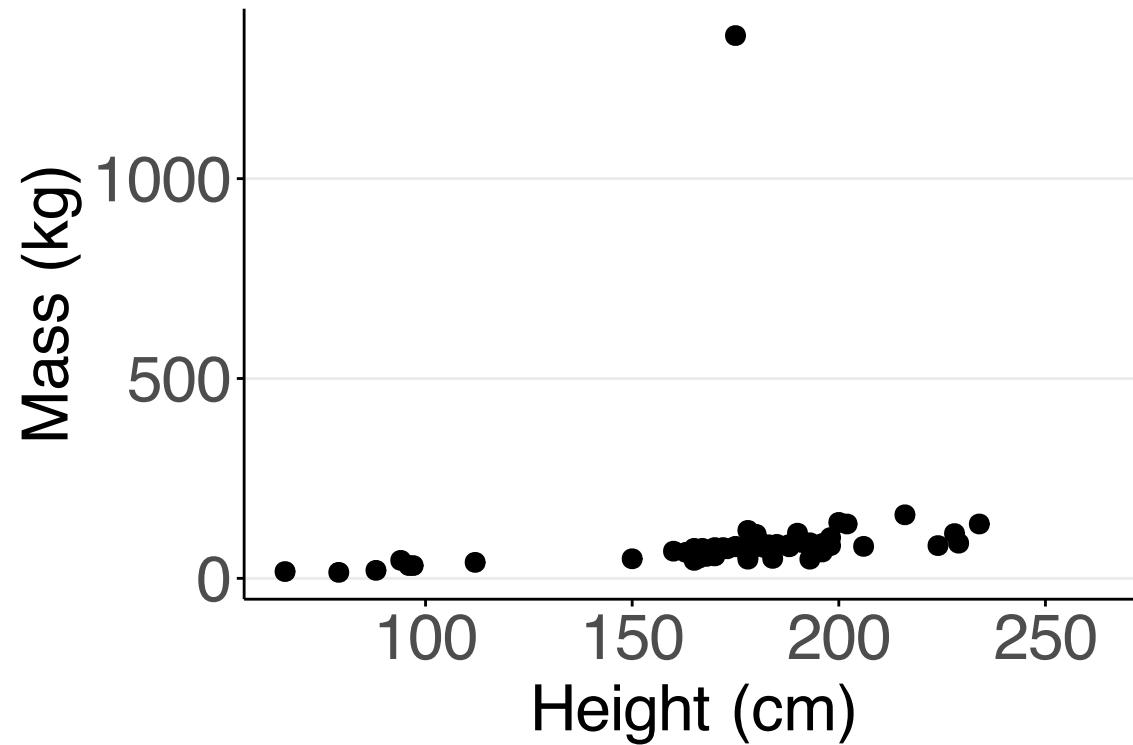
Using regression packages

Suppose we wanted to see what was the effect of height on mass:

$$mass_i = \beta_0 + \beta_1 height_i + \varepsilon_i$$

Using regression packages

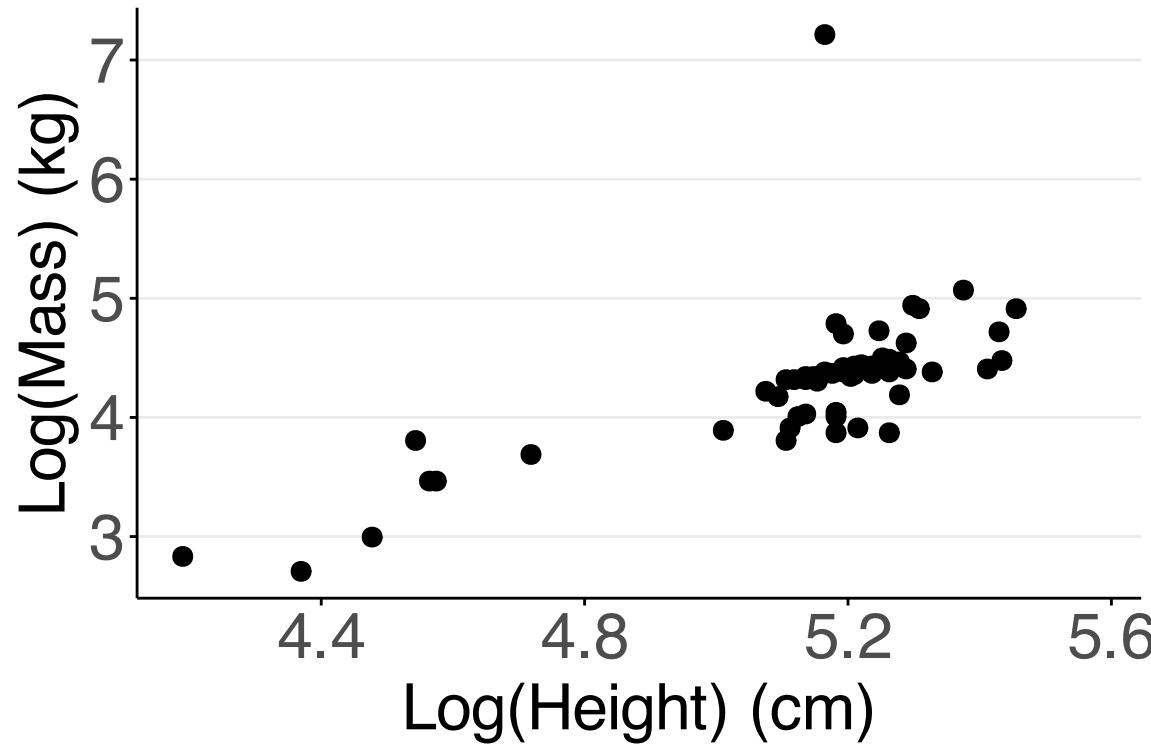
Before we begin lets look at the data and see what the relationship looks like:



Looks like there's an outlier!

Using regression packages

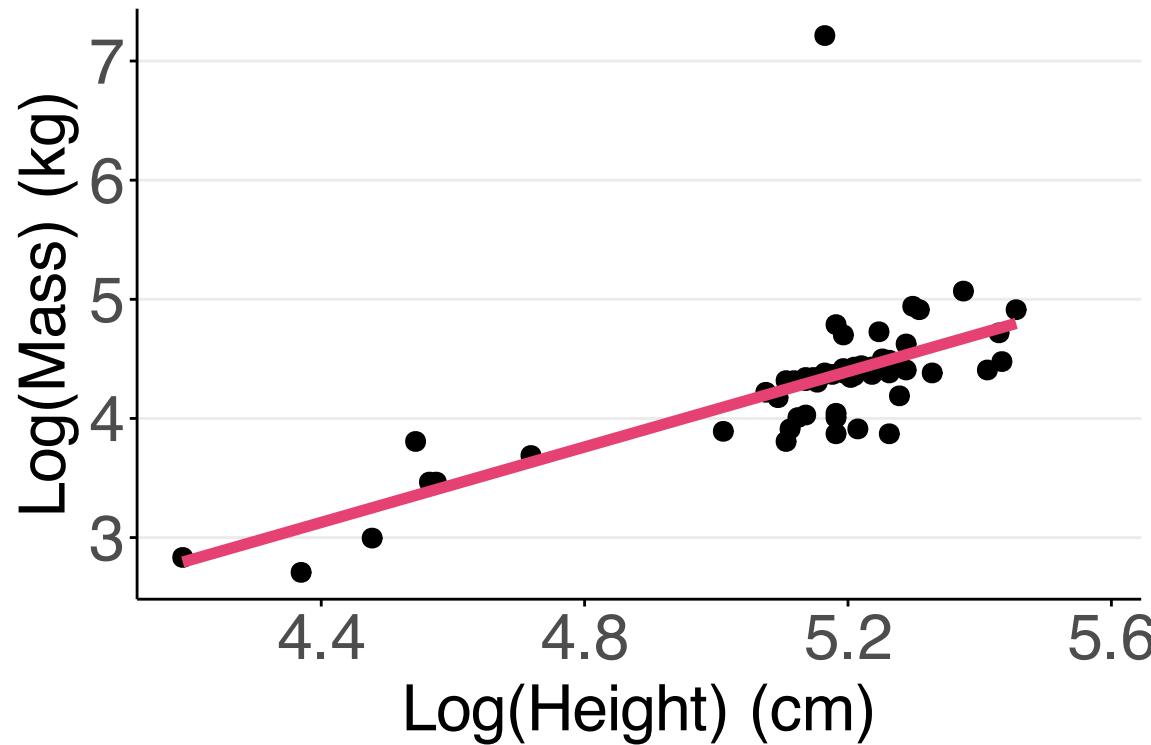
What if we plot it in log units?



That dampens the outlier, the positive association is really clear!

Using regression packages

What if we plot it in log units?



Here's the best fit line, now let's actually estimate β_0, β_1

Using regression packages

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For this example we would write: mass ~ height

Using regression packages

$$mass_i = \beta_0 + \beta_1 height_i + \varepsilon_i$$

We can run the following code:

```
# package_name(formula_here, data = dataframe_here)
lm(mass ~ height, data = starwars)
```

```
##
## Call:
## lm(formula = mass ~ height, data = starwars)
##
## Coefficients:
## (Intercept)      height
## -13.8103        0.6386
```

This gives us the coefficient estimate $\hat{\beta}_0$ (intercept), and $\hat{\beta}_1$ (height)

Using regression packages

We can clean up the output a bit and get other statistics by piping it to

`broom::tidy:`

```
# package_name(formula_here, data = dataframe_here)
lm(mass ~ height, data = starwars) |>
broom::tidy()
```

```
## # A tibble: 2 × 5
##   term      estimate std.error statistic p.value
##   <chr>      <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept) -13.8     111.      -0.124   0.902
## 2 height       0.639     0.626      1.02    0.312
```

The coefficient estimates are now in column `estimate`, and we have a few other things

Using regression packages

The first column gives us our estimates: $\hat{\beta}_0, \hat{\beta}_1$

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Smaller values generally mean it is more likely that height has an effect on mass: the probability that we could have gotten our estimated value if height didn't matter is very low

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Interpreting coefficient estimates

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The estimate for the β on height means: people who are 1cm taller tend to be 0.639kg heavier

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This just comes from our previous example where $\beta_1 = \frac{\partial mass_i}{\partial height_i}$

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Well, it is just the estimated mass, given someone had zero height:

$$\hat{\beta}_0 = \hat{\beta}_0 + \hat{\beta}_1 \times 0$$

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It's kind of a nonsense interpretation here since no one has zero height

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It's kind of a nonsense interpretation here since no one has zero height

Generally we don't read too much into the intercept terms

Interpreting coefficient estimates

Now, what if we changed our model a bit so it was instead:

$$\log(\text{mass}_i) = \beta_0 + \beta_1 \log(\text{height}_i) + \varepsilon_i$$

What does β_1 mean now?

Interpreting coefficient estimates

Now, what if we changed our model a bit so it was instead:

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What does β_1 mean now?

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)}$$

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What does β_1 mean now?

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)}$$

But we can rewrite this as:

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)} = \frac{\partial \log(\text{mass}_i)}{\partial \text{mass}_i} \frac{\partial \text{mass}_i}{\partial \text{height}_i} \frac{\partial \text{height}_i}{\partial \log(\text{height}_i)}$$

Interpreting coefficient estimates

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)} = \frac{\partial \log(\text{mass}_i)}{\partial \text{mass}_i} \frac{\partial \text{mass}_i}{\partial \text{height}_i} \frac{\partial \text{height}_i}{\partial \log(\text{height}_i)}$$

And this is equal to:

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)} = \frac{1}{\text{mass}_i} \frac{\partial \text{mass}_i}{\partial \text{height}_i} \frac{\text{height}_i}{1}$$

Interpreting coefficient estimates

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)} = \frac{\partial \log(\text{mass}_i)}{\partial \text{mass}_i} \frac{\partial \text{mass}_i}{\partial \text{height}_i} \frac{\partial \text{height}_i}{\partial \log(\text{height}_i)}$$

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And finally:

$$\beta_1 = \frac{\partial \log(\text{mass}_i)}{\partial \log(\text{height}_i)} = \frac{\text{height}_i}{\text{mass}_i} \frac{\partial \text{mass}_i}{\partial \text{height}_i}$$

which is the definition of the elasticity of mass with respect to height

Interpreting coefficient estimates

$$\log(\text{mass}_i) = \beta_0 + \beta_1 \log(\text{height}_i) + \varepsilon_i$$

In a *log-log* model, β_1 tells us the percent change in mass, given a percent change in height

Interpreting coefficient estimates

$$\log(\text{mass}_i) = \beta_0 + \beta_1 \log(\text{height}_i) + \varepsilon_i$$

In a *log-log* model, β_1 tells us the percent change in mass, given a percent change in height

Let's run the regression:

```
# package_name(formula_here, data = dataframe_here)
lm(log(mass) ~ log(height), data = starwars) |>
broom::tidy()

## # A tibble: 2 × 5
##   term      estimate std.error statistic    p.value
##   <chr>      <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept) -3.84      1.17     -3.27 0.00181
## 2 log(height)  1.58      0.228      6.93 0.00000000410
```

Interpreting coefficient estimates

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# package_name(formula_here, data = dataframe_here)
lm(log(mass) ~ log(height), data = starwars) |>
broom::tidy()
```

```
## # A tibble: 2 × 5
##   term      estimate std.error statistic    p.value
##   <chr>      <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept) -3.84      1.17     -3.27 0.00181
## 2 log(height)   1.58      0.228      6.93 0.00000000410
```

A 1% increase in height is associated with a 1.58% increase in mass!

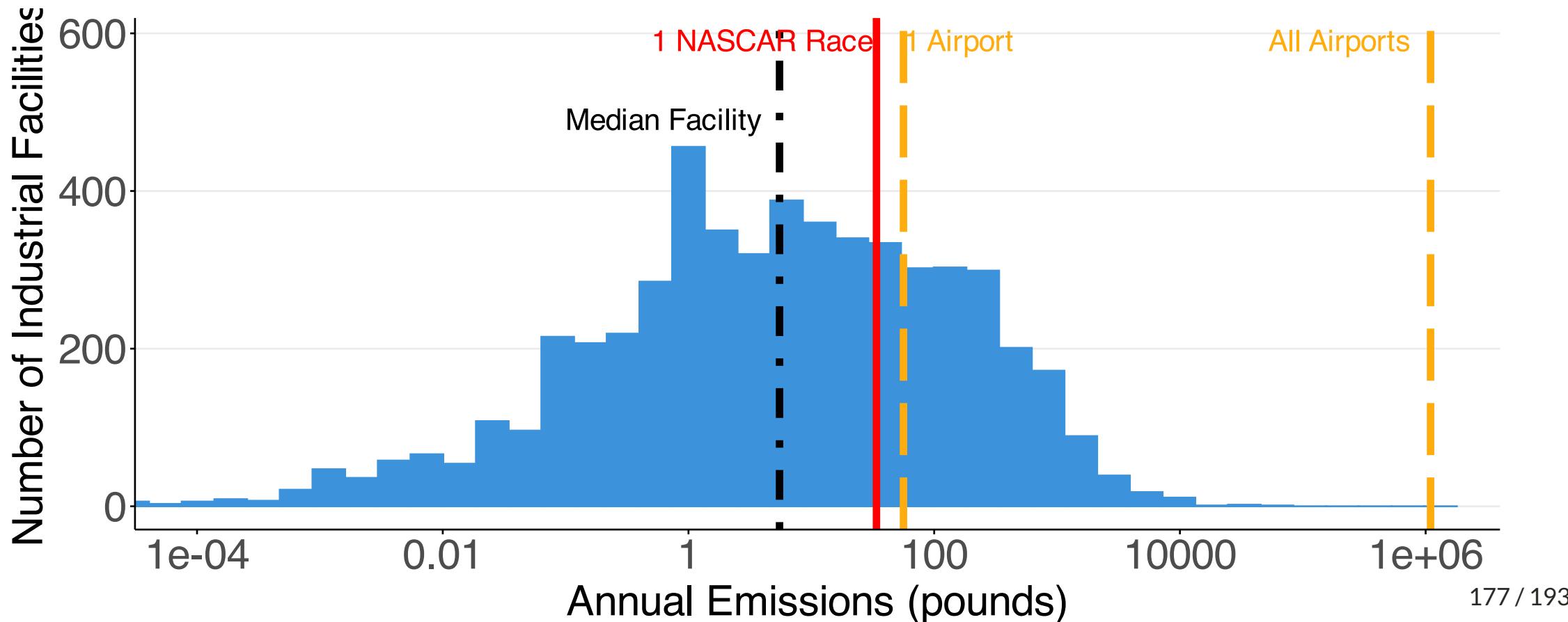
Hands-on pollution education example

Real pollution education example



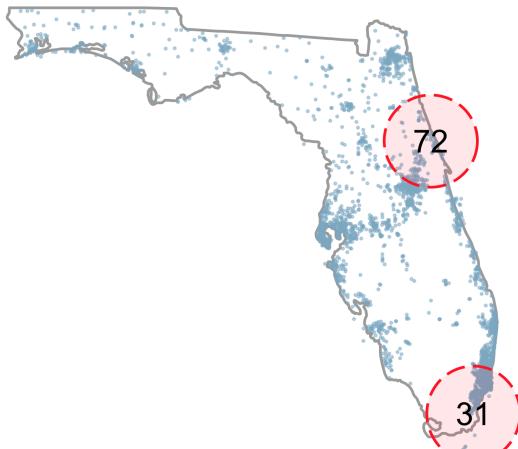
Real pollution education example

In **3 hours**, one NASCAR race emits more lead than a majority of industrial facilities do in an **entire year**

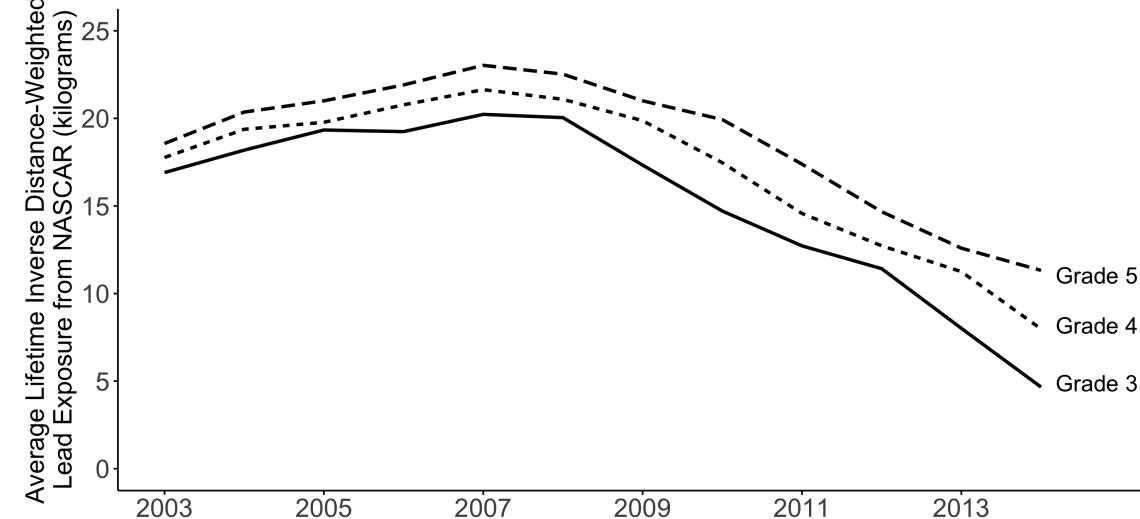


We will look at Florida

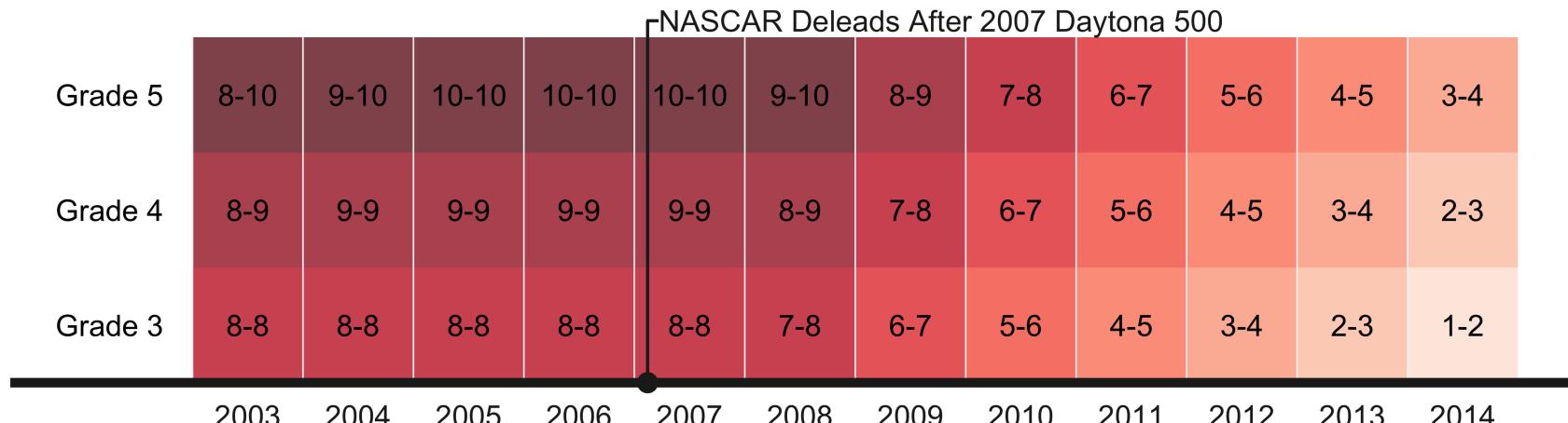
A. Track and School Locations



B. Time Series of Lead Exposure from NASCAR



C. Range of Total Years Exposed to NASCAR Lead By Grade and Year



All the data are public, you can look at scores yourself!



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AAA

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Scores & Reports

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[2004 Score Reports](#)

[2005 Score Reports](#)

[2006 Score Reports](#)

[2007 Score Reports](#)

[2008 Score Reports](#)

[2009 Score Reports](#)

[2010 Score Reports](#)

Scores & Reports

For results by reporting year, use the link for the appropriate year in the left-hand navigation panel. For results by subject area (e.g., reading, science), use one of the links below. [FCAT 2.0 results](#) are also available, and the [interactive reporting](#) resources provide access to databases that allow users to generate reports for the state, districts or schools for certain educational areas.

- [FCAT Reading & Mathematics SSS Scores \(1998-2011\)](#)
- [FCAT Science SSS Scores \(2003-2011\)](#)
- [FCAT Writing Scores \(1997-2012\)](#)
- [FCAT Norm-Referenced Test Scores \(1995-2008\)](#)
- [Longitudinal Data: FWAP / FCAT / HSCT 1995-2000](#)

Additional Resources for Understanding Results

- [Understanding FCAT Reports](#)
- [FCAT Achievement Level Definitions/Tables \(PDF\)](#)
- [Developmental Score Scale Memo \(04/14/02\) \(PDF\)](#)
- [Guidance on Content Area Scores](#)
- [Content Focus Reports](#)

Let's look at the data

```
nascar_df = read_csv("data/10-florida-nascar.csv") |>  
  as_tibble()
```

```
## Rows: 68858 Columns: 12
## — Column specification ——————
## Delimiter: ","
## chr (1): school_name
## dbl (11): school_id, grade, year, zscore, nascar_lead, nascar_lead_weighted, ...
## 
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

nascar_df

My sister is in these observations!

```
nascar_df |> # only keep Saturn Elementary School  
  filter(school_name == "SATURN ELEM")
```

```
## # A tibble: 21 × 12  
##   school_id school_name grade year  zscore nascar_lead nascar_lead_weighted  
##       <dbl> <chr>      <dbl> <dbl>    <dbl>        <dbl>                <dbl>  
## 1     2067 SATURN ELEM     3  2003   0.105         0                   0  
## 2     2067 SATURN ELEM     4  2003  -0.0633        0                   0  
## 3     2067 SATURN ELEM     5  2003   0.163         0                   0  
## 4     2067 SATURN ELEM     3  2004   0.655         0                   0  
## 5     2067 SATURN ELEM     4  2004   0.586         0                   0  
## 6     2067 SATURN ELEM     5  2004   0.679         0                   0  
## 7     2067 SATURN ELEM     3  2005   1.03          0                   0  
## 8     2067 SATURN ELEM     4  2005   0.131          0                   0  
## 9     2067 SATURN ELEM     5  2005   0.696          0                   0  
## 10    2067 SATURN ELEM     3  2006   0.599          0                   0  
## # ... with 11 more rows, and 5 more variables: years_leaded <dbl>,  
## #   industrial_lead <dbl>, median_income <dbl>, unemp_rate <dbl>,  
## #   num_students <dbl>
```

Let's look at the data

```
summary(nascar_df)
```

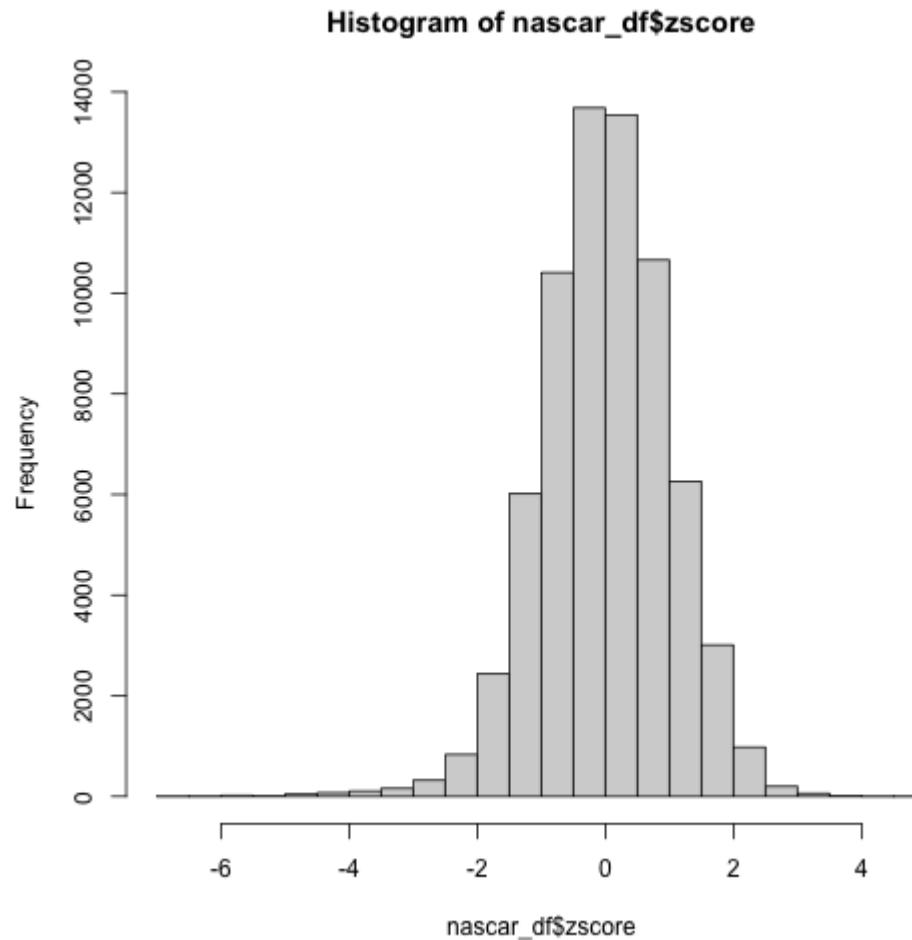
```
##      school_id    school_name          grade        year
##  Min.   :  3    Length:68858    Min.   :3.000  Min.   :2003
##  1st Qu.: 961   Class  :character  1st Qu.:3.000  1st Qu.:2006
##  Median :1811   Mode   :character  Median :4.000  Median :2009
##  Mean   :1832                    Mean   :3.998  Mean   :2009
##  3rd Qu.:2702                    3rd Qu.:5.000  3rd Qu.:2012
##  Max.   :4110                    Max.   :5.000  Max.   :2014
##      zscore       nascar_lead    nascar_lead_weighted  years_leaded
##  Min.   :-6.765987  Min.   : 0.00  Min.   :0.0000  Min.   :0.000
##  1st Qu.:-0.630857  1st Qu.: 0.00  1st Qu.:0.0000  1st Qu.:0.000
##  Median : 0.012807  Median : 0.00  Median :0.0000  Median :0.000
##  Mean   : 0.000358  Mean   :12.88  Mean   :0.5145  Mean   :1.746
##  3rd Qu.: 0.661761  3rd Qu.:16.38  3rd Qu.:0.5528  3rd Qu.:3.000
##  Max.   : 4.884255  Max.   :92.02  Max.   :6.8524  Max.   :8.000
##      industrial_lead  median_income  unemp_rate  num_students
##  Min.   :     0  Min.   :25201  Min.   :0.02000  Min.   : 10.0
##  1st Qu.: 300489  1st Qu.:41184  1st Qu.:0.04000  1st Qu.: 72.0
##  Median : 562856  Median :44635  Median :0.06000  Median :100.0
##  Mean   : 610567.0  Mean   :44635  Mean   :0.06050  Mean   :100.5
```

The variables

- **zscore**: the school's score for the average student in terms of standard deviations above or below the state-wide average
- **nascar lead**: lifetime exposure to lead emissions from NASCAR tracks within 50 miles
- **nascar lead weighted**: same as **nascar lead**, but counts emissions closer to the school more
- **industrial lead**: lead emissions from industrial sources (e.g. factories) within 50 miles
- **unemp rate**: the school district's unemployment rate
- **median income**: the school district's median income
- **num students**: the number of students at the school
- **school id, school name, grade, and year**: self-explanatory

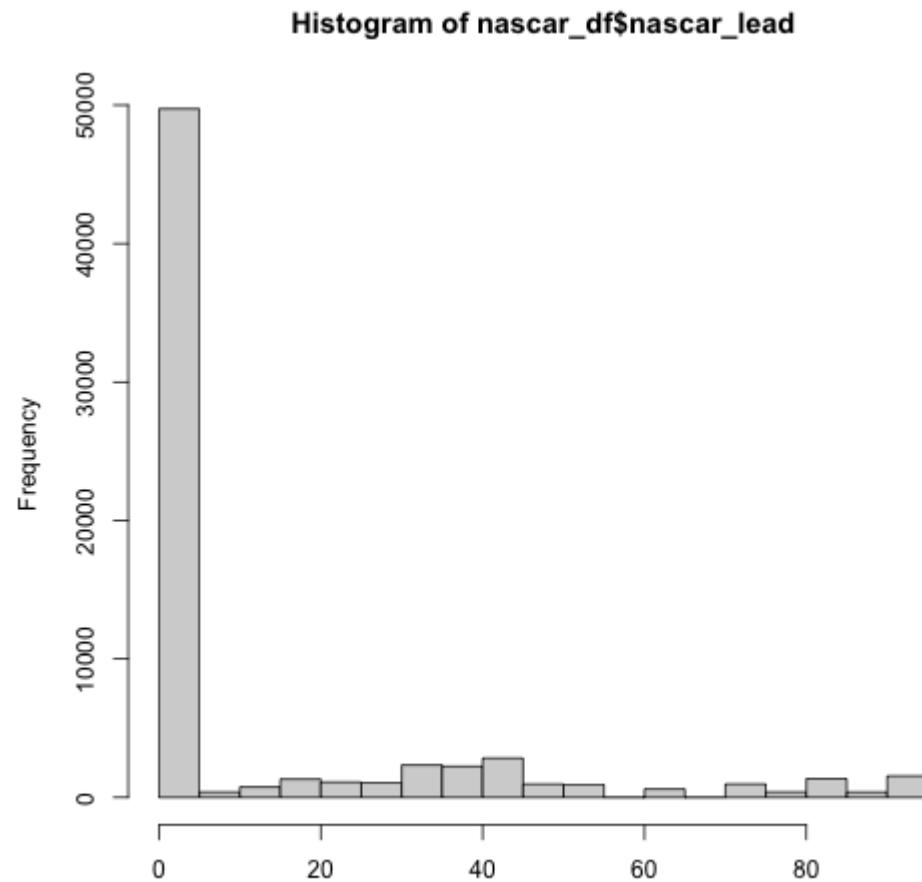
What does the distribution of scores look like?

```
hist(nascar_df$zscore)
```



What about exposure to NASCAR lead

```
hist(nascar_df$nascar_lead)
```



```
hist(nascar_df$nascar_lead)
```

generates a histogram for a variable

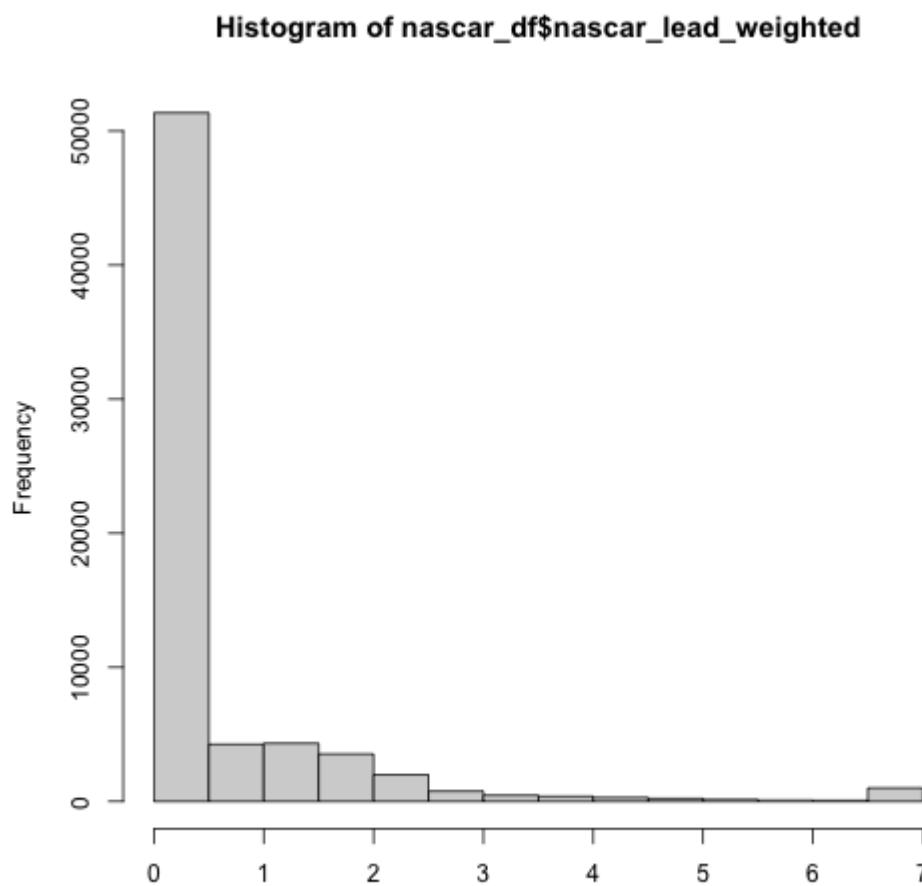
Most schools have zero exposure

Some have a lot

Units are 10s of kilograms

What about exposure to NASCAR lead

```
hist(nascar_df$nascar_lead_weighted)
```

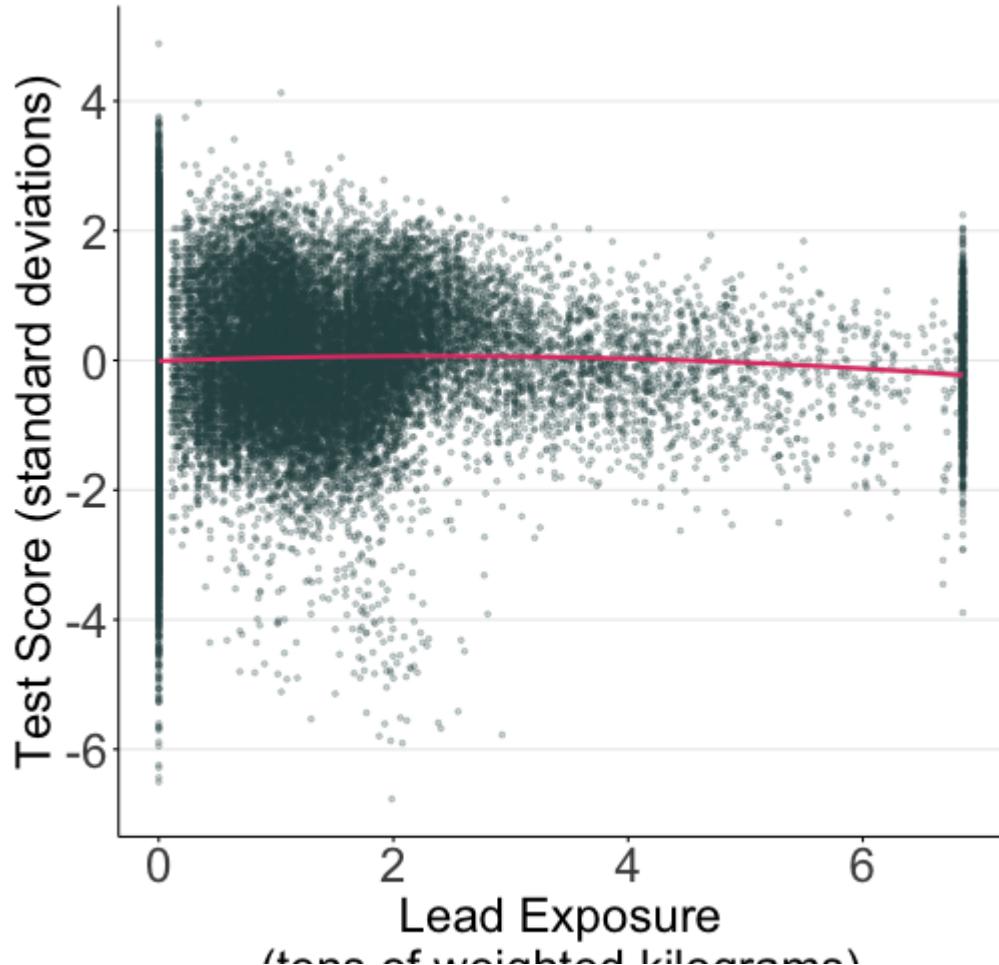


Most schools have zero exposure

Some have a lot

What is the association between lead and scores?

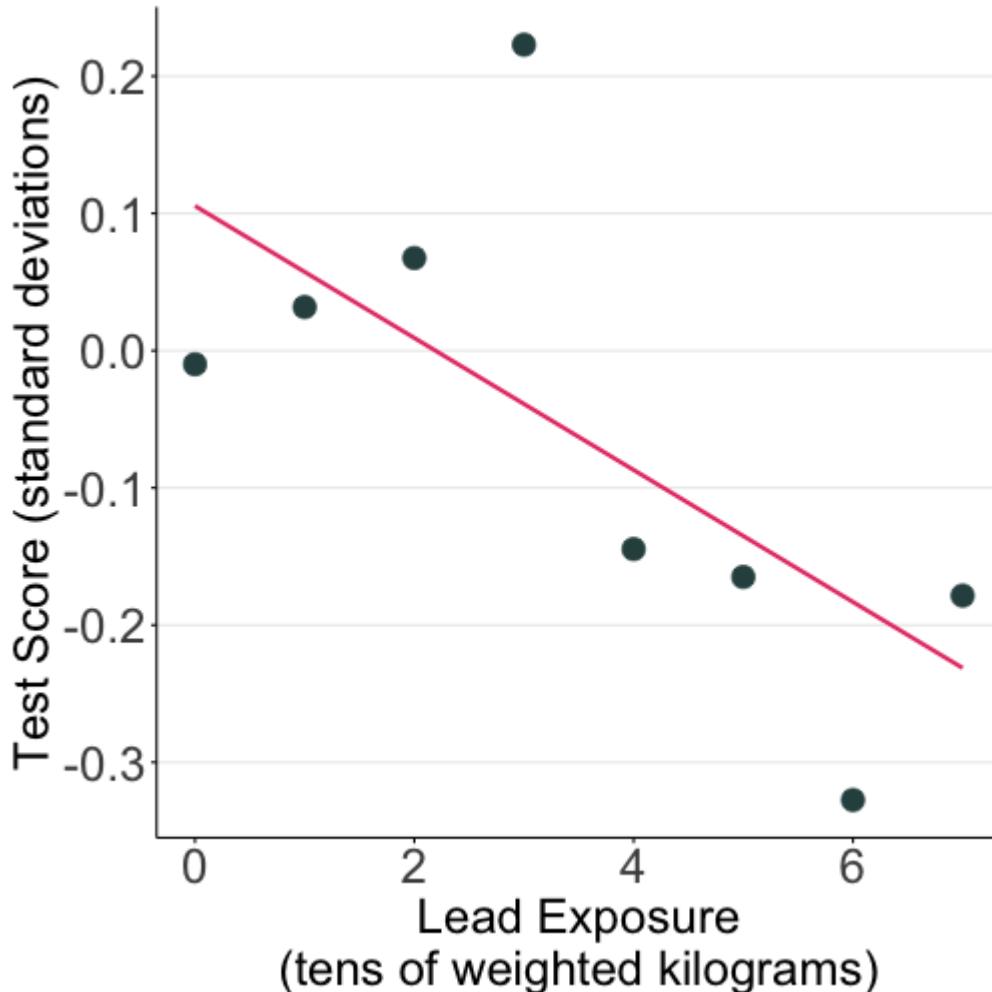
```
## `geom_smooth()` using method = 'gam'
```



Let's look at the pure correlation
between test scores and lead

There's a lot of data so it's kind of
hard to see but it appears there's a
negative association: lead is bad for
test scores

What is the association between lead and scores?



Lets **bin** the data to see the pattern more clearly

All I'm doing is:

- Rounding lead to the nearest integer
- Taking the average of test scores for that bin
- Plot the average scores versus rounded lead

What is the association between lead and scores?

We can get a better sense by running a regression:

$$zscore_{sgy} = \beta_0 + \beta_1 nascarlead_{weighted_{sgy}}$$

(s is school, g is grade, y is year)

```
lm(zscore ~ nascar_lead_weighted, nascar_df) |>  
  broom::tidy()
```

The `broom::tidy()` at the end just makes the results look a bit cleaner on the screen

What is the association between lead and scores?

```
lm(zscore ~ nascar_lead_weighted, nascar_df) |>  
  broom::tidy()
```

```
## # A tibble: 2 × 5  
##   term            estimate  
##   <chr>           <dbl>  
## 1 (Intercept)     0.002  
## 2 nascar_lead_weighted -0.004
```

What does this mean?

An additional 10 kg of lead exposure is associated with a school having an average test score 0.004 standard deviations lower

Do we believe this number?

What's a potential issue with just looking at the raw association?

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Schools near NASCAR tracks are probably a lot different than schools further away

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We want to control for things that are potentially correlated with both test scores and being close to NASCAR

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What's a potential issue with just looking at the raw association?

Schools near NASCAR tracks are probably a lot different than schools further away

We want to control for things that are potentially correlated with both test scores and being close to NASCAR

Two broad important things: lead emissions from other sources, socioeconomic status

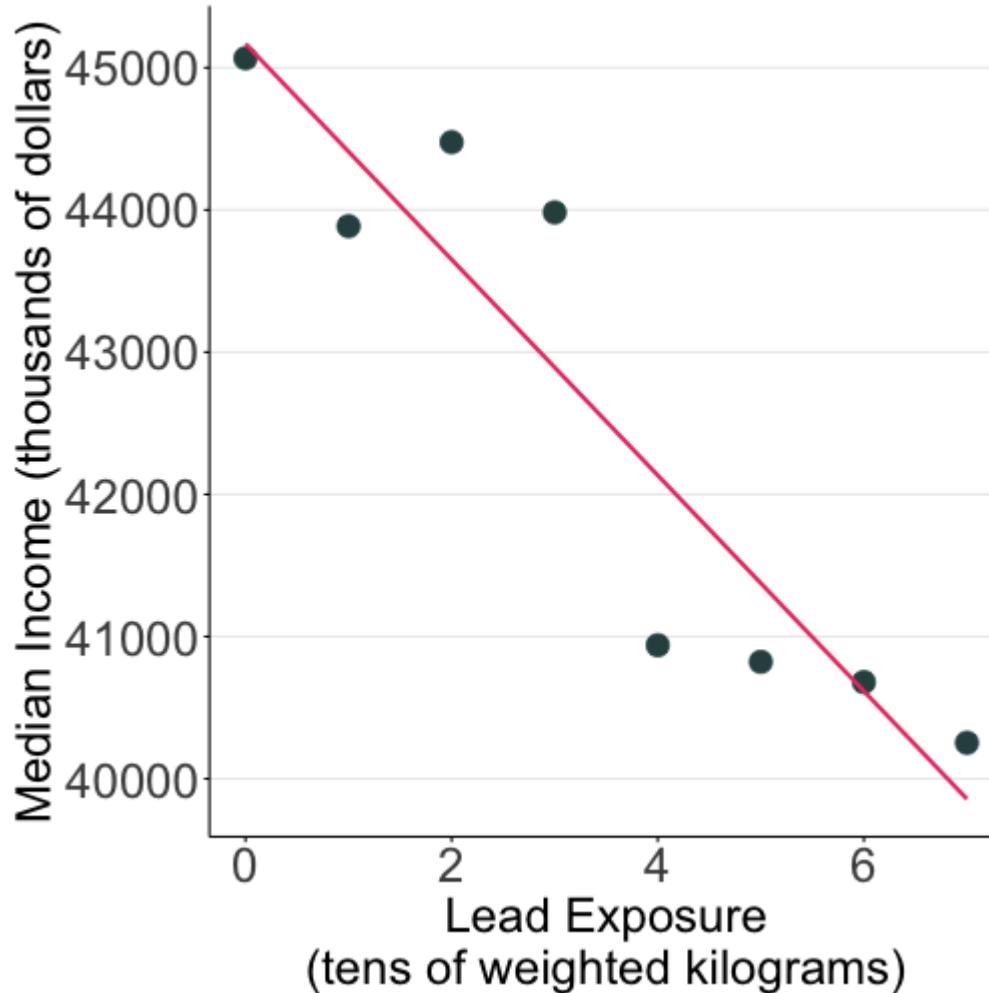
Do we believe this number?

```
lm(zscore ~ nascar_lead_weighted + industrial_lead + unemp_rate + median_income, nascar_df) |>  
broom::tidy()
```

```
## # A tibble: 5 × 5  
##   term            estimate  
##   <chr>           <dbl>  
## 1 (Intercept)     -0.846  
## 2 nascar_lead_weighted -0.0008  (versus -0.004 above)  
## 3 industrial_lead    -0.00000006  
## 4 unemp_rate        -0.640  
## 5 median_income      0.00002
```

Controlling for other things matters: new estimate is 1/4 the size

Why did this matter?



Mainly because places with
NASCAR tracks tend to be poorer:

```
lm(median_income ~ nascar_lead_weighted, nasc
```

```
##  
## Call:  
## lm(formula = median_income ~ nascar_lead_weighted)  
##  
## Coefficients:  
## (Intercept)  nascar_lead_weighted  
##             45057.8                 -672.2
```