Methods Camp

UT Austin, Department of Government

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Class schedule

Date	Time	Location
Mon, Aug. 18	1:00 PM - 5:30 PM	RLP 2.606
Tue, Aug. 19	1:00 PM - 5:30 PM	RLP 2.606
Wed, Aug. 20	9:00 AM - 12:00 PM	RLP1.302D
	1:00 PM - 4:30 PM	BAT 5.108
Thu, Aug. 21	9:00 AM - 12:00 PM	RLP 3.106
	1:00 AM - 4:30 PM	RLP 3.106

On class days, we will have a lunch break from 12:00-1:00 PM. We'll also take short breaks periodically during the morning and afternoon sessions as needed.

Description

Welcome to Introduction to Methods for Political Science, aka "Methods Camp"! Methods Camp is designed to give everyone a chance to brush up on some skills in preparation for the introductory Statistics and Formal Theory courses. The other goal of Methods Camp is to allow you to get to know your cohort. We hope that matrix algebra and the chain rule will still prove to be good bonding exercises!

As you can see from the above schedule, we'll be meeting on Monday, August 18th, through Thursday, August 21st. Classes at UT begin the start of the following week on Monday, August 25th. Below is a tentative schedule outlining what will be covered in the class, although we may rearrange things if we find we're going too slowly or too quickly through the material.

Course outline

1 Monday afternoon: Intro to R

- Introductions
- R and RStudio: basics
- Objects (vectors, matrices, data frames, etc.)

- Basic functions (`mean()`, `length()`, etc.)
- Packages: installation and loading (including the tidyverse)

1 Monday afternoon: Functions

- Definitions
- Functions in R
- Common types of functions
- Logarithms and exponents
- Composite functions

3 Tuesday afternoon: Tidy data analysis I

- Tidy data
- Data wrangling with dplyr
- Data visualization basics with `ggplot2`

4 Tuesday afternoon: Calculus

- Derivatives
- Optimization
- Integrals

5 Wednesday morning: Matrices

- Matrices
- Systems of linear equations
- Matrix operations (multiplication, transpose, inverse, determinant)
- Solving systems of linear equations in matrix form (and why that's cool)
- Introduction to OLS

6 Wednesday afternoon: Tidy data analysis II

- Loading data in different formats (.csv, R, Excel, Stata, SPSS)
- Recoding values (`if_else()`, `case_when()`)
- Handling missing values
- Pivoting data
- Merging data
- Plotting extensions (trend graphs, facets, customization)

7 Thursday morning: Probability

- Probability: basic concepts
- Random variables, probability distributions, and their properties
- Common probability distributions

8 Thursday afternoon: Statistics and simulations

- Statistics: basic concepts
- Random sampling and loops in R
- Simulation example: bootstrapping

11 Thursday afternoon: Wrap-up

- Project management fundamentals
- Self-study resources and materials
- Other software (Overleaf, Zotero, etc.)
- Methods resources at UT

Contact info

If you have any questions during or outside of the methods camp, you can contact us via email. Or if you are curious about our research, you can also check out our respective websites and Twitter accounts (or should we say X…):

- Meiying Xu: xu.meiying@utexas.edu
- Joel Yew: joel.yew@utexas.edu

Acknowledgements

We thank previous Methods Camp instructors for their accumulated experience and materials, upon which we have based ours upon. UT Gov Prof. Max Goplerud gave us amazing feedback for this iteration of Methods Camp (2025). All errors remain our own (and will hopefully be fixed with your help!).

Materials from previous editions

- 2024: co-taught by Andrés Cruz and Meiying Xu.
- 2023: co-taught by Andrés Cruz and Matt Martin.

Setup

Installing R and RStudio

R is a programming language optimized for statistics and data analysis. Most people use R from RStudio, a graphical user interface (GUI) that includes a file pane, a graphics pane, and other goodies. Both R and RStudio are open source, i.e., free as in beer and free as in freedom!

Your first steps should be to install R and RStudio, in that order (if you have installed these programs before, make sure that your versions are up-to-date—if they are not, simply follow the instructions below to re-install them):

1. Download and install R from the official website, CRAN. Click on "Download R for <Windows/MacOS>" and follow the instructions. If you have a Mac, make sure to select the version appropriate for your system (Apple Silicon for newer M1/M2/M3 Macs and Intel for older Macs).
2. Download and install RStudio from the official website. Scroll down and select the installer for your operating system (most likely the .exe for Windows 10/11 or the .dmg for macOS 12+).

After these two steps, you can open RStudio in your system, as you would with any program. You should see something like this:

> **Note for Windows users**
>
> While the installation steps above should be enough for most tasks, we also suggest that Windows users install RTools (click on the "Rtools44 installer" link at the middle of the package to get the .exe file). Rtools is needed on Windows to install some advanced packages, so it is a good idea to have it on your system.

That's it for the installation! We also *strongly* recommend that you change a couple of RStudio's default settings.[1] You can change settings by clicking on `Tools > Global Options` in the menubar. Here are our recommendations:

[1] The idea behind these settings (or at least the first two) is to force R to start from scratch with each new session. No lingering objects from previous coding sessions avoids misunderstandings and helps with reproducibility!

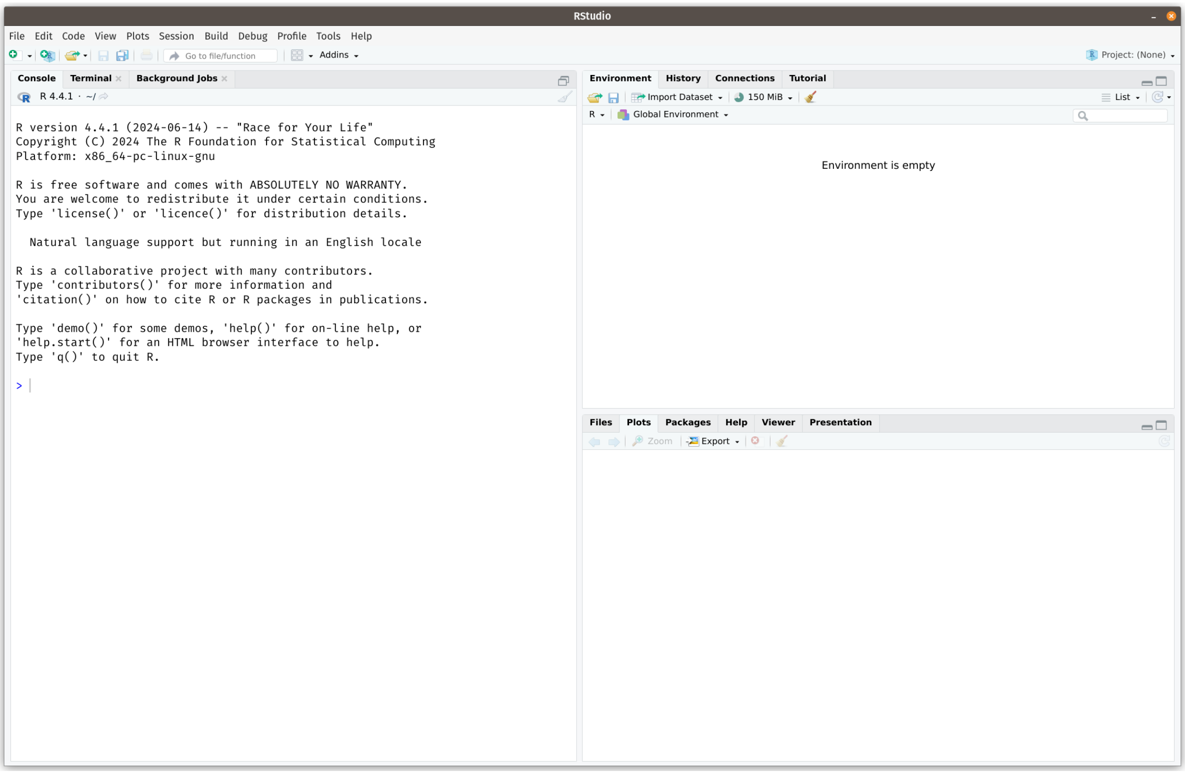


Figure 1: How RStudio looks after a clean installation.

- `General > Uncheck "Restore .RData into workspace at startup"`
- `General > Save workspace to .RData on Exit > Select "Never"`
- `Code > Check "Use native pipe operator"`
- `Tools > Global Options > Appearance` to change to a dark theme, if you want! Pros: better for night sessions, hacker vibes...

Setting up for Methods Camp

All materials for Methods Camp are both on this website and available as RStudio projects for you to execute locally. An RStudio project is simply a folder where one keeps scripts, datasets, and other files needed for a data analysis project.

Below are RStudio projects for you to download, available as .zip compressed files. On MacOS, the file will be uncompressed automatically. On Windows, you should do `Right click > Extract all`.

- Download Part 1 of the class materials.
- Download Part 2 of the class materials.
- Download Part 3 of the class materials.
- Download Part 4 of the class materials.

> ⚠ Warning
>
> Make sure to properly unzip the materials. Double-clicking the .zip file on most Windows systems *will not* unzip the folder—you must do `Right click > Extract all`.

You should now have a folder called `methodscamp_part1/` on your computer. Navigate to the `methodscamp_part1.Rproj` file within it and open it. RStudio should open the project right away. You should see `methodscamp_part1` on the top-right of RStudio—this indicates that you are working in our RStudio project.

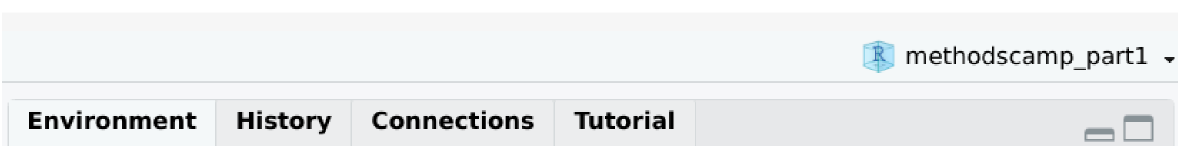


Figure 2: How the bottom-right corner of RStudio looks after opening our project.

That's all for setup! We can now start coding. After opening our RStudio project, we'll begin by opening the `01_r_intro.qmd` file from the "Files" panel, in the bottom-right portion of

RStudio. This is a Quarto document,[2] which contains both code and explanations (you can also read the materials in the next chapter of this website).

[2] Perhaps you have used R Markdown before. Quarto is the next iteration of R Markdown, and is both more flexible and more powerful!

1 Intro to R

In Quarto documents like this one, we can write comments by just using plain text. In contrast, code needs to be within *code blocks*, like the one below. To execute a code block, you can click on the little “Play” button or press `Cmd/Ctrl + Shift + Enter` when your keyboard is hovering the code block.

```
2 + 2
```

```
[1] 4
```

That was our first R command, a simple math operation. Of course, we can also do more complex arithmetic:

```
12345 ^ 2  / (200 + 25 - 6 * 2) # this is an inline comment, see the leading "#"
```

```
[1] 715488.4
```

In order to *create* a code block, you can press `Cmd/Ctrl + Alt + i` or click on the little green “+C” icon on top of the script.

> **Exercise**
>
> Create your own code block below and run a math operation.

1.1 Objects

A huge part of R is working with *objects*. Let’s see how they work:

```
my_object <- 10 # opt/alt + minus sign will make the arrow
```

```
my_object # to print the value of an object, just call its name
```

```
[1] 10
```

We can now use this object in our operations:

```
2 ^ my_object
```

```
[1] 1024
```

Or even create another object out of it:

```
my_object2 <- my_object * 2
```

```
my_object2
```

```
[1] 20
```

You can delete objects with the `rm()` function (for "remove"):

```
rm(my_object2)
```

1.2 Vectors and functions

Objects can be of different types. One of the most useful ones is the *vector*, which holds a series of values. To create one manually, we can use the `c()` function (for "combine"):

```
my_vector <- c(6, -11, my_object, 0, 20)
```

```
my_vector
```

```
[1]   6 -11  10   0  20
```

One can also define vectors by sequences:

```r
3:10
```

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

We can use square brackets to retrieve parts of vectors:

```r
my_vector[4] # fourth element
```

```
[1] 0
```

```r
my_vector[1:2] # first two elements
```

```
[1]   6 -11
```

Let's check out some basic functions we can use with numbers and numeric vectors:

```r
sqrt(my_object) # squared root
```

```
[1] 3.162278
```

```r
log(my_object) # logarithm (natural by default)
```

```
[1] 2.302585
```

```r
abs(-5) # absolute value
```

```
[1] 5
```

```r
mean(my_vector)
```

```
[1] 5
```

```r
median(my_vector)
```

```
[1] 6
```

```r
sd(my_vector) # standard deviation
```

```
[1] 11.53256
```

```r
sum(my_vector)
```

```
[1] 25
```

```r
min(my_vector) # minimum value
```

```
[1] -11
```

```r
max(my_vector) # maximum value
```

```
[1] 20
```

```r
length(my_vector) # length (number of elements)
```

```
[1] 5
```

Notice that if we wanted to save any of these results for later, we would need to *assign* them:

```r
my_mean <- mean(my_vector)
```

```r
my_mean
```

```
[1] 5
```

These functions are quite simple: they take one object and do one operation. A lot of functions are a bit more complex—they take multiple objects or take options. For example, see the `sort()` function, which by default sorts a vector *increasingly*:

```r
sort(my_vector)
```

```
[1] -11   0   6  10  20
```

If we instead want to sort our vector *decreasingly*, we can use the `decreasing = TRUE` argument (`T` also works as an abbreviation for `TRUE`).

```r
sort(my_vector, decreasing = TRUE)
```

```
[1]  20  10   6   0 -11
```

Tip

If you use the argument values in order, you can avoid writing the argument names (see below). This is sometimes useful, but can also lead to confusing code—use it with caution.

```r
sort(my_vector, T)
```

```
[1]  20  10   6   0 -11
```

A useful function to create vectors in sequence is `seq()`. Notice its arguments:

```r
seq(from = 30, to = 100, by = 5)
```

```
 [1]  30  35  40  45  50  55  60  65  70  75  80  85  90  95 100
```

To check the arguments of a function, you can examine its help file: look the function up on the "Help" panel on RStudio or use a command like the following: `?sort`.

Exercise

Examine the help file of the `log()` function. How can we compute the the base-10 logarithm of `my_object`? Your code:

Other than numeric vectors, character vectors are also useful:

```r
my_character_vector <- c("Apple", "Orange", "Watermelon", "Banana")
```

```r
my_character_vector[3]
```

```
[1] "Watermelon"
```

```r
nchar(my_character_vector) # count number of characters
```

```
[1]  5  6 10  6
```

1.3 Data frames and lists

Another useful object type is the *data frame*. Data frames can store multiple vectors in a tabular format. We can manually create one with the `data.frame()` function:

```
my_data_frame <- data.frame(fruit = my_character_vector,
                            calories_per_100g = c(52, 47, 30, 89),
                            water_per_100g = c(85.6, 86.8, 91.4, 74.9))
```

```
my_data_frame
```

```
       fruit calories_per_100g water_per_100g
1      Apple                52           85.6
2     Orange                47           86.8
3 Watermelon                30           91.4
4     Banana                89           74.9
```

Now we have a little 4x3 data frame of fruits with their calorie counts and water composition. We gathered the nutritional information from the USDA (2019).

We can use the `data_frame$column` construct to access the vectors within the data frame:

```
mean(my_data_frame$calories_per_100g)
```

```
[1] 54.5
```

> **Exercise**
>
> Obtain the maximum value of water content per 100g in the data. Your code:

Some useful commands to learn attributes of our data frame:

```
dim(my_data_frame)
```

```
[1] 4 3
```

```
nrow(my_data_frame)
```

```
[1] 4
```

```r
names(my_data_frame) # column names
```

```
[1] "fruit"             "calories_per_100g" "water_per_100g"
```

We will learn much more about data frames in our next module on data analysis.

After talking about vectors and data frames, the last object type that we will cover is the *list*. Lists are super flexible objects that can contain just about anything:

```r
my_list <- list(my_object, my_vector, my_data_frame)
```

```r
my_list
```

```
[[1]]
[1] 10

[[2]]
[1]   6 -11  10   0  20

[[3]]
       fruit calories_per_100g water_per_100g
1      Apple                52           85.6
2     Orange                47           86.8
3 Watermelon                30           91.4
4     Banana                89           74.9
```

To retrieve the elements of a list, we need to use double square brackets:

```r
my_list[[1]]
```

```
[1] 10
```

Lists are sometimes useful due to their flexibility, but are much less common in routine data analysis compared to vectors or data frames.

1.4 Packages

The R community has developed thousands of *packages*, which are specialized collections of functions, datasets, and other resources. To install one, you should use the `install.packages()` command. Below we will install the `tidyverse` package, a suite for data analysis that we will use in the next modules. You just need to install packages once, and then they will be available system-wide.

```
install.packages("tidyverse") # this can take a couple of minutes
```

If you want to use an installed package in your script, you must load it with the `library()` function. Some packages, as shown below, will print descriptive messages once loaded.

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

> **Warning**
>
> Remember that `install.packages("package")` needs to be executed just once, while `library(package)` needs to be in each script in which you plan to use the package. In general, never include `install.packages("package")` as part of your scripts or Quarto documents!

2 Tidy data analysis I

The tidyverse is a suite of packages that streamline data analysis in R. After installing the tidyverse with install.packages("tidyverse") (see the previous module), you can load it with:

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becon
```

> **Tip**
>
> Upon loading, the tidyverse prints a message like the one above. Notice that multiple packages (the constituent elements of the "suite") are actually loaded. For instance, dplyr and tidyr help with data wrangling and transformation, while ggplot2 allows us to draw plots. In most cases, one just loads the tidyverse and forgets about these details, as the constituent packages work together nicely.

Throughout this module, we will use tidyverse functions to load, wrangle, and visualize real data.

2.1 Loading data

Throughout this module we will work with a dataset of senators during the Trump presidency, which was adapted from FiveThirtyEight (2021).

We have stored the dataset in .csv format under the `data/` subfolder. Loading it into R is simple (notice that we need to assign it to an object):

```
trump_scores <- read_csv("data/trump_scores_538.csv")
```

```
Rows: 122 Columns: 8
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (4): bioguide, last_name, state, party
dbl (4): num_votes, agree, agree_pred, margin_trump

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.
```

```
trump_scores
```

```
# A tibble: 122 x 8
   bioguide last_name  state party num_votes agree agree_pred margin_trump
   <chr>    <chr>      <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 A000360  Alexander  TN    R           118 0.890      0.856       26.0  
 2 B000575  Blunt      MO    R           128 0.906      0.787       18.6  
 3 B000944  Brown      OH    D           128 0.258      0.642        8.13 
 4 B001135  Burr       NC    R           121 0.893      0.560        3.66 
 5 B001230  Baldwin    WI    D           128 0.227      0.510        0.764
 6 B001236  Boozman    AR    R           129 0.915      0.851       26.9  
 7 B001243  Blackburn  TN    R           131 0.885      0.889       26.0  
 8 B001261  Barrasso   WY    R           129 0.891      0.895       46.3  
 9 B001267  Bennet     CO    D           121 0.273      0.417       -4.91 
10 B001277  Blumenthal CT    D           128 0.203      0.294      -13.6  
# i 112 more rows
```

Let's review the dataset's columns:

- `bioguide`: A unique ID for each politician, from the Congress Bioguide.
- `last_name`
- `state`
- `party`
- `num_votes`: Number of votes for which data was available.
- `agree`: Proportion (0-1) of votes in which the senator voted in agreement with Trump.
- `agree_pred`: Predicted proportion of vote agreement, calculated using Trump's margin (see next variable).

- `margin_trump`: Margin of victory (percentage points) of Trump in the senator's state.

We can inspect our data by using the interface above. An alternative is to run the command `View(trump_scores)` or click on the object in RStudio's environment panel (in the top-right section).

Do you have any questions about the data?

By the way, the `tidyverse` works amazingly with *tidy data*. If you can get your data to this format (and we will see ways to do this), your life will be much easier:

2.2 Wrangling data with `dplyr`

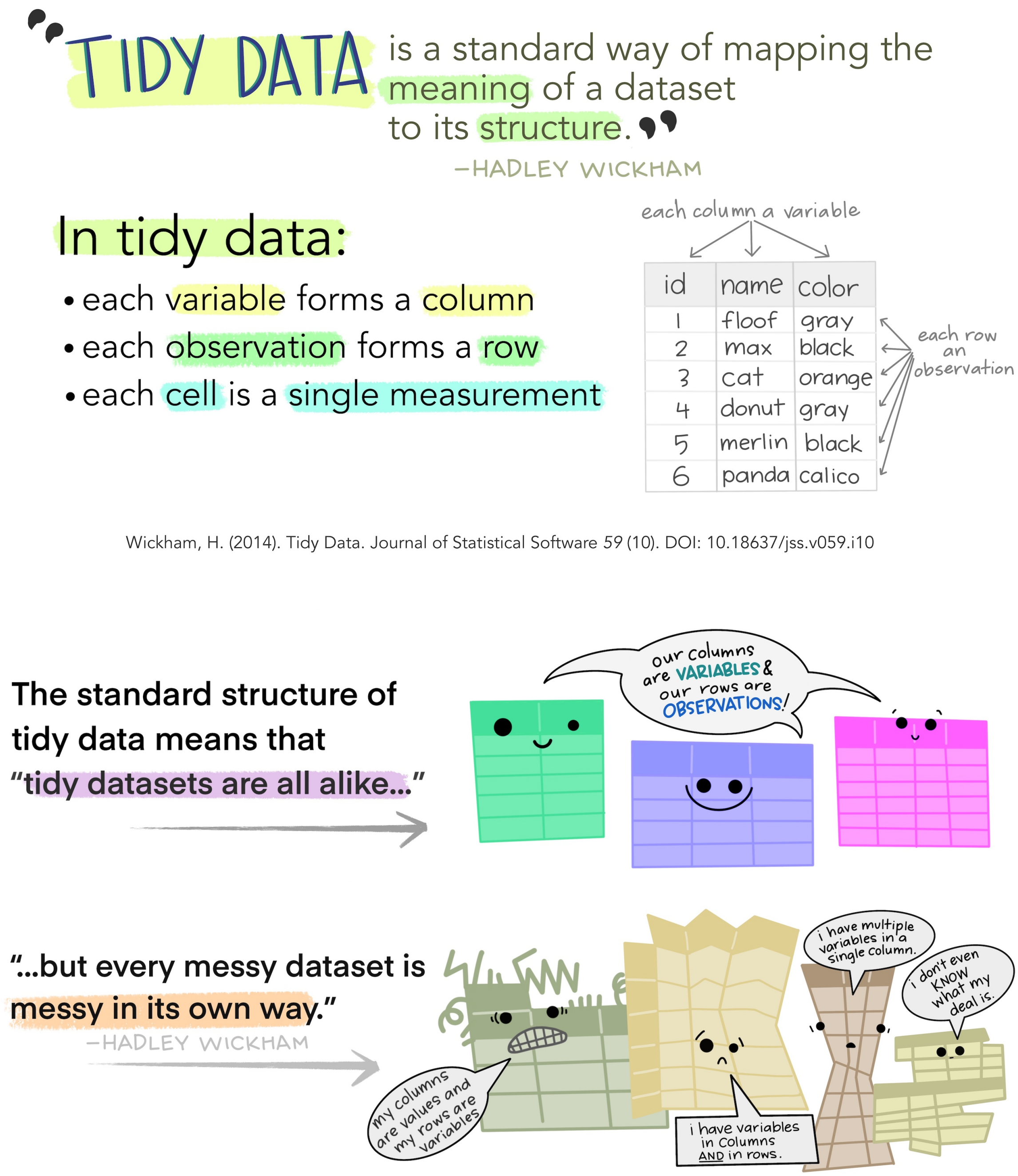
We often need to modify data to conduct our analyses, e.g., creating columns, filtering rows, etc. In the `tidyverse`, these operations are conducted with multiple *verbs*, which we will review now.

2.2.1 Selecting columns

We can select specific columns in our dataset with the `select()` function. All `dplyr` wrangling verbs take a data frame as their first argument—in this case, the columns we want to select are the other arguments.

```r
select(trump_scores, last_name, party)
```

```
# A tibble: 122 x 2
   last_name  party
   <chr>      <chr>
 1 Alexander  R
 2 Blunt      R
 3 Brown      D
 4 Burr       R
 5 Baldwin    D
 6 Boozman    R
 7 Blackburn  R
 8 Barrasso   R
 9 Bennet     D
10 Blumenthal D
# i 112 more rows
```



(a) Source: Illustrations from the Openscapes blog *Tidy Data for reproducibility, efficiency, and collaboration* by Julia Lowndes and Allison Horst.

This is a good moment to talk about "pipes." Notice how the code below produces the same output as the one above, but with a slightly different syntax. Pipes (`|>`) "kick" the object on the left of the pipe to the first argument of the function on the right. One can read pipes as "then," so the code below can be read as "take `trump_scores`, then select the columns `last_name` and `party`." Pipes are very useful to *chain multiple operations*, as we will see in a moment.

```
trump_scores |>
  select(last_name, party)
```

```
# A tibble: 122 x 2
   last_name  party
   <chr>      <chr>
 1 Alexander  R
 2 Blunt      R
 3 Brown      D
 4 Burr       R
 5 Baldwin    D
 6 Boozman    R
 7 Blackburn  R
 8 Barrasso   R
 9 Bennet     D
10 Blumenthal D
# i 112 more rows
```

> Tip
>
> You can insert a pipe with the `Cmd/Ctrl + Shift + M` shortcut. If you have not changed the default RStudio settings, an "old" pipe (`%>%`) might appear. While most of the functionality is the same, the `|>` "new" pipes are more readable and don't need any extra packages (to use `%>%` you need the `tidyverse` or one of its packages). You can change this RStudio option in `Tools > Global Options > Code > Use native pipe operator`. Make sure to check the other suggested settings in our Setup module!

Going back to selecting columns, you can select ranges:

```
trump_scores |>
  select(bioguide:party)
```

```
# A tibble: 122 x 4
   bioguide last_name  state party
```

```
   <chr>    <chr>      <chr> <chr>
 1 A000360  Alexander  TN    R
 2 B000575  Blunt      MO    R
 3 B000944  Brown      OH    D
 4 B001135  Burr       NC    R
 5 B001230  Baldwin    WI    D
 6 B001236  Boozman    AR    R
 7 B001243  Blackburn  TN    R
 8 B001261  Barrasso   WY    R
 9 B001267  Bennet     CO    D
10 B001277  Blumenthal CT    D
# i 112 more rows
```

You can also **de**select columns using a minus sign:

```
trump_scores |>
  select(-last_name)
```

```
# A tibble: 122 x 7
   bioguide state party num_votes agree agree_pred margin_trump
   <chr>    <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 A000360  TN    R           118 0.890      0.856       26.0
 2 B000575  MO    R           128 0.906      0.787       18.6
 3 B000944  OH    D           128 0.258      0.642        8.13
 4 B001135  NC    R           121 0.893      0.560        3.66
 5 B001230  WI    D           128 0.227      0.510        0.764
 6 B001236  AR    R           129 0.915      0.851       26.9
 7 B001243  TN    R           131 0.885      0.889       26.0
 8 B001261  WY    R           129 0.891      0.895       46.3
 9 B001267  CO    D           121 0.273      0.417       -4.91
10 B001277  CT    D           128 0.203      0.294      -13.6
# i 112 more rows
```

And use a few helper functions, like `matches()`:

```
trump_scores |>
  select(last_name, matches("agree"))
```

```
# A tibble: 122 x 3
   last_name  agree agree_pred
   <chr>      <dbl>      <dbl>
```

```
 1 Alexander  0.890      0.856
 2 Blunt      0.906      0.787
 3 Brown      0.258      0.642
 4 Burr       0.893      0.560
 5 Baldwin    0.227      0.510
 6 Boozman    0.915      0.851
 7 Blackburn  0.885      0.889
 8 Barrasso   0.891      0.895
 9 Bennet     0.273      0.417
10 Blumenthal 0.203      0.294
# i 112 more rows
```

Or `everything()`, which we usually use to reorder columns:

```r
trump_scores |>
  select(last_name, everything())
```

```
# A tibble: 122 x 8
   last_name  bioguide state party num_votes agree agree_pred margin_trump
   <chr>      <chr>    <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 Alexander  A000360  TN    R           118 0.890      0.856       26.0
 2 Blunt      B000575  MO    R           128 0.906      0.787       18.6
 3 Brown      B000944  OH    D           128 0.258      0.642        8.13
 4 Burr       B001135  NC    R           121 0.893      0.560        3.66
 5 Baldwin    B001230  WI    D           128 0.227      0.510        0.764
 6 Boozman    B001236  AR    R           129 0.915      0.851       26.9
 7 Blackburn  B001243  TN    R           131 0.885      0.889       26.0
 8 Barrasso   B001261  WY    R           129 0.891      0.895       46.3
 9 Bennet     B001267  CO    D           121 0.273      0.417       -4.91
10 Blumenthal B001277  CT    D           128 0.203      0.294      -13.6
# i 112 more rows
```

Tip

Notice that all these commands have not edited our existent objects—they have just printed the requested outputs to the screen. In order to modify objects, you need to use the assignment operator (`<-`). For example:

```r
trump_scores_reduced <- trump_scores |>
  select(last_name, matches("agree"))
```

```r
trump_scores_reduced
```

```
# A tibble: 122 x 3
   last_name  agree agree_pred
   <chr>      <dbl>      <dbl>
 1 Alexander  0.890      0.856
 2 Blunt      0.906      0.787
 3 Brown      0.258      0.642
 4 Burr       0.893      0.560
 5 Baldwin    0.227      0.510
 6 Boozman    0.915      0.851
 7 Blackburn  0.885      0.889
 8 Barrasso   0.891      0.895
 9 Bennet     0.273      0.417
10 Blumenthal 0.203      0.294
# i 112 more rows
```

Exercise

Select the variables `last_name`, `party`, `num_votes`, and `agree` from the data frame. Your code:

2.2.2 Renaming columns

We can use the `rename()` function to rename columns, with the syntax `new_name = old_name`. For example:

```r
trump_scores |>
  rename(prop_agree = agree, prop_agree_pred = agree_pred)
```

```
# A tibble: 122 x 8
  bioguide last_name state party num_votes prop_agree prop_agree_pred
  <chr>    <chr>     <chr> <chr>     <dbl>      <dbl>           <dbl>
1 A000360  Alexander TN    R           118      0.890           0.856
2 B000575  Blunt     MO    R           128      0.906           0.787
3 B000944  Brown     OH    D           128      0.258           0.642
4 B001135  Burr      NC    R           121      0.893           0.560
5 B001230  Baldwin   WI    D           128      0.227           0.510
6 B001236  Boozman   AR    R           129      0.915           0.851
7 B001243  Blackburn TN    R           131      0.885           0.889
```

```
 8 B001261   Barrasso   WY     R             129      0.891            0.895
 9 B001267   Bennet     CO     D             121      0.273            0.417
10 B001277   Blumenthal CT     D             128      0.203            0.294
# i 112 more rows
# i 1 more variable: margin_trump <dbl>
```

This is a good occasion to show how pipes allow us to chain operations. How do we read the following code out loud? (Remember that pipes are read as "then").

```
trump_scores |>
  select(last_name, matches("agree")) |>
  rename(prop_agree = agree, prop_agree_pred = agree_pred)
```

```
# A tibble: 122 x 3
   last_name  prop_agree prop_agree_pred
   <chr>           <dbl>           <dbl>
 1 Alexander       0.890           0.856
 2 Blunt           0.906           0.787
 3 Brown           0.258           0.642
 4 Burr            0.893           0.560
 5 Baldwin         0.227           0.510
 6 Boozman         0.915           0.851
 7 Blackburn       0.885           0.889
 8 Barrasso        0.891           0.895
 9 Bennet          0.273           0.417
10 Blumenthal      0.203           0.294
# i 112 more rows
```

2.2.3 Creating columns

It is common to want to create columns, based on existing ones. We can use `mutate()` to do so. For example, we could want our main variables of interest in terms of percentages instead of proportions:

```
trump_scores |>
  select(last_name, agree, agree_pred) |> # select just for clarity
  mutate(pct_agree = 100 * agree,
         pct_agree_pred = 100 * agree_pred)
```

```
# A tibble: 122 x 5
   last_name  agree agree_pred pct_agree pct_agree_pred
   <chr>      <dbl>      <dbl>     <dbl>          <dbl>
 1 Alexander  0.890      0.856      89.0           85.6
 2 Blunt      0.906      0.787      90.6           78.7
 3 Brown      0.258      0.642      25.8           64.2
 4 Burr       0.893      0.560      89.3           56.0
 5 Baldwin    0.227      0.510      22.7           51.0
 6 Boozman    0.915      0.851      91.5           85.1
 7 Blackburn  0.885      0.889      88.5           88.9
 8 Barrasso   0.891      0.895      89.1           89.5
 9 Bennet     0.273      0.417      27.3           41.7
10 Blumenthal 0.203      0.294      20.3           29.4
# i 112 more rows
```

We can also use multiple columns for creating a new one. For example, let's retrieve the total *number* of votes in which the senator agreed with Trump:

```r
trump_scores |>
  select(last_name, num_votes, agree) |> # select just for clarity
  mutate(num_votes_agree = num_votes * agree)
```

```
# A tibble: 122 x 4
   last_name  num_votes agree num_votes_agree
   <chr>          <dbl> <dbl>           <dbl>
 1 Alexander        118 0.890           105
 2 Blunt            128 0.906           116
 3 Brown            128 0.258            33
 4 Burr             121 0.893           108
 5 Baldwin          128 0.227            29
 6 Boozman          129 0.915           118
 7 Blackburn        131 0.885           116
 8 Barrasso         129 0.891           115
 9 Bennet           121 0.273            33.0
10 Blumenthal       128 0.203            26
# i 112 more rows
```

2.2.4 Filtering rows

Another common operation is to filter rows based on logical conditions. We can do so with the `filter()` function. For example, we can filter to only get Democrats:

```r
trump_scores |>
  filter(party == "D")
```

```
# A tibble: 55 x 8
   bioguide last_name  state party num_votes agree agree_pred margin_trump
   <chr>    <chr>      <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 B000944  Brown      OH    D           128 0.258      0.642        8.13
 2 B001230  Baldwin    WI    D           128 0.227      0.510        0.764
 3 B001267  Bennet     CO    D           121 0.273      0.417       -4.91
 4 B001277  Blumenthal CT    D           128 0.203      0.294      -13.6
 5 B001288  Booker     NJ    D           119 0.160      0.290      -14.1
 6 C000127  Cantwell   WA    D           128 0.242      0.276      -15.5
 7 C000141  Cardin     MD    D           128 0.25       0.209      -26.4
 8 C000174  Carper     DE    D           129 0.295      0.318      -11.4
 9 C001070  Casey      PA    D           129 0.287      0.508        0.724
10 C001088  Coons      DE    D           128 0.289      0.319      -11.4
# i 45 more rows
```

Notice that `==` here is a *logical operator*, read as "is equal to." So our full chain of operations says the following: take `trump_scores`, then filter it to get rows where party is equal to "D".

There are other logical operators:

Logical operator	Meaning
`==`	"is equal to"
`!=`	"is not equal to"
`>`	"is greater than"
`<`	"is less than"
`>=`	"is greater than or equal to"
`<=`	"is less than or equal to"
`%in%`	"is contained in"
`&`	"and" (intersection)
`|`	"or" (union)

Let's see a couple of other examples.

```r
trump_scores |>
  filter(agree > 0.5)
```

```
# A tibble: 69 x 8
   bioguide last_name state party num_votes agree agree_pred margin_trump
   <chr>    <chr>     <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 A000360  Alexander TN    R           118 0.890      0.856        26.0
 2 B000575  Blunt     MO    R           128 0.906      0.787        18.6
 3 B001135  Burr      NC    R           121 0.893      0.560         3.66
 4 B001236  Boozman   AR    R           129 0.915      0.851        26.9
 5 B001243  Blackburn TN    R           131 0.885      0.889        26.0
 6 B001261  Barrasso  WY    R           129 0.891      0.895        46.3
 7 B001310  Braun     IN    R            44 0.909      0.713        19.2
 8 C000567  Cochran   MS    R            68 0.971      0.830        17.8
 9 C000880  Crapo     ID    R           125 0.904      0.870        31.8
10 C001035  Collins   ME    R           129 0.651      0.441        -2.96
# i 59 more rows
```

```r
trump_scores |>
  filter(state %in% c("CA", "TX"))
```

```
# A tibble: 4 x 8
  bioguide last_name state party num_votes agree agree_pred margin_trump
  <chr>    <chr>     <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
1 C001056  Cornyn    TX    R           129 0.922      0.659         9.00
2 C001098  Cruz      TX    R           126 0.921      0.663         9.00
3 F000062  Feinstein CA    D           128 0.242      0.201       -30.1
4 H001075  Harris    CA    D           116 0.164      0.209       -30.1
```

```r
trump_scores |>
  filter(state == "WV" & party == "D")
```

```
# A tibble: 1 x 8
  bioguide last_name state party num_votes agree agree_pred margin_trump
  <chr>    <chr>     <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
1 M001183  Manchin   WV    D           129 0.504      0.893         42.2
```

Exercise

1. Add a new column to the data frame, called `diff_agree`, which subtracts `agree` and `agree_pred`. How would you create `abs_diff_agree`, defined as the absolute value of `diff_agree`? Your code:

2. Filter the data frame to only get senators for which we have information on fewer

than (or equal to) five votes. Your code:

3. Filter the data frame to only get Democrats who agreed with Trump in at least 30% of votes. Your code:

2.2.5 Ordering rows

The `arrange()` function allows us to order rows according to values. For example, let's order based on the `agree` variable:

```
trump_scores |>
  arrange(agree)
```

```
# A tibble: 122 x 8
   bioguide last_name    state party num_votes agree agree_pred margin_trump
   <chr>    <chr>        <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 H000273  Hickenlooper CO    D             2 0         0.0302        -4.91
 2 H000601  Hagerty      TN    R             2 0         0.115         26.0
 3 L000570  Luján        NM    D           186 0.124     0.243         -8.21
 4 G000555  Gillibrand   NY    D           121 0.124     0.242        -22.5
 5 M001176  Merkley      OR    D           129 0.155     0.323        -11.0
 6 W000817  Warren       MA    D           116 0.155     0.216        -27.2
 7 B001288  Booker       NJ    D           119 0.160     0.290        -14.1
 8 S000033  Sanders      VT    D           112 0.161     0.221        -26.4
 9 H001075  Harris       CA    D           116 0.164     0.209        -30.1
10 M000133  Markey       MA    D           127 0.165     0.213        -27.2
# i 112 more rows
```

Maybe we only want senators with more than a few data points. Remember that we can chain operations:

```
trump_scores |>
  filter(num_votes >= 10) |>
  arrange(agree)
```

```
# A tibble: 115 x 8
   bioguide last_name  state party num_votes agree agree_pred margin_trump
   <chr>    <chr>      <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 L000570  Luján      NM    D           186 0.124      0.243        -8.21
 2 G000555  Gillibrand NY    D           121 0.124      0.242       -22.5
```

```
 3 M001176  Merkley    OR    D              129 0.155      0.323        -11.0
 4 W000817  Warren     MA    D              116 0.155      0.216        -27.2
 5 B001288  Booker     NJ    D              119 0.160      0.290        -14.1
 6 S000033  Sanders    VT    D              112 0.161      0.221        -26.4
 7 H001075  Harris     CA    D              116 0.164      0.209        -30.1
 8 M000133  Markey     MA    D              127 0.165      0.213        -27.2
 9 W000779  Wyden      OR    D              129 0.186      0.323        -11.0
10 B001277  Blumenthal CT    D              128 0.203      0.294        -13.6
# i 105 more rows
```

By default, `arrange()` uses increasing order (like `sort()`). To use decreasing order, add a minus sign:

```r
trump_scores |>
  filter(num_votes >= 10) |>
  arrange(-agree)
```

```
# A tibble: 115 x 8
   bioguide last_name state party num_votes agree agree_pred margin_trump
   <chr>    <chr>     <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 M001198  Marshall  KS    R           183 0.973      0.933        20.6
 2 C000567  Cochran   MS    R            68 0.971      0.830        17.8
 3 H000338  Hatch     UT    R            84 0.964      0.825        18.1
 4 M001197  McSally   AZ    R           136 0.949      0.562         3.55
 5 P000612  Perdue    GA    R           119 0.941      0.606         5.16
 6 C001096  Cramer    ND    R           135 0.941      0.908        35.7
 7 R000307  Roberts   KS    R           127 0.937      0.818        20.6
 8 C001056  Cornyn    TX    R           129 0.922      0.659         9.00
 9 H001061  Hoeven    ND    R           129 0.922      0.883        35.7
10 C001047  Capito    WV    R           127 0.921      0.896        42.2
# i 105 more rows
```

You can also order rows by more than one variable. What this does is to order by the first variable, and resolve any ties by ordering by the second variable (and so forth if you have more than two ordering variables). For example, let's first order our data frame by party, and then within party order by agreement with Trump:

```r
trump_scores |>
  filter(num_votes >= 10) |>
  arrange(party, agree)
```

```
# A tibble: 115 x 8
   bioguide last_name  state party num_votes agree agree_pred margin_trump
   <chr>    <chr>      <chr> <chr>     <dbl> <dbl>      <dbl>        <dbl>
 1 L000570  Luján      NM    D           186 0.124      0.243        -8.21
 2 G000555  Gillibrand NY    D           121 0.124      0.242       -22.5
 3 M001176  Merkley    OR    D           129 0.155      0.323       -11.0
 4 W000817  Warren     MA    D           116 0.155      0.216       -27.2
 5 B001288  Booker     NJ    D           119 0.160      0.290       -14.1
 6 S000033  Sanders    VT    D           112 0.161      0.221       -26.4
 7 H001075  Harris     CA    D           116 0.164      0.209       -30.1
 8 M000133  Markey     MA    D           127 0.165      0.213       -27.2
 9 W000779  Wyden      OR    D           129 0.186      0.323       -11.0
10 B001277  Blumenthal CT    D           128 0.203      0.294       -13.6
# i 105 more rows
```

> **Exercise**
>
> Arrange the data by `diff_pred`, the difference between agreement and predicted agreement with Trump. (You should have code on how to create this variable from the last exercise). Your code:

2.2.6 Summarizing data

`dplyr` makes summarizing data a breeze using the `summarize()` function:

```
trump_scores |>
  summarize(mean_agree = mean(agree),
            mean_agree_pred = mean(agree_pred))
```

```
# A tibble: 1 x 2
  mean_agree mean_agree_pred
       <dbl>           <dbl>
1      0.592           0.572
```

To make summaries, we can use any function that takes a vector and returns one value. Another example:

```
trump_scores |>
  filter(num_votes >= 5) |> # to filter out senators with few data points
  summarize(max_agree = max(agree),
            min_agree = min(agree))
```

```
# A tibble: 1 x 2
  max_agree min_agree
      <dbl>     <dbl>
1         1     0.124
```

Grouped summaries allow us to disaggregate summaries according to other variables (usually categorical):

```
trump_scores |>
  filter(num_votes >= 5) |> # to filter out senators with few data points
  summarize(mean_agree = mean(agree),
            max_agree = max(agree),
            min_agree = min(agree),
            .by = party) # to group by party
```

```
# A tibble: 2 x 4
  party mean_agree max_agree min_agree
  <chr>      <dbl>     <dbl>     <dbl>
1 R          0.876     1         0.651
2 D          0.272     0.548     0.124
```

> **Exercise**
>
> Obtain the maximum absolute difference in agreement with Trump (the `abs_diff_agree` variable from before) for each party.

2.2.7 Overview

Function	Purpose
`select()`	Select columns
`rename()`	Rename columns
`mutate()`	Creating columns
`filter()`	Filtering rows
`arrange()`	Ordering rows
`summarize()`	Summarizing data
`summarize(…, .by = )`	Summarizing data (by groups)

2.3 Visualizing data with `ggplot2`

`ggplot2` is the package in charge of data visualization in the `tidyverse`. It is extremely flexible and allows us to draw bar plots, box plots, histograms, scatter plots, and many other types of plots (see examples at R Charts).

Throughout this module we will use a subset of our data frame, which only includes senators with more than a few data points:

```
trump_scores_ss <- trump_scores |>
  filter(num_votes >= 10)
```

The `ggplot2` syntax provides a unifying interface (the "grammar of graphics" or "gg") for drawing all different types of plots. One draws plots by adding different "layers," and the core code always includes the following:

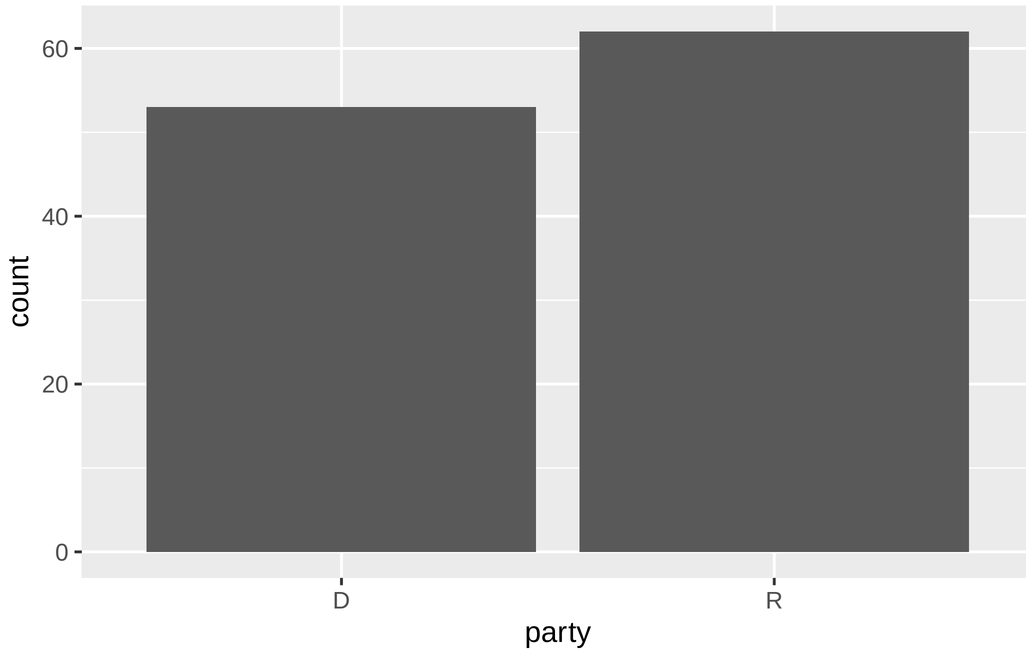
- A `ggplot()` command with a `data =` argument specifying a data frame and a `mapping = aes()` argument specifying "aesthetic mappings," i.e., how we want to use the columns in the data frame in the plot (for example, in the x-axis, as color, etc.).
- "geoms," such as `geom_bar()` or `geom_point()`, specifying what to draw on the plot.

So *all* `ggplot2` commands will have at least three elements: data, aesthetic mappings, and geoms.

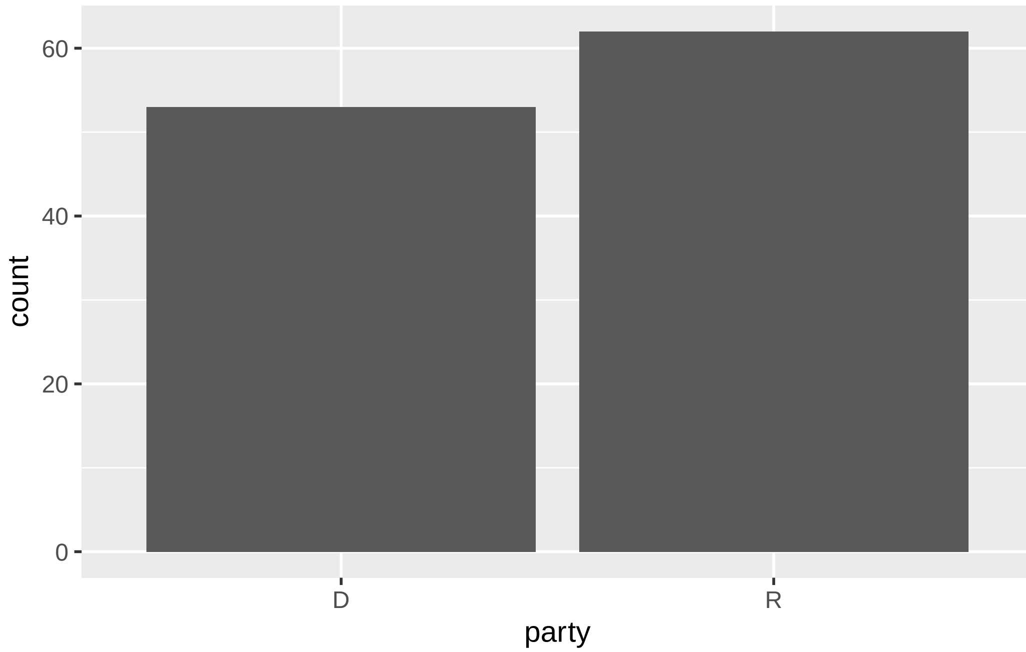
2.3.1 Univariate plots: categorical

Let's see an example of a bar plot with a categorical variable:

```
ggplot(data = trump_scores_ss, mapping = aes(x = party)) +
  geom_bar()
```

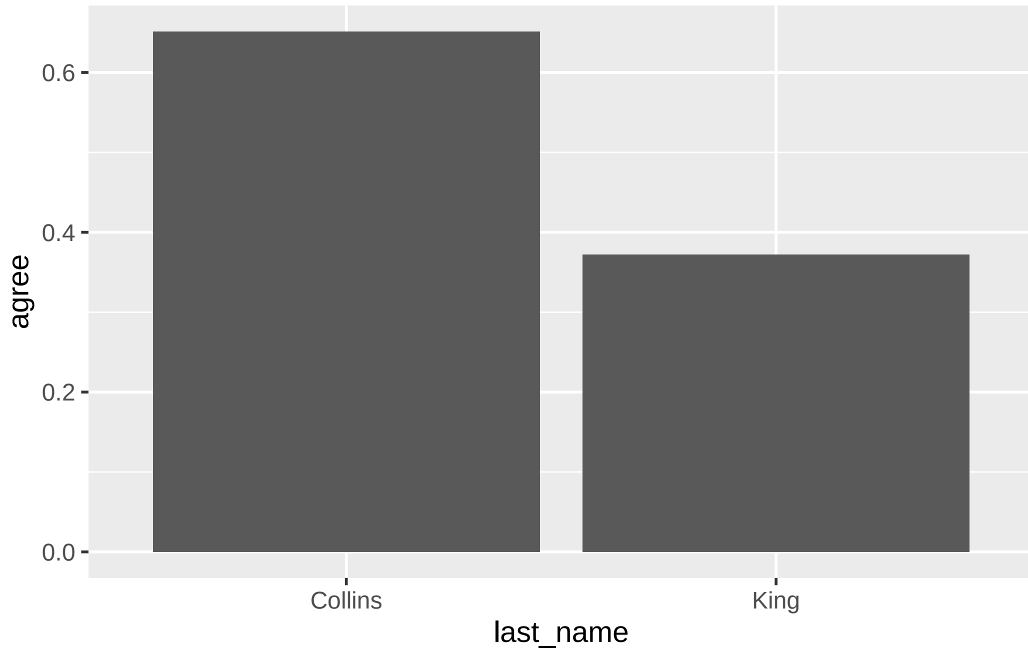


> **Tip**
>
> As with any other function, we can drop the argument names if we specify the argument values in order. This is common in `ggplot2` code:
>
> ```
> ggplot(trump_scores_ss, aes(x = party)) +
>   geom_bar()
> ```



Notice how `geom_bar()` automatically computes the number of observations in each category for us. Sometimes we want to use numbers in our data frame as part of a bar plot. Here we can use the `geom_col()` geom specifying both `x` and `y` aesthetic mappings, in which is sometimes called a "column plot:"

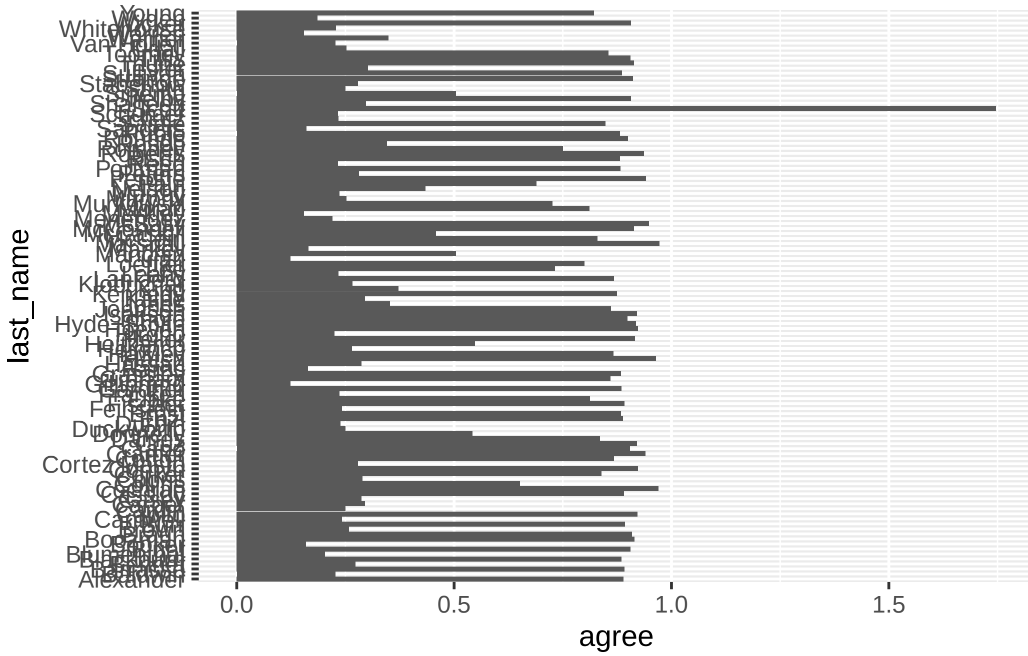
```
ggplot(trump_scores_ss |> filter(state == "ME"),
       aes(x = last_name, y = agree)) +
  geom_col()
```



> **Exercise**
>
> Draw a column plot with the agreement with Trump of Bernie Sanders and Ted Cruz. What happens if you use `last_name` as the `y` aesthetic mapping and `agree` in the `x` aesthetic mapping? Your code:

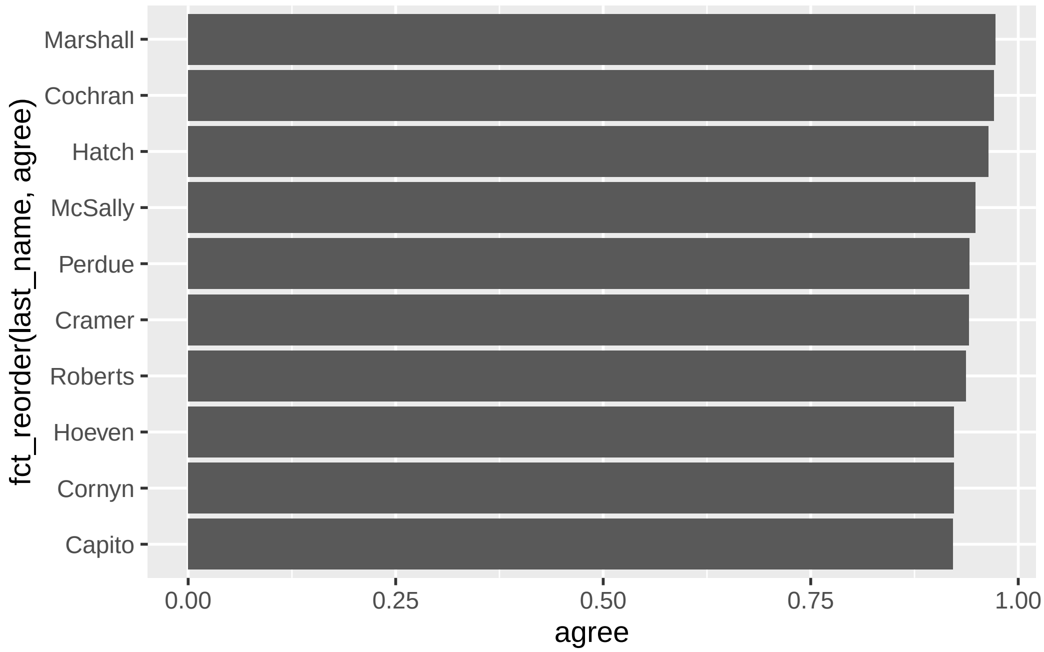
A common use of `geom_col()` is to create "ranking plots." For example, who are the senators with highest agreement with Trump? We can start with something like this:

```
ggplot(trump_scores_ss,
       aes(x = agree, y = last_name)) +
  geom_col()
```



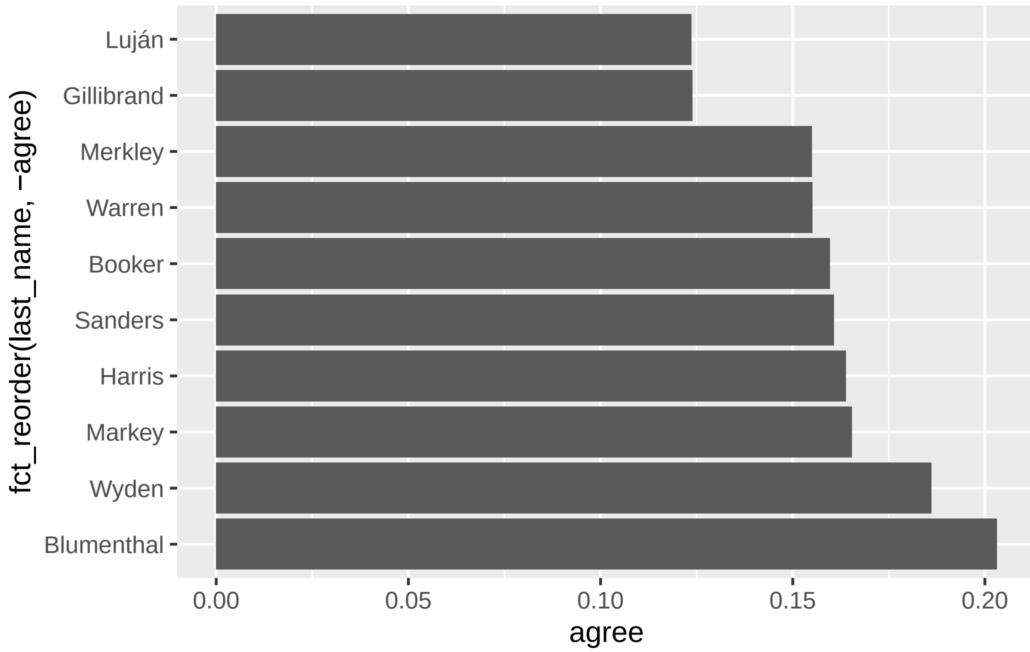
We might want to (1) select the top 10 observations and (2) order the bars according to the `agree` values. We can do these operations with `slice_max()` and `fct_reorder()`, as shown below:

```
ggplot(trump_scores_ss |> slice_max(agree, n = 10),
       aes(x = agree, y = fct_reorder(last_name, agree))) +
  geom_col()
```



We can also plot the senators with the *lowest* agreement with Trump using `slice_min()` and `fct_reorder()` with a minus sign in the ordering variable:

```
ggplot(trump_scores_ss |> slice_min(agree, n = 10),
       aes(x = agree, y = fct_reorder(last_name, -agree))) +
  geom_col()
```

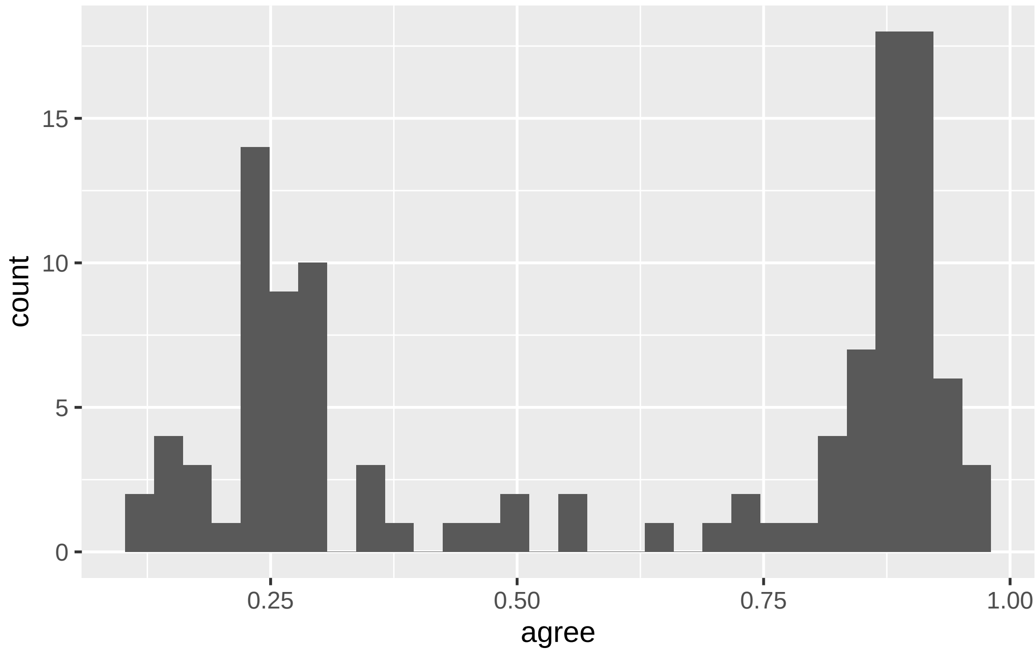


2.3.2 Univariate plots: numerical

We can draw a histogram with `geom_histogram()`:

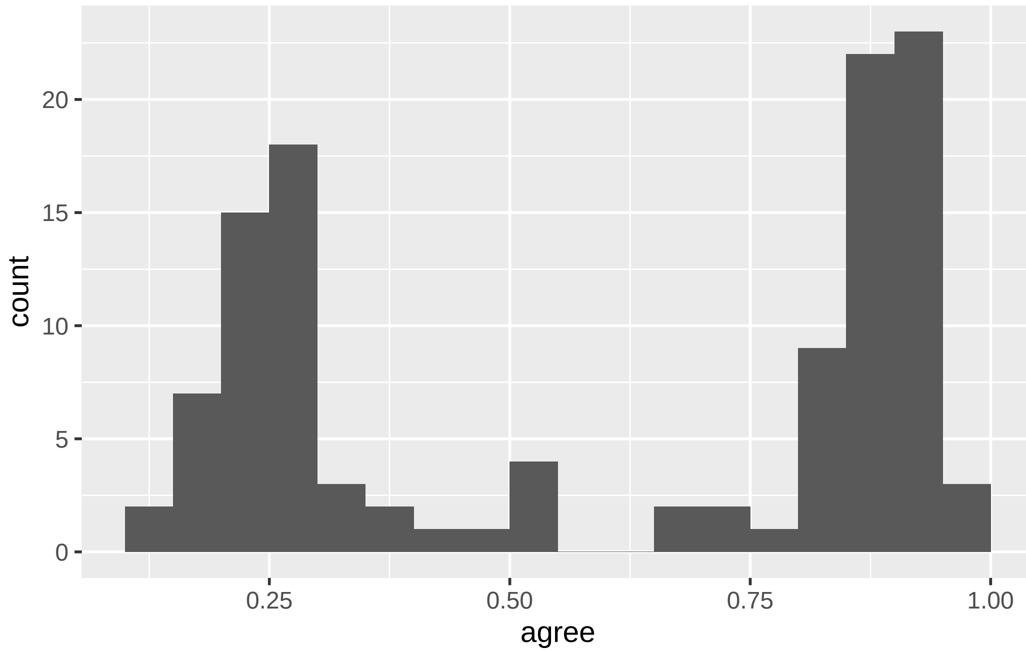
```
ggplot(trump_scores_ss, aes(x = agree)) +
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



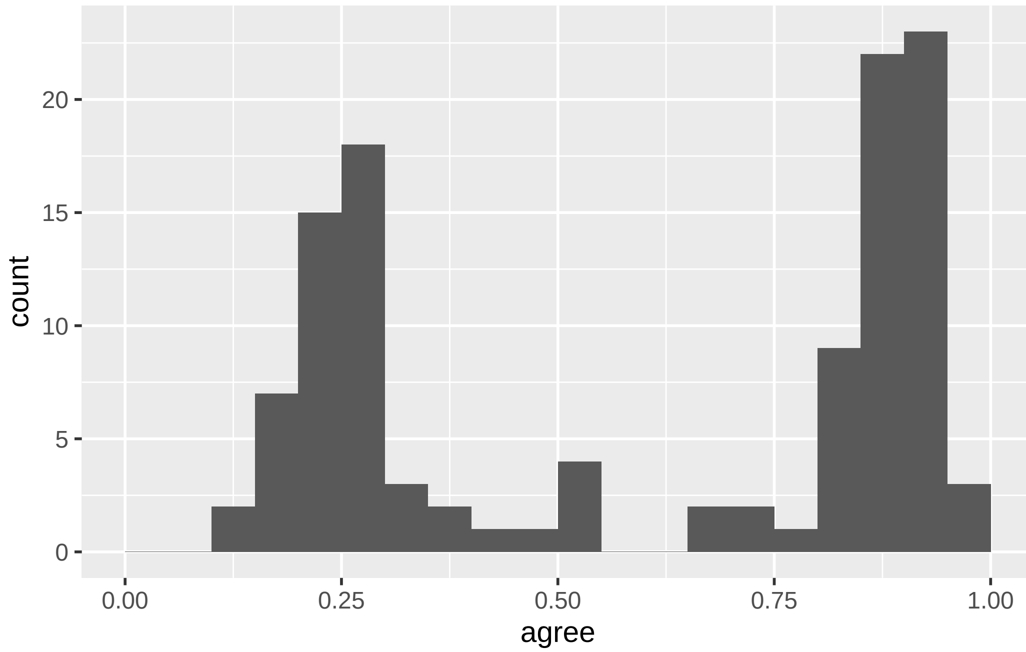
Notice the warning message above. It's telling us that, by default, `geom_histogram()` will draw 30 bins. Sometimes we want to modify this behavior. The following code has some common options for `geom_histogram()` and their explanations:

```
ggplot(trump_scores_ss, aes(x = agree)) +
  geom_histogram(binwidth = 0.05,   # draw bins every 0.05 jumps in x
                 boundary = 0,      # don't shift bins to integers
                 closed   = "left") # close bins on the left
```



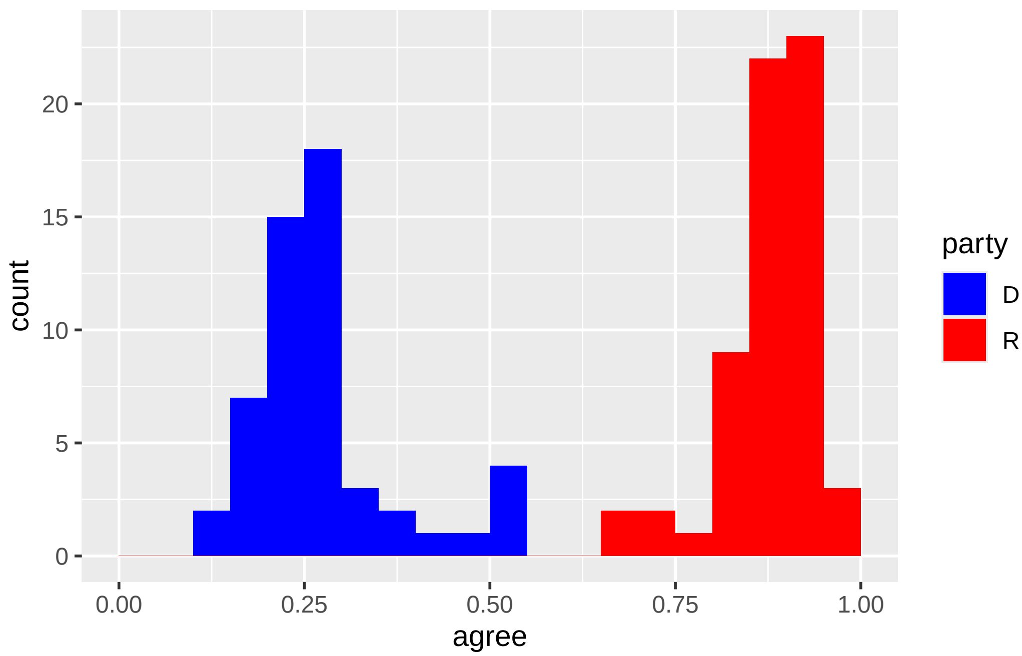
Sometimes we want to manually alter a scale. This is accomplished with the `scale_*()` family of `ggplot2` functions. Here we use the `scale_x_continuous()` function to make the x-axis go from 0 to 1:

```
ggplot(trump_scores_ss, aes(x = agree)) +
  geom_histogram(binwidth = 0.05, boundary = 0, closed   = "left") +
  scale_x_continuous(limits = c(0, 1))
```



Adding the `fill` aesthetic mapping to a histogram will divide it according to a categorical variable. This is actually a bivariate plot!

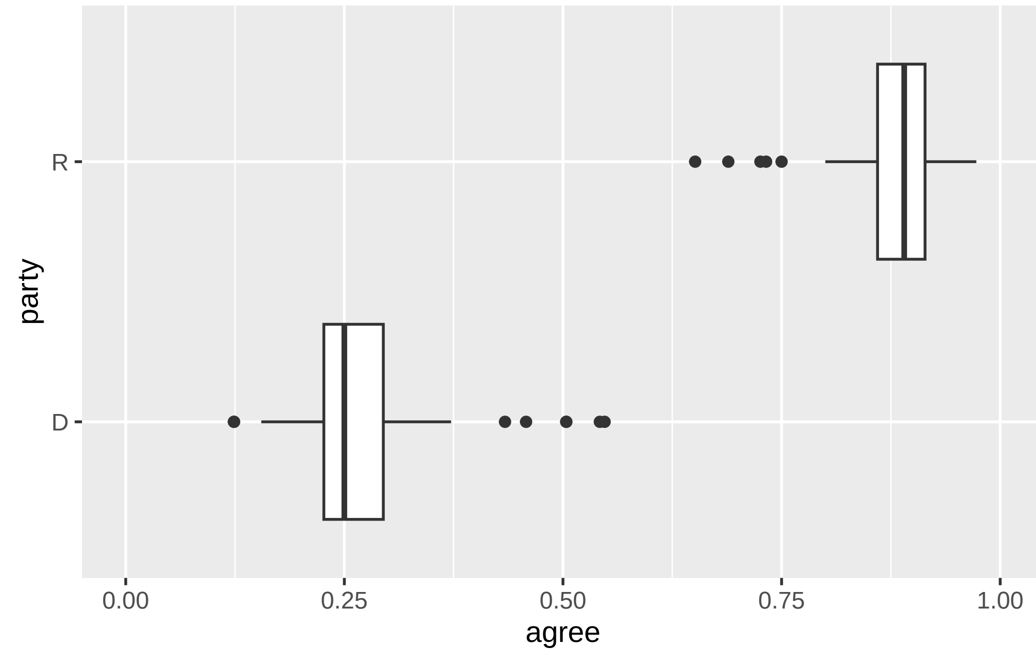
```
ggplot(trump_scores_ss, aes(x = agree, fill = party)) +
  geom_histogram(binwidth = 0.05, boundary = 0, closed   = "left") +
  scale_x_continuous(limits = c(0, 1)) +
  # change default colors:
  scale_fill_manual(values = c("D" = "blue", "R" = "red"))
```



2.3.3 Bivariate plots

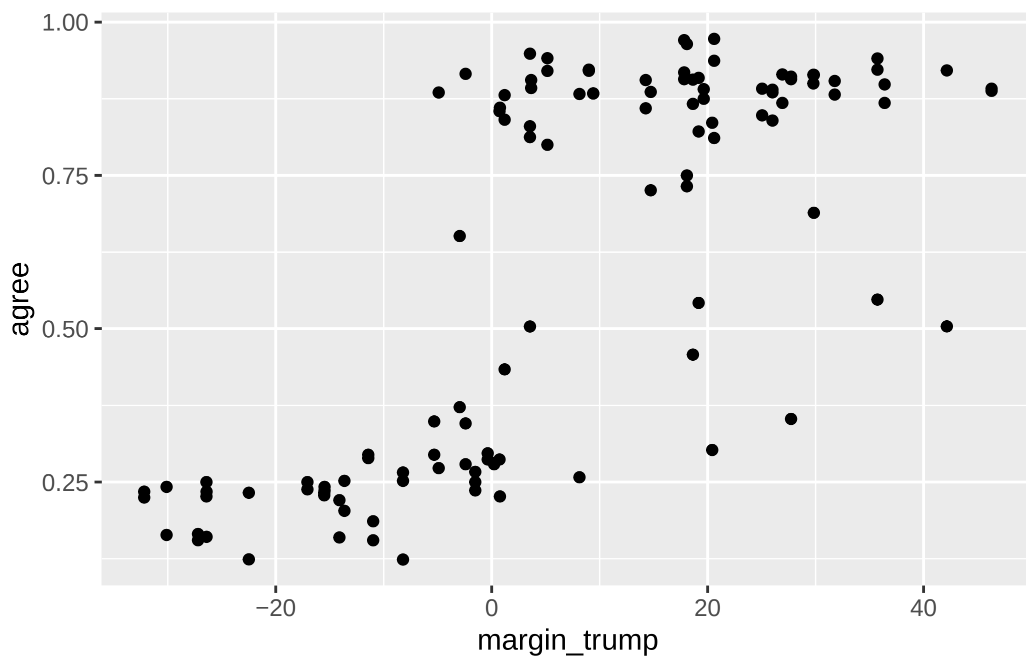
Another common bivariate plot for categorical and numerical variables is the grouped box plot:

```
ggplot(trump_scores_ss, aes(x = agree, y = party)) +
  geom_boxplot() +
  scale_x_continuous(limits = c(0, 1)) # same change as before
```



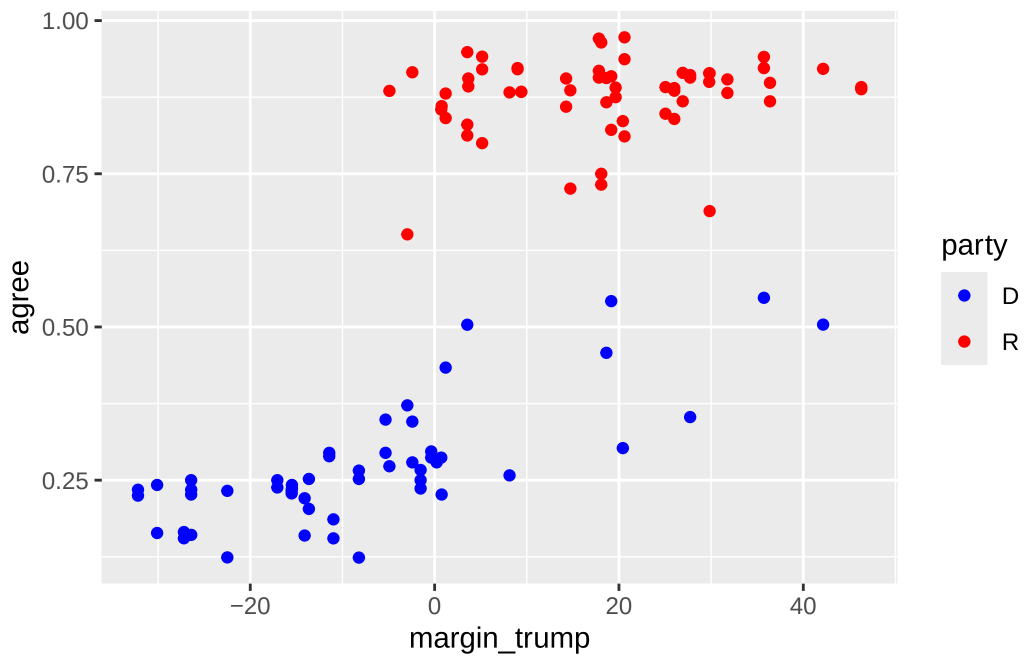
For bivariate plots of numerical variables, scatter plots are made with `geom_point()`:

```
ggplot(trump_scores_ss, aes(x = margin_trump, y = agree)) +
  geom_point()
```



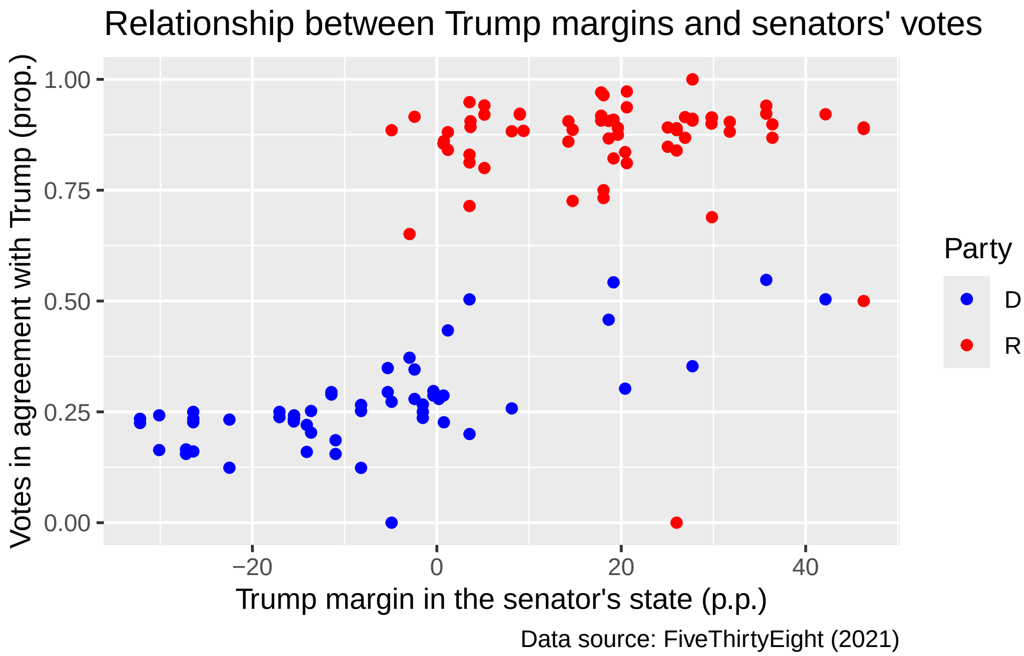
We can add the `color` aesthetic mapping to add a third variable:

```
ggplot(trump_scores_ss, aes(x = margin_trump, y = agree, color = party)) +
  geom_point() +
  scale_color_manual(values = c("D" = "blue", "R" = "red"))
```



Let's finish our plot with the `labs()` function, which allows us to add labels to our aesthetic mappings, as well as titles and notes:

```
ggplot(trump_scores, aes(x = margin_trump, y = agree, color = party)) +
  geom_point() +
  scale_color_manual(values = c("D" = "blue", "R" = "red")) +
  labs(x = "Trump margin in the senator's state (p.p.)",
       y = "Votes in agreement with Trump (prop.)",
       color = "Party",
       title = "Relationship between Trump margins and senators' votes",
       caption = "Data source: FiveThirtyEight (2021)")
```



We will review a few more customization options, including text labels and facets, in a subsequent module.

3 Functions

3.1 Basics

3.1.1 What is a function?

Informally, a function is anything that takes input(s) and gives one defined output. There are always three main parts:

- The input (x values, or each value in the domain)
- The relationship of interest
- The output (y values, or a unique value in the range)

Note

"$f(x) =$ ... is the classic notation for writing a function, but we can also use"$y =$ ...". This is because y is"a function of" x, so $y = f(x)$.

Let's take a look at an example and break down the structure:

$$f(x) = 3x + 4$$

- x is the *input* (some value) that the function takes.
- For any x, we multiply by three and add 4, which is the *relationship*.
- Finally, $f(x)$ or y is the unique result, or the *output*.

The most common name to give a function is, predictably, "f", but we can have other names such as "g" or "h". The choice is yours.

Important

When reading out loud, we say "[name of function] of x equals [relationship]. For example, $f(x) = x^2$ is referred to as"f of x equals x squared."

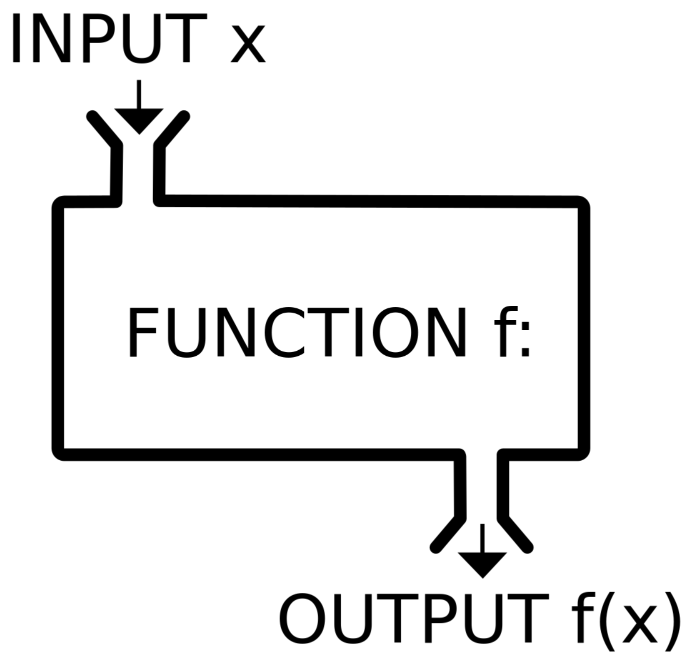


Figure 3.1: Function machine. Source: Bill Bailey on Wikimedia Commons.

3.1.2 Vertical line test

Exercise

When graphed, vertical lines cannot touch functions at more than one point. Why? Which of the following represent functions?

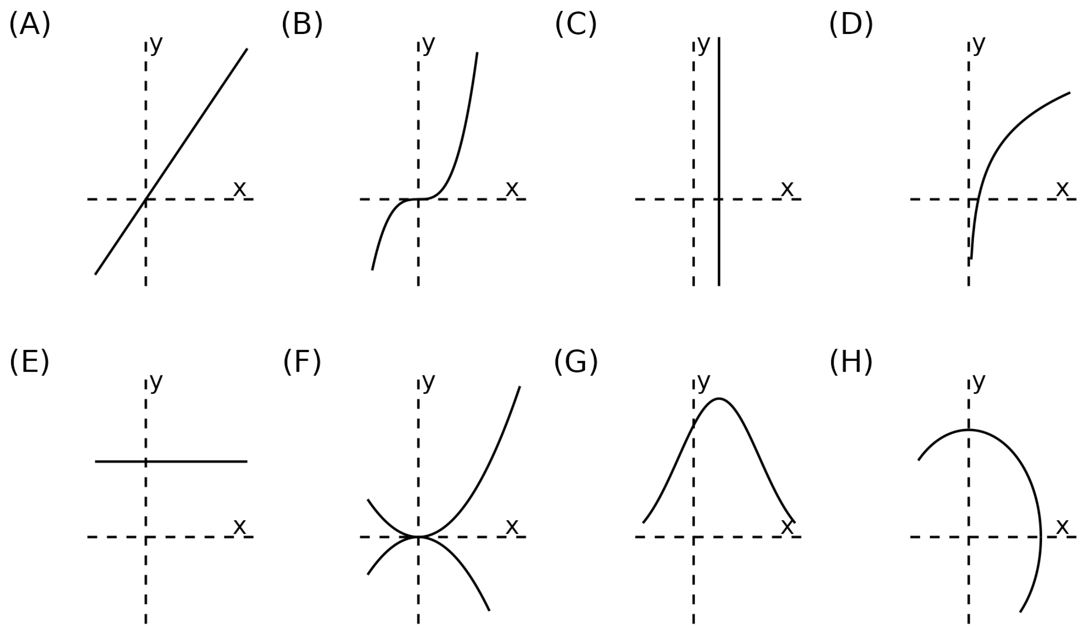


Figure 3.2: Vertical line test: examples.

3.2 Functions in R

Often we need to create our own functions in R. To build them: we use the keyword `function` alongside the following syntax: `function_name <- function(argumentnames){ operation }`

- `function_name`: the name of the function, that will be stored as an object in the R environment. Make the name concise and memorable!
- `function(argumentnames)`: the inputs of the function.
- `{ operation }`: a set of commands that are run in a predefined order every time we call the function.

For example, we can create a function that multiplies a number by 2:

```
mult_by_two <- function(x){x * 2}
```

```
mult_by_two(x = 5) # we can also omit the argument name (x =)
```

```
[1] 10
```

If the function body works for vectors, our custom function will do too:

```
mult_by_two(1:10)
```

```
 [1]  2  4  6  8 10 12 14 16 18 20
```

We can also automate more complicated tasks such as calculating the area of a circle from its radius:

```
circ_area_r <- function(r){
    pi * r ^ 2
}
circ_area_r(r = 3)
```

```
[1] 28.27433
```

> **Exercise**
>
> Create a function that calculates the area of a circle *from its diameter*. So `your_function(d = 6)` should yield the same result as the example above. Your code:

Functions can take more than one argument/input. In a silly example, let's generalize our first function:

```
mult_by <- function(x, mult){x * mult}
```

```
mult_by(x = 1:5, mult = 10)
```

```
[1] 10 20 30 40 50
```

```r
mult_by(1:5, mult = 10)
```

```
[1] 10 20 30 40 50
```

```r
mult_by(1:5, 10)
```

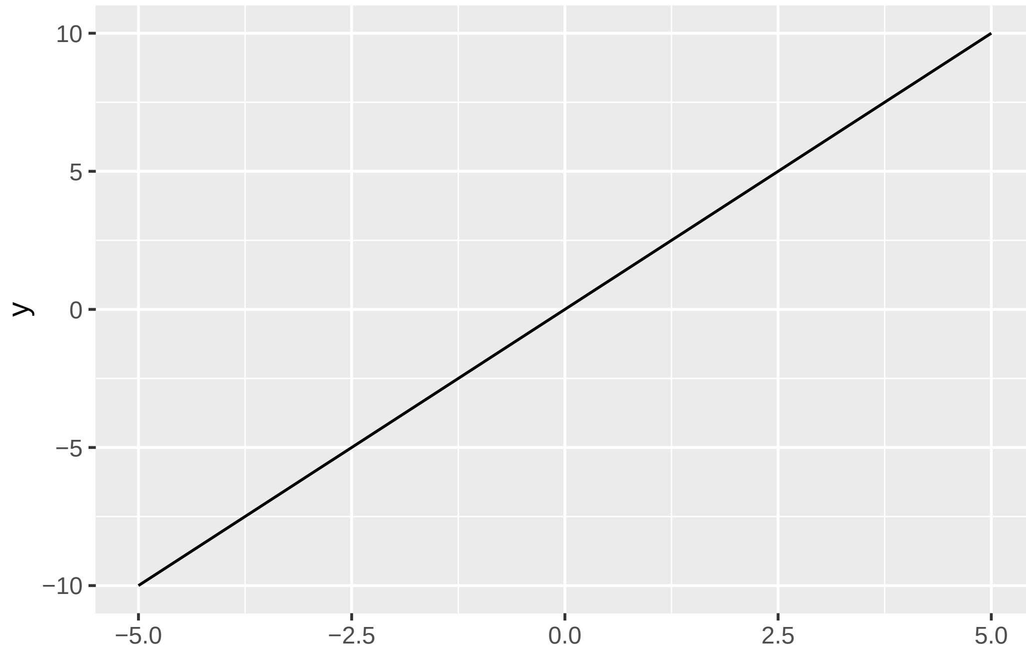
```
[1] 10 20 30 40 50
```

To graph a function, we'll use our friend `ggplot2` and `stat_function()`:

```r
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```r
ggplot() +
  stat_function(fun = mult_by_two,
               xlim = c(-5, 5)) # domain over which we will plot the function
```



User-defined functions have endless possibilities! We encourage you to get creative and try to automate new tasks when possible, especially if they are repetitive.

> **Tip**
>
> Functions in R can also take non-numeric inputs. For example:
>
> ```
> say_my_name <- function(my_name){paste("My name is", my_name)}
> ```
>
> ```
> say_my_name("Inigo Montoya")
> ```
>
> ```
> [1] "My name is Inigo Montoya"
> ```

3.3 Common types of functions

3.3.1 Linear functions

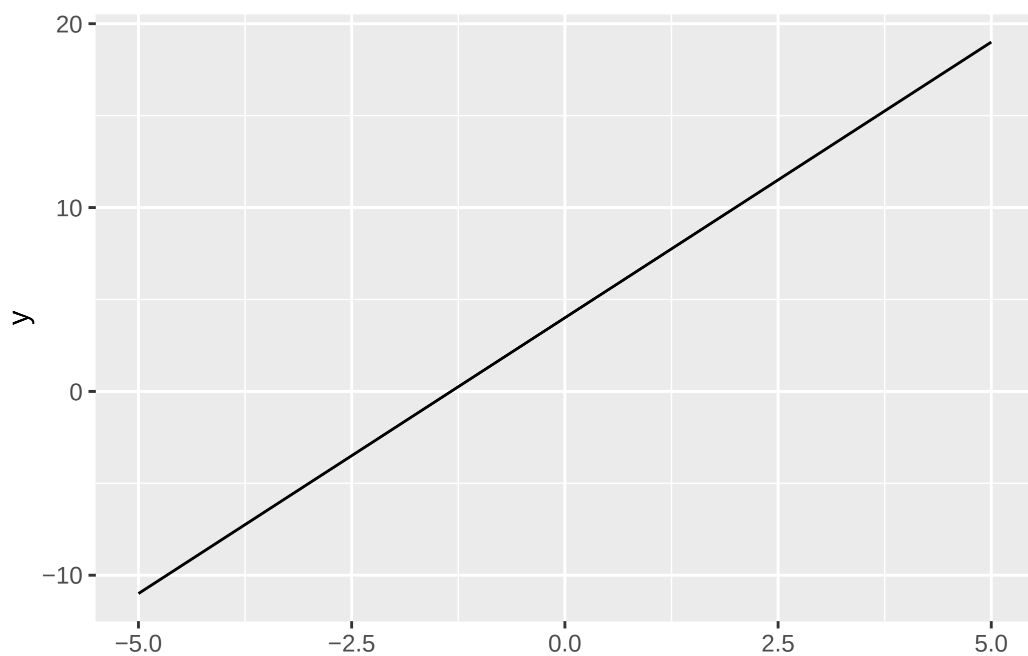
$$y = mx + b$$

Linear functions are those whose graph is a straight line (in two dimensions).

- m is the slope, or the rate of change (common interpretation: for every one unit increase in x, y increases m units).
- b is the y intercept, or the constant term (the value of y when $x = 0$).

Below is a graph of the function $y = 3x + 4$:

```
ggplot() +
  stat_function(fun = function(x){3 * x + 4}, # we don't need to create an object
                xlim = c(-5, 5))
```



3.3.2 Quadratic functions

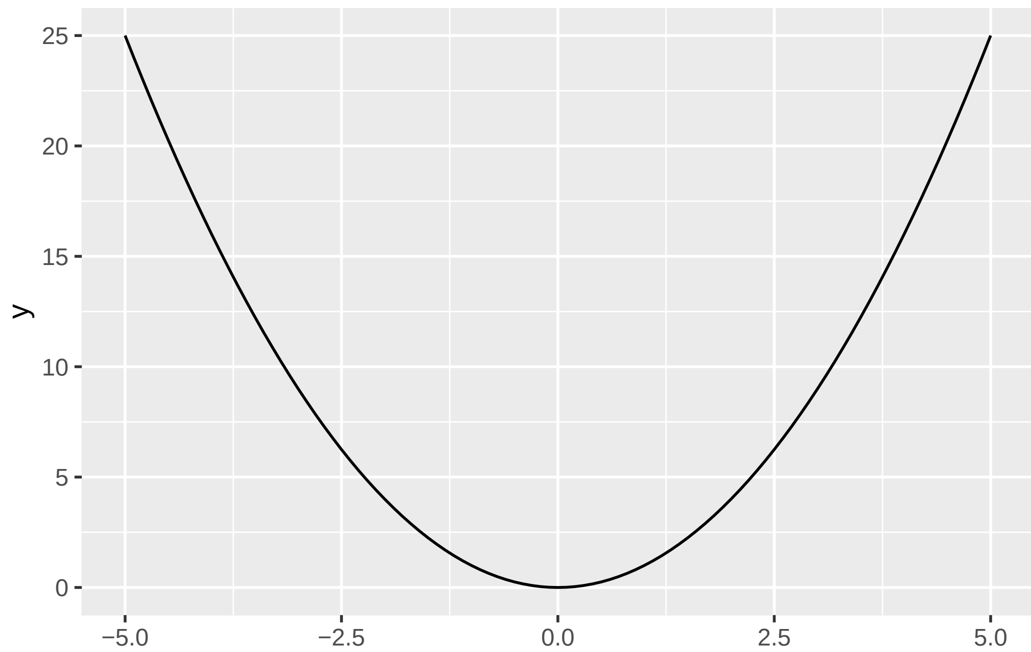
$$y = ax^2 + bx + c$$

Quadratic functions take "U" forms. If a is positive, it is a regular "U" shape. If a is negative, it is an "inverted U" shape.

Note that x^2 always returns positive values (or zero).

Below is a graph of the function $y = x^2$:

```r
ggplot() +
  stat_function(fun = function(x){x ^ 2},
                xlim = c(-5, 5))
```



Exercise

Social scientists commonly use linear or quadratic functions as theoretical simplifications of social phenomena. Can you give any examples?

Exercise

Graph the function $y = x^2 + 2x - 10$, i.e., a quadratic function with $a = 1$, $b = 2$, and $c = -10$.
Next, try switching up these values and the `xlim =` argument. How do they each alter the function (and plot)?

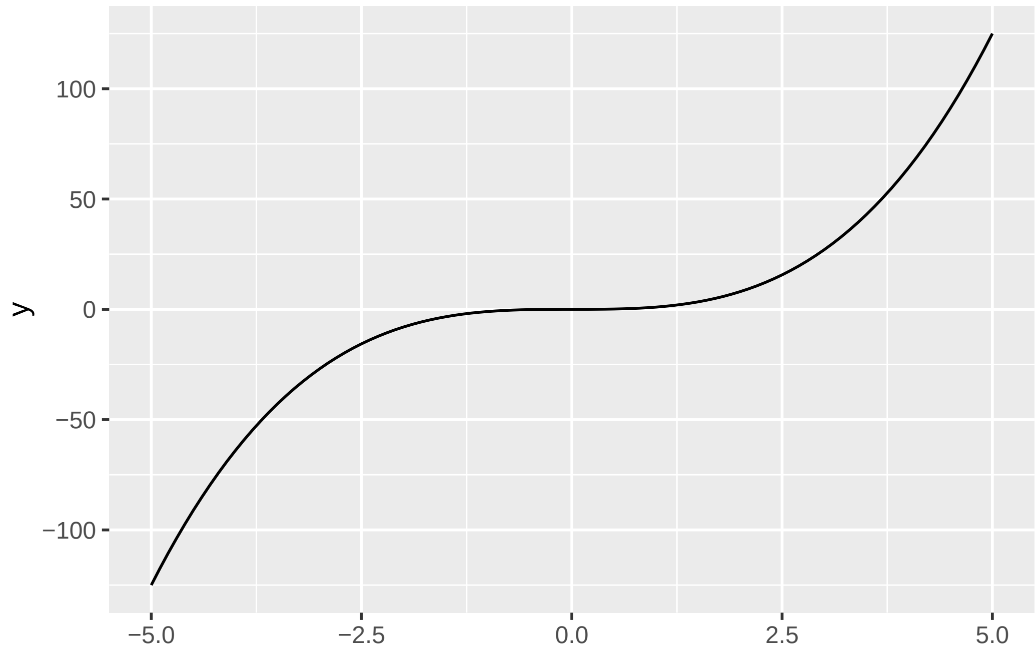
3.3.3 Cubic functions

$$y = ax^3 + bx^2 + cx + d$$

These lines (generally) have two curves (inflection points).

Below is a graph of the function $y = x^3$:

```
ggplot() +
  stat_function(fun = function(x){x ^ 3},
                xlim = c(-5, 5))
```



Exercise

We'll briefly introduce Desmos, an online graphing calculator. Use Desmos to graph the following function $y = 1x^3 + 1x^2 + 1x + 1$. What happens when you change the a, b, c, and d parameters?

3.3.4 Polynomial functions

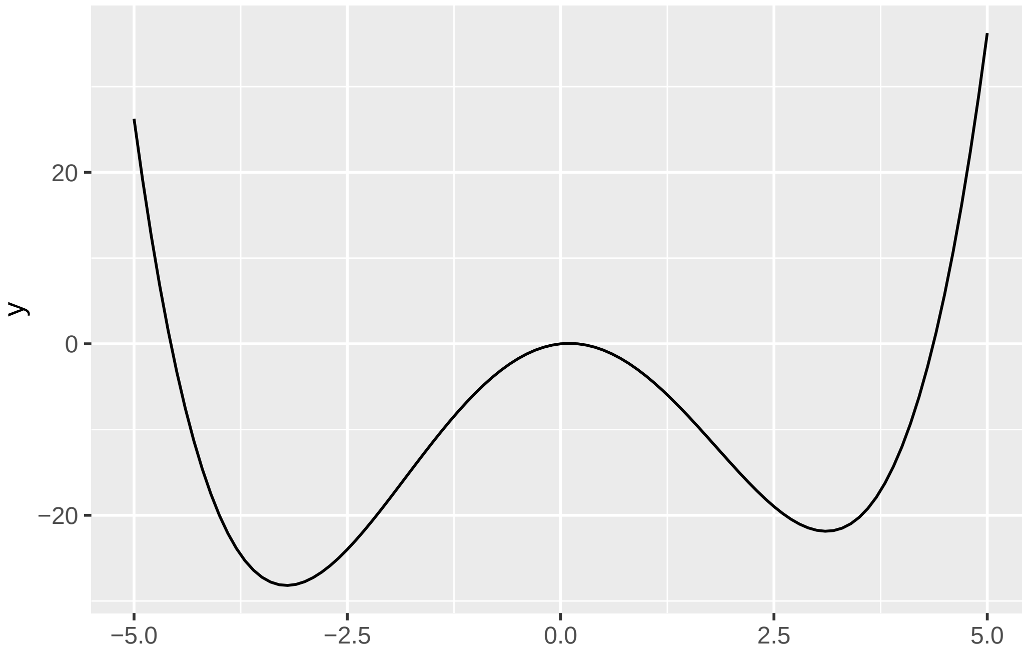
$$y = ax^n + bx^{n-1} + ... + c$$

These functions have (a maximum of) $n - 1$ changes in direction (turning points). They also have (a maximum of) n x-intercepts.

High-order polynomials can be made arbitrarily precise!

Below is a graph of the function $y = \frac{1}{4}x^4 - 5x^2 + x$.

```r
ggplot() +
  stat_function(fun = function(x){1/4 * x ^ 4 - 5 * x ^ 2 + x},
                xlim = c(-5, 5))
```



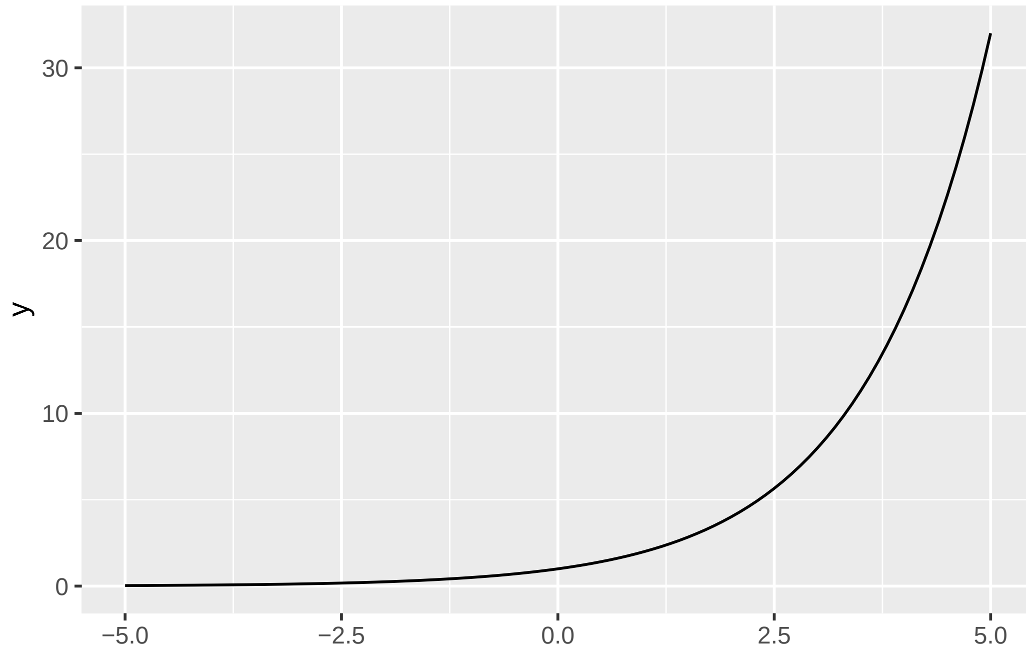
3.3.5 Exponential functions

$$y = ab^x$$

Here our input (x), is the exponent.

Below is a graph of the function $y = 2^x$:

```r
ggplot() +
  stat_function(fun = function(x){2 ^ x},
                xlim = c(-5, 5))
```



Exercise

Exponential *growth* appears quite frequently social science theories. Which variables can be theorized to have exponential growth over time?

3.4 Logarithms and exponents

3.4.1 Logarithms

Logarithms are the opposite/inverse of exponents. They ask how many times you must raise the base to get x.

So $log_a(b) = x$ is asking "a raised to what power x gives b?" For example, $\log_3(81) = 4$ because $3^4 = 81$.

Warning

Logarithms are *undefined* if the base is ≤ 0 (at least in the real numbers).

3.4.2 Relationships

If,

$$log_a x = b$$

then,

$$a^{log_a x} = a^b$$

and

$$x = a^b$$

3.4.3 Basic rules

- Change of Base rule: $\dfrac{\log_x n}{\log_x m} = \log_m n$
- Product Rule: $\log_x (ab) = \log_x a + \log_x b$
- Quotient Rule: $\log_x \left(\frac{a}{b}\right) = \log_x a - \log_x b$
- Power Rule: $\log_x a^b = b \log_x a$
- Logarithm of 1: $\log_x 1 = 0$
- Logarithm of the Base: $log_x x = 1$
- Exponential Identity: $m^{\log_m (a)} = a$

3.4.4 Natural logarithms

- We most often use natural logarithms for our purposes.
- This means $log_e(x)$, which is usually written as $ln(x)$.

> **!** Important
>
> $e \approx 2.7183$.

- $ln(x)$ and its exponent opposite, e^x, have nice properties when we perform calculus.

3.4.5 Illustration of e

Imagine you invest $1 in a bank and receive 100% interest for one year, and the bank pays you back once a year:

$$(1+1)^1 = 2$$

.

When it pays you twice a year with compound interest:

$$(1+1/2)^2 = 2.25$$

If it pays you three times a year:

$$(1+1/3)^3 = 2.37...$$

What will happen when the bank pays you once a month? Once a day?

$$(1+\frac{1}{n})^n$$

However, there is limit to what you can get.

$$\lim_{n\to\infty}(1+\frac{1}{n})^n = 2.7183... = e$$

For any interest rate k and number of times the bank pays you t:

$$\lim_{n\to\infty}(1+\frac{k}{n})^{nt} = e^{kt}$$

> e is important for defining *exponential growth*. Since $ln(e^x) = x$, the natural logarithm helps us turn exponential functions into linear ones.

Exercise

Solve the problems below, simplifying as much as you can.

$$log_{10}(1000)$$

$$log_2(\frac{8}{32})$$

$$10^{log_{10}(300)}$$

$$ln(1)$$

$$ln(e^2)$$

$$ln(5e)$$

3.4.6 Logarithms in R

By default, R's `log()` function computes natural logarithms:

```
log(100)
```

```
[1] 4.60517
```

We can change this behavior with the `base =` argument:

```
log(100, base = 10)
```

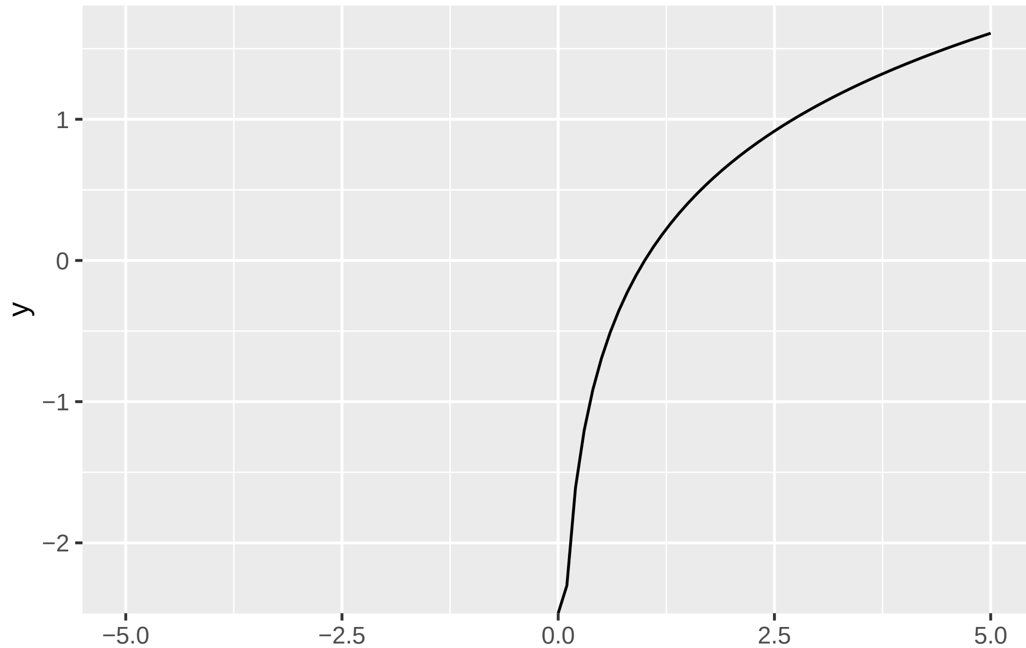
```
[1] 2
```

We can also plot logarithms. Remember that $ln(x)\ \forall x < 0$ is undefined (at least in the real numbers), and `ggplot2` displays a nice warning letting us know!

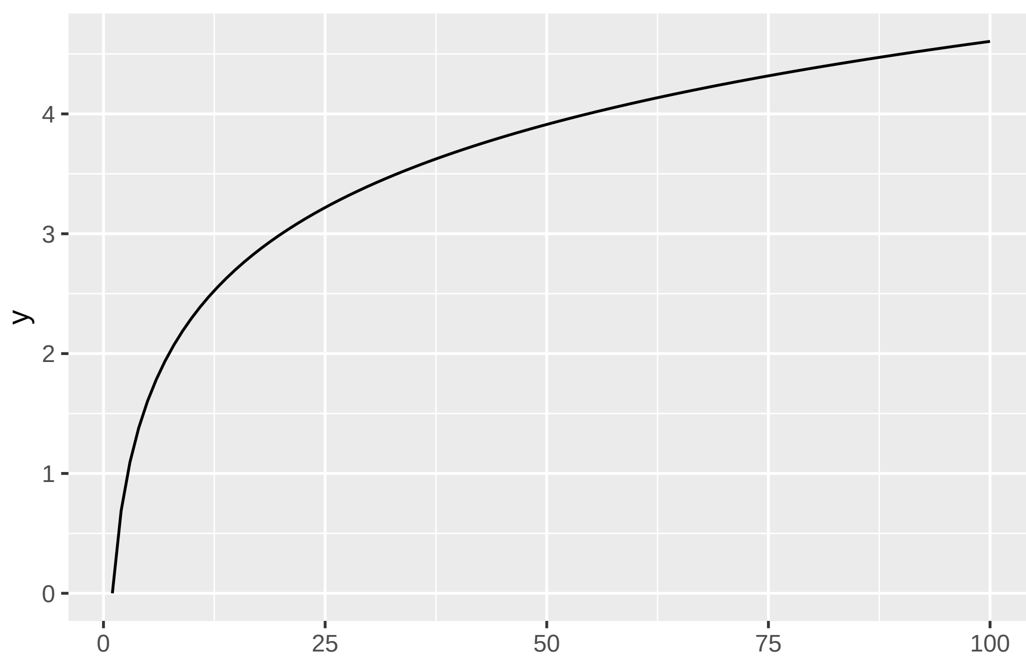
```
ggplot() +
  stat_function(fun = function(x){log(x)},
                xlim = c(-5, 5))
```

```
Warning in log(x): NaNs produced
```

```
Warning: Removed 50 rows containing missing values or values outside the scale range
(`geom_function()`).
```




```
ggplot() +
  stat_function(fun = function(x){log(x)},
                xlim = c(1, 100))
```



3.5 Composite functions (functions of functions)

Functions can take other functions as inputs, e.g., $f(g(x))$. This means that the outside function takes the output of the inside function as its input.

Say we have the exterior function

$$f(x) = x^2$$

and the interior function

$$g(x) = x - 3$$

.

Then if we want $f(g(x))$, we would subtract 3 from any input, and then square the result or

$$f(g(x)) = (x - 3)^2$$

.

> ⚠ Warning
>
> We write this as $(x - 3)^2$, not $x^2 - 3$!

R can handle this just fine:

```
f <- function(x){x ^ 2}
g <- function(x){x - 3}
```

```
f(g(5))
```

```
[1] 4
```

Here we can also use pipes to make this code more readable (imagine if we were chaining multiple functions…). Remember that pipes can be inserted with the `Cmd/Ctrl + Shift + M` shortcut.

```
# compute g(5), THEN f() of that
g(5) |> f()
```

```
[1] 4
```

Exercise

Compute `g(f(5))` using the definitions above. First do it manually, and then check your answer with R.

4 Calculus

In this section we'll focus on three big ideas from calculus: derivatives, optimization, and integrals.

4.1 Derivatives

Derivatives are about (instantaneous) rate of change.

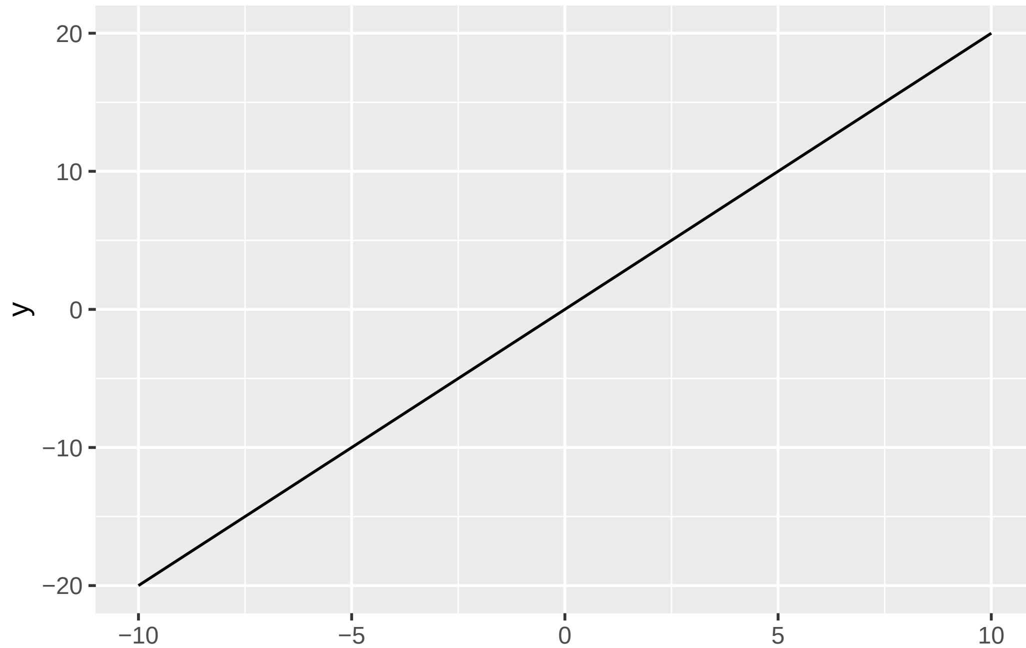
> "In the fall of 1972 President Nixon announced that the rate of increase of inflation was decreasing. This was the first time a sitting president used the third derivative to advance his case for reelection" (Rossi 1996)

Let's dissect what Nixon might have said:

> Inflation's [first derivative, of prices] rate of increase [second derivative] is going down [third derivative].

A more graphical way to think about a derivatives is as a *slope*. Let's consider a linear function of the form $y = 2x$:

```
library(tidyverse) # could also just do library(ggplot2)
ggplot() +
  stat_function(fun = function(x){2 * x},
                xlim = c(-10, 10))
```

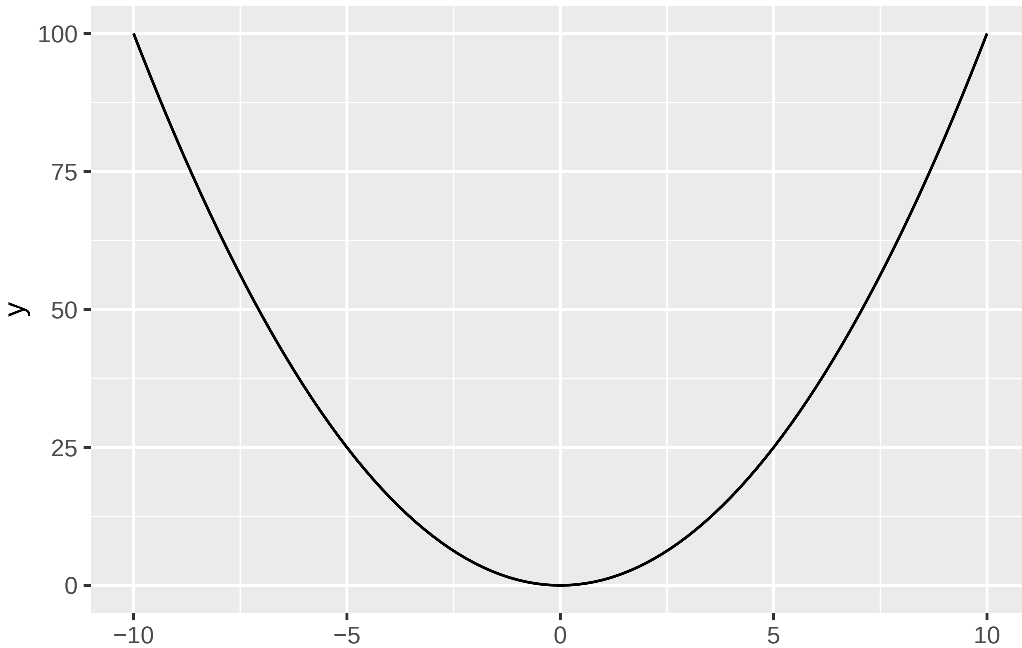


We can imagine any political variables in the x- and y-axes. What is the rate of change? In other words, what is the derivative? Remember that we can calculate the slope with:

$$m = \frac{f(x_2) - f(x_1)}{x_2 - x_1}$$

Now consider another slightly more complicated function, a quadratic one, $y = x^2$:

```
ggplot() +
  stat_function(fun = function(x){x ^ 2},
                xlim = c(-10, 10))
```



What happens when we apply our slope function?

> **Exercise**
>
> 1) Use the slope formula to calculate the rate of change between 5 and 6.
> 2) Use the slope formula to calculate the rate of change between 5 and 5.5.
> 3) Use the slope formula to calculate the rate of change between 5 and 5.1.

Takeaway: here the derivative depends on the value of x. It is actually $2x$.

Differential calculus is about finding these derivatives in a more straightforward manner! We can generalize our slope formula as follows:

$$m = \frac{f(x_1 + \Delta x) - f(x_1)}{\Delta x}$$

The point is that when Δx is arbitrarily small, we'll get our rate of change. Formalizing this:

$$\lim_{\Delta x \to 0} \frac{f(x_1 + \Delta x) - f(x_1)}{\Delta x} = \frac{d}{dx} f(x) = \frac{dy}{dx} = f'(x)$$

A few points on notation:

- $\frac{d}{dx}f(x)$ is read "The derivative of f of x with respect to x."
  - The variable with respect to which we're differentiating is the one that appears in the bottom (in the case above, this is x).

> **Warning**
>
> While the above looks like a fraction, it's really not. Do not try to cancel out the ds!

- $f'(x)$ (read: "f prime x") is the derivative of $f(x)$. This is a more compact form to refer to derivatives when you have defined $f(x)$ elsewhere.

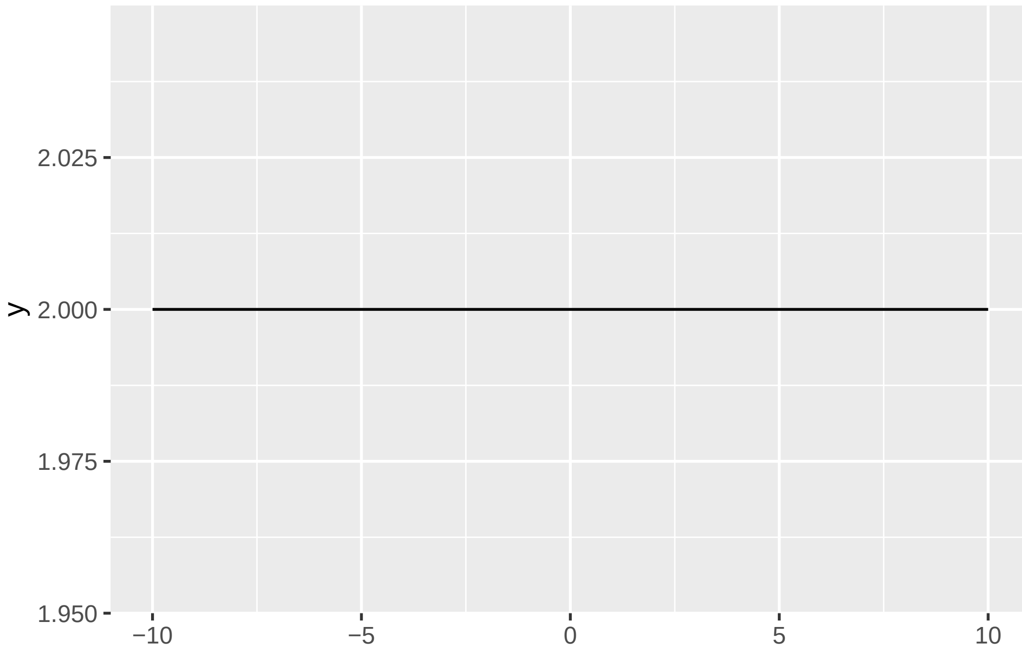
4.1.1 Rules of differentiation

How to compute derivatives? Sometimes you can try a bunch of numbers and get at the answer. Sometimes you can use the limit-based formula above, if you know a few properties of limits. But in most cases you will either use software (more on this later) or the **rules of differentiation**, which we will cover now.

Constant rule: $(c)' = 0$.

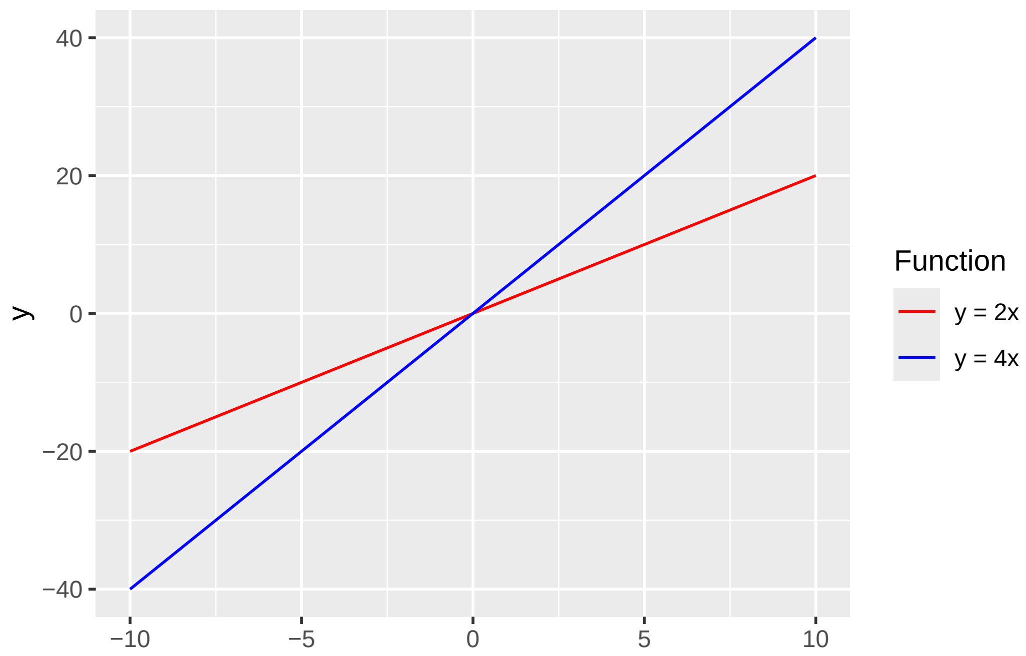
There is no change in a constant:

```
ggplot() +
  stat_function(fun = function(x){2}, xlim = c(-10, 10))
```



Coefficient rule: $(c \cdot f(x))' = c \cdot f'(x)$.

```
ggplot() +
  stat_function(fun = function(x){2 * x}, xlim = c(-10, 10), aes(color = "y = 2x")) +
  stat_function(fun = function(x){4 * x}, xlim = c(-10, 10), aes(color = "y = 4x")) +
  scale_color_manual("Function", values = c("red", "blue"))
```



Sum/difference rule: $(f(x) \pm g(x))' = f'(x) \pm g'(x)$.

The two rules above give us that the derivative is a *linear operator*.

Power rule: $(x^n)' = nx^{(n-1)}$

Remember when we wanted to calculate the derivative of $y = x^2$ above? We can use the power rule, with $n = 2$: $nx^{(n-1)} = 2x^{(2-1)} = 2x$. Let's try out $\frac{d}{dx}4x^3$ and $\frac{d}{dx}(x^2 + 2x)$ on the board.

> **Exercise**
>
> Use the differentiation rules we have covered so far to calculate the derivatives of y with respect to x of the following functions:
>
> 1) $y = 2x^2 + 10$
> 2) $y = 5x^4 - \frac{2}{3}x^3$
> 3) $y = 9\sqrt{x}$
> 4) $y = \frac{4}{x^2}$
> 5) $y = ax^3 + b$, where a and b are constants.
> 6) $y = \frac{2w}{5}$

Exponent and logarithm rules:

$$(c^x)' = c^x \cdot ln(c), \quad \forall x > 0$$
$$(e^x)' = e^x$$

$$(log_a(x))' = \frac{1}{x \cdot ln(a)}, \quad \forall x > 0$$
$$(ln(x))' = \frac{1}{x}, \quad \forall x > 0$$

We saw previously how Euler's number (e) arises from compound interest. The properties above make it very useful in a lot of calculus applications!

> **Exercise**
>
> Compute the following:
>
> 1) $\frac{d}{dx}(10e^x)$
> 2) $\frac{d}{dx}(ln(x) - \frac{e^2}{3})$

Now we'll get to a couple of more advanced (and powerful) rules.

- **Product rule:** $(f(x)g(x))' = f'(x)g(x) + g'(x)f(x)$
- **Quotient rule:** $(\dfrac{f(x)}{g(x)})' = \dfrac{f'(x)g(x) + g'(x)f(x)}{[g(x)]^2}$
- **Chain rule:** $(f(g(x))' = f'(g(x)) \cdot g'(x)$

  Let's calculate $\frac{d}{dx}(3 \cdot ln(x) \cdot x^2)$ on the board.

  Let's compute $\frac{d}{dx}(e^{x^2})$ on the board.

> **Exercise**
>
> Use the differentiation rules we have covered so far to calculate the derivatives of y with respect to x of the following functions:
>
> 1) $x^3 \cdot x$
> 2) $e^x \cdot x^2$
> 3) $(3x^4 - 8)^2$

4.1.2 Higher-order derivatives

We saw how politicians can refer to higher-order derivatives. To compute them, you simply "pass the outputs," starting from the lowest order and going up.

The second derivative tells us whether the slope of a function is increasing, decreasing, or staying the same at any point x on the function's domain. For example, when driving a car:

- $f(x)$ = distance traveled at time x
- $f'(x)$ = speed at time x
- $f''(x)$ = acceleration at time x

Let's compute the following second derivative:

$$f''(x^4) = \frac{d^2(x^4)}{dx^2}$$

- First, we take the first derivative: $f'(x^4) = 4x^3$
- Then we use that output to take the second derivative: $f''(x^4) = f'(4x^3) = 12x^2$
- We can keep going… for example, the third derivative:

$$f'''(x^4) = f'(12x^2) = 24x$$

Exercise

Compute the following:

1) $\frac{d^3}{dx^3}(x^5)$
2) $f''(4x^{3/2})$
3) $f''(4 \cdot ln(x))$

4.1.3 Partial derivatives

For a function $f(x, z)$, we might want to know how the function changes with respect to x. We call this a *partial derivative*:

$$\frac{\partial}{\partial_x} f(x, z) = \frac{\partial_y}{\partial_x} = \partial_x f$$

To obtain a partial derivative, we treat all other variables as constants and take the derivative with respect to the variable of interest (here x). For example:

$$y = f(x,z) = xz$$
$$\frac{\partial_y}{\partial_x} = z$$

What is $\frac{\partial_y}{\partial_z}$?

Let's solve $\frac{\partial(x^2y + xy^2 - x)}{\partial x}$ and $\frac{\partial(x^2y + xy^2 - x)}{\partial y}$ on the board.

Example

Let's say that y is how much I like a movie, d is how many dogs a movie has, and e is how many explosions a movie has. I claim that how much I like a movie can be expressed by a function of the type $y = f(d,e)$. Evaluate the following situations:

1. I like dogs and I don't care about action. So I believe that the true relationship is $y = f(d,e) = 3 \cdot d$. What is $\frac{\partial_y}{\partial_d}$, and how can we interpret it?
2. I like dogs and I like action. So I believe that the true relationship is $y = f(d,e) = 3 \cdot d + 1 \cdot e$. What is $\frac{\partial_y}{\partial_d}$, and how can we interpret it?
3. I like dogs and I like action. *But I definitely don't like them together*—I don't want the dogs to be in danger! So I believe that the true relationship is $y = f(d,e) = 3 \cdot d + 1 \cdot e - 10 \cdot d \cdot e$. What is $\frac{\partial_y}{\partial_d}$, and how can we interpret it?

Exercise

Take the partial derivative with respect to x and with respect to z of the following functions. What would the notation for each look like?

1) $y = 3xz - x$
2) $x^3 + z^3 + x^4z^4$
3) e^{xz}

4.1.4 Differentiability of functions

Not all functions are differentiable at every point of their domains!

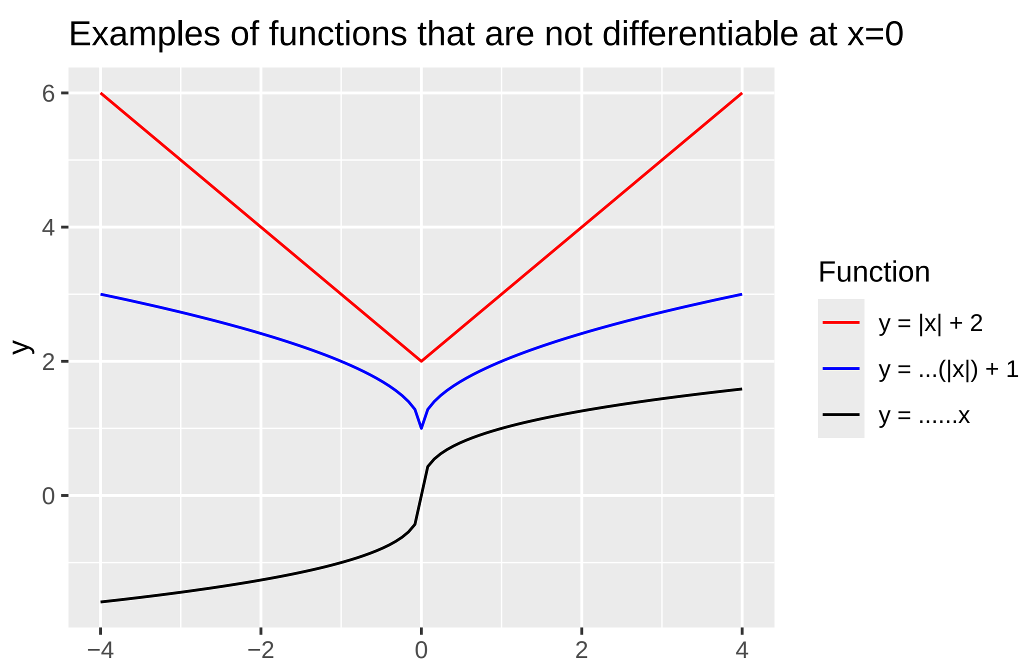
An important concept here is whether functions are **continuous** at a point:

- Informally: A function is continuous at a point if its graph has no holes or breaks at that point
- Formally: A function is continuous at a point a if: $\lim_{x \to a} f(x) = f(a)$

When is a function **differentiable** at a point?

- If a function is differentiable at a point, it is also continuous at that point.
- If a function is continuous at a point, it is *not* necessarily differentiable at that point.
    - Impossible to calculate derivative at sharp turns, cusps, or vertical tangents.

```
ggplot() +
  stat_function(fun = function(x){abs(x) + 2}, xlim = c(-4, 4),
                aes(color = "y = |x| + 2")) +
  stat_function(fun = function(x){sqrt(abs(x)) + 1}, xlim = c(-4, 4),
                aes(color = "y = √(|x|) + 1")) +
  stat_function(fun = function(x){sign(x) * abs(x)^(1 / 3)}, xlim = c(-4, 4),
                aes(color = "y = ∛x")) +
  scale_colour_manual("Function", values = c("red", "blue", "black")) +
  labs(title = "Examples of functions that are not differentiable at x=0")
```



Informally, functions need to be continuous and reasonably smooth to be differentiable.

4.1.5 How do computers calculate derivatives?

In quite a few statistics and machine learning problems, computers need to compute derivatives of arbitrarily complex functions, perhaps millions of times. How do they do it? (see Baydin et al. 2018 for discussion of these three approaches)

- Symbolic differentiation: automatically combine the rules of differentiation (power rule, product rule, etc.). It is what math solvers use, e.g., WolframAlpha or (presumably) Symbolab.
- Numerical differentiation: infer the derivative by computing the function at different sample values (like we did with $y = x^2$ before. This is what, for example, R's `optim()` function does behind the scenes.

```r
# minimize the x^2 + 5 function:
optim(par = 0, fn = function(x){x ^ 2 + 5}, method = "L-BFGS-B")
```

```
$par
[1] 0

$value
[1] 5

$counts
function gradient
       1        1

$convergence
[1] 0

$message
[1] "CONVERGENCE: NORM OF PROJECTED GRADIENT <= PGTOL"
```

- Automatic differentiation: track how every function is constructed from (differentiable) elementary computer operations (e.g., binary arithmetic), and get the result using the chain rule. Implemented in the `torch` R package, the `TensorFlow`, `PyTorch`, and `JAX` Python libraries, and the `ReverseDiff.jl` and `Zygote.jl` Julia packages.

```
julia> function pow(x, n)
         r = 1
         for i = 1:n
           r *= x
         end
         return r
       end
pow (generic function with 1 method)

julia> gradient(x -> pow(x, 3), 5)
(75.0,)

julia> pow2(x, n) = n <= 0 ? 1 : x*pow2(x, n-1)
pow2 (generic function with 1 method)

julia> gradient(x -> pow2(x, 3), 5)
(75.0,)
```

Figure 4.1: An example of computing the gradient of an esoteric function using Zygote.jl (from its documentation)

4.2 Optimization

Optimization allows us to find the minimum or maximum values (or *extrema*) a function takes. It has many applications in the social sciences:

- Formal theory: utility maximization, continuous choices
- Ordinary Least Squares (OLS): Focuses on *minimizing* the squared errors between observed data and model-estimated values
- Maximum Likelihood Estimation (MLE): Focuses on *maximizing* a likelihood function, given observed values.

4.2.1 Extrema

On **extrema**: informally, a maximum is just the highest value a function takes, and a minimum is the lowest value.

In some situations, it can be easy to identify extrema intuitively by looking at a graph of the function.

- Maxima are high points ("peaks")
- Minima are low points ("valleys")

We can use derivatives (rates of change!) to get at extrema.

4.2.2 Critical points and the First-Order Condition

At critical points (or stationary points), the derivative is zero or fails to exist. At these, the function has *usually* reached a (local) maximum or minimum.

- At a maximum, the function must be increasing before the point and decreasing after it.
- At a minimum, the function must be decreasing before the point and increasing after it.

> ⚠ Warning
>
> Local extrema occur at critical points, but not all critical points are extrema. For instance, sometimes the graph is changing between concave and convex ("inflection points"). Or sometimes the function is not differentiable at that point for other reasons.

We can find the local maxima and/or minima of a function by taking the derivative, setting it equal to zero, and solving for x (or whatever variable). This gives us the First-Order Condition (FOC).

$$FOC : f'(x) = 0$$

4.2.3 Second-Order Condition

Notice that after this we only know that there is a critical point. **BUT** we don't know if we've found a maximum or minimum, or even if we've found an extremum.

To determine whether a we are seeing a (local) maximum or minimum, we can use the **Second Derivative Test**:

- Start by identifying $f''(x)$

- Substitute in the stationary points (x^*) identified from the FOC.
  - $f''(x^*) > 0$ we have a local minimum
  - $f''(x^*) < 0$ we have a local maximum
  - $f''(x^*) = 0$ we (may) have an inflection point - need to calculate higher-order derivatives (don't worry about this now)

Collectively these give us the **Second-Order Condition (SOC)**.

Let's do this procedure and obtain the FOC and SOC for $y = \frac{1}{2}x^3 + 3x^2 - 2$ on the board. What do we learn? Compare this with the plot of the function on Desmos.

4.2.4 Local or global extrema?

Now when it comes to knowing whether extrema are local or global:

- Here we use the **Extreme value theorem**, which states that if a real-valued function is continuous on a closed and bounded (i.e., finite) interval, the function must have a global minimum and a global minimum on that interval at least once. Importantly, in this situation the global extrema exist, and **they are either at the local extrema or at the boundaries** (where we cannot even find critical points).
- So to find the minimum/maximum on some interval, compare the local min/max to the value of the function at the interval's endpoints. So, e.g., if the interval is $(-\infty, +\infty)$, check the function's limits as it approaches $-\infty$ and $+\infty$.

Let's try this last step for our example above, $y = \frac{1}{2}x^3 + 3x^2 - 2$, to get the global extrema in the entire domain.

> **Exercise**
>
> Identify the global extrema of the function $\frac{x^3}{3} - \frac{3}{2}x^2 - 10x$ in the interval $[-6, 6]$.

4.3 Integrals

Informally, we can think of integrals as the flip side of derivatives.

We can motivate integrals as a way of finding the area under a curve. Sometimes finding the area is easy. What's the area under the curve between $x = -1$ and $x = 1$ for this function?

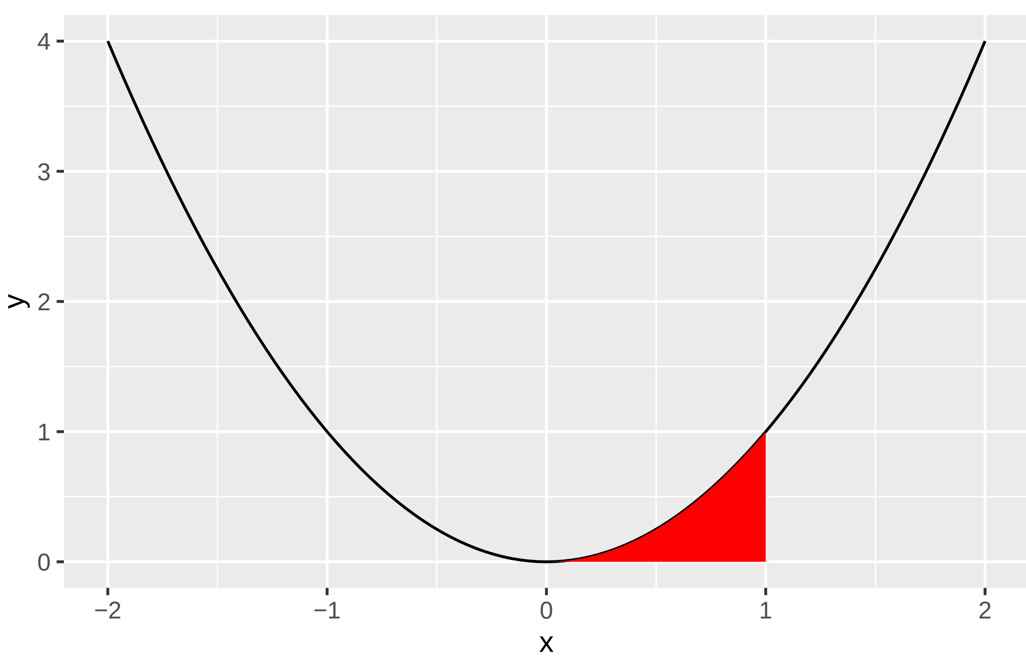
$$f(x) = \begin{cases} \frac{1}{3} & \text{for } x \in [0, 3] \\ 0 & \text{otherwise} \end{cases}$$

Normally, finding the area under a curve is much harder. But this is basically the question behind integration.

4.3.1 Integrals are about infinitesimals too

Let's say we have a function $y = x^2$ And we want to find the area under the curve from $x = 0$ to $x = 1$. How would we do this?

```
ggplot() +
  # draw main function
  stat_function(fun = function(x){x ^ 2}, xlim = c(-2, 2)) +
  # fill area under the curve between x = 0 and x = 1
  geom_area(mapping = aes(x = 0), stat = "function",
            fun = function(x){x ^ 2}, xlim = c(0, 1), fill = "red")
```



One way to approximate this area is by drawing narrow rectangles that cover the area in red. Let's draw this on the board.

Our approximation is rough, but it gets better and better the narrower the rectangles are:

$$Area = lim_{\Delta x \to 0} \sum_{i}^{n} f(x) \cdot \Delta x$$

, where Δx is the width of the rectangles and n is their number.

This is actually one way to define the **definite integral**, $\int_a^b f(x)dx$ (also known as the Riemann integral). We'll learn how to compute these in a few moments.

4.3.2 Indefinite integrals as antiderivatives

The **indefinite integral**, also known as the **antiderivative**, $F(x)$ is the inverse of the function $f'(x)$.

$$F(x) = \int f(x)\ dx$$

This means if you take the derivative of $F(x)$, you wind up back at $f(x)$.

$$F' = f \text{ or } \frac{dF(x)}{dx} = f(x)$$

For example, what is the antiderivative for a constant function $f(x) = 1$? Is there just one? (this example comes from Moore and Siegel, 2013, p. 137).

This process is called *anti-differentiation*. We can use this concept to help us solve definite integrals!

4.3.3 Solving definite integrals

One way to calculate definite integrals, known as the "fundamental theorem of calculus," is shown below:

$$\int_a^b f(x)\ dx = F(b) - F(a) = F(x)\Big|_a^b$$

First we determine the antiderivative (indefinite integral) of $f(x)$ (and represent it $F(x)$), substitute the upper limit first and then the lower limit one by one, and subtract the results in order.

> **Warning**
>
> C in the following definitions and rules is the called the "constant of integration." We need to add it when we define *all* antiderivatives (integrals) of a function because the anti-derivative "undoes" the derivative.
> Remember that the derivative of any constant is zero. So if we find an integral $F(x)$ whose derivative is $f(x)$, adding (or subtracting) any constant will give us another integral $F(x) + C$ whose derivative is *also* $f(x)$.

4.3.4 Rules of integration

Many of the rules of integetration have counterparts in differentiation.

Coefficient rule: $\int cf(x)\,dx = c\int f(x)\,dx$

Sum/difference rule: $\int (f(x) \pm g(x))\,dx = \int f(x)\,dx \pm \int g(x)\,dx$

Constant rule: $\int c\,dx = cx + C$

Power rule: $\int x^n\,dx = \frac{x^{n+1}}{n+1} + C \qquad \forall n \neq -1$

Reciprocal rule: $\int \frac{1}{x}\,dx = \ln(x) + C$

Exponent and logarithm rules:

$$\int e^x\,dx = e^x + C$$
$$\int c^x\,dx = \frac{c^x}{ln(c)} + C$$

$$\int ln(x)\,dx = x \cdot ln(x) - x + C$$
$$\int log_c(x)\,dx = \frac{x \cdot log_c(x) - x}{log_c(x)} + C$$

The final two rules are analog to the product rule and the chain rule:

Integration by parts: $\int f(x)g'(x)\,dx = f(x)g(x) - \int f'(x)g(x)\,dx$

Integration by substitution:

1. Have $\displaystyle\int f(g(x))g'(x)\,dx$
2. Set u=g(x)
3. Compute $\displaystyle\int f(u)\,du$
4. Replace u for g(x)

Let's do an example on the board: $\displaystyle\int e^{x^2} 2x\,dx$.

4.3.5 Solving the problem

Remember our function $y = x^2$ and our goal of finding the area under the curve from $x = 0$ to $x = 1$. We can describe this problem as $\displaystyle\int_0^1 x^2 dx$

Find the indefinite integral, $F(x)$:

$$\int x^2\ dx = \frac{x^3}{3} + C$$

Now we'll use the fundamental theory of calculus. Evaluate at our lowest and highest points, $F(0)$ and $F(1)$:

- $F(0) = 0$
- $F(1) = \frac{1}{3}$
- Technically $0 + C$ and $\frac{1}{3} + C$, but the C's will fall out in the next step

Calculate $F(1) - F(0)$

$$\frac{1}{3} - 0 = \frac{1}{3}$$

Exercise

Solve the following indefinite integrals:

1. $\int x^2\ dx$
2. $\int 3x^2\ dx$
3. $\int x\ dx$

4. $\int (3x^2 + 2x - 7\ ) dx$

5. $\int \frac{2}{x}\ dx$

And solve the following definite integrals:

1. $\displaystyle\int_1^7 x^2\ dx$

2. $\displaystyle\int_1^{10} 3x^2\ dx$

3. $\displaystyle\int_7^7 x\ dx$

4. $\displaystyle\int_1^5 3x^2 + 2x - 7\ dx$

5. $\int_1^e \frac{2}{x}\ dx$

5 Matrices

Matrices are rectangular collections of numbers. In this module we will introduce them and review some basic operators, to then introduce a sneak peek of why matrices are useful (and cool).

5.1 Introduction

5.1.1 Scalars

One number (for example, 12) is referred to as a scalar.

$$a = 12$$

5.1.2 Vectors

We can put several scalars together to make a vector. Here is an example:

$$\vec{b} = \begin{bmatrix} 12 \\ 14 \\ 15 \end{bmatrix}$$

Since this is a column of numbers, we cleverly refer to it as a *column vector*.

Here is another example of a vector, this time represented as a *row vector*:

$$\vec{c} = \begin{bmatrix} 12 & 14 & 15 \end{bmatrix}$$

Column vectors are possibly more common and useful, but we sometimes write things down using row vectors to

Vectors are fairly easy to construct in R. As we saw before, we can use the `c()` function to combine elements:

```r
c(5, 25, -2, 1)
```

```
[1]  5 25 -2  1
```

> **Warning**
>
> Remember that the code above does not *create* any objects. To do so, you'd need to use the assignment operator (`<-`):
>
> ```r
> vector_example <- c(5, 25, -2, 1)
> vector_example
> ```
>
> ```
> [1]  5 25 -2  1
> ```

Or we can also create vectors from sequences with the `:` operator or the `seq()` function:

```r
10:20
```

```
 [1] 10 11 12 13 14 15 16 17 18 19 20
```

```r
seq(from = 3, to = 27, by = 3)
```

```
[1]  3  6  9 12 15 18 21 24 27
```

5.2 Operators

5.2.1 Summation

The summation operator $\sum$ (i.e., the uppercase Sigma letter) lets us perform an operation on a sequence of numbers, which is often but not always a vector.

$$\vec{d} = \begin{bmatrix} 12 & 7 & -2 & 3 & -1 \end{bmatrix}$$

We can then calculate the sum of the first three elements of the vector, which is expressed as follows:

$$\sum_{i=1}^{3} d_i$$

Then we do the following math:

$$12 + 7 + (-2) = 17$$

It is also common to use n in the superscript to indicate that we want to sum all elements:

$$\sum_{i=1}^{n} d_i = 12 + 7 + (-2) + 3 + (-1) = 19$$

We can perform these operations using the `sum()` function in R:

```
vector_d <- c(12, 7, -2, 3, -1)
```

```
sum(vector_d[1:3])
```

```
[1] 17
```

```
sum(vector_d)
```

```
[1] 19
```

5.2.2 Product

The product operator $\prod$ (i.e., the uppercase Pi letter) can also perform operations over a sequence of elements in a vector. Recall our previous vector:

$$\vec{d} = \begin{bmatrix} 12 & 7 & -2 & 3 & 1 \end{bmatrix}$$

We might want to calculate the product of all its elements, which is expressed as follows:

$$\prod_{i=1}^{n} d_i = 12 \cdot 7 \cdot (-2) \cdot 3 \cdot (-1) = 504$$

In R, we can compute products using the `prod()` function:

```
prod(vector_d)
```

```
[1] 504
```

Exercise

Get the product of the first three elements of vector d. Write the notation by hand and use R to obtain the number.

5.3 Matrices

5.3.1 Basics

We can append vectors together to form a matrix:

$$A = \begin{bmatrix} 12 & 14 & 15 \\ 115 & 22 & 127 \\ 193 & 29 & 219 \end{bmatrix}$$

The number of rows and columns of a matrix constitute the *dimensions* of the matrix. The first number is the number of rows ("r") and the second number is the number of columns ("c") in the matrix.

Important

Find a way to remember "r x c" *permanently*. The order of the dimensions never changes.

Matrix A above, for example, is a 3×3 matrix. Sometimes we'd refer to it as $A_{3 \times 3}$.

Tip

It is common to use capital letters (sometimes **bold-faced**) to represent matrices. In contrast, vectors are usually represented with either bold lowercase letters or lowercase letters with an arrow on top (e.g., $\vec{v}$).

Constructing matrices in R

There are different ways to create matrices in R. One of the simplest is via `rbind()` or `cbind()`, which paste vectors together (either by **r**ows or by **c**olumns):

```
# Create some vectors
vector1 <- 1:4
vector2 <- 5:8
```

```r
vector3 <- 9:12
vector4 <- 13:16
```

```r
# Using rbind(), each vector will be a row
rbind_mat <- rbind(vector1, vector2, vector3, vector4)
rbind_mat
```

```
        [,1] [,2] [,3] [,4]
vector1    1    2    3    4
vector2    5    6    7    8
vector3    9   10   11   12
vector4   13   14   15   16
```

```r
# Using cbind(), each vector will be a column
cbind_mat <- cbind(vector1, vector2, vector3, vector4)
cbind_mat
```

```
     vector1 vector2 vector3 vector4
[1,]       1       5       9      13
[2,]       2       6      10      14
[3,]       3       7      11      15
[4,]       4       8      12      16
```

An alternative is to use to properly named `matrix()` function. The basic syntax is `matrix(data, nrow, ncol, byrow)`:

- `data` is the input vector which becomes the data elements of the matrix.
- `nrow` is the number of rows to be created.
- `ncol` is the number of columns to be created.
- `byrow` is a logical clue. If `TRUE` then the input vector elements are arranged by row. By default (`FALSE`), elements are arranged by column.

Let's see some examples:

```r
# Elements are arranged sequentially by row.
M <- matrix(c(1:12), nrow = 4, byrow = T)
M
```

```
     [,1] [,2] [,3]
[1,]    1    2    3
```

```
[2,]    4    5    6
[3,]    7    8    9
[4,]   10   11   12
```

```r
# Elements are arranged sequentially by column (byrow = F by default).
N <- matrix(c(1:12), nrow = 4)
N
```

```
     [,1] [,2] [,3]
[1,]    1    5    9
[2,]    2    6   10
[3,]    3    7   11
[4,]    4    8   12
```

5.3.2 Structure

How do we refer to specific elements of the matrix? For example, matrix A is an $m \times n$ matrix where $m = n = 3$. This is sometimes called a *square matrix*.

More generally, matrix B is an $m \times n$ matrix where the elements look like this:

$$B = \begin{bmatrix} b_{11} & b_{12} & b_{13} & \dots & b_{1n} \\ b_{21} & b_{22} & b_{23} & \dots & b_{2n} \\ \vdots & \vdots & \vdots & \dots & \vdots \\ b_{m1} & b_{m2} & b_{m3} & \dots & b_{mn} \end{bmatrix}$$

Thus b_{23} refers to the second unit down and third across. More generally, we refer to row indices as i and to column indices as j.

In R, we can access a matrix's elements using square brackets:

```r
# In matrix N, access the element at 1st row and 3rd column.
N[1,3]
```

```
[1] 9
```

```r
# In matrix N, access the element at 4th row and 2nd column.
N[4,2]
```

```
[1] 8
```

Tip

When trying to identify a specific element, the first subscript is the element's row and the second subscript is the element's column (*always* in that order).

Warning

In R, indexing is 1-based, meaning that the first element of a vector, matrix, or any other data structure is accessed with index 1. In other programming tools such as Python, indexing is 0-based, meaning that the first element of a list, array, or any other data structure is accessed with index 0.

```
# Create a 2x2 matrix in R
matrix_A <- matrix(1:4, nrow = 2, ncol = 2)

# Access the element in the first row, first column
element <- matrix_A[1, 1]  # This will return 1
```

```
# Create a list in Python
vector = [10, 20, 30, 40]

# Access the first element
first_element = vector[0]  # This will return 10
import numpy as np

# Create a 2x2 matrix in Python with NumPy
matrix_A = np.array([[1, 2], [3, 4]])

# Access the element in the first row, first column
element = matrix_A[0, 0]  # This will return 1
```

5.4 Matrix operations

5.4.1 Addition and subtraction

- Addition and subtraction are straightforward operations.
- Matrices must have *exactly* the same dimensions for both of these operations.
- We add or subtract each element with the corresponding element from the other matrix.

- This is expressed as follows:

$$A \pm B = C$$

$$c_{ij} = a_{ij} \pm b_{ij} \ \forall i, j$$

$$\begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix} \pm \begin{bmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ b_{31} & b_{32} & b_{33} \end{bmatrix}$$
$$=$$
$$\begin{bmatrix} a_{11} \pm b_{11} & a_{12} \pm b_{12} & a_{13} \pm b_{13} \\ a_{21} \pm b_{21} & a_{22} \pm b_{22} & a_{23} \pm b_{23} \\ a_{31} \pm b_{31} & a_{32} \pm b_{32} & a_{33} \pm b_{33} \end{bmatrix}$$

Addition and subtraction in R

We start by creating two 2x3 matrices:

$$A = \begin{bmatrix} 3 & -1 & 2 \\ 9 & 4 & 6 \end{bmatrix}$$

```r
# Create two 2x3 matrices.
matrix1 <- matrix(c(3, 9, -1, 4, 2, 6), nrow = 2)
matrix1
```

```
     [,1] [,2] [,3]
[1,]    3   -1    2
[2,]    9    4    6
```

And

$$B = \begin{bmatrix} 5 & 2 & 0 \\ 9 & 3 & 4 \end{bmatrix}$$

```r
matrix2 <- matrix(c(5, 2, 0, 9, 3, 4), nrow = 2)
matrix2
```

```
     [,1] [,2] [,3]
[1,]    5    0    3
[2,]    2    9    4
```

We can simply use the + and - operators for addition and substraction:

```
matrix1 + matrix2
```

```
     [,1] [,2] [,3]
[1,]    8   -1    5
[2,]   11   13   10
```

```
matrix1 - matrix2
```

```
     [,1] [,2] [,3]
[1,]   -2   -1   -1
[2,]    7   -5    2
```

Exercise

(Use code for one of these and do the other one by hand!)
1) Calculate $A + B$

$$A = \begin{bmatrix} 1 & 0 \\ -2 & -1 \end{bmatrix}$$

$$B = \begin{bmatrix} 5 & 1 \\ 2 & -1 \end{bmatrix}$$

2) Calculate $A - B$

$$A = \begin{bmatrix} 6 & -2 & 8 & 12 \\ 4 & 42 & 8 & -6 \end{bmatrix}$$

$$B = \begin{bmatrix} 18 & 42 & 3 & 7 \\ 0 & -42 & 15 & 4 \end{bmatrix}$$

5.4.2 Scalar multiplication

Scalar multiplication is very intuitive. As we know, a scalar is a single number. We multiply each value in the matrix by the scalar to perform this operation.

Formally, this is expressed as follows:

$$A = \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix}$$

$$cA = \begin{bmatrix} ca_{11} & ca_{12} & ca_{13} \\ ca_{21} & ca_{22} & ca_{23} \\ ca_{31} & ca_{32} & ca_{33} \end{bmatrix}$$

In R, all we need to do is take an established matrix and multiply it by some scalar:

```
# matrix1 from our previous example
matrix1
```

```
     [,1] [,2] [,3]
[1,]    3   -1    2
[2,]    9    4    6
```

```
matrix1 * 3
```

```
     [,1] [,2] [,3]
[1,]    9   -3    6
[2,]   27   12   18
```

Exercise

Calculate $2 \times A$ and $-3 \times B$. Again, do one by hand and the other one using R.

$$A = \begin{bmatrix} 1 & 4 & 8 \\ 0 & -1 & 3 \end{bmatrix}$$

$$B = \begin{bmatrix} -15 & 1 & 5 \\ 2 & -42 & 0 \\ 7 & 1 & 6 \end{bmatrix}$$

5.4.3 Matrix multiplication

- Multiplying matrices is slightly trickier than multiplying scalars.
- Two matrices must be *conformable* for them to be multiplied together. This means that the number of columns in the first matrix equals the number of rows in the second.
- When multiplying $A \times B$, if A is $m \times n$, B must have n rows.

> **Important**
>
> The conformability requirement *never* changes. Before multiplying anything, check to make sure the matrices are indeed conformable.

- The resulting matrix will have the same number of rows as the first matrix and the number of columns in the second. For example, if A is $i \times k$ and B is $k \times j$, then $A \times B$ will be $i \times j$.

Which of the following can we multiply? What will be the dimensions of the resulting matrix?

$$B_{4\times 1} = \begin{bmatrix} 2 \\ 3 \\ 4 \\ 1 \end{bmatrix} M_{3\times 3} = \begin{bmatrix} 1 & 0 & 2 \\ 1 & 2 & 4 \\ 2 & 3 & 2 \end{bmatrix} L_{2\times 3} = \begin{bmatrix} 6 & 5 & -1 \\ 1 & 4 & 3 \end{bmatrix}$$

The only valid multiplication based on the provided matrices is $L \times M$, which results in a 2×3 matrix.

Why can't we multiply in the opposite order?

The non-commutative property of matrix multiplication is a fundamental aspect in matrix algebra. The multiplication of matrices is sensitive to the order in which the matrices are multiplied due to the requirements of dimensional compatibility, the resulting dimensions, and the computation process itself.

> **Warning**
>
> When multiplying matrices, *order matters*. Even if multiplication is possible in both directions, in general $AB \neq BA$.

Multiplication steps

- Multiply each row by each column, summing up each pair of multiplied terms.

> **Tip**
>
> This is sometimes to referred to as the "dot product," where we multiply matching members, then sum up.

- The element in position ij is the sum of the products of elements in the ith row of the first matrix (A) and the corresponding elements in the jth column of the second matrix (B).

$$c_{ij} = \sum_{k=1}^{n} a_{ik} b_{kj}$$

Example

Suppose a company manufactures two kinds of furniture: chairs and sofas.

- A chair costs \$100 for wood, \$270 for cloth, and \$130 for feathers.
- Each sofa costs \$150 for wood, \$420 for cloth, and \$195 for feathers.

	Chair	Sofa
Wood	100	150
Cloth	270	420
Feathers	130	195

The same information about unit cost (C) can be presented as a matrix.

$$C = \begin{bmatrix} 100 & 150 \\ 270 & 420 \\ 130 & 195 \end{bmatrix}$$

Note that each of the three rows of this 3 x 2 matrix represents a material (wood, cloth, or feathers), and each of the two columns represents a product (chair or coach). The elements are the unit cost (in USD).

Now, suppose that the company will produce 45 chairs and 30 sofas this month. This production quantity can be represented in the following table, and also as a 2 x 1 matrix (Q):

Product	Quantity
Chair	45
Sofa	30

$$Q = \begin{bmatrix} 45 \\ 30 \end{bmatrix}$$

What will be the company's total cost? The "total expenditure" is equal to the "unit cost" times the "production quantity" (the number of units).

The total expenditure (E) for each material this month is calculated by multiplying these two matrices.

$$E = CQ = \begin{bmatrix} 100 & 150 \\ 270 & 420 \\ 130 & 195 \end{bmatrix} \begin{bmatrix} 45 \\ 30 \end{bmatrix} = \begin{bmatrix} (100)(45) + (150)(30) \\ (270)(45) + (420)(30) \\ (130)(45) + (195)(30) \end{bmatrix} = \begin{bmatrix} 9,000 \\ 24,750 \\ 11,700 \end{bmatrix}$$

Multiplying the 3x2 Cost matrix (C) times the 2x1 Quantity matrix (Q) yields the 3x1 Expenditure matrix (E).

As a result of this matrix multiplication, we determine that this month the company will incur expenditures of:

- $9,000 for wood
- $24,750 for cloth
- $11,700 for feathers.

Matrix multiplication in R

Before attempting matrix multiplication, we must make sure the matrices are conformable (as we do for our manual calculations).

Then we can multiply our matrices together using the `%*%` operator.

```
C <- matrix(c(100, 270, 130, 150, 420, 195), nrow = 3)
C
```

```
     [,1] [,2]
[1,]  100  150
[2,]  270  420
[3,]  130  195
```

```
Q <- matrix(c(45, 30), nrow = 2)
Q
```

```
     [,1]
[1,]   45
[2,]   30
```

```r
C %*% Q
```

```
      [,1]
[1,]  9000
[2,] 24750
[3,] 11700
```

> **Warning**
>
> If you have a missing value or `NA` in one of the matrices you are trying to multiply (something we will discuss in further detail in the next module), you will have `NA`s in your resulting matrix.

5.4.4 Properties of operations

- Addition and subtraction:
  - Associative: $(A \pm B) \pm C = A \pm (B \pm C)$
  - Communicative: $A \pm B = B \pm A$
- Multiplication:
  - $AB \neq BA$
  - $A(BC) = (AB)C$
  - $A(B + C) = AB + AC$
  - $(A + B)C = AC + BC$

5.5 Special matrices

Square matrix

$$A = \begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \\ 7 & 8 & 9 \end{bmatrix}$$

- In a square matrix, the number of rows equals the number of columns ($m = n$):
- The *diagonal* of a matrix is a set of numbers consisting of the elements on the line from the upper-left-hand to the lower-right-hand corner of the matrix, as in $ d(A)=[1,5,9] $. Diagonals are particularly useful in square matrices.
- The *trace* of a matrix, denoted as $tr(A)$, is the sum of the diagonal elements of the matrix. $tr(A) = 1 + 5 + 9 = 15$

Diagonal matrix:

- In a diagonal matrix, all of the elements of the matrix that are not on the diagonal are equal to zero.
$$D = \begin{bmatrix} 4 & 0 & 0 \\ 0 & 5 & 0 \\ 0 & 0 & 6 \end{bmatrix}$$

Scalar matrix:

- A scalar matrix is a diagonal matrix where the diagonal elements are all equal to each other. In other words, we're really only concerned with one scalar (or element) held in the diagonal.

$$S = \begin{bmatrix} 7 & 0 & 0 \\ 0 & 7 & 0 \\ 0 & 0 & 7 \end{bmatrix}$$

Identity matrix:

$$I = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

- The identity matrix is a scalar matrix with all of the diagonal elements equal to one.
- Remember that, as with all diagonal matrices, the off-diagonal elements are equal to zero.

- The capital letter I is reserved for the identity matrix. For convenience, a 3x3 identity matrix can be denoted as I_3.

5.6 Transpose

The transpose is the original matrix with the rows and the columns interchanged.

The notation is either J' ("J prime") or J^T ("J transpose").

$$J = \begin{bmatrix} 4 & 5 \\ 3 & 0 \\ 7 & -2 \end{bmatrix}$$

$$J' = J^T = \begin{bmatrix} 4 & 3 & 7 \\ 5 & 0 & -2 \end{bmatrix}$$

In R, we use `t()` to get the transpose.

```
J <- matrix(c(4, 3, 7, 5, 0, -2), ncol = 2)
J
```

```
     [,1] [,2]
[1,]    4    5
[2,]    3    0
[3,]    7   -2
```

```
t(J)
```

```
     [,1] [,2] [,3]
[1,]    4    3    7
[2,]    5    0   -2
```

5.7 Inverse

- Just like a number has a reciprocal, a matrix has an inverse.
- When we multiply a matrix by its inverse we get the identity matrix (which is like "1" for matrices).

$$A \times A^{-1} = I$$

- The inverse of A is A^{-1} only when:

$$AA^{-1} = A^{-1}A = I$$

- Sometimes there is no inverse at all.

> **Note**
>
> For now, don't worry about calculating the inverse of a matrix manually. This is the type of task we use R for.

- In R, we use the `solve()` function to calculate the inverse of a matrix:

```
A <- matrix(c(3, 2, 5, 2, 3, 2, 5, 2, 4), ncol = 3)
A
```

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

```
solve(A)
```

```
            [,1]        [,2]       [,3]
[1,] -0.29629630 -0.07407407  0.4074074
[2,] -0.07407407  0.48148148 -0.1481481
[3,]  0.40740741 -0.14814815 -0.1851852
```

5.8 Linear systems and matrices

- A system of equations can be represented by an *augmented matrix*.
- System of equations:

$$3x + 6y = 12$$

$$5x + 10y = 25$$

- In an augmented matrix, each row represents one equation in the system and each column represents a variable or the constant terms.

$$\begin{bmatrix} 3 & 6 & 12 \\ 5 & 10 & 25 \end{bmatrix}$$

5.9 OLS and matrices

- We can use the logic above to calculate estimates for our ordinary least squares (OLS) models.
- OLS is a linear regression technique used to find the best-fitting line for a set of data points (observations) by minimizing the residuals (the differences between the observed and predicted values).
- We minimize the *sum of the squared errors.*

5.9.1 Dependent variable

- Suppose, for example, we have a sample consisting of n observations.
- The dependent variable is denoted as an $n \times 1$ column vector.

$$Y = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_n \end{bmatrix}$$

5.9.2 Independent variables

- Suppose there are k independent variables and a constant term, meaning $k+1$ columns and n rows.
- We can represent these variables as an $n \times (k+1)$ matrix, expressed as follows:

$$X = \begin{bmatrix} 1 & x_{11} & \dots & x_{1k} \\ 1 & x_{21} & \dots & x_{2k} \\ \vdots & \vdots & \dots & \vdots \\ 1 & x_{n1} & \dots & x_{nk} \end{bmatrix}$$

- x_{ij} is the i-th observation of the j-th independent variable.

5.9.3 Linear regression model

- Let's say we have 173 observations (n = 173) and 2 IVs (k = 3).
- This can be expressed as the following linear equation:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \epsilon$$

- In matrix form, we have:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_{11} & x_{21} \\ 1 & x_{21} & x_{22} \\ \vdots & \vdots & \vdots \\ 1 & x_{1173} & x_{2173} \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_{173} \end{bmatrix}$$

- All 173 equations can be represented by:

$$y = X\beta + \epsilon$$

5.9.4 Estimates

- Without getting too much into the mechanics, we can calculate our coefficient estimates with matrix algebra using the following equation:

$$\hat{\beta} = (X'X)^{-1}X'Y$$

- Read aloud, we say "X prime X inverse, X prime Y".
- The little hat on our beta ($\hat{\beta}$) signifies that these are estimates.
- Remember, the OLS method is to choose $\hat{\beta}$ such that the sum of squared residuals ("SSR") is minimized.

5.9.4.1 Example in R

- We will load the `mtcars` data set (our favorite) for this example, which contains data about many different car models.

```
cars_df <- mtcars
```

- Now, we want to estimate the association between `hp` (horsepower) and `wt` (weight), our independent variables, and `mpg` (miles per gallon), our dependent variable.

- First, we transform our dependent variable into a matrix, using the `as.matrix` function and specifying the column of the `mtcars` data set to create a column vector of our observed values for the DV.

```
Y <- as.matrix(cars_df$mpg)
Y
```

```
      [,1]
 [1,] 21.0
 [2,] 21.0
 [3,] 22.8
 [4,] 21.4
 [5,] 18.7
 [6,] 18.1
 [7,] 14.3
 [8,] 24.4
 [9,] 22.8
[10,] 19.2
[11,] 17.8
[12,] 16.4
[13,] 17.3
[14,] 15.2
[15,] 10.4
[16,] 10.4
[17,] 14.7
[18,] 32.4
[19,] 30.4
[20,] 33.9
[21,] 21.5
[22,] 15.5
[23,] 15.2
[24,] 13.3
[25,] 19.2
[26,] 27.3
[27,] 26.0
[28,] 30.4
[29,] 15.8
[30,] 19.7
[31,] 15.0
[32,] 21.4
```

- Next, we do the same thing for our independent variables of interest, and our constant.

```
# create two separate matrices for IVs
X1 <- as.matrix(cars_df$hp)
X2 <- as.matrix(cars_df$wt)

# create constant column

# bind them altogether into one matrix
constant <-  rep(1, nrow(cars_df))
X <- cbind(constant, X1, X2)
X
```

```
      constant
 [1,]        1 110 2.620
 [2,]        1 110 2.875
 [3,]        1  93 2.320
 [4,]        1 110 3.215
 [5,]        1 175 3.440
 [6,]        1 105 3.460
 [7,]        1 245 3.570
 [8,]        1  62 3.190
 [9,]        1  95 3.150
[10,]        1 123 3.440
[11,]        1 123 3.440
[12,]        1 180 4.070
[13,]        1 180 3.730
[14,]        1 180 3.780
[15,]        1 205 5.250
[16,]        1 215 5.424
[17,]        1 230 5.345
[18,]        1  66 2.200
[19,]        1  52 1.615
[20,]        1  65 1.835
[21,]        1  97 2.465
[22,]        1 150 3.520
[23,]        1 150 3.435
[24,]        1 245 3.840
[25,]        1 175 3.845
[26,]        1  66 1.935
[27,]        1  91 2.140
[28,]        1 113 1.513
[29,]        1 264 3.170
[30,]        1 175 2.770
```

```
[31,]        1 335 3.570
[32,]        1 109 2.780
```

- Next, we calculate $X'X$, $X'Y$, and $(X'X)^{-1}$.

Don't forget to use **%*%** for matrix multiplication!

```
# X prime X
XpX <- t(X) %*% X

# X prime X inverse
XpXinv <- solve(XpX)

# X prime Y
XpY <- t(X) %*% Y

# beta coefficient estimates
bhat <- XpXinv %*% XpY
bhat
```

```
                [,1]
constant 37.22727012
         -0.03177295
         -3.87783074
```

6 Tidy data analysis II

In this session, we'll cover a few more advanced topics related to data wrangling. Again we'll use the `tidyverse`:

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becon
```

6.1 Loading data in different formats.

In this module we will use cross-national data from the Quality of Government (QoG) project (Dahlberg et al., 2023).

Notice how in the `data/` folder we have multiple versions of the same dataset (a subset of the QOG basic dataset): .csv (comma-separated values), .rds (R), .xlsx (Excel), .dta (Stata), and .sav (SPSS).

6.1.1 CSV and R data files

We can use the `read_csv()` and `read_rds()` functions from the `tidyverse`[1] to read the .csv and .rds (R) data files:

[1]Technically, the `read_csv()` and `read_rds()` functions come from `readr`, one of the `tidyverse` constituent packages.

```r
qog_csv <- read_csv("data/sample_qog_bas_ts_jan23.csv")
```

```
Rows: 1085 Columns: 8
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (4): cname, ccodealp, region, ht_colonial
dbl (4): year, wdi_pop, vdem_polyarchy, vdem_corr

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.
```

```r
qog_rds <- read_rds("data/sample_qog_bas_ts_jan23.rds")
```

For reading files from other software (Excel, Stata, or SPSS), we need to load additional packages. Luckily, they are automatically installed when one installs the `tidyverse`.

6.1.2 Excel data files

For Excel files (.xls or .xlsx files), the `readxl` package has a handy `read_excel()` function.

```r
library(readxl)
qog_excel <- read_excel("data/sample_qog_bas_ts_jan23.xlsx")
```

> Tip
>
> Useful arguments of the `read_excel()` function include `sheet =`, which reads particular sheets (specified via their positions or sheet names), and `range =`, which extracts a particular cell range (e.g., 'A5:E25').

6.1.3 Stata and SPSS data files

To load files from Stata (.dta) or SPSS (.spss), one needs the `haven` package and its properly-named `read_stata()` and `read_spss()` functions:

```r
library(haven)
qog_stata <- read_stata("data/sample_qog_bas_ts_jan23.dta")
qog_spss <- read_spss("data/sample_qog_bas_ts_jan23.sav")
```

> **Tip**
>
> Datasets from Stata and SPSS can have additional properties, like variable labels and special types of missing values. To learn more about this, check out the "Labelled data" chapter from Danny Smith's *Survey Research Datasets and R* (2020).

6.1.4 Our data for this session

We will rename one of our objects to `qog`:

```r
qog <- qog_csv
qog
```

```
# A tibble: 1,085 x 8
   cname      ccodealp   year region wdi_pop vdem_polyarchy vdem_corr ht_colonial
   <chr>      <chr>     <dbl> <chr>    <dbl>          <dbl>     <dbl> <chr>
 1 Antigua a~ ATG        1990 Carib~   63328             NA        NA British
 2 Antigua a~ ATG        1991 Carib~   63634             NA        NA British
 3 Antigua a~ ATG        1992 Carib~   64659             NA        NA British
 4 Antigua a~ ATG        1993 Carib~   65834             NA        NA British
 5 Antigua a~ ATG        1994 Carib~   67072             NA        NA British
 6 Antigua a~ ATG        1995 Carib~   68398             NA        NA British
 7 Antigua a~ ATG        1996 Carib~   69798             NA        NA British
 8 Antigua a~ ATG        1997 Carib~   71218             NA        NA British
 9 Antigua a~ ATG        1998 Carib~   72572             NA        NA British
10 Antigua a~ ATG        1999 Carib~   73821             NA        NA British
# i 1,075 more rows
```

This dataset is a small sample of QOG, which contains data for countries in the Americas from 1990 to 2020. The observational unit is thus country-year. You can access the full codebook online. The variables are as follows:

Variable	Description
`cname`	Country name
`ccodealp`	Country code (ISO-3 character convention)
`year`	Year
`region`	Region (following legacy WDI convention). Added to QOG by us.
`wdi_pop`	Total population, from the World Development Indicators
`vdem_polyarchy`	V-Dem's polyarchy index (electoral democracy)

Variable	Description
`vdem_corr`	V-Dem's corruption index
`ht_colonial`	Former colonial ruler

6.2 Recoding variables

Take a look at the `ht_colonial` variable. We can do a simple tabulation with `count()`:

```
qog |>
  count(ht_colonial)
```

```
# A tibble: 6 x 2
  ht_colonial         n
  <chr>           <int>
1 British           372
2 Dutch              31
3 French             31
4 Never colonized    62
5 Portuguese         31
6 Spanish           558
```

> **Tip**
>
> Another common way to compute quick tabulations in R is with the `table()` function. Be aware that this takes a *vector* as the input:
>
> ```
> table(qog$ht_colonial)
> ```
>
> ```
>
>         British           Dutch          French Never colonized      Portuguese
>             372              31              31              62              31
>         Spanish
>             558
> ```

We might want to recode this variable. For instance, we could create a *dummy/binary* variable for whether the country was a British colony. We can do this with `if_else()`, which works with logical conditions:

```
qog |>
  # the arguments are condition, true (what to do if true), false
  mutate(d_britishcol = if_else(ht_colonial == "British", 1, 0)) |>
  count(d_britishcol)
```

```
# A tibble: 2 x 2
  d_britishcol     n
         <dbl> <int>
1            0   713
2            1   372
```

Instead of a numeric classification (0 and 1), we could use characters:

```
qog |>
  mutate(cat_britishcol = if_else(ht_colonial == "British", "British", "Other")) |>
  count(cat_britishcol)
```

```
# A tibble: 2 x 2
  cat_britishcol     n
  <chr>          <int>
1 British          372
2 Other            713
```

`if_else()` is great for binary recoding. But sometimes we want to create more than two categories. We can use `case_when()`:

```
qog |>
  # syntax is condition ~ value
  mutate(cat_col = case_when(
    ht_colonial == "British" ~ "British",
    ht_colonial == "Spanish" ~ "Spanish",
    .default = "Other" # what to do in all other cases
  )) |>
  count(cat_col)
```

```
# A tibble: 3 x 2
  cat_col     n
  <chr>   <int>
1 British   372
2 Other     155
3 Spanish   558
```

The `.default =` argument in `case_when()` can also be used to leave the variable as-is for non-specified cases. For example, let's combine Portuguese and Spanish colonies:

```
qog |>
  # syntax is condition ~ value
  mutate(cat_col = case_when(
    ht_colonial %in% c("Spanish", "Portuguese") ~ "Spanish/Portuguese",
    .default = ht_colonial # what to do in all other cases
  )) |>
  count(cat_col)
```

```
# A tibble: 5 x 2
  cat_col                n
  <chr>              <int>
1 British              372
2 Dutch                 31
3 French                31
4 Never colonized       62
5 Spanish/Portuguese   589
```

Exercise

1. Create a dummy variable, `d_large_pop`, for whether the country-year has a population of more than 1 million. Then compute its mean. Your code:

2. Which countries are recorded as "Never colonized"? Change their values to other reasonable codings and compute a tabulation with `count()`. Your code:

6.3 Missing values

Missing values are commonplace in real datasets. In R, missing values are a special type of value in vectors, denoted as `NA`.

Warning

The special value `NA` is different from the character value "NA". For example, notice that a numeric vector can have `NA`s, while it obviously cannot hold the character value "NA":

```
c(5, 4.6, NA, 8)
```

```
[1] 5.0 4.6  NA 8.0
```

A quick way to check for missing values in small datasets is with the `summary()` function:

```r
summary(qog)
```

```
    cname             ccodealp              year          region         
 Length:1085        Length:1085        Min.   :1990   Length:1085       
 Class :character   Class :character   1st Qu.:1997   Class :character  
 Mode  :character   Mode  :character   Median :2005   Mode  :character  
                                       Mean   :2005                     
                                       3rd Qu.:2013                     
                                       Max.   :2020                     
                                                                        
    wdi_pop           vdem_polyarchy     vdem_corr       ht_colonial       
 Min.   :    40542   Min.   :0.0710   Min.   :0.0260   Length:1085       
 1st Qu.:   389131   1st Qu.:0.5570   1st Qu.:0.1890   Class :character  
 Median :  5687744   Median :0.7030   Median :0.5550   Mode  :character  
 Mean   : 25004057   Mean   :0.6569   Mean   :0.4922                     
 3rd Qu.: 16195902   3rd Qu.:0.8030   3rd Qu.:0.7540                     
 Max.   :331501080   Max.   :0.9160   Max.   :0.9630                     
                     NA's   :248      NA's   :248                        
```

Notice that we have missingness in the `vdem_polyarchy` and `vdem_corr` variables. We might want to filter the dataset to see which observations are in this situation:

```r
qog |>
  filter(vdem_polyarchy == NA | vdem_corr == NA)
```

```
# A tibble: 0 x 8
# i 8 variables: cname <chr>, ccodealp <chr>, year <dbl>, region <chr>,
#   wdi_pop <dbl>, vdem_polyarchy <dbl>, vdem_corr <dbl>, ht_colonial <chr>
```

But the code above doesn't work! To refer to missing values in logical conditions, we cannot use `== NA`. Instead, we need to use the `is.na()` function:

```r
qog |>
  filter(is.na(vdem_polyarchy) | is.na(vdem_corr))
```

```
# A tibble: 248 x 8
   cname      ccodealp  year region wdi_pop vdem_polyarchy vdem_corr ht_colonial
   <chr>      <chr>    <dbl> <chr>    <dbl>          <dbl>     <dbl> <chr>      
```

```
 1 Antigua a~ ATG       1990 Carib~   63328              NA         NA British
 2 Antigua a~ ATG       1991 Carib~   63634              NA         NA British
 3 Antigua a~ ATG       1992 Carib~   64659              NA         NA British
 4 Antigua a~ ATG       1993 Carib~   65834              NA         NA British
 5 Antigua a~ ATG       1994 Carib~   67072              NA         NA British
 6 Antigua a~ ATG       1995 Carib~   68398              NA         NA British
 7 Antigua a~ ATG       1996 Carib~   69798              NA         NA British
 8 Antigua a~ ATG       1997 Carib~   71218              NA         NA British
 9 Antigua a~ ATG       1998 Carib~   72572              NA         NA British
10 Antigua a~ ATG       1999 Carib~   73821              NA         NA British
# i 238 more rows
```

Notice that, in most R functions, missing values are "contagious." This means that any missing value will contaminate the operation and carry over to the results. For example:

```r
qog |>
  summarize(mean_vdem_polyarchy = mean(vdem_polyarchy))
```

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

Sometimes we'd like to perform our operations even in the presence of missing values, simply excluding them. Most basic R functions have an `na.rm =` argument to do this:

```r
qog |>
  summarize(mean_vdem_polyarchy = mean(vdem_polyarchy, na.rm = T))
```

```
# A tibble: 1 x 1
  mean_vdem_polyarchy
                <dbl>
1               0.657
```

> **Exercise**
>
> Calculate the median value of the corruption variable for each region (i.e., perform a grouped summary). Your code:

6.4 Pivoting data

We will now load another time-series cross-sectional dataset, but in a slightly different format. It's adapted from the World Bank's World Development Indicators (WDI) (2023) and records gross domestic product at purchasing power parity (GDP PPP).

```
gdp <- read_excel("data/wdi_gdp_ppp.xlsx")
```

```
gdp
```

```
# A tibble: 266 x 35
   country_name        country_code   `1990`   `1991`   `1992`   `1993`   `1994`
   <chr>               <chr>           <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
 1 Aruba               ABW           2.03e 9  2.19e 9  2.32e 9  2.48e 9  2.69e 9
 2 Africa Eastern and~ AFE           9.41e11  9.42e11  9.23e11  9.19e11  9.35e11
 3 Afghanistan         AFG          NA       NA       NA       NA       NA
 4 Africa Western and~ AFW           5.76e11  5.84e11  5.98e11  5.92e11  5.91e11
 5 Angola              AGO           6.85e10  6.92e10  6.52e10  4.95e10  5.02e10
 6 Albania             ALB           1.59e10  1.14e10  1.06e10  1.16e10  1.26e10
 7 Andorra             AND          NA       NA       NA       NA       NA
 8 Arab World          ARB           2.19e12  2.25e12  2.35e12  2.41e12  2.48e12
 9 United Arab Emirat~ ARE           2.01e11  2.03e11  2.10e11  2.12e11  2.27e11
10 Argentina           ARG           4.61e11  5.04e11  5.43e11  5.88e11  6.22e11
# i 256 more rows
# i 28 more variables: `1995` <dbl>, `1996` <dbl>, `1997` <dbl>, `1998` <dbl>,
#   `1999` <dbl>, `2000` <dbl>, `2001` <dbl>, `2002` <dbl>, `2003` <dbl>,
#   `2004` <dbl>, `2005` <dbl>, `2006` <dbl>, `2007` <dbl>, `2008` <dbl>,
#   `2009` <dbl>, `2010` <dbl>, `2011` <dbl>, `2012` <dbl>, `2013` <dbl>,
#   `2014` <dbl>, `2015` <dbl>, `2016` <dbl>, `2017` <dbl>, `2018` <dbl>,
#   `2019` <dbl>, `2020` <dbl>, `2021` <dbl>, `2022` <dbl>
```

Note how the information is recorded differently. Here columns are not variables, but years. We call datasets like this one **wide**, in contrast to the **long** datasets we have seen before. In general, R and the `tidyverse` work much nicer with long datasets. Luckily, the `tidyr` package of the `tidyverse` makes it easy to convert datasets between these two formats.

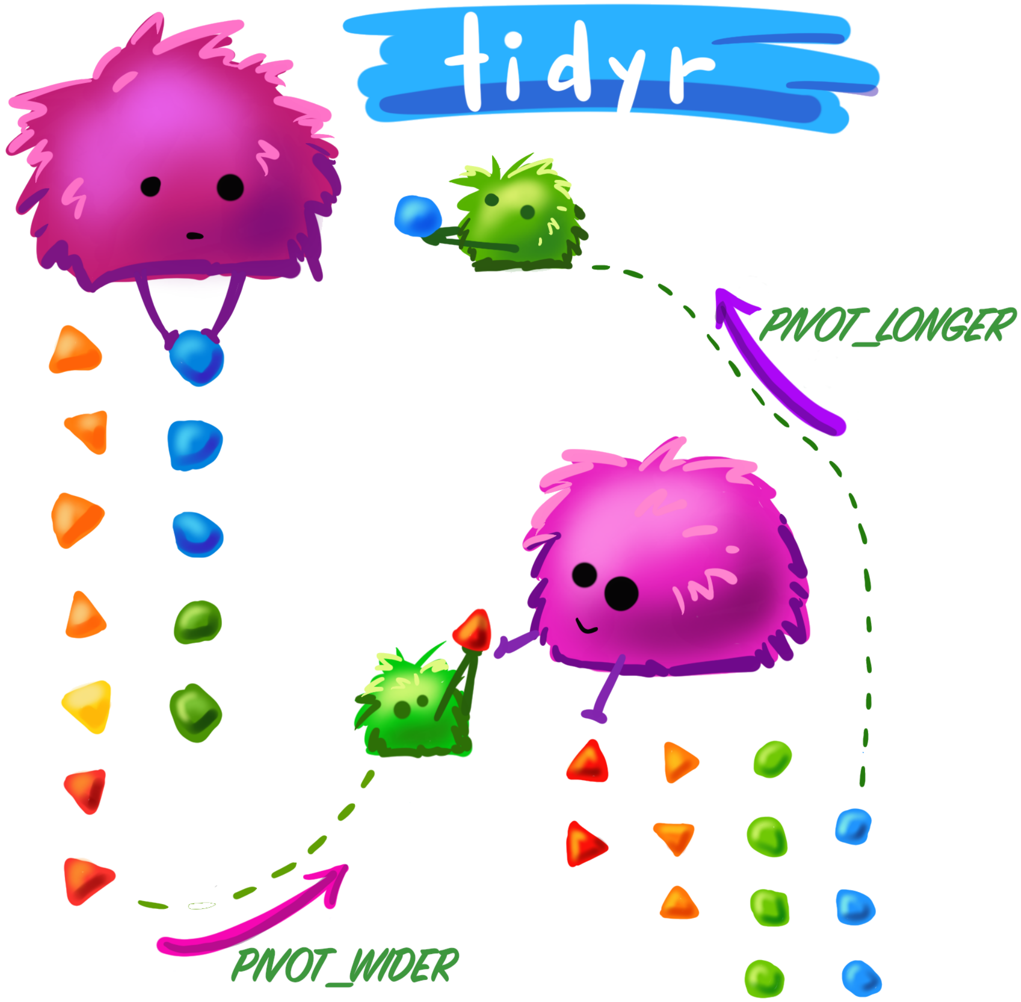


Figure 6.1: Source: Illustration by Allison Horst, adapted by Peter Higgins.

We will use the `pivot_longer()` function:

```
gdp_long <- gdp |>
  pivot_longer(cols = -c(country_name, country_code), # cols to not pivot
               names_to = "year", # how to name the column with names
               values_to = "wdi_gdp_ppp",  # how to name the column with values
```

```r
               names_transform = as.integer) # make sure that years are numeric
gdp_long
```

```
# A tibble: 8,778 x 4
   country_name country_code  year wdi_gdp_ppp
   <chr>        <chr>        <int>       <dbl>
 1 Aruba        ABW           1990 2025472682.
 2 Aruba        ABW           1991 2186758474.
 3 Aruba        ABW           1992 2315391348.
 4 Aruba        ABW           1993 2484593045.
 5 Aruba        ABW           1994 2688426606.
 6 Aruba        ABW           1995 2756904694.
 7 Aruba        ABW           1996 2789595753.
 8 Aruba        ABW           1997 2986175079.
 9 Aruba        ABW           1998 3045659222.
10 Aruba        ABW           1999 3083365758.
# i 8,768 more rows
```

Done! This is a much friendlier format to work with. For example, we can now do summaries:

```r
gdp_long |>
  summarize(mean_gdp_ppp = mean(wdi_gdp_ppp, na.rm = T), .by = country_name)
```

```
# A tibble: 266 x 2
   country_name                mean_gdp_ppp
   <chr>                              <dbl>
 1 Aruba                            3.38e 9
 2 Africa Eastern and Southern      1.61e12
 3 Afghanistan                      5.56e10
 4 Africa Western and Central       1.15e12
 5 Angola                           1.38e11
 6 Albania                          2.56e10
 7 Andorra                        NaN
 8 Arab World                       4.22e12
 9 United Arab Emirates             4.29e11
10 Argentina                        8.06e11
# i 256 more rows
```

Exercise

Convert back `gdp_long` to a wide format using `pivot_wider()`. Check out the help file using `?pivot_wider`. Your code:

6.5 Merging datasets

It is extremely common to want to integrate data from multiple sources. Combining information from two datasets is called *merging* or *joining*.

To do this, we need ID variables in common between the two data sets. Using our QOG and WDI datasets, these variables will be country code (which in this case is shared between the two datasets) and year.

Tip

Standardized unit codes (like country codes) are extremely useful when merging data. It's harder than expected for a computer to realize that "Bolivia (Plurinational State of)" and "Bolivia" refer to the same unit. By default, these units will not be matched.[2]

Okay, now to the merging. Imagine we want to add information about GDP to our QOG main dataset. To do so, we can use the `left_join()` function, from the `tidyverse`'s `dplyr` package:

```
qog_plus <- left_join(qog, # left data frame, which serves as a "base"
                      gdp_long, # right data frame, from which to draw new columns
                      by = c("ccodealp" = "country_code", # can define name equivalencies!
                             "year"))
```

```
qog_plus |>
  # select variables for clarity
  select(cname, ccodealp, year, wdi_pop, wdi_gdp_ppp)
```

```
# A tibble: 1,085 x 5
   cname               ccodealp  year wdi_pop wdi_gdp_ppp
   <chr>               <chr>    <dbl>   <dbl>       <dbl>
 1 Antigua and Barbuda ATG       1990   63328  966660878.
```

[2]There are R packages to deal with these complications. `fuzzyjoin` matches units by their approximate distance, using some clever algorithms. `countrycode` allows one to standardize country names and country codes across different conventions.

```
 2 Antigua and Barbuda ATG       1991   63634  987701012.
 3 Antigua and Barbuda ATG       1992   64659  999143284.
 4 Antigua and Barbuda ATG       1993   65834 1051896837.
 5 Antigua and Barbuda ATG       1994   67072 1122128908.
 6 Antigua and Barbuda ATG       1995   68398 1073208718.
 7 Antigua and Barbuda ATG       1996   69798 1144088355.
 8 Antigua and Barbuda ATG       1997   71218 1206688391.
 9 Antigua and Barbuda ATG       1998   72572 1263778328.
10 Antigua and Barbuda ATG       1999   73821 1310634399.
# i 1,075 more rows
```

Tip

Most of the time, you'll want to do a `left_join()`, which is great for adding new information to a "base" dataset, without dropping information from the latter. In limited situations, other types of joins can be helpful. To learn more about them, you can read Jenny Bryan's excellent tutorial on `dplyr` joins.

Exercise

There is a dataset on country's CO2 emissions, again from the World Bank (2023), in "data/wdi_co2.csv". Load the dataset into R and add a new variable with its information, `wdi_co2`, to our `qog_plus` data frame. Finally, compute the average values of CO2 emissions *per capita*, by country. Tip: this exercise requires you to do many steps—plan ahead before you start coding! Your code:

6.5.1 Sanity checks

Sanity checks are small tests to make sure that your code is doing what you think it's doing. They are especially important in complex operations like joins, but the idea can be extended to pretty much any command.

The `tidylog` package gives more information about `tidyverse` operations, and it's an easy/automatic way to check your work:

```
library(tidylog)
```

```
qog_plus <- left_join(qog, # left data frame, which serves as a "base"
                      gdp_long, # right data frame, from which to draw new columns
                      by = c("ccodealp" = "country_code", # can define name equivalencies!
                             "year"))
```

```
left_join: added 2 columns (country_name, wdi_gdp_ppp)
           > rows only in qog            0
           > rows only in gdp_long (7,693)
           > matched rows            1,085
           >                       =======
           > rows total              1,085
```

You can also construct sanity checks manually. For instance, we know that a left join shouldn't modify a data frame's number of rows:

```r
nrow(qog) == nrow(qog_plus)
```

```
[1] TRUE
```

6.6 Plotting extensions: trend graphs, facets, and customization

> **Exercise**
>
> Draw a scatterplot with time in the x-axis and democracy scores in the y-axis. Your code:

How can we visualize trends effectively? One alternative is to use a trend graph. Let's start by computing the yearly averages for democracy in the whole region:

```r
dem_yearly <- qog |>
  summarize(mean_dem = mean(vdem_polyarchy, na.rm = T), .by = year)
```

```
summarize: now 31 rows and 2 columns, ungrouped
```

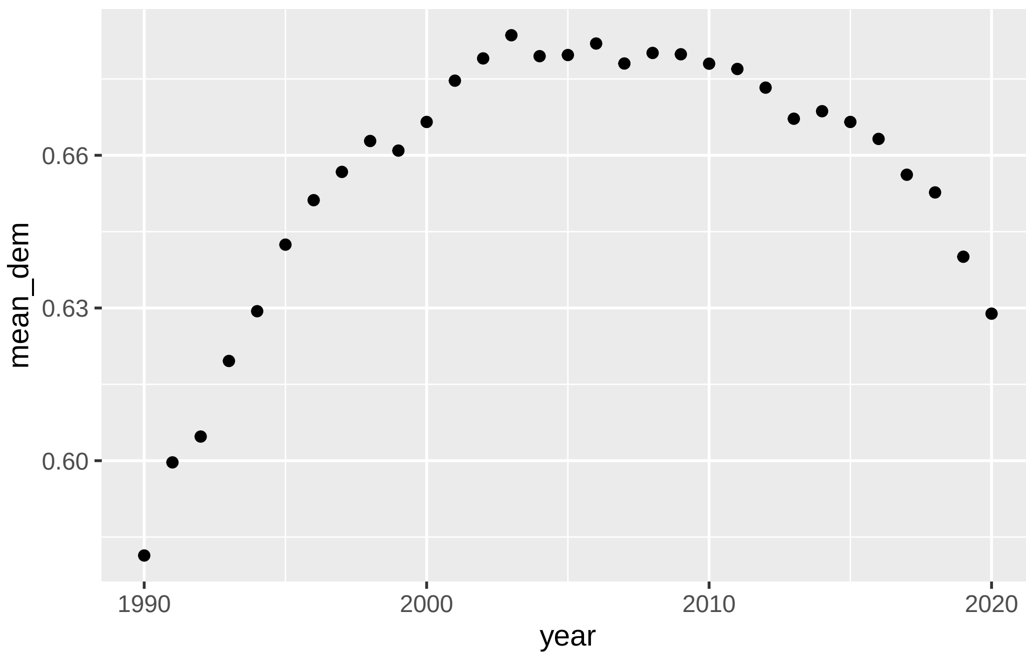
```r
dem_yearly
```

```
# A tibble: 31 x 2
    year mean_dem
   <dbl>    <dbl>
 1  1990    0.581
 2  1991    0.600
 3  1992    0.605
 4  1993    0.620
 5  1994    0.629
```

```
 6  1995     0.642
 7  1996     0.651
 8  1997     0.657
 9  1998     0.663
10  1999     0.661
# i 21 more rows
```

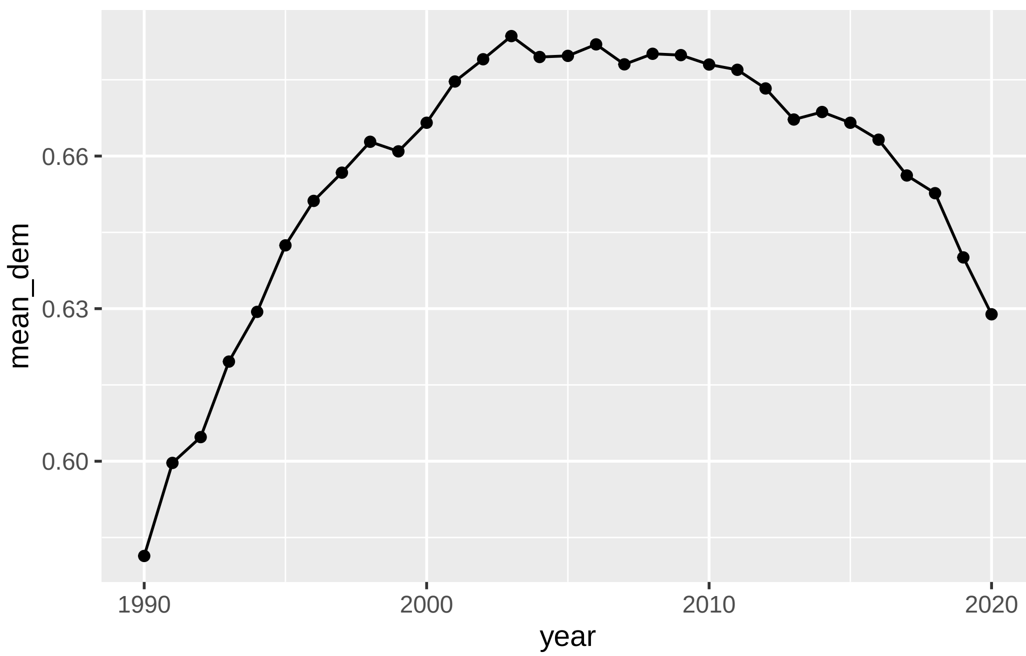
Now we can plot them with a scatterplot:

```
ggplot(dem_yearly, aes(x = year, y = mean_dem)) +
  geom_point()
```



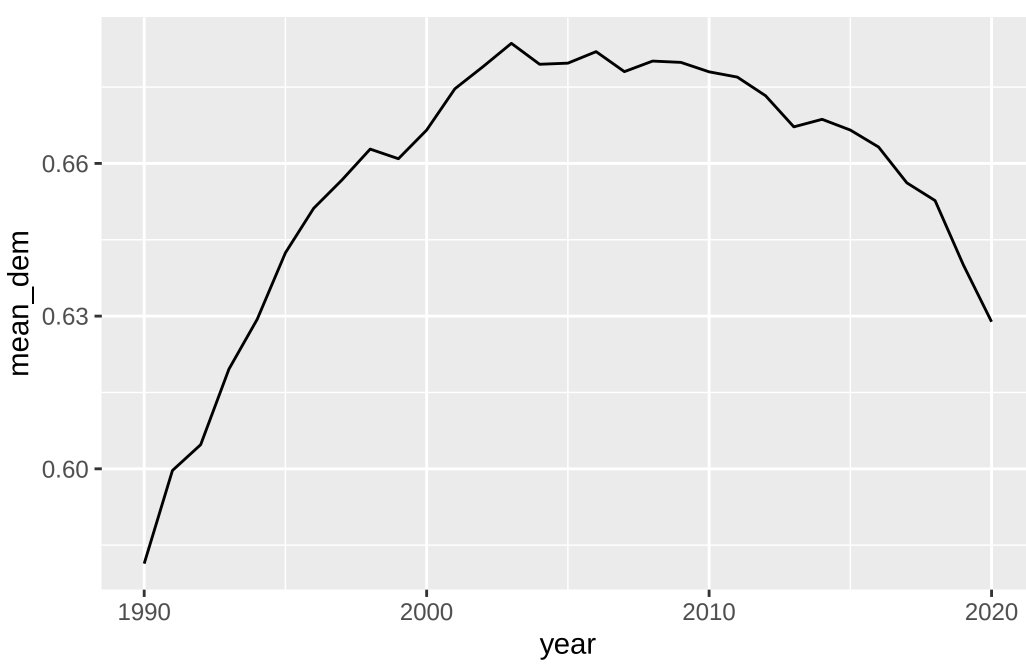
We can add `geom_line()` to connect the dots:

```
ggplot(dem_yearly, aes(x = year, y = mean_dem)) +
  geom_point() +
  geom_line()
```



We can, of course, remove to points to only keep the line:

```
ggplot(dem_yearly, aes(x = year, y = mean_dem)) +
  geom_line()
```

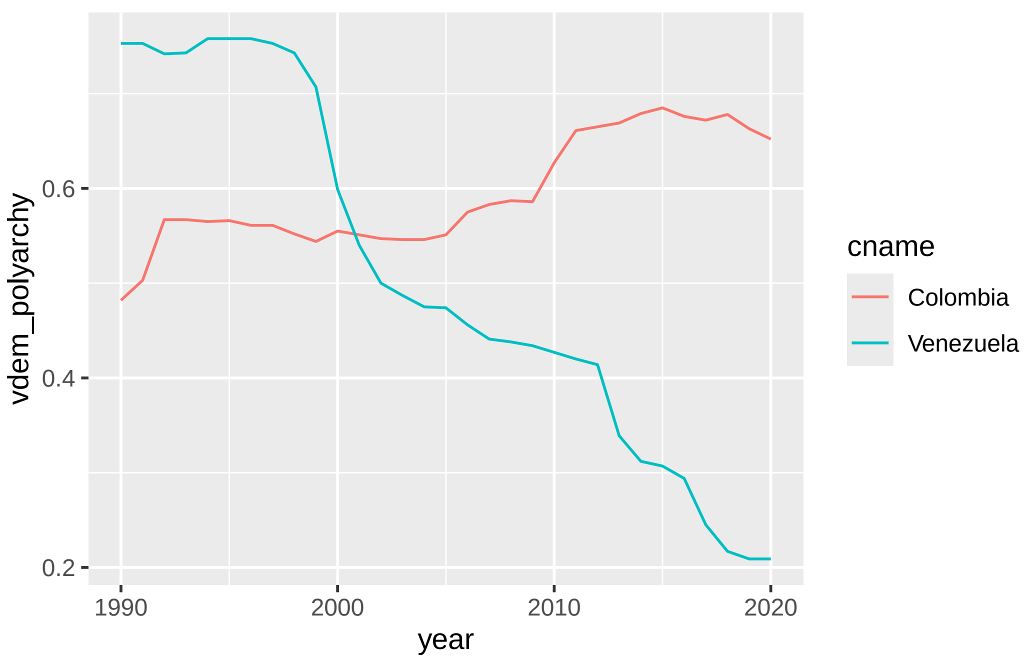


What if we want to plot trends for different countries? We can use the `group` and `color` aesthetic mappings (no need to do a summary here! data is already at the country-year level):

```
# filter to only get Colombia and Venezuela
dem_yearly_countries <- qog |>
  filter(ccodealp %in% c("COL", "VEN"))
```

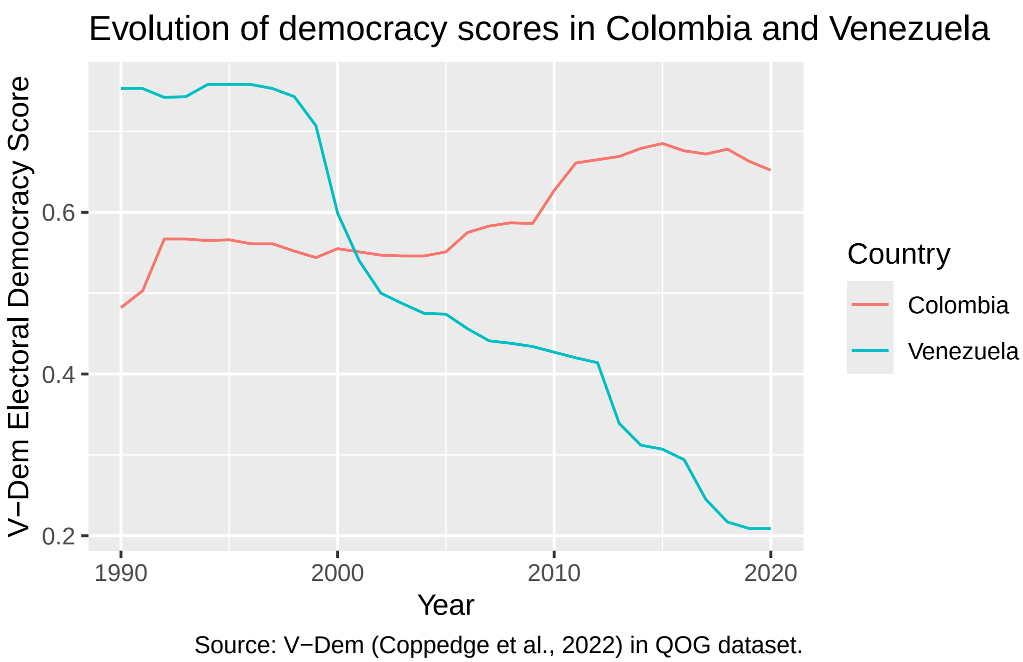
```
filter: removed 1,023 rows (94%), 62 rows remaining
```

```
ggplot(dem_yearly_countries, aes(x = year, y = vdem_polyarchy, color = cname)) +
  geom_line()
```



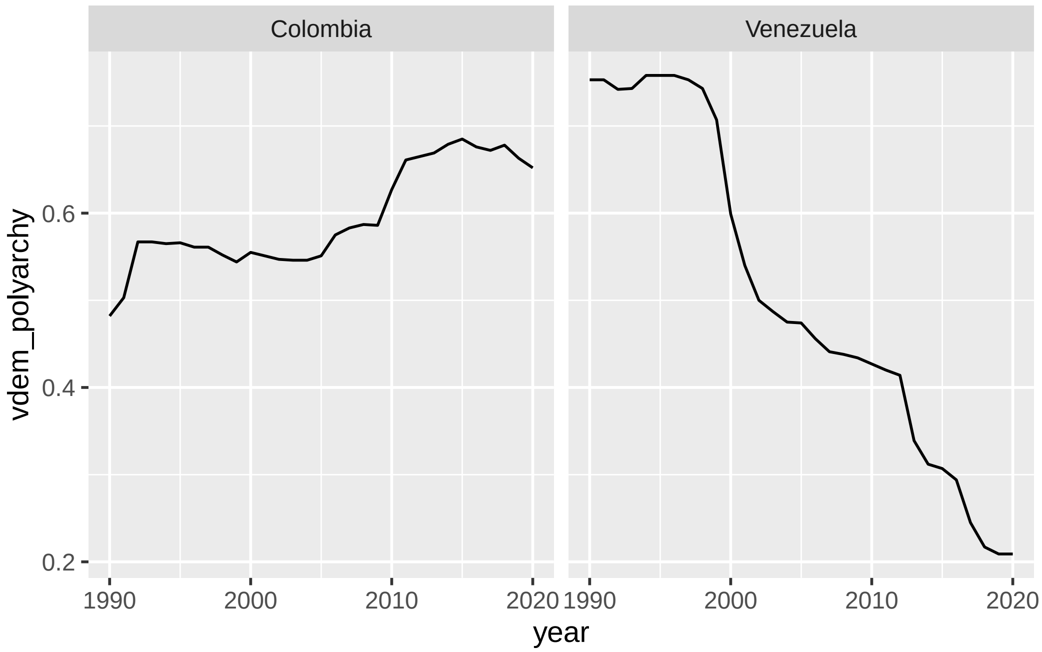
Remember that we can use the `labs()` function to add labels:

```
ggplot(dem_yearly_countries, aes(x = year, y = vdem_polyarchy, color = cname)) +
  geom_line() +
  labs(x = "Year", y = "V-Dem Electoral Democracy Score", color = "Country",
       title = "Evolution of democracy scores in Colombia and Venezuela",
       caption = "Source: V-Dem (Coppedge et al., 2022) in QOG dataset.")
```



Another way to display these trends is by using *facets*, which divide a plot into small boxes according to a categorical variable (no need to add color here):

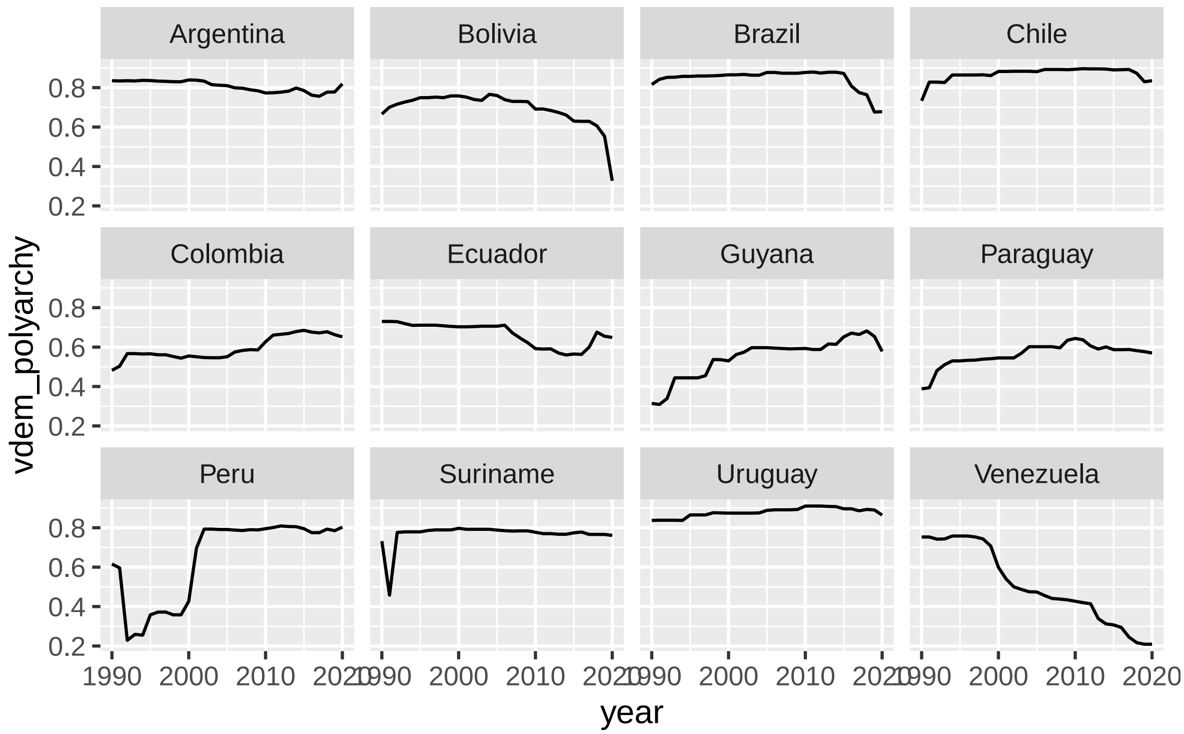
```
ggplot(dem_yearly_countries, aes(x = year, y = vdem_polyarchy)) +
  geom_line() +
  facet_wrap(~cname)
```



Facets are particularly useful for many categories (where the number of distinguishable colors reaches its limit):

```
ggplot(qog |> filter(region == "South America"),
       aes(x = year, y = vdem_polyarchy)) +
  geom_line() +
  facet_wrap(~cname)
```

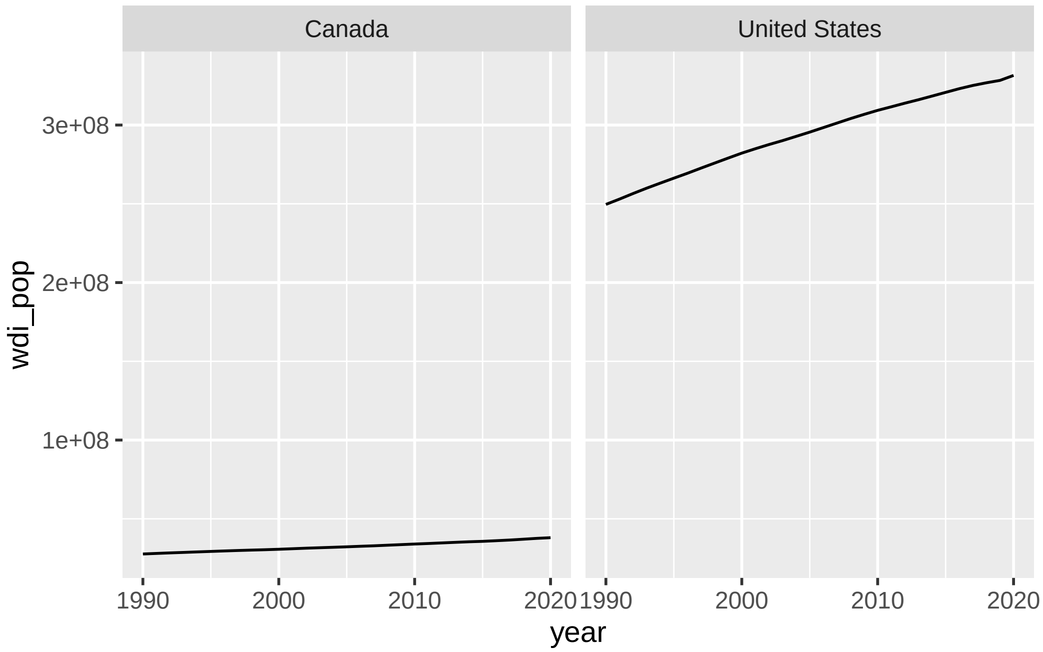
```
filter: removed 713 rows (66%), 372 rows remaining
```



With facets, one can control whether each facet picks its own scales or if all facets share the same scale. For example, let's plot the populations of Canada and the US:

```
ggplot(qog |> filter(cname %in% c("Canada", "United States")),
       aes(x = year, y = wdi_pop)) +
  geom_line() +
  facet_wrap(~cname)
```

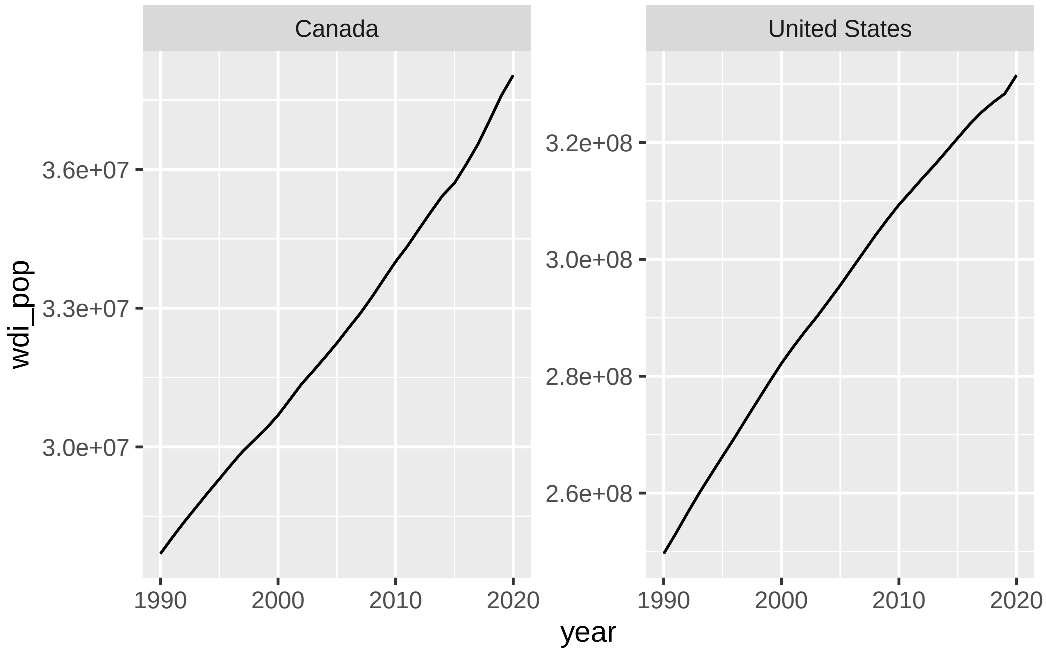
```
filter: removed 1,023 rows (94%), 62 rows remaining
```



The scales are so disparate that unifying them yields a plot that's hard to interpret. But if we're interested in within-country trends, we can let each facet have its own scale with the `scales =` argument (which can be "fixed", "free_x", "free_y", or "free"):

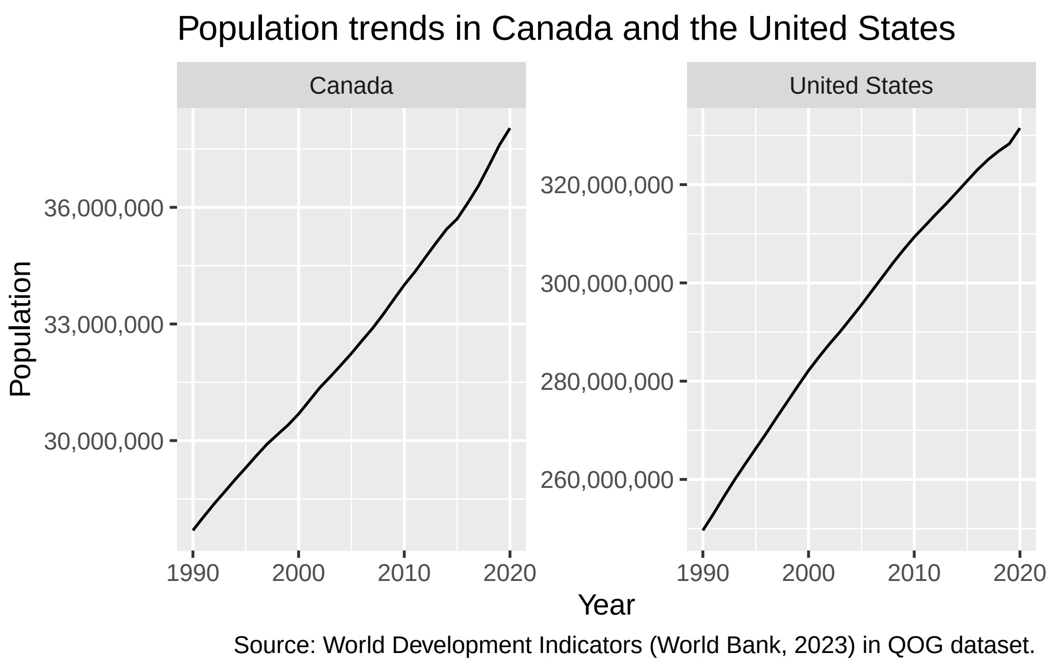
```
ggplot(qog |> filter(cname %in% c("Canada", "United States")),
       aes(x = year, y = wdi_pop)) +
  geom_line() +
  facet_wrap(~cname, scales = "free_y")
```

```
filter: removed 1,023 rows (94%), 62 rows remaining
```



This ability to visualize *within* time trends also makes facets appealing in many situations.

> **Tip**
>
> Plots made with `ggplot2` are extremely customizable. For example, we could want to change the y-axis labels in the last plot to something more readable:
>
> ```
> # create as object "p" to use later
> p <- ggplot(qog |> filter(cname %in% c("Canada", "United States")),
>        aes(x = year, y = wdi_pop)) +
>   geom_line() +
>   facet_wrap(~cname, scales = "free_y") +
>   scale_y_continuous(labels = scales::label_number(big.mark = ",")) +
>   # also add labels
>   labs(x = "Year", y = "Population",
>        title = "Population trends in Canada and the United States",
>        caption = "Source: World Development Indicators (World Bank, 2023) in QOG dataset.")
> ```
>
> ```
> filter: removed 1,023 rows (94%), 62 rows remaining
> ```
>
> ```
> p
> ```



While it's impossible for us to review all the customization options you might need, a fantastic reference is the "ggplot2: Elegant Graphics for Data Analysis" book by Hadley Wickham, Danielle Navarro, and Thomas Lin Pedersen.

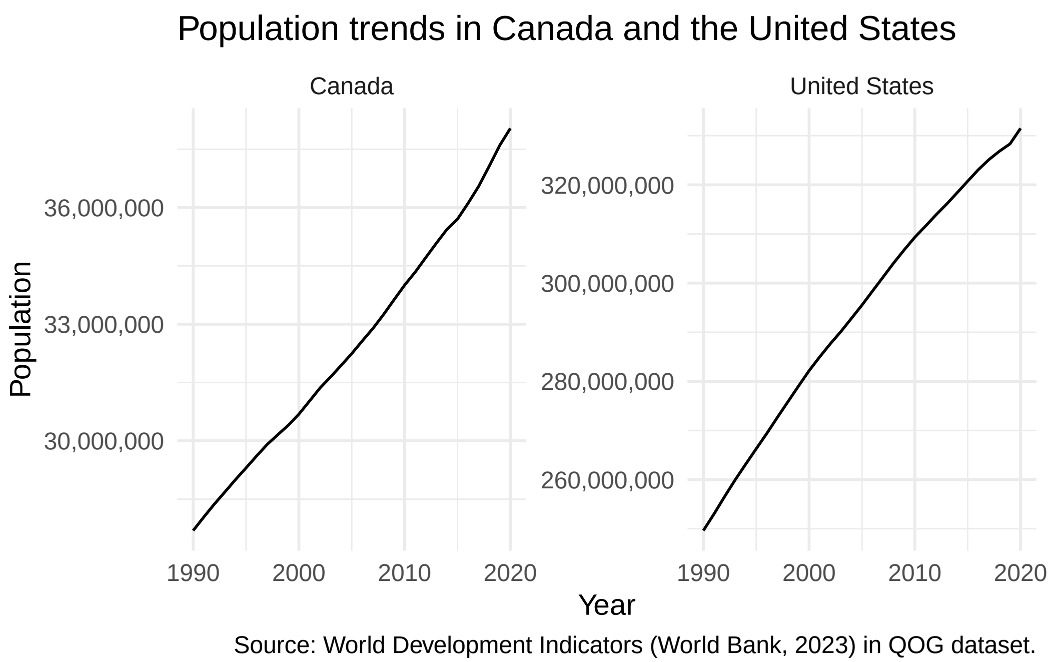
Exercise

Using your merged dataset from the previous section, plot the trajectories of C02 per capita emissions for the US and Haiti. Use adequate scales.

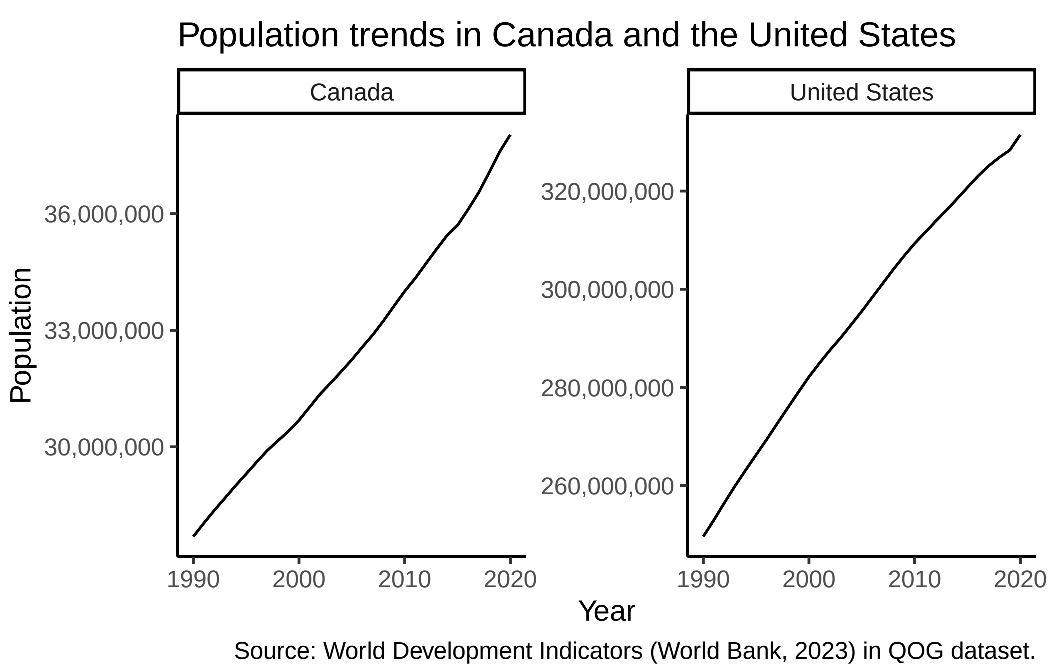
6.6.1 Themes

We can change the overall aspect of a `ggplot2` figure by changing its theme:

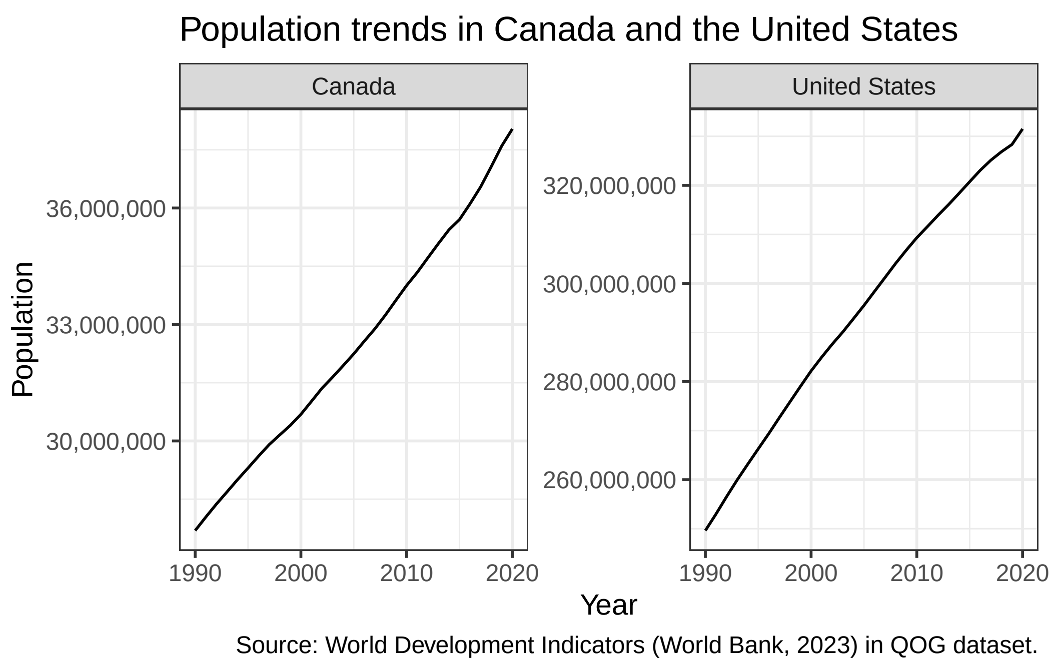
```
p +
  theme_minimal()
```




```
p +
  theme_classic()
```

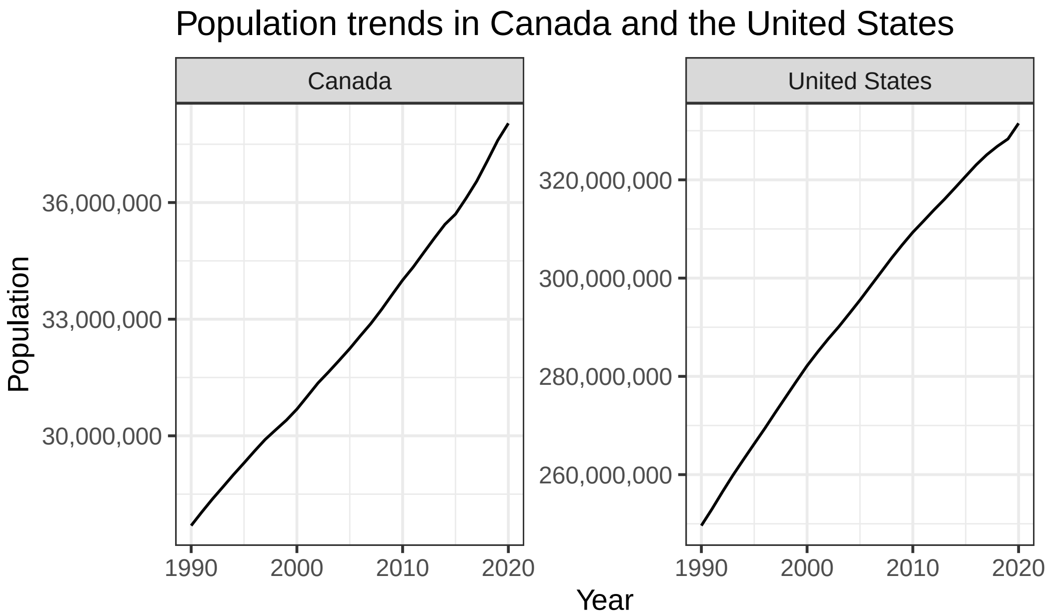


```r
p +
  theme_bw()
```



If you are going to make multiple plots in a script, you can set the theme at the beginning with `theme_bw()`:

```r
theme_set(theme_bw())
p
```



Source: World Development Indicators (World Bank, 2023) in QOG dataset.

7 Probability

7.1 What is probability?

- Informally, a probability is a number that describes how likely an event is.
  - It is, by definition, between 0 and 1.
  - What is the probability that a fair coin flip will result in heads?
- We can also think of a probability as an outcome's **relative frequency** after repeating an "experiment" many times.[1]
  - In this setting, an experiment is "an action or a set of actions that produce stochastic [random] events of interest" (Imai and Williams 2022, p. 281). Not to confuse with scientific experiments!
  - If we were to flip a million fair coins, what will be the proportion of heads?
- A *probability space* (Ω, S, P) is a formal way to talk about a random process:
  - The sample space (Ω) is the set of all possible outcomes.
  - The event space (S) is a collection of events (an event is a subset of Ω).
  - The probability measure (P) is a function that assigns a probability in $\mathbb{R}$ to every event in S. So $P : S \to \mathbb{R}$.
- We can formalize our intuitions with the **probability axioms** (sometimes called Kolmogorov's axioms):
  - $P(A) \geq 0, \ \forall A \in S$.
    - Probabilities must be non-negative.
  - $P(\Omega) = 1$.
    - Something has to happen!
    - Probabilities sum/integrate to 1.
  - $P(A \cup B) = P(A) + P(B), \ \forall A, B \in S, \ A \cup B = \emptyset$.
    - The probability of disjoint (mutually exclusive) events is equal to the sum of their individual probabilities.

[1] This is sometimes called the *frequentist* interpretation of probability. There are other possibilities, such as *Bayesian* interpretations of probability, which describe probabilities as degrees of belief.

7.2 Definitions and properties of probability

- Joint probability: $P(A \cap B)$. The probability that the two events will occur in one realization of the experiment.
- Law of total probability: $P(A) = P(A \cap B) + P(A \cap B^C)$.
- Addition rule: $P(A \cup B) = P(A) + P(B) - P(A \cap B)$.
- Conditional probability: $P(A|B) = \dfrac{P(A \cap B)}{P(B)}$
  - the probability of event A occurring given that event B has already occurred is the probability that both A and B occur together devided by the probability that event B occurs
- Bayes theorem: $P(A|B) = \dfrac{P(A) \cdot P(B|A)}{P(B)}$
  - $P(A|B)$: the probability of event A occurring given that B is true
  - $P(B|A)$: the probability of event B occurring given that A is true.

7.3 Random variables and probability distributions

- A **random variable** is a function ($X : \Omega \to \mathbb{R}$) of the outcome of a random generative process. Informally, it is a “placeholder” for whatever will be the output of a process we're studying.
- A **probability distribution** describes the probabilities associated with the values of a random variable.
- Random variables (and probability distributions) can be **discrete** or **continuous**.

7.3.1 Discrete random variables and probability distributions

- A sample space in which there are a (finite or infinite) countable number of outcomes
- Each realization of random process has a discrete probability of occurring.
  - $f(X = x_i) = P(X = x_i)$ is the probability the variable takes the value x_i.

An example

- What's the probability that we'll roll a 3 on one die roll:

$$Pr(y = 3) = \frac{1}{6}$$

- If one roll of the die is an "experiment," we can think of a 3 as a "success."
- $Y \sim Bernoulli\left(\frac{1}{6}\right)$
- Fair coins are $\sim Bernoulli(.5)$, for example.
- More generally, $Bernoulli(\pi)$. We'll talk about other probability distributions soon.
  - π represents the probability of success.

Let's do another example on the board, using the sum of two fair dice.

> Exercise:
>
> What's the probability that the sum of two fair dice equals 7?

7.3.2 Continuous random variables and probability distributions

- What happens when our outcome is continuous?
- There are an infinite number of outcomes. This makes the denominator of our fraction difficult to work with.
- The probability of the whole space must equal 1.
- The domain may not span -∞ to ∞.
  - Even space between 0 and 1 is infinite!
- Two common examples are the uniform and normal probability distributions, which we will discuss below.

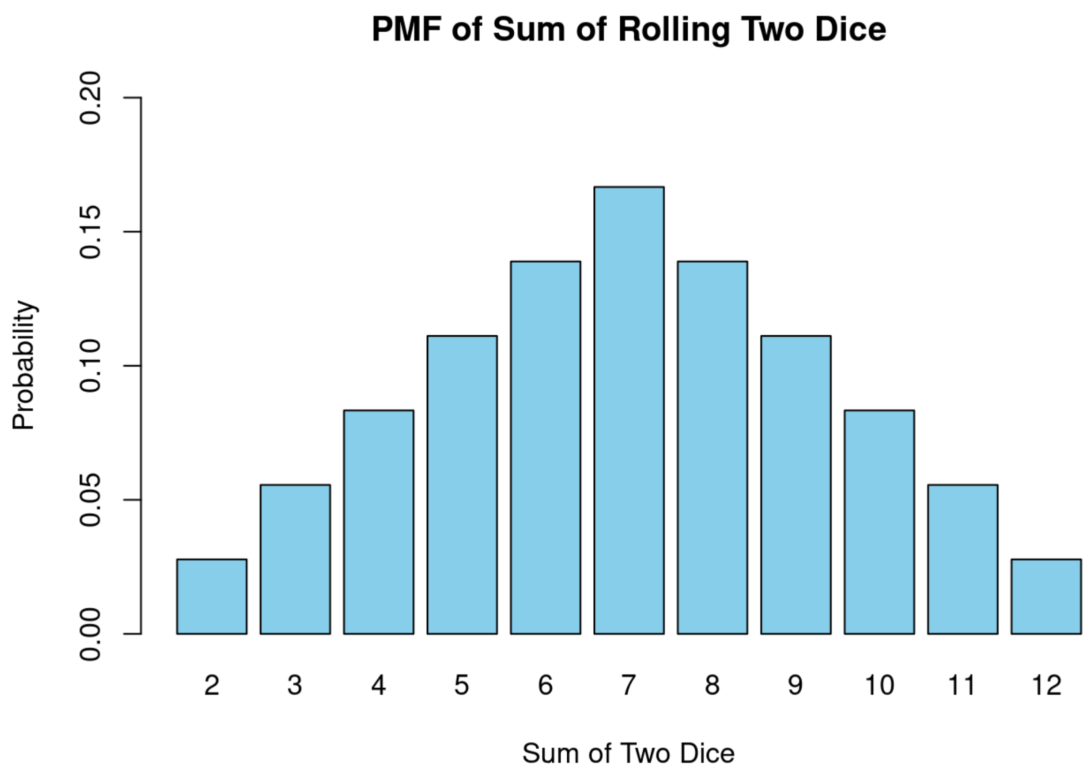
7.4 Functions describing probability distributions

7.4.1 Probability Mass Function (PMF) – Discrete Variables

Probability of each occurrence encoded in probability mass function (PMF)

- $0 \leq f(x_i) \leq 1$: Probability of any value occurring must be between 0 and 1.

- $\sum_{x} f(x_i) = 1$: Probabilities of all values must sum to 1.

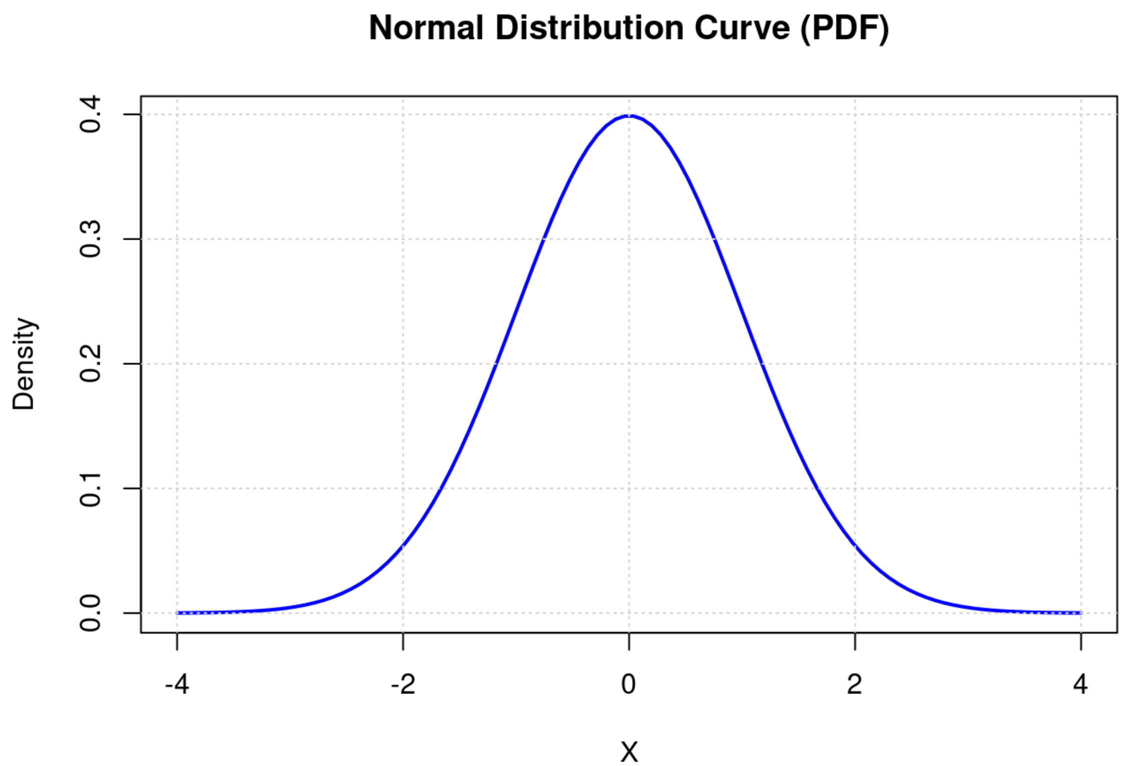


7.4.2 Probability Density Function (PDF) – Continuous Variables

- Similar to PMF from before, but for continuous variables.
- Using integration, it gives the probability a value falls within a particular interval

$$P[a \leq X \leq b] = \int_{a}^{b} f(x)\, dx$$

- Total area under the curve is 1.
- $P(a < X < b)$ is the area under the curve between a and b (where $b > a$).


Normal Distribution Curve (PDF)
Density
0.0
0.1
0.2
0.3
0.4
-4
-2
0
2
4
X

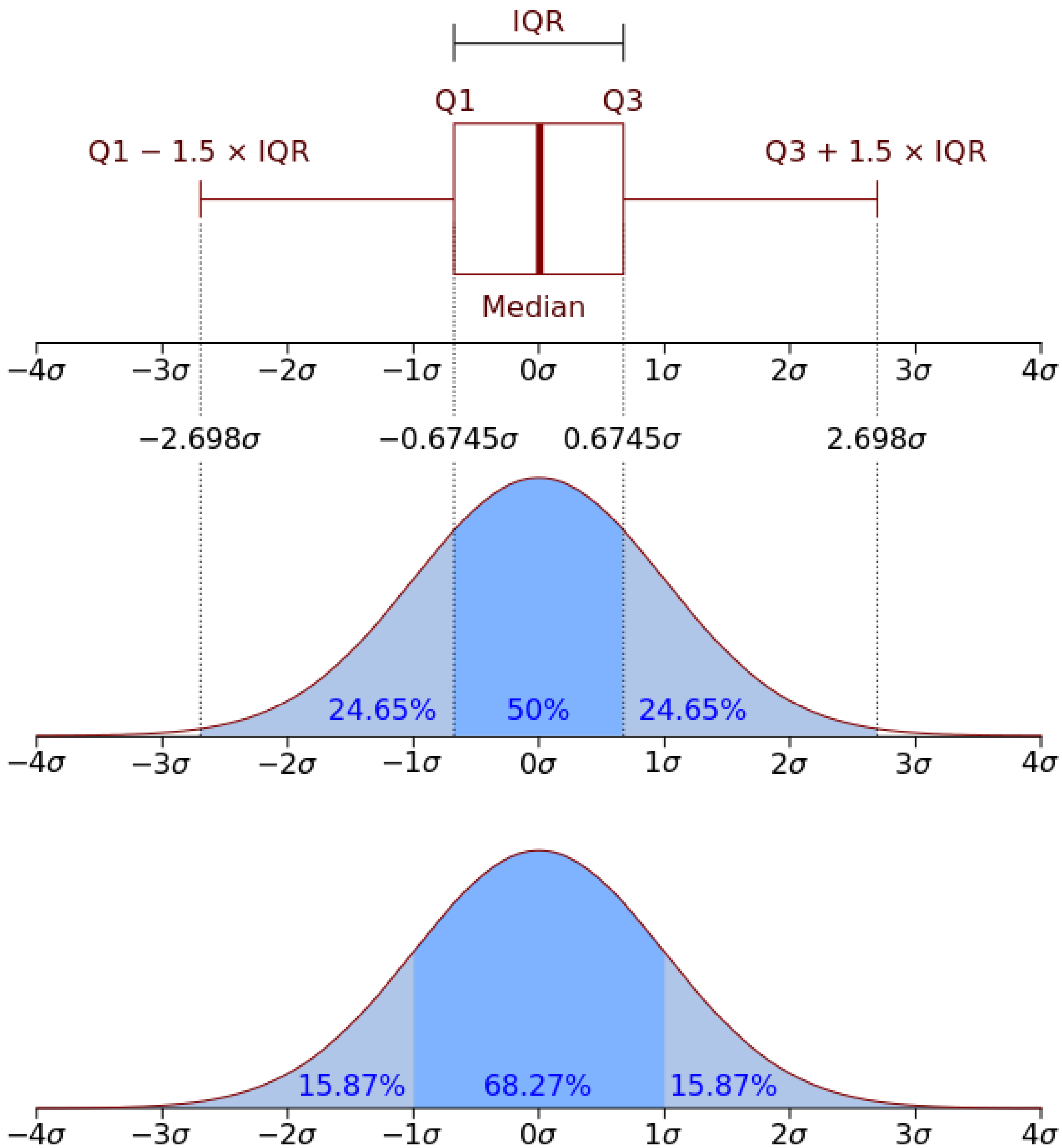


Figure 7.1: Box plot and PDF of a normal distribution $N(0, \sigma^2)$

Source: Wikipedia Commons

7.4.3 Cumulative Density Function (CDF)

Discrete

- Cumulatve density function is probability X will take a value of x or lower.
- PDF is written $f(x)$, and CDF is written $F'(x)$.

$$F_X(x) = Pr(X \leq x)$$

- For discrete CDFs, that means summing up over all values.

> Exercise:
>
> What is the probability of rolling a 6 or lower with two dice? $F(6) = ?$

Continuous

- We can't sum probabilities for continuous distributions (remember the 0 problem).
- Solution: integration

$$F_Y(y) = \int_{-\infty}^{y} f(y)dy$$

- Examples of uniform distribution.

7.5 Common types of probability distributions

There are many useful probability distributions. In this section we will cover three of the most common ones: the binomial, uniform, and normal distributions.

7.5.1 Binomial distribution

A Binomial distribution is defined as follow: $X \sim Binomial(n, p)$

PMF:

$$\binom{n}{k} p^k (1-p)^{n-k}$$

, where n is the number of trials, p is the probability of success, and k is the number of successes.

Remember that:

$$\binom{n}{k} = \frac{n!}{k!(n-k)!}$$

For example, let's say that voters choose some candidate with probability 0.02. What is the probability of seeing exactly 0 voters of the candidate in a sample of 100 people?

We can compute the PMF of a binomial distribution using R's `dbinom()` function.

```r
dbinom(x = 0, size = 100, prob = 0.02)
```

```
[1] 0.1326196
```

```r
dbinom(x = 1, size = 100, prob = 0.02)
```

```
[1] 0.2706522
```

Similarly, we can compute the CDF using R's `pbinom()` function:

```r
pbinom(q = 0, size = 100, prob = 0.02)
```

```
[1] 0.1326196
```

```r
pbinom(q = 100, size = 100, prob = 0.02)
```

```
[1] 1
```

```r
pbinom(q = 1, size = 100, prob = 0.02)
```

```
[1] 0.4032717
```

> **Exercise**
>
> Compute the probability of seeing between 1 and 10 voters of the candidate in a sample of 100 people.

7.5.2 Uniform distribution

A uniform distribution has two parameters: a minimum and a maximum. So $X \sim U(a, b)$.

- PDF:

$$\begin{cases} \frac{1}{b-a} & , x \in [a, b] \\ 0 & , \text{otherwise} \end{cases}$$

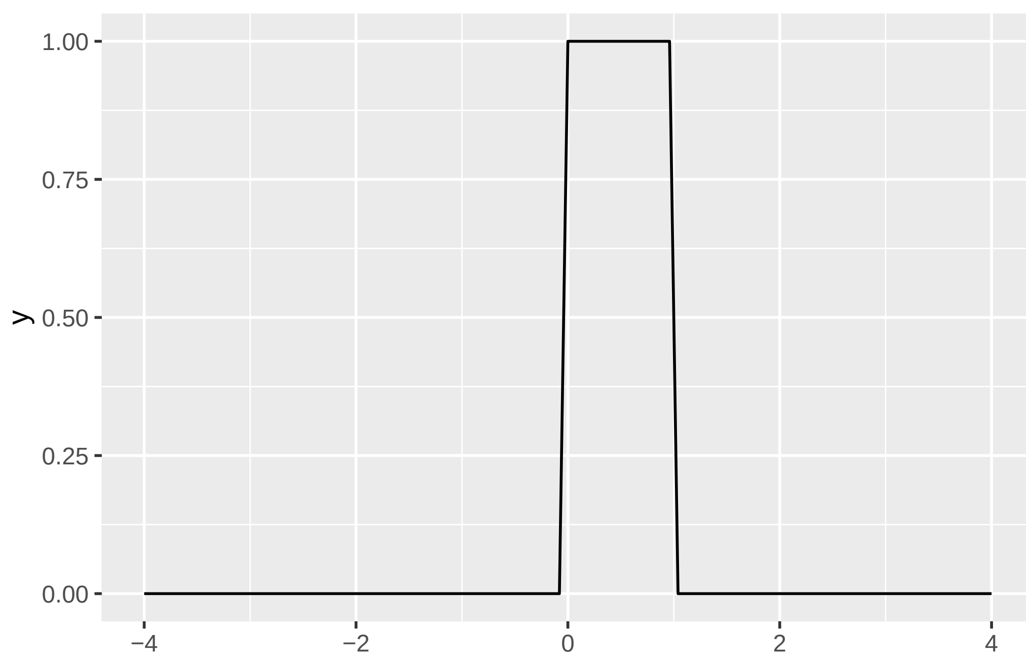
- CDF:

$$\begin{cases} 0 & , x < a \\ \frac{x-a}{b-a} & , x \in [a, b] \\ 1 & , x > b \end{cases}$$

In R, `dunif()` gives the PDF of a uniform distribution. By default, it is $X \sim U(0, 1)$.

```
library(tidyverse)
```

```
ggplot() +
  stat_function(fun = dunif, xlim = c(-4, 4))
```



Meanwhile, `punif()` evaluates the CDF of a uniform distribution.

```
punif(q = .3)
```

```
[1] 0.3
```

> **Exercise**
>
> Evaluate the CDF of $Y \sim U(-2, 2)$ at point $y = 1$. Use the formula and `punif()`.

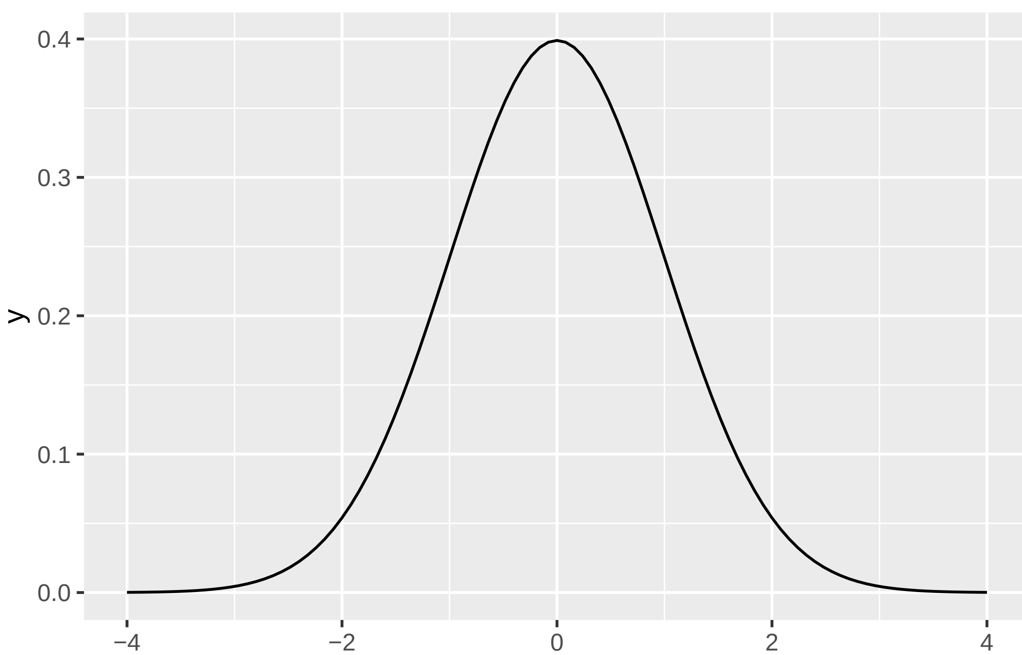
7.5.3 Normal distribution

A normal distribution has two parameters: a mean and a standard deviation. So $X \sim N(\mu, \sigma)$.

- PDF: $2\frac{1}{\sigma\sqrt{2\pi}}e^{-\frac{1}{2}(\frac{x-\mu}{\sigma})^2}$

In R, `dnorm()` gives us the PDF of a standard normal distribution ($Z \sim N(0, 1)$):

```
ggplot() +
  stat_function(fun = dnorm, xlim = c(-4, 4))
```



Like you might expect, `pnorm()` computes the CDF of a normal distribution (by default, the standard normal).

```
pnorm(0)
```

```
[1] 0.5
```

```
pnorm(1) - pnorm(-1)
```

```
[1] 0.6826895
```

> **Exercise**
>
> What is the probability of obtaining a value above 1.96 or below -1.96 in a standard normal probability distribution? Hint: use the `pnorm()` function.

8 Statistics and simulations

```
library(tidyverse)
```

8.1 Random sampling

Before we jump to statistics and simulations, we'll cover how to do random sampling in R.

8.1.1 Random sampling from theoretical distributions

Uniform distribution

For the uniform distribution, the arguments specify how many draws we want and the boundaries

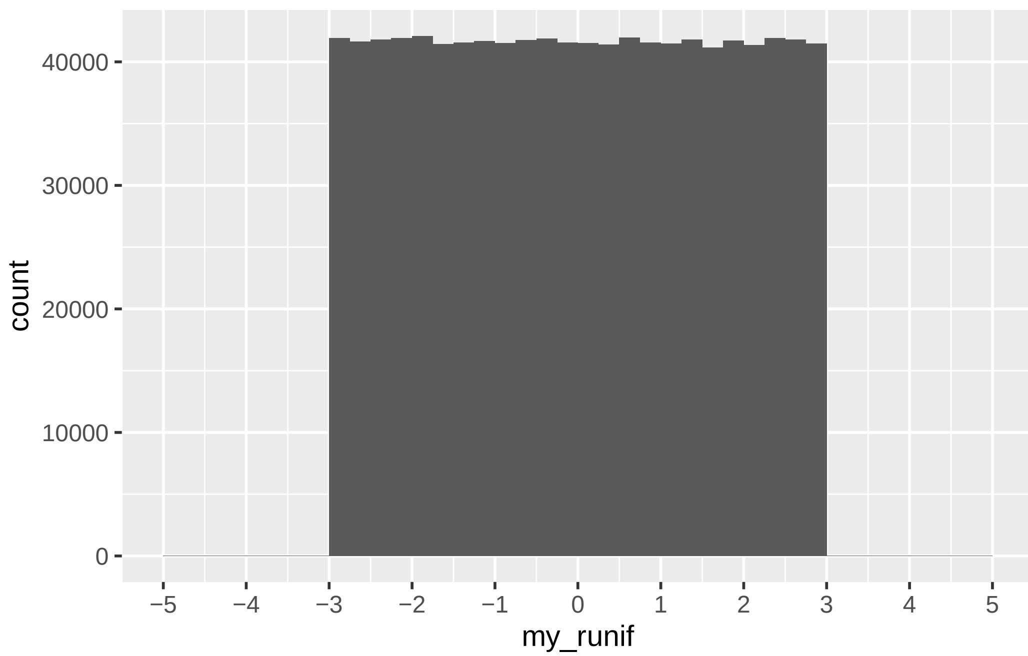
```
runif(n = 20, min = -3, max = 3)
```

```
 [1]  1.8296946 -2.8675775  0.1479456  2.0746701  0.6505194 -2.7358402
 [7] -0.9232697  0.5528655 -1.8622765 -2.6383892  1.4122433  1.7811805
[13]  1.0443270  0.5272953 -1.4213804 -0.8412322  1.9827302  1.7462656
[19]  1.5447222 -1.6104076
```

When we draw a million times from the distribution, we can then plot it and see that it does look as we would expect:

```
set.seed(123)
my_runif <- runif(n = 1000000, min = -3, max = 3)
```

```
ggplot(data.frame(my_runif), aes(x = my_runif)) +
  geom_histogram(binwidth = 0.25, boundary = 0, closed = "right") +
  scale_x_continuous(breaks = seq(-5, 5, 1), limits = c(-5, 5))
```



Binomial distribution

For the binomial distribution, we can specify the number of draws, how many trials each draw will have, and the probability of success.

For instance, we can ask R to do the following twenty times: flip a fair coin one hundred times, and count the number of tails.

```
rbinom(n = 20, size = 100, prob = 0.5)
```

```
 [1] 48 45 54 50 58 50 42 58 48 57 53 49 52 51 49 40 57 53 52 41
```

With `prob =` , we can implement unfair coins:

```
rbinom(n = 20, size = 100, prob = 0.9)
```

```
 [1] 88 87 93 95 93 92 91 94 87 91 90 92 93 89 90 95 91 90 86 88
```

Normal distribution

For the Normal or Gaussian distribution, we specify the number of draws, the mean, and standard deviation:

```
rnorm(n = 20, mean = 0, sd = 1)
```

```
 [1]  1.10455864  0.06386693 -1.59684275  1.86298270 -0.90428935 -1.55158044
 [7]  1.27986282 -0.32420495 -0.70015076  2.17271578  0.89778913 -0.01338538
[13] -0.74074395  0.36772316 -0.66453402 -1.11498344 -1.15067439 -0.55098894
[19]  0.10503154 -0.27183645
```

> **Exercise**
>
> Compute and plot `my_rnorm`, a vector with 10,000 draws from a Normal distribution X with mean equal to -10 and standard deviation equal to 2 ($X \sim N(-10, 2)$). You can recycle code!

8.1.2 Random sampling from data

In this section we will work with good ol' `mtcars`, one of R's most notable default datasets. We'll assign it to an object so it shows in our Environment pane:

```
my_mtcars <- mtcars
```

> **Tip**
>
> Default datasets such as `mtcars` and `iris` are useful because they are available to everyone, and once you become familiar with them, you can start thinking about the code instead of the intricacies of the data. These qualities also make default datasets ideal for building **reproducible examples** (see Wickham 2014)

We can use the function `sample()` to obtain random values from a vector. The `size =` argument specifies how many values we want. For example, let's get one random value of the "mpg" column:

```
sample(my_mtcars$mpg, size = 1)
```

```
[1] 24.4
```

Every time we run this command, we can get a different result:

```
sample(my_mtcars$mpg, size = 1)
```

```
[1] 14.7
```

```
sample(my_mtcars$mpg, size = 1)
```

```
[1] 15.5
```

In some occasions we do want to get the same result consistently after running some random process multiple times. In this case, we *set a seed*, which takes advantage of R's pseudo-random number generator capabilities. No matter how many times we run the following code block, the result will be the same:

```
set.seed(123)
sample(my_mtcars$mpg, size = 1)
```

```
[1] 15
```

Sampling *with replacement* means that we can get the same value multiple times. For example:

```
set.seed(12)
sample(c("Banana", "Apple", "Orange"), size = 3, replace = T)
```

```
[1] "Apple"  "Apple"  "Orange"
```

```
sample(my_mtcars$mpg, size = 100, replace = T)
```

```
  [1] 26.0 15.2 18.7 18.7 30.4 21.0 24.4 26.0 32.4 15.8 32.4 19.2 18.1 16.4 19.2
 [16] 27.3 14.3 10.4 17.3 13.3 21.4 13.3 19.2 24.4 15.0 27.3 17.8 15.2 15.8 14.3
 [31] 19.7 16.4 18.7 15.8 19.2 21.0 14.3 15.2 14.3 27.3 21.4 33.9 33.9 21.4 30.4
 [46] 33.9 21.4 17.3 17.3 10.4 26.0 18.7 15.2 30.4 10.4 10.4 15.5 14.3 26.0 17.3
 [61] 33.9 26.0 24.4 18.7 30.4 32.4 21.5 30.4 15.2 27.3 13.3 17.3 21.4 24.4 13.3
 [76] 22.8 33.9 13.3 21.5 14.3 19.2 30.4 24.4 26.0 15.8 10.4 24.4 14.3 15.2 10.4
 [91] 19.2 21.0 16.4 19.2 24.4 19.7 18.7 10.4 18.7 17.8
```

In order to sample not from a vector but from a data frame's rows, we can use the `slice_sample()` function from `dplyr`:

```r
my_mtcars |>
  slice_sample(n = 2) # a number of rows
```

```
                  mpg cyl disp  hp drat   wt  qsec vs am gear carb
Dodge Challenger 15.5   8  318 150 2.76 3.52 16.87  0  0    3    2
Datsun 710       22.8   4  108  93 3.85 2.32 18.61  1  1    4    1
```

```r
my_mtcars |>
  slice_sample(prop = 0.5) # a proportion of rows
```

```
                     mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
Merc 450SE          16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3
Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
```

Again, we can also use seeds here to ensure that we'll get the same result each time:

```r
set.seed(123)
my_mtcars |>
  slice_sample(prop = 0.5)
```

```
                    mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Maserati Bora      15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
Cadillac Fleetwood 10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
Honda Civic        30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
Merc 450SLC        15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3
Datsun 710         22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
```

```
Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
```

> **Exercise**
>
> Use `slice_sample()` to sample 32 rows from `mtcars` *with replacement*.

8.2 Statistics

> The problems considered by probability and statistics are inverse to each other. In probability theory we consider some underlying process which has some randomness or uncertainty modeled by random variables, and we figure out what happens. In statistics we observe something that has happened, and try to figure out what underlying process would explain those observations. (quote attributed to Persi Diaconis)

- In statistics we try to learn about a **data-generating process** (DGP) using our observed data. Examples: surveys, GDP statistics.
- Usually we are restrained to **samples**, while our DGPs of interest are **population-based**.
  - So we use **random sampling** or refer to **superpopulations** as a way to justify how the data we observe can approximate the population.
- Statistics has two main targets:
  - **Estimation**: how we find a reasonable guess of an unknown property (parameter) of a DGP
  - **Inference**: how we describe uncertainty about our estimate
- We use an **estimator** $\hat{\theta}(\cdot)$, which is a function that summarizes data, as a guess about a parameter θ. A guess generated by an estimator in a given sample is called an **estimate**.

> **Exercise**
>
> Suppose there's a uniform distribution $X \sim U(0, \text{unknown})$ out there.[1] We want to use a sample from this distribution (let's say of n=30 observations) to estimate the unknown upper bound.
> Discuss: would the sample maximum be a good estimator? Why or why not?

- Theoretical statistics is all about finding "good" estimators. A few properties of good estimators:
  - **Unbiasedness**: Across multiple random samples, an unbiased estimator gets the right answer on average.
  - **Low variance**: Across multiple random samples, a low-variance estimator is more concentrated around the true parameter.
  - BUT it's sometimes hard to get both unbiasedness and low variance. So we have to make sacrifices. We usually quantify this via the mean squared error: $MSE = bias^2 + variance$. Comparing two estimators, the one with the lowest MSE is said to be more **efficient**.
  - **Consistency**: A consistent estimator converges in probability to the true value. "If we had enough data, the probability that our estimate would be far from the truth would be close to zero" (Aronow and Miller 2019, p. 105).
- Applied statistics is about using these techniques reasonably in messy real-world situations…

8.3 Simulations

- In simulations, we generate fake data following standard procedures. Why?
  - To better understand how our estimators work in different settings (the methods reason)
  - To get insights about complex processes with many moving parts (the substantive reason) (let's talk about gerrymandering).

> **Exercise**
>
> Simulate drawing an n=30 random sample from a $X \sim U(0, 10)$ distribution and take its maximum value.

[1] This is a fascinating distribution with a rich history, and it is used in many statistical textbooks (Whittinghill and Hogg, 2001). It is thoroughly covered in the UT SDS Mathematical Statistics sequence.

8.3.1 Loops

Loops allow us to repeat operations in R. The most common construct is the for-loop:

```r
for (i in 1:10){
  print(i)
}
```

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

It's common to perform operations at each step and save the results. We typically create an empty object and "fill it in" at each step:

```r
results <- double(10)
for (i in 1:10){
  results[i] <- i ^ 2
}
```

```r
results
```

```
 [1]   1   4   9  16  25  36  49  64  81 100
```

Functional loops

Another way to do loops is with the `*apply()` family of functions:

```r
sapply(1:10, function(x){x ^ 2})
```

```
 [1]   1   4   9  16  25  36  49  64  81 100
```

We talked about loops and various extensions in one of our methods workshops last year: Speedy R.

8.3.2 An example simulation

We will simulate our exercise from above 10,000 times:

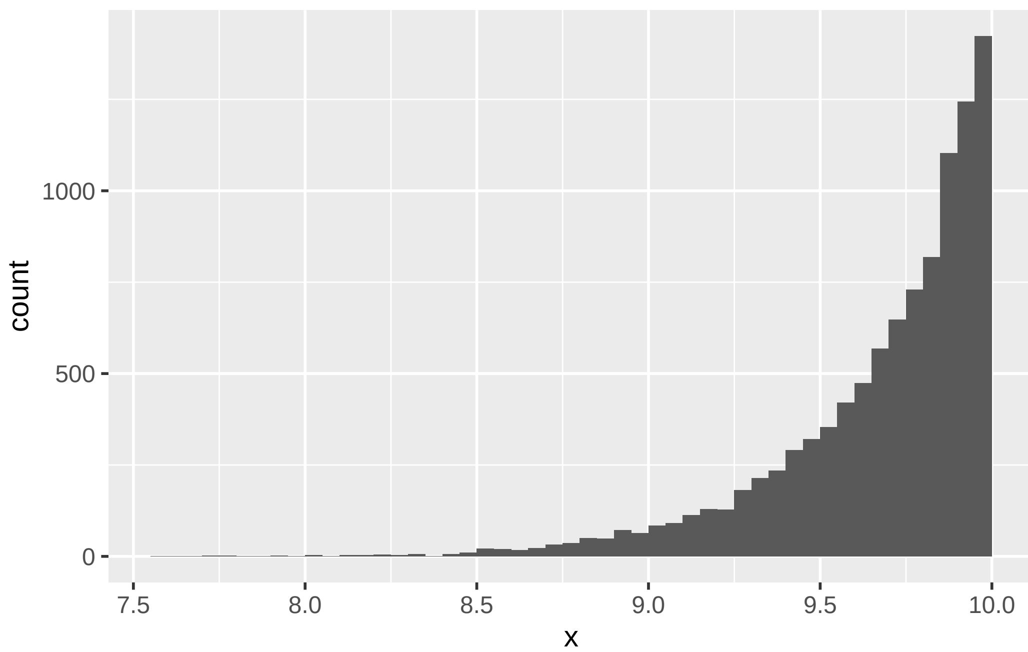
```
set.seed(1)
k <- 10000 # number of simulations
n <- 30    # number of observations in each simulation

# define an empty numeric object
simulated_estimates <- double(k)

# loop: at each step draw a random n=30 sample and get its maximum
for (i in 1:k){
  random_sample <- runif(n, 0, 10)
  simulated_estimates[i] <- max(random_sample)
}
```

Now we can analyze our simulated estimates:

```
mean(simulated_estimates)
```

```
[1] 9.677225
```

```
ggplot(data.frame(x = simulated_estimates), aes(x = x)) +
  geom_histogram(binwidth = 0.05, boundary = 0, closed = "right")
```



Exercise

We just simulated to evaluate the sample maximum as an estimator. Modify the code above to evaluate the following two estimators:

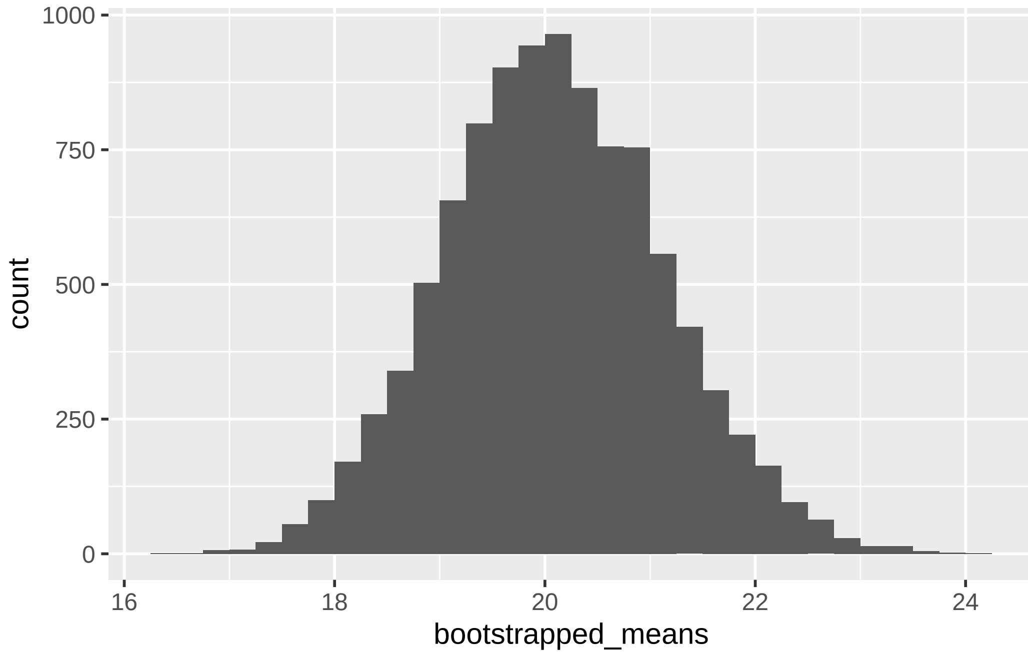
- $\text{(sample maximum)} \cdot \dfrac{(n+1)}{n}$
- $2 \cdot \text{(sample mean)}$

8.3.3 Another example simulation: bootstrapping

Bootstrap (and its relatives) is one way in which we can do *inference*, i.e., assess uncertainty. (We'll go through the intuition on the board.)

```
# set seed an number of simulations
set.seed(1)
k <- 10000
bootstrapped_means <- double(k)
for (i in 1:k){
  m <- my_mtcars |> slice_sample(prop = 1, replace = T)
  bootstrapped_means[i] <- mean(m$mpg)
}
```

```
ggplot(data.frame(bootstrapped_means), aes(x = bootstrapped_means)) +
  geom_histogram(binwidth = 0.25, boundary = 0, closed = "right")
```



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