Quantitive Social Science: The R Tidyverse Code

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Contents

Preface

This is tidyverse R code to supplement the book, Quantitative Social Science: An Introduction, by Kosuke Imai.

The R code included with the text of *QSS* and the supplementary materials relies mostly on base R functions. This translates the code examples provided with *QSS* to tidyverse R code. Tidyverse refers to a set of packages (**ggplot2**, **dplyr**, **tidyr**, **readr**, **purrr**, **tibble**, and a few others) that share common data representations, especially the use of data frames for return values.

This is not a complete introduction to R and the tidyverse. I suggest pairing it with R for Data Science by Hadley Wickham and Garrett Grolemond.

These materials are supplement to replace the existing *QSS* code with the tidvyerse dialect of R. Thus it does not replicate the substantive material, and not meant to be used independently of the *QSS* text. However, the provided code is not merely a translation of the *QSS* code. It often uses the topics in *QSS* to delve deeper into data science, data visualization, and computational topics.

I wrote this code while teaching course that employed both texts in order to make the excellent examples and statistical material in *QSS* more compatible with the modern data science using R approach in *R4DS*.

Colophon

To install the R packages used in this work run the following code, installs the **qsstidy** package which contains no code or data, but will install the needed dependencies.

```r
install.packages("devtools")
install_github("jrnold/qss-tidy")
```

Additionally, the gganimate package requires installing ffmpeg with libvpx support.

The source of the book is available here and was built with versions of packages below:

```
#> Session info -------------------------------------------------------------
#>  setting  value
#>  version  R version 3.4.3 (2017-11-30)
#>  system   x86_64, darwin15.6.0
#>  ui       X11
#>  language (EN)
#>  collate  en_US.UTF-8
#>  tz       America/Los_Angeles
#>  date     2017-12-22
#> Packages -----------------------------------------------------------------
#>  package    * version date       source
#>  animation  * 2.5     2017-03-30 cran (@2.5)
#>  assertthat   0.2.0   2017-04-11 CRAN (R 3.4.0)
#>  backports    1.1.2   2017-12-13 CRAN (R 3.4.3)
#>  base       * 3.4.3   2017-12-07 local
#>  bindr        0.1     2016-11-13 CRAN (R 3.4.0)
#>  bindrcpp     0.2     2017-06-17 CRAN (R 3.4.0)
#>  bookdown     0.5     2017-08-20 CRAN (R 3.4.1)
#>  broom        0.4.3   2017-11-20 CRAN (R 3.4.3)
#>  cellranger   1.1.0   2016-07-27 CRAN (R 3.4.0)
#>  cli          1.0.0   2017-11-05 cran (@1.0.0)
#>  colorspace   1.3-2   2016-12-14 CRAN (R 3.4.0)
#>  compiler     3.4.3   2017-12-07 local
#>  crayon       1.3.4   2017-09-16 CRAN (R 3.4.1)
#>  datasets   * 3.4.3   2017-12-07 local
#>  devtools     1.13.4  2017-11-09 CRAN (R 3.4.2)
#>  digest       0.6.13  2017-12-14 CRAN (R 3.4.3)
#>  dplyr      * 0.7.4   2017-09-28 CRAN (R 3.4.2)
#>  evaluate     0.10.1  2017-06-24 CRAN (R 3.4.1)
#>  forcats    * 0.2.0   2017-01-23 CRAN (R 3.4.0)
#>  foreign      0.8-69  2017-06-22 CRAN (R 3.4.3)
#>  ggplot2    * 2.2.1   2016-12-30 CRAN (R 3.4.0)
#>  glue         1.2.0   2017-10-29 CRAN (R 3.4.2)
#>  graphics   * 3.4.3   2017-12-07 local
#>  grDevices  * 3.4.3   2017-12-07 local
#>  grid         3.4.3   2017-12-07 local
#>  gtable       0.2.0   2016-02-26 CRAN (R 3.4.0)
#>  haven        1.1.0   2017-07-09 CRAN (R 3.4.1)
#>  hms          0.4.0   2017-11-23 CRAN (R 3.4.3)
#>  htmltools    0.3.6   2017-04-28 CRAN (R 3.4.0)
#>  httr         1.3.1   2017-08-20 CRAN (R 3.4.1)
#>  jsonlite     1.5     2017-06-01 CRAN (R 3.4.0)
#>  knitr        1.17    2017-08-10 CRAN (R 3.4.1)
#>  lattice      0.20-35 2017-03-25 CRAN (R 3.4.3)
#>  lazyeval     0.2.1   2017-10-29 CRAN (R 3.4.2)
#>  lubridate    1.7.1   2017-11-03 cran (@1.7.1)
#>  magrittr     1.5     2014-11-22 CRAN (R 3.4.0)
#>  memoise      1.1.0   2017-04-21 CRAN (R 3.4.0)
#>  methods      3.4.3   2017-12-07 local
#>  mnormt       1.5-5   2016-10-15 CRAN (R 3.4.0)
#>  modelr       0.1.1   2017-07-24 CRAN (R 3.4.1)
#>  munsell      0.4.3   2016-02-13 CRAN (R 3.4.0)
#>  nlme         3.1-131 2017-02-06 CRAN (R 3.4.3)
#>  parallel     3.4.3   2017-12-07 local
#>  pkgconfig    2.0.1   2017-03-21 CRAN (R 3.4.0)
#>  plyr         1.8.4   2016-06-08 CRAN (R 3.4.0)
#>  psych        1.7.8   2017-09-09 CRAN (R 3.4.1)
#>  purrr      * 0.2.4   2017-10-18 cran (@0.2.4)
#>  R6           2.2.2   2017-06-17 CRAN (R 3.4.0)
#>  Rcpp         0.12.14 2017-11-23 CRAN (R 3.4.3)
#>  readr      * 1.1.1   2017-05-16 CRAN (R 3.4.0)
#>  readxl       1.0.0   2017-04-18 CRAN (R 3.4.0)
#>  reshape2     1.4.3   2017-12-11 CRAN (R 3.4.3)
#>  rlang        0.1.4   2017-11-05 CRAN (R 3.4.2)
#>  rmarkdown    1.8     2017-11-17 CRAN (R 3.4.2)
#>  rprojroot    1.3-1   2017-12-18 CRAN (R 3.4.3)
#>  rstudioapi   0.7     2017-09-07 CRAN (R 3.4.1)
#>  rvest        0.3.2   2016-06-17 CRAN (R 3.4.0)
#>  scales       0.5.0   2017-08-24 CRAN (R 3.4.1)
#>  stats      * 3.4.3   2017-12-07 local
#>  stringi      1.1.6   2017-11-17 CRAN (R 3.4.2)
#>  stringr    * 1.2.0   2017-02-18 CRAN (R 3.4.0)
#>  tibble     * 1.3.4   2017-08-22 CRAN (R 3.4.1)
#>  tidyr      * 0.7.2   2017-10-16 cran (@0.7.2)
#>  tidyverse  * 1.2.1   2017-11-14 CRAN (R 3.4.2)
#>  tools        3.4.3   2017-12-07 local
#>  utils      * 3.4.3   2017-12-07 local
#>  withr        2.1.1   2017-12-19 cran (@2.1.1)
#>  xml2         1.1.1   2017-01-24 CRAN (R 3.4.0)
#>  yaml         2.1.16  2017-12-12 CRAN (R 3.4.3)
```

Chapter 1

Introduction

Prerequisites

In this and other chapters we will make use of data from the `qss` package, which is available on github. Install it using the `install_github()` function from the library `devtools`.

```
devtools::install_github("kosukeimai/qss-package")
```

```
library("qss")
```

In the prerequisites section of each chapter, we'll load any packages needed for the chapter, possibly define some functions, and possibly load data. It is good practice to load necessary libraries at the start of an R markdown file or script.

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

We also load the **readr** package to load `csv` files,

```
library("readr")
```

the **haven** package to load Stata `dta` files,

```
library("haven")
```

and the **rio** package to load multiple types of files

```
library("rio")
```

1.1 Overview of the Book

*This sections contains no code to translate – see*QSS* text.*

1.2 How to use the Book

*This sections contains no code to translate – see*QSS* text.*

1.3 Introduction to R

These notes do not aim to completely teach R and the tidyverse. However, there are many other resources for that.

R for Data Science is a comprehensive introduction to R using the tidyverse.

Data Camp has interactive courses. In particular, I recommend starting with the following two courses.

- Introduction to R
- Introduction to the Tidyverse

1.3.1 Arithmetic Operations

This sections contains no code to translate—see *QSS* text.

1.3.2 Objects

This sections contains no code to translate—see *QSS* text.

Also see R4DS: Workflow basics.

1.3.3 Vectors

This sections contains no code to translate—see *QSS* text.

Also see R4DS: Vectors. In *R for Data Science* vectors are introduced much later, after data frames.

1.3.4 Functions

This sections contains no code to translate—see *QSS* text.

Also see R4DS: Functions.

1.3.5 Data Files

Rather than using `setwd()` in scripts, data analysis should be organized in projects. Read the introduction on RStudio projects in R4DS.[1]

Datasets used in R are accessed in two ways.

- Datasets can be distributed with R packages. These are often smaller datasets used in examples and tutorials in packages. These are loaded with the `data()` function. For example you can load UN data on demographic statistics from the **qss** library, which distributes the data sets used in the *QSS* textbook. (The function `data()` called without any arguments will list all the datasets distributed with installed packages.)

```
data("UNpop", package = "qss")
```

- Datasets can be loaded from external files including both stored R objects (`.RData`, `.rda`) and other formats (`.csv`, `.dta`, `.sav`). To read a csv file into R use the `read_csv` function from the **readr** library, part of the tidyverse.

[1] For more on using projects read Project-oriented workflow.

```
UNpop_URL <- "https://raw.githubusercontent.com/kosukeimai/qss/master/INTRO/UNpop.csv"
UNpop <- read_csv(UNpop_URL)
#> Parsed with column specification:
#> cols(
#>   year = col_integer(),
#>   world.pop = col_integer()
#> )
```

We use the readr functionread_csv() instead of the base R function read.csv() used in the *QSS* text. It is slightly faster, and returns a tibble instead of a data frame. Check this by calling class() on the new object.

```
class(UNpop)
#> [1] "tbl_df"     "tbl"        "data.frame"
UNpop
#> # A tibble: 7 x 2
#>    year world.pop
#>   <int>     <int>
#> 1  1950   2525779
#> 2  1960   3026003
#> 3  1970   3691173
#> 4  1980   4449049
#> 5  1990   5320817
#> 6  2000   6127700
#> # ... with 1 more row
```

See R for Data Science Ch 11: Data Import for more discussion.

Note that in the previous code we loaded the file directly from a URL, but we could also work with local files on your computer, e.g.

```
UNpop <- read_csv("INTRO/UNpop.csv")
```

See R for Data Science Ch 10: Tibbles for a deeper discussion of data frames.

The single bracket, [, is useful to select rows and columns in simple cases.

```
UNpop[c(1, 2, 3), ]
#> # A tibble: 3 x 2
#>    year world.pop
#>   <int>     <int>
#> 1  1950   2525779
#> 2  1960   3026003
#> 3  1970   3691173
```

There are **dplyr** functions to select rows by number, to select rows by certain criteria, or to select columns.

To select rows 1–3, use slice().

```
slice(UNpop, 1:3)
#> # A tibble: 3 x 2
#>    year world.pop
#>   <int>     <int>
#> 1  1950   2525779
#> 2  1960   3026003
#> 3  1970   3691173
```

Base R allows you to choose the column world.pop column from the UNpop data frame:

```
UNpop[, "world.pop"]
#> # A tibble: 7 x 1
#>   world.pop
#>       <int>
#> 1   2525779
#> 2   3026003
#> 3   3691173
#> 4   4449049
#> 5   5320817
#> 6   6127700
#> # ... with 1 more row
UNpop$world.pop
#> [1] 2525779 3026003 3691173 4449049 5320817 6127700 6916183
UNpop[["world.pop"]]
#> [1] 2525779 3026003 3691173 4449049 5320817 6127700 6916183
select(UNpop, world.pop)
#> # A tibble: 7 x 1
#>   world.pop
#>       <int>
#> 1   2525779
#> 2   3026003
#> 3   3691173
#> 4   4449049
#> 5   5320817
#> 6   6127700
#> # ... with 1 more row
```

Unlike `[`, the `[[` and `$` operators can only select a single column and return a vector.[2] The `dplyr` function `select()` **always** returns a tibble (data frame), and never a vector, even if only one column is selected.

Select rows 1–3 of the `year` column:

```
UNpop[1:3, "year"]
#> # A tibble: 3 x 1
#>    year
#>   <int>
#> 1  1950
#> 2  1960
#> 3  1970
```

or,

```
select(slice(UNpop, 1:3), year)
#> # A tibble: 3 x 1
#>    year
#>   <int>
#> 1  1950
#> 2  1960
#> 3  1970
```

The same series of functions can be performed using the pipe operator, `%>%`.

```
UNpop %>%
  slice(1:3) %>%
  select(year)
```

[2] See the discussion in R for Data Science on how `tibble` objects differ from base `data.frame` objects in how `[` is handled.

```
#> # A tibble: 3 x 1
#>    year
#>   <int>
#> 1  1950
#> 2  1960
#> 3  1970
```

This example may seem verbose, but later we can produce more complicated transformations of the data by chaining together simple functions.

Select every other row from `UNpop`:

```
UNpop$world.pop[seq(from = 1, to = nrow(UNpop), by = 2)]
#> [1] 2525779 3691173 5320817 6916183
```

or

```
UNpop %>%
  slice(seq(1, n(), by = 2)) %>%
  select(world.pop)
#> # A tibble: 4 x 1
#>   world.pop
#>       <int>
#> 1   2525779
#> 2   3691173
#> 3   5320817
#> 4   6916183
```

or

```
UNpop %>%
  filter(row_number() %% 2 == 1)
#> # A tibble: 4 x 2
#>    year world.pop
#>   <int>     <int>
#> 1  1950   2525779
#> 2  1970   3691173
#> 3  1990   5320817
#> 4  2010   6916183
```

The function `n()` when used in a **dplyr** function returns the number of rows in the data frame (or the number of rows in the group if used with `group_by()`). The function `row_number()` returns the row number of an observation. The `%%` operator returns the modulus, i.e. division remainder.

1.3.6 Saving Objects

It is not recommended that you save the entire R workspace using `save.image` due to the negative and unexpected impacts it can have on reproducibility.See the R for Data Science chapter Workflow Projects.

You should uncheck the options in RStudio to avoid saving and restoring from `.RData` files (go to `Tools > Global Options > General`). This will help ensure that your R code runs the way you think it does, instead of depending on some long forgotten code that is only saved in the workspace image. Everything important should be in a script. Anything saved or loaded from file should be done explicitly.

Your motto should be that the **source is real**, not the objects created by it.

> The source code is real. The objects are realizations of the source code. Source for EVERY user modified object is placed in a particular directory or directories, for later editing and retrieval. –

from the ESS manual

This means that while you should not save the entire workplace it is perfectly fine practice to run a script and save or load R objects to files, using or .

As with reading CSV files, use the readr package functions. In this case, `write_csv()` writes a csv file and takes at least two objects: the data that you want to write to a csv and the name that you want to give the file.

```
write_csv(UNpop, "UNpop.csv")
```

1.3.7 Programming and Learning Tips

Use the haven package to read and write Stata (`.dta`) and SPSS (`.sav`) files. Stata and SPSS are two other statistical programs commonly used in social science. Even if you don't ever use them, you'll almost certainly encounter data stored in their native formats.

```
UNpop_dta_url <- "https://github.com/kosukeimai/qss/raw/master/INTRO/UNpop.dta"
UNpop <- read_dta(UNpop_dta_url)
UNpop
#> # A tibble: 7 x 2
#>    year world_pop
#>   <dbl>     <dbl>
#> 1 1950.     2526.
#> 2 1960.     3026.
#> 3 1970.     3691.
#> 4 1980.     4449.
#> 5 1990.     5321.
#> 6 2000.     6128.
#> # ... with 1 more row
```

There is also the equivalent `write_dta()` function to create Stata datasets.

```
write_dta(UNpop, "UNpop.dta")
```

While Stata and SPSS data sets are quite similar to data frames, they differ slightly in definitions of acceptable data types of columns and what metadata they store with the data. +Be careful when reading and writing from these formats to ensure that information is not lost.

Also see the rio package which makes loading data even easier with smart defaults.

You can use the `import()` function to load many types of files:

```
import("https://github.com/kosukeimai/qss/raw/master/INTRO/UNpop.csv")
#>   year world.pop
#> 1 1950   2525779
#> 2 1960   3026003
#> 3 1970   3691173
#> 4 1980   4449049
#> 5 1990   5320817
#> 6 2000   6127700
#> 7 2010   6916183

import("https://github.com/kosukeimai/qss/raw/master/INTRO/UNpop.RData")
#>   year world.pop
#> 1 1950   2525779
#> 2 1960   3026003
#> 3 1970   3691173
#> 4 1980   4449049
#> 5 1990   5320817
#> 6 2000   6127700
#> 7 2010   6916183

import("https://github.com/kosukeimai/qss/raw/master/INTRO/UNpop.dta")
#>   year world_pop
#> 1 1950      2526
#> 2 1960      3026
#> 3 1970      3691
#> 4 1980      4449
#> 5 1990      5321
#> 6 2000      6128
#> 7 2010      6916
```

R also includes the **foreign** package, which contains functions for reading and writing files using **haven**. One reason to use these packages is that they are better maintained. For example, the R function `read.dta()` does not read files created by the most recent versions of Stata (13+), whereas **haven** does.

1.3.8 Style Guide

Following a consistent coding style is important for your code to be readable by you and others. The preferred style is the tidyverse style guide, which differs slightly from Google's R style guide.

- The lintr package will check files for style errors.
- The styler package provides functions for automatically formatting R code according to style guides.
- In RStudio, go to the `Tools > Global Options > Code > Diagnostics` pane and check the box to activate style warnings. On this pane, there are other options that can be set in order to increase or decrease the amount of warnings while writing R code in RStudio.

Chapter 2

Causality

Prerequisites

```
library("tidyverse")
library("stringr")
```

2.1 Racial Discrimination in the Labor Market

Load the data from the **qss** package.

```
data("resume", package = "qss")
```

In addition to the `dim()`, `summary()`, and `head()` functions shown in the text,

```
dim(resume)
#> [1] 4870    4
summary(resume)
#>   firstname              sex                 race                 call
#>  Length:4870         Length:4870         Length:4870         Min.   :0.00
#>  Class :character    Class :character    Class :character    1st Qu.:0.00
#>  Mode  :character    Mode  :character    Mode  :character    Median :0.00
#>                                                              Mean   :0.08
#>                                                              3rd Qu.:0.00
#>                                                              Max.   :1.00
head(resume)
#>   firstname    sex  race call
#> 1   Allison female white    0
#> 2   Kristen female white    0
#> 3   Lakisha female black    0
#> 4   Latonya female black    0
#> 5    Carrie female white    0
#> 6       Jay   male white    0
```

we can also use `glimpse()` to get a quick understanding of the variables in the data frame:

```
glimpse(resume)
#> Observations: 4,870
#> Variables: 4
#> $ firstname <chr> "Allison", "Kristen", "Lakisha", "Latonya", "Carrie"...
#> $ sex       <chr> "female", "female", "female", "female", "female", "m...
#> $ race      <chr> "white", "white", "black", "black", "white", "white"...
#> $ call      <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
```

The code in *QSS* uses `table()` and `addmargins()` to construct the table. However, this can be done easily with the **dplyr** package using grouping and summarizing.

Use `group_by()` to identify each combination of `race` and `call`, and then `count()` the observations:

```
race_call_tab <-
  resume %>%
  group_by(race, call) %>%
  count()
race_call_tab
#> # A tibble: 4 x 3
#> # Groups:   race, call [4]
#>    race  call     n
#>   <chr> <int> <int>
#> 1 black     0  2278
#> 2 black     1   157
#> 3 white     0  2200
#> 4 white     1   235
```

If we want to calculate callback rates by race, we can use the `mutate()` function from **dplyr**.

```
race_call_rate <-
  race_call_tab %>%
  group_by(race) %>%
  mutate(call_rate =  n / sum(n)) %>%
  filter(call == 1) %>%
  select(race, call_rate)
race_call_rate
#> # A tibble: 2 x 2
#> # Groups:   race [2]
#>    race call_rate
#>   <chr>     <dbl>
#> 1 black    0.0645
#> 2 white    0.0965
```

If we want the overall callback rate, we can calculate it from the original data. Use the `summarise()` function from **dplyr**.

```
resume %>%
  summarise(call_back = mean(call))
#>   call_back
#> 1    0.0805
```

2.2 Subsetting Data in R

2.2.1 Subsetting

Create a new object of all individuals whose `race` variable equals `black` in the `resume` data:

```
resumeB <-
  resume %>%
  filter(race == "black")
```

```
glimpse(resumeB)
#> Observations: 2,435
#> Variables: 4
#> $ firstname <chr> "Lakisha", "Latonya", "Kenya", "Latonya", "Tyrone", ...
#> $ sex       <chr> "female", "female", "female", "female", "male", "fem...
#> $ race      <chr> "black", "black", "black", "black", "black", "black"...
#> $ call      <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
```

Calculate the callback rate for black individuals:

```
resumeB %>%
  summarise(call_rate = mean(call))
#>   call_rate
#> 1    0.0645
```

You can combine the `filter()` and `select()` functions with multiple conditions. For example, to keep the call and first name variables for female individuals with stereotypically black names:

```
resumeBf <-
  resume %>%
  filter(race == "black", sex == "female") %>%
  select(call, firstname)
head(resumeBf)
#>   call firstname
#> 1    0   Lakisha
#> 2    0   Latonya
#> 3    0     Kenya
#> 4    0   Latonya
#> 5    0     Aisha
#> 6    0     Aisha
```

Now we can calculate the gender gap by group.

Now we can calculate the gender gap by group. Doing so may seem to require a little more code, but we will not duplicate as much as in *QSS*, and this would easily scale to more than two categories.

First, group by race and sex and calculate the callback rate for each group:

```
resume_race_sex <-
  resume %>%
  group_by(race, sex) %>%
  summarise(call = mean(call))
head(resume_race_sex)
#> # A tibble: 4 x 3
#> # Groups:   race [2]
#>   race  sex      call
#>   <chr> <chr>   <dbl>
#> 1 black female 0.0663
#> 2 black male   0.0583
#> 3 white female 0.0989
#> 4 white male   0.0887
```

Use `spread()` from the **tidyr** package to make each value of `race` a new column:

```
resume_sex <-
  resume_race_sex %>%
  ungroup() %>%
  spread(race, call)
resume_sex
#> # A tibble: 2 x 3
#>   sex     black  white
#>   <chr>   <dbl>  <dbl>
#> 1 female 0.0663 0.0989
#> 2 male   0.0583 0.0887
```

Now we can calculate the race wage differences by sex as before,

```
resume_sex %>%
  mutate(call_diff = white - black)
#> # A tibble: 2 x 4
#>   sex     black  white call_diff
#>   <chr>   <dbl>  <dbl>     <dbl>
#> 1 female 0.0663 0.0989    0.0326
#> 2 male   0.0583 0.0887    0.0304
```

This could be combined into a single chain with only six lines of code:

```
resume %>%
  group_by(race, sex) %>%
  summarise(call = mean(call)) %>%
  ungroup() %>%
  spread(race, call) %>%
  mutate(call_diff = white - black)
#> # A tibble: 2 x 4
#>   sex     black  white call_diff
#>   <chr>   <dbl>  <dbl>     <dbl>
#> 1 female 0.0663 0.0989    0.0326
#> 2 male   0.0583 0.0887    0.0304
```

For more information on a way to do this using the spread and gather functions from tidyr package, see the R for Data Science chapter "Tidy Data".

WARNING The function ungroup removes the groupings in group_by. The function `spread` will not allow a grouping variable to be reshaped. Since many **dplyr** functions work differently depending on whether the data frame is grouped or not, I find that I can encounter many errors due to forgetting that a data frame is grouped. As such, I tend to `ungroup` data frames as soon as I am no longer are using the groupings.

Alternatively, we could have used `summarise` and the `diff` function:

```
resume %>%
  group_by(race, sex) %>%
  summarise(call = mean(call)) %>%
  group_by(sex) %>%
  arrange(race) %>%
  summarise(call_diff = diff(call))
#> # A tibble: 2 x 2
#>   sex    call_diff
#>   <chr>      <dbl>
#> 1 female    0.0326
#> 2 male      0.0304
```

I find the `spread` code preferable since the individual race callback rates are retained in the data, and since there is no natural ordering of the `race` variable (unlike if it were a time-series), it is not obvious from reading the code whether `call_diff` is `black - white` or `white - black`.

2.2.2 Simple conditional statements

dlpyr has three conditional statement functions `if_else`, `recode` and `case_when`.

The function `if_else` is like `ifelse` but corrects inconsistent behavior that `ifelse` exhibits in certain cases.

Create a variable `BlackFemale` using `if_else()` and confirm it is only equal to `1` for black and female observations:

```
resume %>%
  mutate(BlackFemale = if_else(race == "black" & sex == "female", 1, 0)) %>%
  group_by(BlackFemale, race, sex) %>%
  count()
#> # A tibble: 4 x 4
#> # Groups:   BlackFemale, race, sex [4]
#>   BlackFemale race  sex        n
#>         <dbl> <chr> <chr>  <int>
#> 1          0. black male     549
#> 2          0. white female  1860
#> 3          0. white male     575
#> 4          1. black female  1886
```

Warning The function `if_else` is more strict about the variable types than `ifelse`. While most R functions are forgiving about variables types, and will automatically convert integers to numeric or vice-versa, they are distinct. For example, these examples will produce errors:

```
resume %>%
  mutate(BlackFemale = if_else(race == "black" & sex == "female", TRUE, 0))
#> Error in mutate_impl(.data, dots): Evaluation error: `false` must be type logical, not double.
```

because `TRUE` is logical and `0` is numeric.

```
resume %>%
  mutate(BlackFemale = if_else(race == "black" & sex == "female", 1L, 0))
#> Error in mutate_impl(.data, dots): Evaluation error: `false` must be type integer, not double.
```

because `1L` is an integer and `0` is numeric vector (floating-point number). The distinction between integers and numeric variables is often invisible because most functions coerce variables between integer and numeric vectors.

```
class(1)
#> [1] "numeric"
class(1L)
#> [1] "integer"
```

The `:` operator returns integers and `as.integer` coerces numeric vectors to integer vectors:

```
class(1:5)
#> [1] "integer"
class(c(1, 2, 3))
#> [1] "numeric"
class(as.integer(c(1, 2, 3)))
#> [1] "integer"
```

2.2.3 Factor Variables

For more on factors see the R for Data Science chapter “Factors” and the package forcats. Also see the R for Data Science chapter “Strings” for working with strings.

The function `case_when` is a generalization of the `if_else` function to multiple conditions. For example, to create categories for all combinations of race and sex,

```
resume %>%
  mutate(
    race_sex = case_when(
      race == "black" & sex == "female" ~ "black, female",
      race == "white" & sex == "female" ~ "white female",
      race == "black" & sex == "male" ~ "black male",
      race == "white" & sex == "male" ~ "white male"
    )
  ) %>%
  head()
#>   firstname    sex  race call      race_sex
#> 1   Allison female white    0  white female
#> 2   Kristen female white    0  white female
#> 3   Lakisha female black    0 black, female
#> 4   Latonya female black    0 black, female
#> 5    Carrie female white    0  white female
#> 6       Jay   male white    0    white male
```

Each condition is a formula (an R object created with the “tilde” `~`). You will see formulas used extensively in the modeling section. The condition is on the left-hand side of the formula. The value to assign to observations meeting that condition is on the right-hand side. Observations are given the value of the first matching condition, so the order of these can matter.

The `case_when` function also supports a default value by using a condition `TRUE` as the last condition. This will match anything not already matched. For example, if you wanted three categories (“black male”, “black female”, “white”):

```
resume %>%
  mutate(
    race_sex = case_when(
      race == "black" & sex == "female" ~ "black female",
      race == "black" & sex == "male" ~ "black male",
      TRUE ~ "white"
    )
  ) %>%
  head()
#>   firstname    sex  race call     race_sex
#> 1   Allison female white    0        white
#> 2   Kristen female white    0        white
#> 3   Lakisha female black    0 black female
#> 4   Latonya female black    0 black female
#> 5    Carrie female white    0        white
#> 6       Jay   male white    0        white
```

Alternatively, we could have created this variable using string manipulation functions. Use `mutate()` to create a new variable, `type`, str_to_title to capitalize `sex` and `race`, and str_c to concatenate these vectors.

```
resume <-
  resume %>%
  mutate(type = str_c(str_to_title(race), str_to_title(sex)))
```

Some of the reasons given in *QSS* for using factors in this chapter are less important due to the functionality of modern **tidyverse** packages. For example, there is no reason to use `tapply`, as you can use `group_by` and `summarise`,

```
resume %>%
  group_by(type) %>%
  summarise(call = mean(call))
#> # A tibble: 4 x 2
#>   type          call
#>   <chr>        <dbl>
#> 1 BlackFemale 0.0663
#> 2 BlackMale   0.0583
#> 3 WhiteFemale 0.0989
#> 4 WhiteMale   0.0887
```

or,

```
resume %>%
  group_by(race, sex) %>%
  summarise(call = mean(call))
#> # A tibble: 4 x 3
#> # Groups:   race [?]
#>   race  sex      call
#>   <chr> <chr>   <dbl>
#> 1 black female 0.0663
#> 2 black male   0.0583
#> 3 white female 0.0989
#> 4 white male   0.0887
```

What's nice about this approach is that we wouldn't have needed to create the factor variable first as in *QSS*.

We can use that same approach to calculate the mean of first names, and use `arrange()` to sort in ascending order.

```
resume %>%
  group_by(firstname) %>%
  summarise(call = mean(call)) %>%
  arrange(call)
#> # A tibble: 36 x 2
#>   firstname   call
#>   <chr>      <dbl>
#> 1 Aisha     0.0222
#> 2 Rasheed   0.0299
#> 3 Keisha    0.0383
#> 4 Tremayne  0.0435
#> 5 Kareem    0.0469
#> 6 Darnell   0.0476
#> # ... with 30 more rows
```

Tip: General advice for working (or not) with factors:

- Use character vectors instead of factors. They are easier to manipulate with string functions.
- Use factor vectors only when you need a specific ordering of string values in a variable, e.g. in a model or a plot.

2.3 Causal Affects and the Counterfactual

Load the social dataset included in the **qss** package.

```
data("social", package = "qss")
summary(social)
#>      sex             yearofbirth    primary2004      messages        
#>  Length:305866      Min.   :1900   Min.   :0.000   Length:305866     
#>  Class :character   1st Qu.:1947   1st Qu.:0.000   Class :character  
#>  Mode  :character   Median :1956   Median :0.000   Mode  :character  
#>                     Mean   :1956   Mean   :0.401                     
#>                     3rd Qu.:1965   3rd Qu.:1.000                     
#>                     Max.   :1986   Max.   :1.000                     
#>   primary2006        hhsize    
#>  Min.   :0.000   Min.   :1.00  
#>  1st Qu.:0.000   1st Qu.:2.00  
#>  Median :0.000   Median :2.00  
#>  Mean   :0.312   Mean   :2.18  
#>  3rd Qu.:1.000   3rd Qu.:2.00  
#>  Max.   :1.000   Max.   :8.00  
```

Calculate the mean turnout by message:

```
turnout_by_message <-
  social %>%
  group_by(messages) %>%
  summarize(turnout = mean(primary2006))
turnout_by_message
#> # A tibble: 4 x 2
#>   messages   turnout
#>   <chr>        <dbl>
#> 1 Civic Duty   0.315
#> 2 Control      0.297
#> 3 Hawthorne    0.322
#> 4 Neighbors    0.378
```

Since we want to calculate the difference by group, spread() the data set so each group is a column, then use mutate() to calculate the difference of each from the control group. Finally, use select() and matches() to return a dataframe with only those new variables that you have created:

```
turnout_by_message %>%
  spread(messages, turnout) %>%
  mutate(diff_civic_duty = `Civic Duty` - Control,
         diff_Hawthorne = Hawthorne - Control,
         diff_Neighbors = Neighbors - Control) %>%
  select(matches("diff_"))
#> # A tibble: 1 x 3
#>   diff_civic_duty diff_Hawthorne diff_Neighbors
#>             <dbl>          <dbl>          <dbl>
#> 1          0.0179         0.0257         0.0813
```

Find the mean values of age, 2004 turnout, and household size for each group:

```
social %>%
  mutate(age = 2006 - yearofbirth) %>%
  group_by(messages) %>%
  summarise(primary2004 = mean(primary2004),
            age = mean(age),
            hhsize = mean(hhsize))
#> # A tibble: 4 x 4
#>   messages   primary2004   age hhsize
#>   <chr>            <dbl> <dbl>  <dbl>
#> 1 Civic Duty       0.399  49.7   2.19
#> 2 Control          0.400  49.8   2.18
#> 3 Hawthorne        0.403  49.7   2.18
#> 4 Neighbors        0.407  49.9   2.19
```

The function summarise_at allows you to summarize multiple variables, using multiple functions, or both.

```
social %>%
  mutate(age = 2006 - yearofbirth) %>%
  group_by(messages) %>%
  summarise_at(vars(primary2004, age, hhsize), funs(mean))
#> # A tibble: 4 x 4
#>   messages   primary2004   age hhsize
#>   <chr>            <dbl> <dbl>  <dbl>
#> 1 Civic Duty       0.399  49.7   2.19
#> 2 Control          0.400  49.8   2.18
#> 3 Hawthorne        0.403  49.7   2.18
#> 4 Neighbors        0.407  49.9   2.19
```

2.4 Observational Studies

Load and inspect the minimum wage data from the **qss** package:

```
data("minwage", package = "qss")
glimpse(minwage)
#> Observations: 358
#> Variables: 8
#> $ chain      <chr> "wendys", "wendys", "burgerking", "burgerking", "kf...
#> $ location   <chr> "PA", "PA", "PA", "PA", "PA", "PA", "PA", "PA", "PA...
#> $ wageBefore <dbl> 5.00, 5.50, 5.00, 5.00, 5.25, 5.00, 5.00, 5.00, 5.0...
#> $ wageAfter  <dbl> 5.25, 4.75, 4.75, 5.00, 5.00, 5.00, 4.75, 5.00, 4.5...
#> $ fullBefore <dbl> 20.0, 6.0, 50.0, 10.0, 2.0, 2.0, 2.5, 40.0, 8.0, 10...
#> $ fullAfter  <dbl> 0.0, 28.0, 15.0, 26.0, 3.0, 2.0, 1.0, 9.0, 7.0, 18....
#> $ partBefore <dbl> 20.0, 26.0, 35.0, 17.0, 8.0, 10.0, 20.0, 30.0, 27.0...
#> $ partAfter  <dbl> 36, 3, 18, 9, 12, 9, 25, 32, 39, 10, 20, 4, 13, 20,...
summary(minwage)
#>      chain             location           wageBefore     wageAfter
#>  Length:358         Length:358         Min.   :4.25   Min.   :4.25
#>  Class :character   Class :character   1st Qu.:4.25   1st Qu.:5.05
#>  Mode  :character   Mode  :character   Median :4.50   Median :5.05
#>                                        Mean   :4.62   Mean   :4.99
#>                                        3rd Qu.:4.99   3rd Qu.:5.05
#>                                        Max.   :5.75   Max.   :6.25
#>    fullBefore     fullAfter      partBefore     partAfter
#>  Min.   : 0.0   Min.   : 0.0   Min.   : 0.0   Min.   : 0.0
#>  1st Qu.: 2.1   1st Qu.: 2.0   1st Qu.:11.0   1st Qu.:11.0
#>  Median : 6.0   Median : 6.0   Median :16.2   Median :17.0
#>  Mean   : 8.5   Mean   : 8.4   Mean   :18.8   Mean   :18.7
#>  3rd Qu.:12.0   3rd Qu.:12.0   3rd Qu.:25.0   3rd Qu.:25.0
#>  Max.   :60.0   Max.   :40.0   Max.   :60.0   Max.   :60.0
```

First, calculate the proportion of restaurants by state whose hourly wages were less than the minimum wage in NJ, $5.05, for `wageBefore` and `wageAfter`:

Since the NJ minimum wage was $5.05, we'll define a variable with that value. Even if you use them only once or twice, it is a good idea to put values like this in variables. It makes your code closer to self-documenting, i.e. easier for others (including you, in the future) to understand what the code does.

```
NJ_MINWAGE <- 5.05
```

Later, it will be easier to understand `wageAfter < NJ_MINWAGE` without any comments than it would be to understand `wageAfter < 5.05`. In the latter case you'd have to remember that the new NJ minimum wage was 5.05 and that's why you were using that value. Using `5.05` in your code, instead of assigning it to an object called `NJ_MINWAGE`, is an example of a magic number; try to avoid them.

Note that the variable `location` has multiple values: PA and four regions of NJ. So we'll add a state variable to the data.

```
minwage %>%
  count(location)
#> # A tibble: 5 x 2
#>   location      n
#>   <chr>     <int>
#> 1 centralNJ    45
#> 2 northNJ     146
#> 3 PA           67
#> 4 shoreNJ      33
#> 5 southNJ      67
```

We can extract the state from the final two characters of the location variable using thestringr function str_sub:

```
minwage <-
  mutate(minwage, state = str_sub(location, -2L))
```

Alternatively, since `"PA"` is the only value that an observation in Pennsylvania takes in `location`, and since all other observations are in New Jersey:

```
minwage <-
  mutate(minwage, state = if_else(location == "PA", "PA", "NJ"))
```

Let's confirm that the restaurants followed the law:

```
minwage %>%
  group_by(state) %>%
  summarise(prop_after = mean(wageAfter < NJ_MINWAGE),
            prop_Before = mean(wageBefore < NJ_MINWAGE))
#> # A tibble: 2 x 3
#>   state prop_after prop_Before
#>   <chr>      <dbl>       <dbl>
#> 1 NJ       0.00344       0.911
#> 2 PA       0.955         0.940
```

Create a variable for the proportion of full-time employees in NJ and PA after the increase:

```
minwage <-
  minwage %>%
  mutate(totalAfter = fullAfter + partAfter,
         fullPropAfter = fullAfter / totalAfter)
```

Now calculate the average proportion of full-time employees for each state:

```
full_prop_by_state <-
  minwage %>%
  group_by(state) %>%
  summarise(fullPropAfter = mean(fullPropAfter))
full_prop_by_state
#> # A tibble: 2 x 2
#>   state fullPropAfter
#>   <chr>         <dbl>
#> 1 NJ            0.320
#> 2 PA            0.272
```

We could compute the difference in means between NJ and PA by

```
(filter(full_prop_by_state, state == "NJ")[["fullPropAfter"]] -
  filter(full_prop_by_state, state == "PA")[["fullPropAfter"]])
#> [1] 0.0481
```

or

```
spread(full_prop_by_state, state, fullPropAfter) %>%
  mutate(diff = NJ - PA)
#> # A tibble: 1 x 3
#>      NJ    PA   diff
#>   <dbl> <dbl>  <dbl>
#> 1 0.320 0.272 0.0481
```

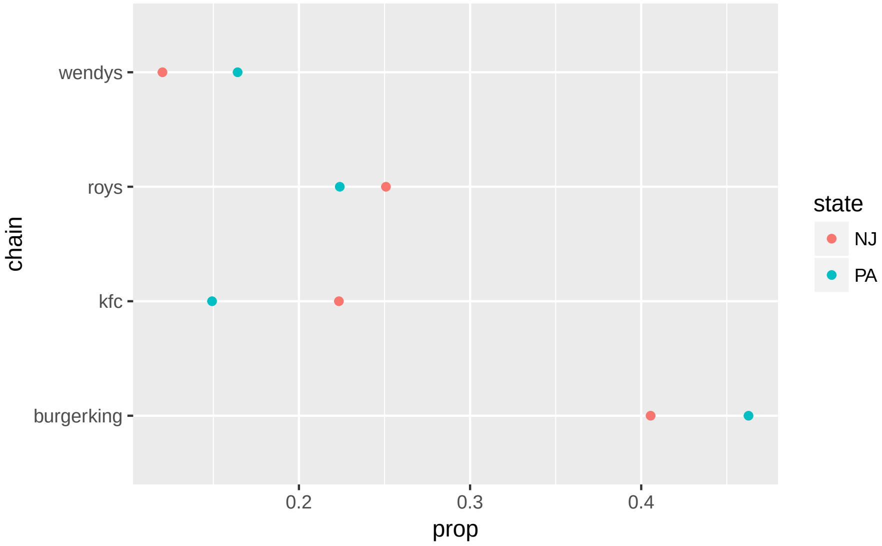
2.4.1 Confounding Bias

We can calculate the proportion of each chain out of all fast-food restaurants in each state:

```
chains_by_state <-
  minwage %>%
  group_by(state) %>%
  count(chain) %>%
  mutate(prop = n / sum(n))
```

We can easily compare these using a dot-plot:

```
ggplot(chains_by_state, aes(x = chain, y = prop, colour = state)) +
  geom_point() +
  coord_flip()
```

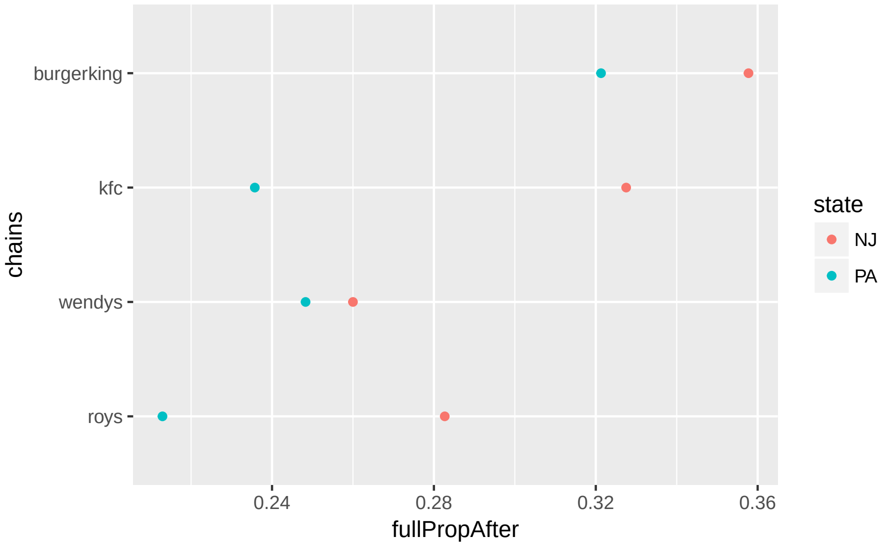


In the *QSS* text, only Burger King restaurants are compared. However, **dplyr** makes comparing all restaurants not much more complicated than comparing two. All we have to do is change the `group_by` statement we used previously so that we group by chain restaurants and states:

```
full_prop_by_state_chain <-
  minwage %>%
  group_by(state, chain) %>%
  summarise(fullPropAfter = mean(fullPropAfter))
full_prop_by_state_chain
#> # A tibble: 8 x 3
#> # Groups:   state [?]
#>   state chain      fullPropAfter
#>   <chr> <chr>              <dbl>
#> 1 NJ    burgerking         0.358
#> 2 NJ    kfc                0.328
#> 3 NJ    roys               0.283
#> 4 NJ    wendys             0.260
#> 5 PA    burgerking         0.321
#> 6 PA    kfc                0.236
#> # ... with 2 more rows
```

We can plot and compare the proportions easily in this format. In general, ordering categorical variables alphabetically is useless, so we'll order the chains by the average of the NJ and PA `fullPropAfter`, using fct_reorder function:

```
ggplot(full_prop_by_state_chain,
       aes(x = forcats::fct_reorder(chain, fullPropAfter),
           y = fullPropAfter,
           colour = state)) +
  geom_point() +
  coord_flip() +
  labs(x = "chains")
```



To calculate the difference between states in the proportion of full-time employees after the change:

```
full_prop_by_state_chain %>%
  spread(state, fullPropAfter) %>%
  mutate(diff = NJ - PA)
#> # A tibble: 4 x 4
#>   chain         NJ    PA   diff
#>   <chr>      <dbl> <dbl>  <dbl>
#> 1 burgerking 0.358 0.321 0.0364
#> 2 kfc        0.328 0.236 0.0918
#> 3 roys       0.283 0.213 0.0697
#> 4 wendys     0.260 0.248 0.0117
```

2.4.2 Before and After and Difference-in-Difference Designs

To compute the estimates in the before and after design first create an additional variable for the proportion of full-time employees before the minimum wage increase.

```
minwage <-
  minwage %>%
  mutate(totalBefore = fullBefore + partBefore,
         fullPropBefore = fullBefore / totalBefore)
```

The before-and-after analysis is the difference between the full-time employment before and after the minimum wage law passed looking only at NJ:

```
minwage %>%
  filter(state == "NJ") %>%
  summarise(diff = mean(fullPropAfter) - mean(fullPropBefore))
#>     diff
#> 1 0.0239
```

The difference-in-differences design uses the difference in the before-and-after differences for each state.

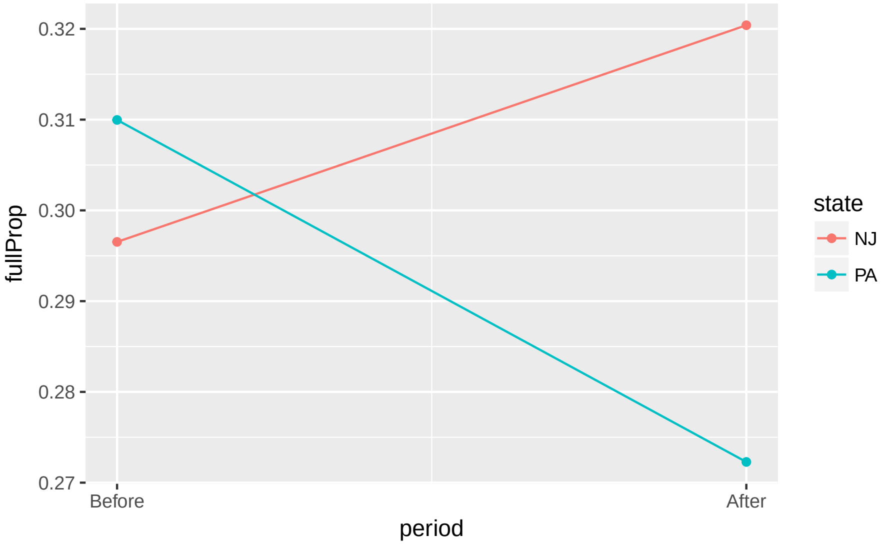
```
minwage %>%
  group_by(state) %>%
  summarise(diff = mean(fullPropAfter) - mean(fullPropBefore)) %>%
  spread(state, diff) %>%
  mutate(diff_in_diff = NJ - PA)
#> # A tibble: 1 x 3
#>       NJ      PA diff_in_diff
#>    <dbl>   <dbl>        <dbl>
#> 1 0.0239 -0.0377       0.0616
```

Let's create a single dataset with the mean values of each state before and after to visually look at each of these designs:

```
full_prop_by_state <-
  minwage %>%
  group_by(state) %>%
  summarise_at(vars(fullPropAfter, fullPropBefore), mean) %>%
  gather(period, fullProp, -state) %>%
  mutate(period = recode(period, fullPropAfter = 1, fullPropBefore = 0))
full_prop_by_state
#> # A tibble: 4 x 3
#>   state period fullProp
#>   <chr>  <dbl>    <dbl>
#> 1 NJ        1.    0.320
#> 2 PA        1.    0.272
#> 3 NJ        0.    0.297
#> 4 PA        0.    0.310
```

Now plot this new dataset:

```
ggplot(full_prop_by_state, aes(x = period, y = fullProp, colour = state)) +
  geom_point() +
  geom_line() +
  scale_x_continuous(breaks = c(0, 1), labels = c("Before", "After"))
```



2.5 Descriptive Statistics for a Single Variable

To calculate the summary for the variables `wageBefore` and `wageAfter` for New Jersey only:

```
minwage %>%
  filter(state == "NJ") %>%
  select(wageBefore, wageAfter) %>%
  summary()
#>    wageBefore     wageAfter
#>  Min.   :4.25   Min.   :5.00
#>  1st Qu.:4.25   1st Qu.:5.05
#>  Median :4.50   Median :5.05
#>  Mean   :4.61   Mean   :5.08
#>  3rd Qu.:4.87   3rd Qu.:5.05
#>  Max.   :5.75   Max.   :5.75
```

We calculate the interquartile range for each state's wages after the passage of the law using the same grouped summarize as we used before:

```
minwage %>%
  group_by(state) %>%
  summarise(wageAfter = IQR(wageAfter),
            wageBefore = IQR(wageBefore))
#> # A tibble: 2 x 3
#>   state wageAfter wageBefore
#>   <chr>     <dbl>      <dbl>
#> 1 NJ        0.         0.620
#> 2 PA        0.575      0.750
```

Calculate the variance and standard deviation of `wageAfter` and `wageBefore` for each state:

```
minwage %>%
  group_by(state) %>%
  summarise(wageAfter_sd = sd(wageAfter),
               wageAfter_var = var(wageAfter),
               wageBefore_sd = sd(wageBefore),
               wageBefore_var = var(wageBefore))
#> # A tibble: 2 x 5
#>   state wageAfter_sd wageAfter_var wageBefore_sd wageBefore_var
#>   <chr>        <dbl>         <dbl>         <dbl>          <dbl>
#> 1 NJ           0.106        0.0112         0.343          0.118
#> 2 PA           0.359        0.129          0.358          0.128
```

Here we can see again how using summarise_at allows for more compact code to specify variables and summary statistics that would be the case using just `summarise`:

```
minwage %>%
  group_by(state) %>%
  summarise_at(vars(wageAfter, wageBefore), funs(sd, var))
#> # A tibble: 2 x 5
#>   state wageAfter_sd wageBefore_sd wageAfter_var wageBefore_var
#>   <chr>        <dbl>         <dbl>         <dbl>          <dbl>
#> 1 NJ           0.106         0.343        0.0112          0.118
#> 2 PA           0.359         0.358        0.129           0.128
```

Chapter 3

Measurement

Prerequisites

```
library("tidyverse")
library("forcats")
library("broom")
library("tidyr")
```

3.1 Measuring Civilian Victimization during Wartime

```
data("afghan", package = "qss")
```

Summarize the variables of interest

```
afghan %>%
  select(age, educ.years, employed, income) %>%
  summary()
#>       age          educ.years     employed        income
#>  Min.   :15.0   Min.   : 0   Min.   :0.000   Length:2754
#>  1st Qu.:22.0   1st Qu.: 0   1st Qu.:0.000   Class :character
#>  Median :30.0   Median : 1   Median :1.000   Mode  :character
#>  Mean   :32.4   Mean   : 4   Mean   :0.583
#>  3rd Qu.:40.0   3rd Qu.: 8   3rd Qu.:1.000
#>  Max.   :80.0   Max.   :18   Max.   :1.000
```

Loading data with either `data()` or`read_csv()` does not convert strings to factors by default; see below with `income`. To get a summary of the different levels, either convert it to a factor (see R4DS Ch 15), or use `count()`:

```
count(afghan, income)
#> # A tibble: 6 x 2
#>   income              n
#>   <chr>           <int>
#> 1 10,001-20,000     616
#> 2 2,001-10,000     1420
#> 3 20,001-30,000      93
#> 4 less than 2,000   457
#> 5 over 30,000        14
#> 6 <NA>              154
```

Use count to calculate the proportion of respondents who answer that they were harmed by the ISAF or the Taliban (`violent.exp.ISAF` and `violent.exp.taliban`, respectively):

```
afghan %>%
  group_by(violent.exp.ISAF, violent.exp.taliban) %>%
  count() %>%
  ungroup() %>%
  mutate(prop = n / sum(n))
#> # A tibble: 9 x 4
#>   violent.exp.ISAF violent.exp.taliban     n    prop
#>              <int>               <int> <int>   <dbl>
#> 1                0                   0  1330 0.483
#> 2                0                   1   354 0.129
#> 3                0                  NA    22 0.00799
#> 4                1                   0   475 0.172
#> 5                1                   1   526 0.191
#> 6                1                  NA    22 0.00799
#> # ... with 3 more rows
```

We need to use `ungroup()` in order to ensure that `sum(n)` sums over the entire dataset as opposed to only within categories of `violent.exp.ISAF`. Unlike `prop.table()`, the code above does not drop missing values. We can drop those values by adding `filter()` and `!is.na()` to test for missing values in those variables:

```
afghan %>%
  filter(!is.na(violent.exp.ISAF), !is.na(violent.exp.taliban)) %>%
  group_by(violent.exp.ISAF, violent.exp.taliban) %>%
  count() %>%
  ungroup() %>%
  mutate(prop = n / sum(n))
#> # A tibble: 4 x 4
#>   violent.exp.ISAF violent.exp.taliban     n  prop
#>              <int>               <int> <int> <dbl>
#> 1                0                   0  1330 0.495
#> 2                0                   1   354 0.132
#> 3                1                   0   475 0.177
#> 4                1                   1   526 0.196
```

3.2 Handling Missing Data in R

We already observed the issues with `NA` values in calculating the proportion answering the "experienced violence" questions. You can filter rows with specific variables having missing values using `filter()` as shown above.

```
head(afghan$income, n = 10)
#>  [1] "2,001-10,000"  "2,001-10,000"  "2,001-10,000"  "2,001-10,000"
#>  [5] "2,001-10,000"  NA              "10,001-20,000" "2,001-10,000"
#>  [9] "2,001-10,000"  NA
head(is.na(afghan$income), n = 10)
#>  [1] FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE  TRUE
```

Counts and proportion of missing values of `income`:

```
summarise(afghan,
          n_missing = sum(is.na(income)),
          p_missing = mean(is.na(income)))
#>   n_missing p_missing
#> 1       154    0.0559
```

Mean, and other functions, do not by default exclude missing values. Use `na.rm = TRUE` in these cases.

```
x <- c(1, 2, 3, NA)
mean(x)
#> [1] NA
mean(x, na.rm = TRUE)
#> [1] 2
```

Table of proportions of individuals harmed by the ISAF and Taliban that includes missing (`NA`) values:

```
violent_exp_prop <-
  afghan %>%
  group_by(violent.exp.ISAF, violent.exp.taliban) %>%
  count() %>%
  ungroup() %>%
  mutate(prop = n / sum(n)) %>%
  select(-n)
violent_exp_prop
#> # A tibble: 9 x 3
#>   violent.exp.ISAF violent.exp.taliban    prop
#>              <int>               <int>   <dbl>
#> 1                0                   0 0.483
#> 2                0                   1 0.129
#> 3                0                  NA 0.00799
#> 4                1                   0 0.172
#> 5                1                   1 0.191
#> 6                1                  NA 0.00799
#> # ... with 3 more rows
```

The data frame above can be reorganized so that rows are ISAF and the columns are Taliban as follows:

```
violent_exp_prop %>%
  spread(violent.exp.taliban, prop)
#> # A tibble: 3 x 4
#>   violent.exp.ISAF     `0`     `1`  `<NA>`
#>              <int>   <dbl>   <dbl>   <dbl>
#> 1                0 0.483   0.129   0.00799
#> 2                1 0.172   0.191   0.00799
#> 3               NA 0.00254 0.00290 0.00363
```

`drop_na` is an alternative to `na.omit` that allows for removing missing values,

```
drop_na(afghan)
```

Tip There are multiple types of missing values.

```
NA  # logical
#> [1] NA
NA_integer_ # integer
#> [1] NA
NA_real_ # double
#> [1] NA
```

```
NA_character_ # character
#> [1] NA
```

In many cases, this distinction does not matter since many functions will coerce these missing values to the correct vector type. However, you will need to use these in some tidyverse functions that require the outputs to be the same type, e.g. `map()` and most of the other purrr functions, and `if_else()`. The code below produces an error, since the `TRUE` case returns an integer value (`x` is an integer), but the `FALSE` case does not specify the type of `NA`.

```
x <- 1:5
class(x)
#> [1] "integer"
if_else(x < 3, x, NA)
#> Error: `false` must be type integer, not logical
```

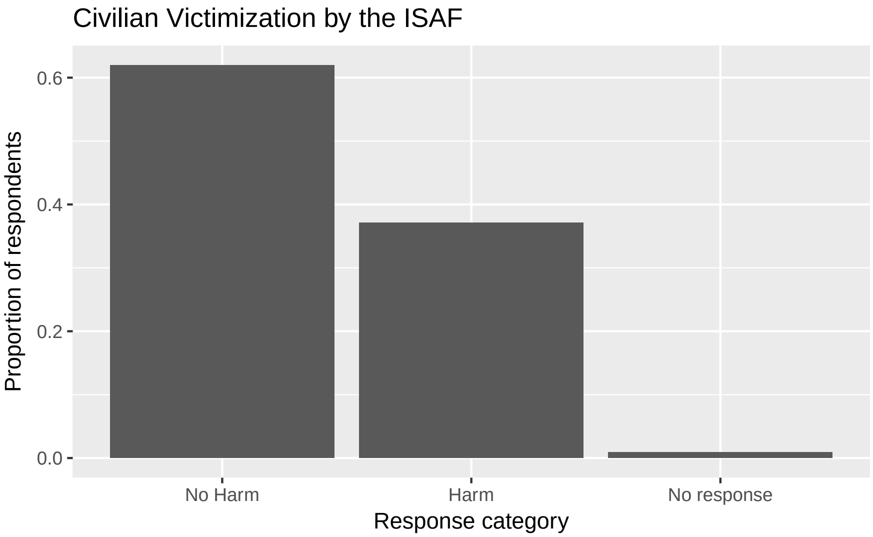
So instead of `NA`, use `NA_integer_`:

```
if_else(x < 3, x, NA_integer_)
#> [1]  1  2 NA NA NA
```

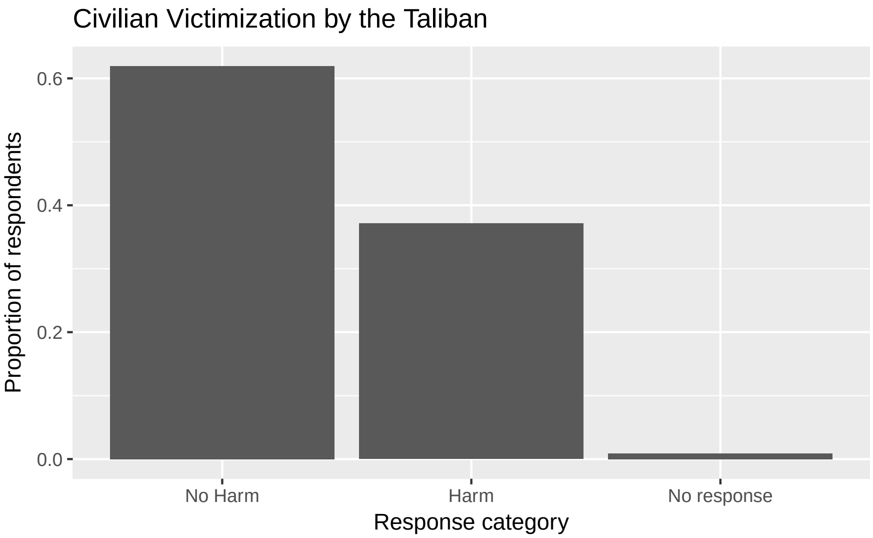
3.3 Visualizing the Univariate Distribution

3.3.1 Barplot

```
afghan <-
  afghan %>%
  mutate(violent.exp.ISAF.fct =
           fct_explicit_na(fct_recode(factor(violent.exp.ISAF),
                                      Harm = "1", "No Harm" = "0"),
                           "No response"))
ggplot(afghan, aes(x = violent.exp.ISAF.fct, y = ..prop.., group = 1)) +
  geom_bar() +
  xlab("Response category") +
  ylab("Proportion of respondents") +
  ggtitle("Civilian Victimization by the ISAF")
```

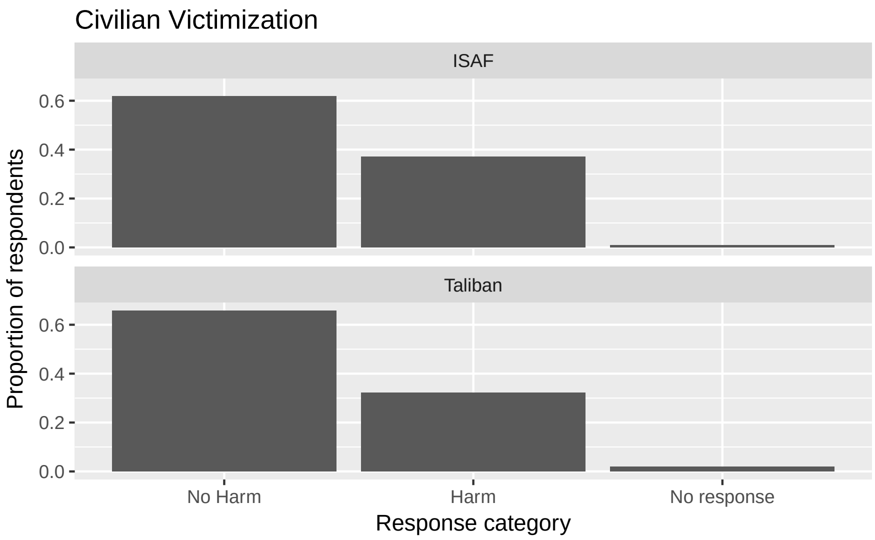


```
afghan <-
  afghan %>%
  mutate(violent.exp.taliban.fct =
           fct_explicit_na(fct_recode(factor(violent.exp.taliban),
                                          Harm = "1", "No Harm" = "0"),
                           "No response"))
ggplot(afghan, aes(x = violent.exp.ISAF.fct, y = ..prop.., group = 1)) +
  geom_bar() +
  xlab("Response category") +
  ylab("Proportion of respondents") +
  ggtitle("Civilian Victimization by the Taliban")
```



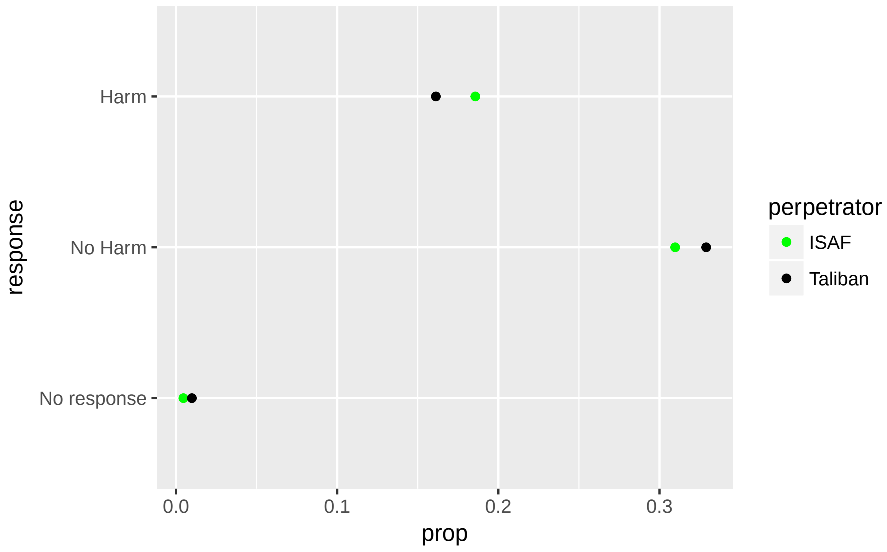
Instead of creating two separate box-plots, create a single plot facetted by ISAF and Taliban:

```
select(afghan, violent.exp.ISAF, violent.exp.taliban) %>%
  gather(variable, value) %>%
  mutate(value = fct_explicit_na(fct_recode(factor(value),
                                 Harm = "1", "No Harm" = "0"),
                                 "No response"),
         variable = recode(variable,
                           violent.exp.ISAF = "ISAF",
                           violent.exp.taliban = "Taliban")) %>%
  ggplot(aes(x = value, y = ..prop.., group = 1)) +
  geom_bar() +
  facet_wrap(~ variable, ncol = 1) +
  xlab("Response category") +
  ylab("Proportion of respondents") +
  ggtitle("Civilian Victimization")
```



This plot could improved by plotting the two values simultaneously to be able to better compare them. This will require creating a data frame that has the following columns: perpetrator (`ISAF`, `Taliban`) and response (`No Harm`, `Harm`, `No response`).

```
violent_exp <-
  afghan %>%
  select(violent.exp.ISAF, violent.exp.taliban) %>%
  gather(perpetrator, response) %>%
  mutate(perpetrator = str_replace(perpetrator, "violent\\.exp\\.", ""),
         perpetrator = str_replace(perpetrator, "taliban", "Taliban"),
         response = fct_recode(factor(response), "Harm" = "1", "No Harm" = "0"),
         response = fct_explicit_na(response, "No response"),
         response = fct_relevel(response, c("No response", "No Harm"))
         ) %>%
  count(perpetrator, response) %>%
  mutate(prop = n / sum(n))
ggplot(violent_exp, aes(x = prop, y = response, color = perpetrator)) +
  geom_point() +
  scale_color_manual(values = c(ISAF = "green", Taliban = "black"))
```

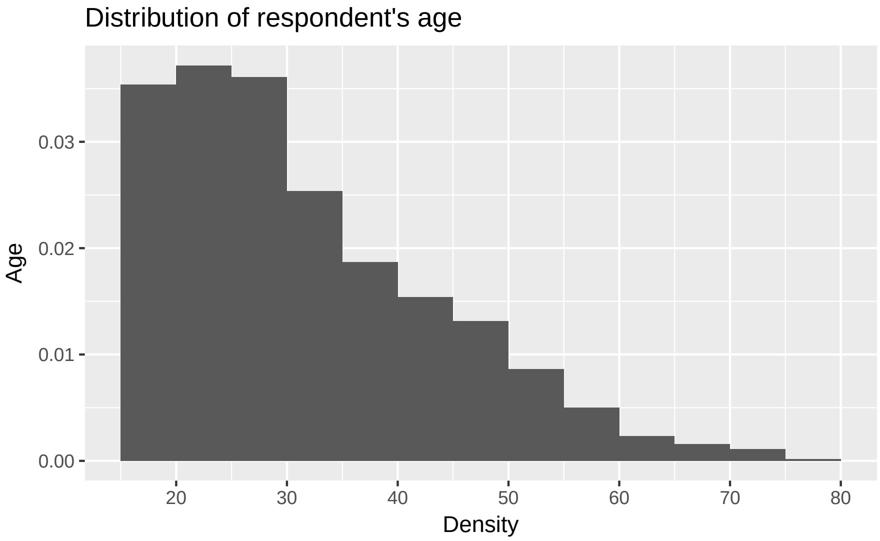


Black was chosen for the Taliban, and Green for ISAF because they are the colors of their respective flags.

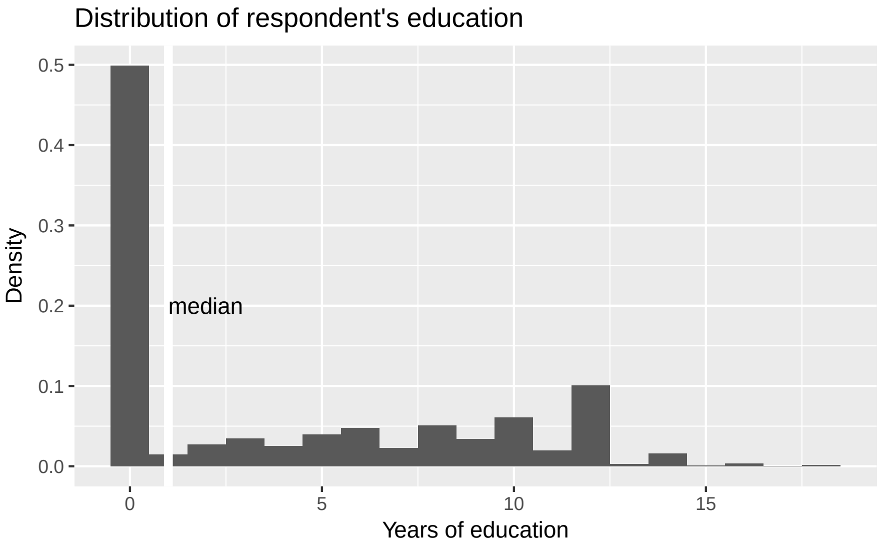
3.3.2 Histogram

See the documentation for geom_histogram.

```
ggplot(afghan, aes(x = age, y = ..density..)) +
  geom_histogram(binwidth = 5, boundary = 0) +
  scale_x_continuous(breaks = seq(20, 80, by = 10)) +
  labs(title = "Distribution of respondent's age",
       y = "Age", x = "Density")
```



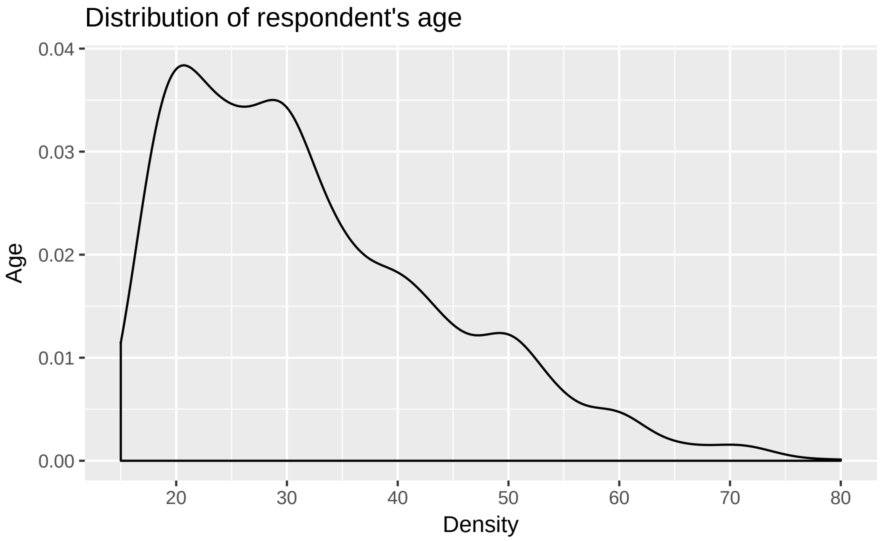
```
ggplot(afghan, aes(x = educ.years, y = ..density..)) +
  geom_histogram(binwidth = 1, center = 0) +
  geom_vline(xintercept = median(afghan$educ.years),
             color = "white", size = 2) +
  annotate("text", x = median(afghan$educ.years),
           y = 0.2, label = "median", hjust = 0) +
  labs(title = "Distribution of respondent's education",
       x = "Years of education",
       y = "Density")
```



There are several alternatives to the histogram.

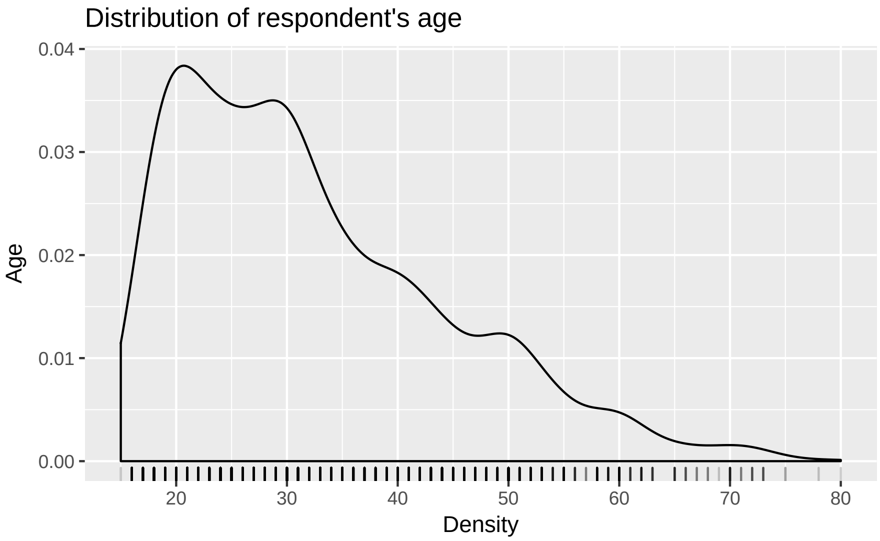
Density plots (geom_density):

```
dens_plot <- ggplot(afghan, aes(x = age)) +
  geom_density() +
  scale_x_continuous(breaks = seq(20, 80, by = 10)) +
  labs(title = "Distribution of respondent's age",
       y = "Age", x = "Density")
dens_plot
```



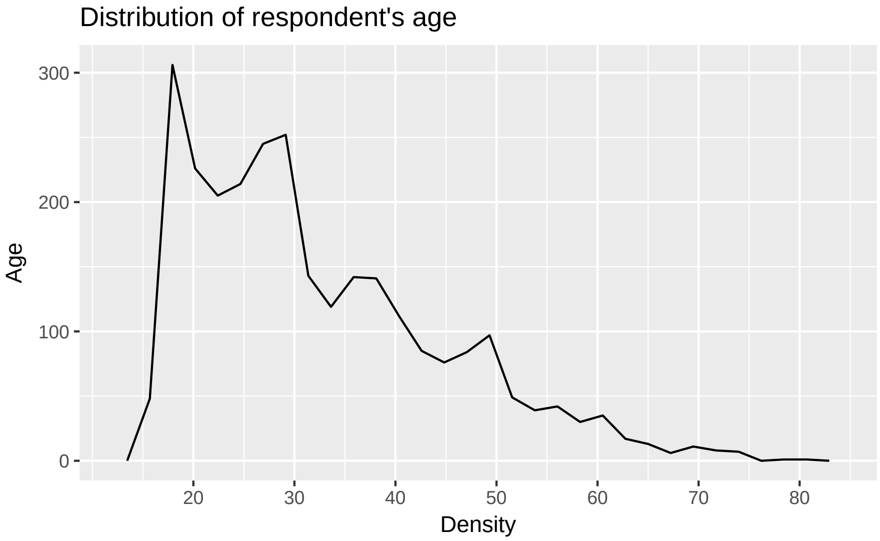
which can be combined with a geom_rug to create a rug plot, which puts small lines on the axis to represent the value of each observation. It can be combined with a scatter or density plot to add extra detail. Adjust the `alpha` to modify the color transparency of the rug and address overplotting.

```
dens_plot + geom_rug(alpha = .2)
```



Frequency polygons (geom_freqpoly): See R for Data Science EDA.

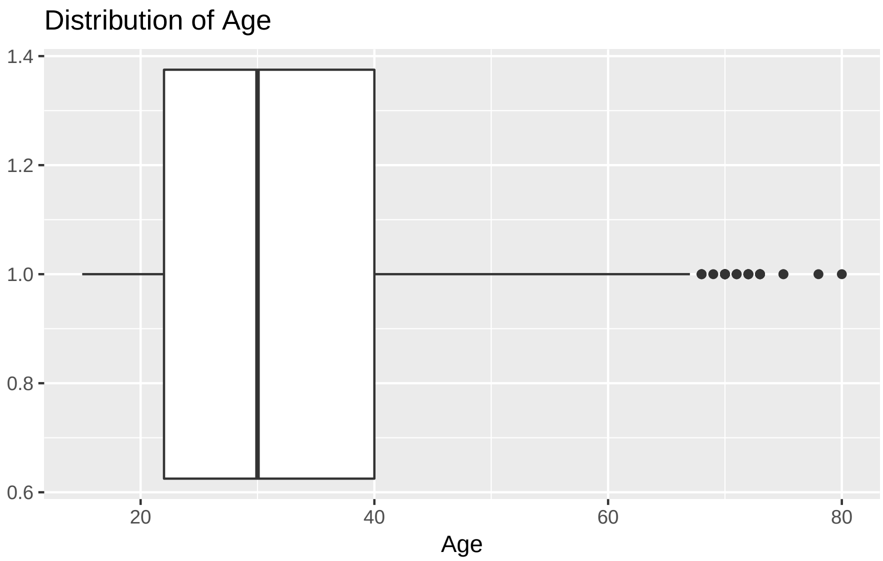
```r
ggplot(afghan, aes(x = age)) +
  geom_freqpoly() +
  scale_x_continuous(breaks = seq(20, 80, by = 10)) +
  labs(title = "Distribution of respondent's age",
       y = "Age", x = "Density")
#> `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



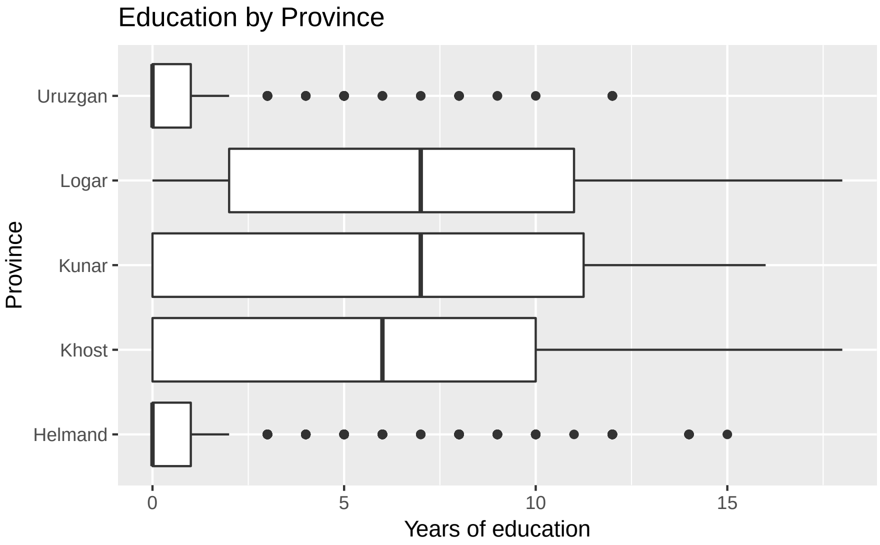
3.3.3 Boxplot

See the documentation for geom_boxplot.

```r
ggplot(afghan, aes(x = 1, y = age)) +
  geom_boxplot() +
  coord_flip() +
  labs(y = "Age", x = "", title = "Distribution of Age")
```



```
ggplot(afghan, aes(y = educ.years, x = province)) +
  geom_boxplot() +
  coord_flip() +
  labs(x = "Province", y = "Years of education",
       title = "Education by Province")
```



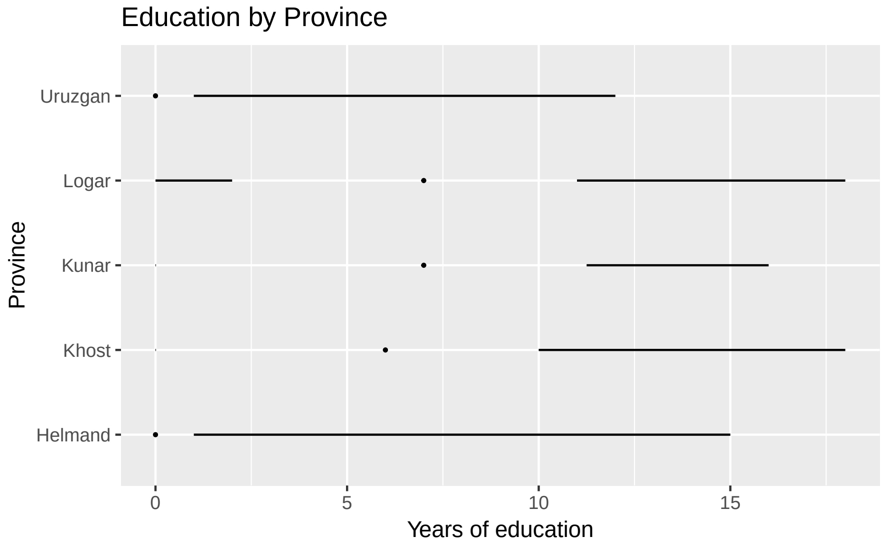
Helmand and Uruzgan have much lower levels of education than the other provinces, and also report higher levels of violence.

```
afghan %>%
  group_by(province) %>%
  summarise(educ.years = mean(educ.years, na.rm = TRUE),
            violent.exp.taliban =
              mean(violent.exp.taliban, na.rm = TRUE),
            violent.exp.ISAF =
              mean(violent.exp.ISAF, na.rm = TRUE)) %>%
  arrange(educ.years)
#> # A tibble: 5 x 4
#>   province educ.years violent.exp.taliban violent.exp.ISAF
#>   <chr>         <dbl>              <dbl>           <dbl>
#> 1 Uruzgan        1.04              0.455           0.496
#> 2 Helmand        1.60              0.504           0.541
#> 3 Khost          5.79              0.233           0.242
#> 4 Kunar          5.93              0.303           0.399
#> 5 Logar          6.70              0.0802          0.144
```

An alternatives to the traditional boxplot:

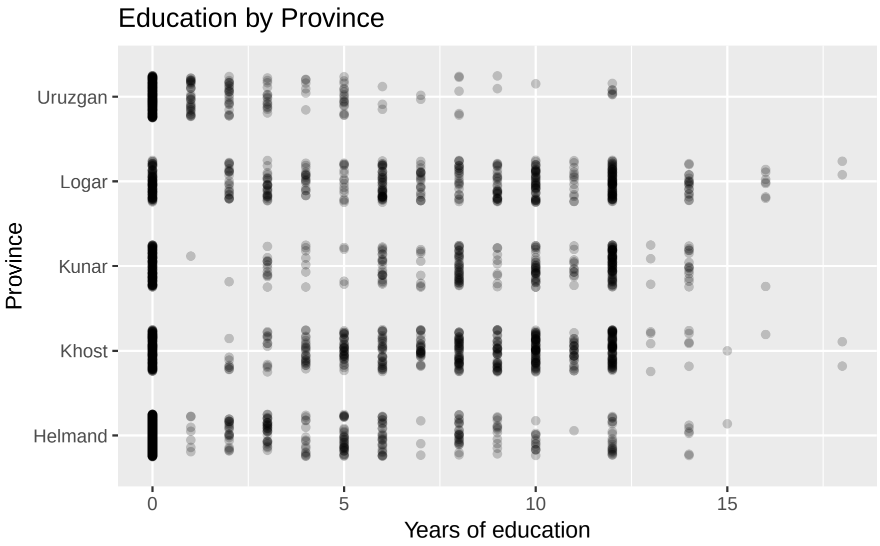
The Tufte boxplot:

```
library("ggthemes")
ggplot(afghan, aes(y = educ.years, x = province)) +
  geom_tufteboxplot() +
  coord_flip() +
  labs(x = "Province", y = "Years of education",
       title = "Education by Province")
```



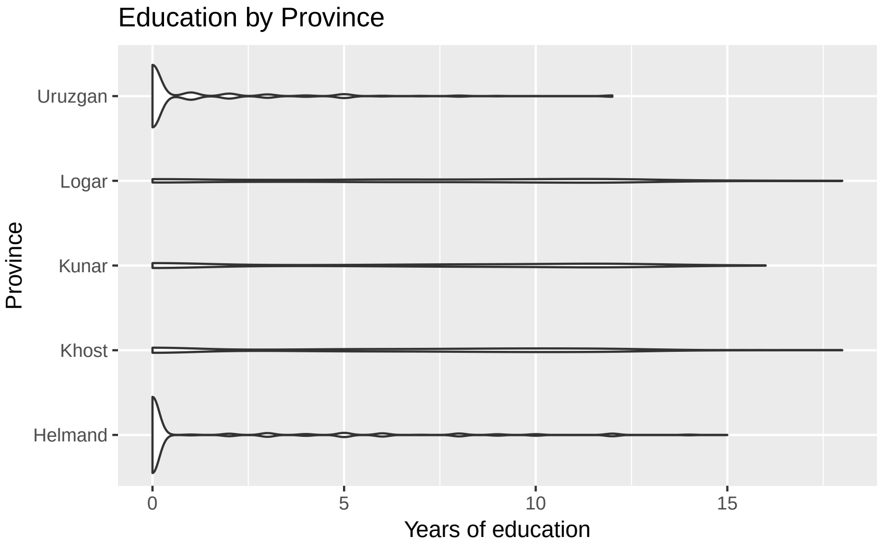
Dot plot with jitter and adjusted alpha to avoid overplotting:

```
ggplot(afghan, aes(y = educ.years, x = province)) +
  geom_point(position = position_jitter(width = 0.25, height = 0),
             alpha = .2) +
  coord_flip() +
  labs(x = "Province", y = "Years of education",
       title = "Education by Province")
```



A violin plot:

```
ggplot(afghan, aes(y = educ.years, x = province)) +
  geom_violin() +
  coord_flip() +
  labs(x = "Province", y = "Years of education",
       title = "Education by Province")
```



3.3.4 Printing and saving graphics

Use the function `rdoc ("ggplot2", "ggsave")` to save ggplot2 graphics. Also, R Markdown files have their own means of creating and saving plots created by code-chunks.

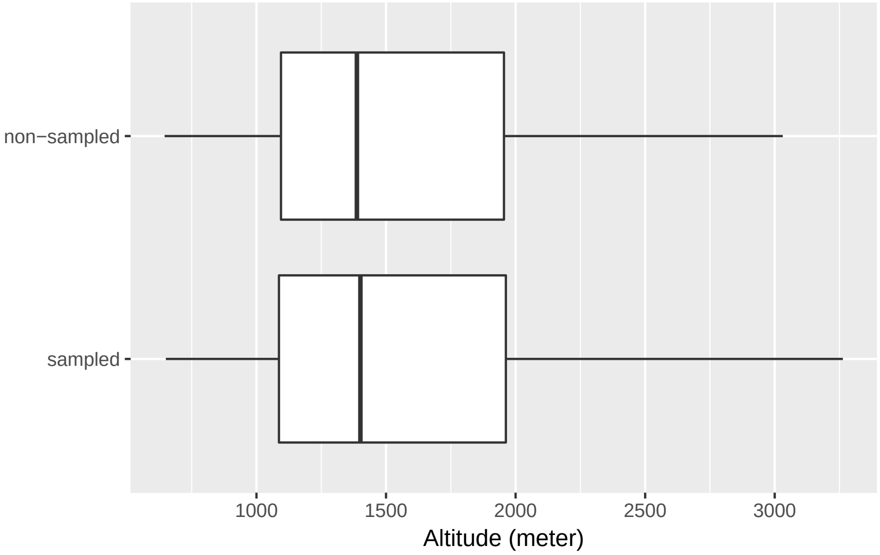
3.4 Survey Sampling

3.4.1 The Role of Randomization

```
data("afghan.village", package = "qss")
```

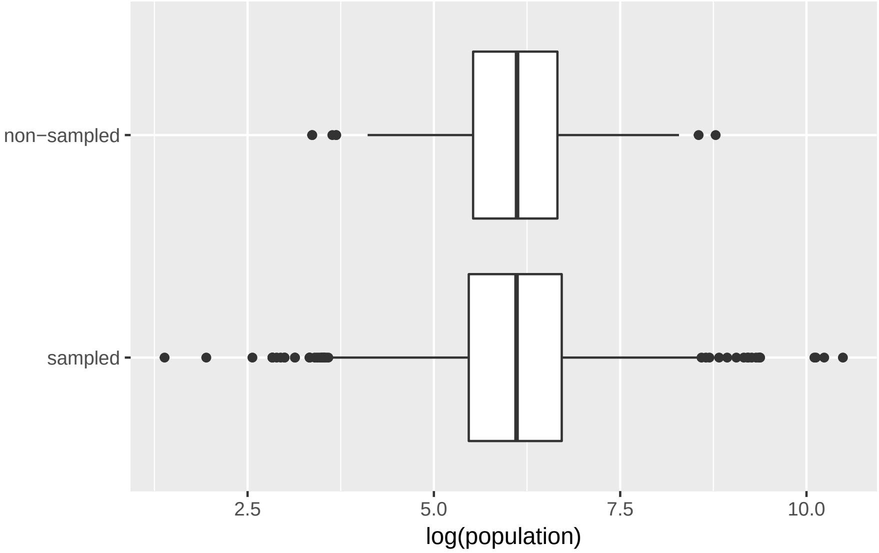
Box-plots of altitude

```
ggplot(afghan.village, aes(x = factor(village.surveyed,
                                      labels = c("sampled", "non-sampled")),
                           y = altitude)) +
  geom_boxplot() +
  labs(y = "Altitude (meter)", x = "") +
  coord_flip()
```



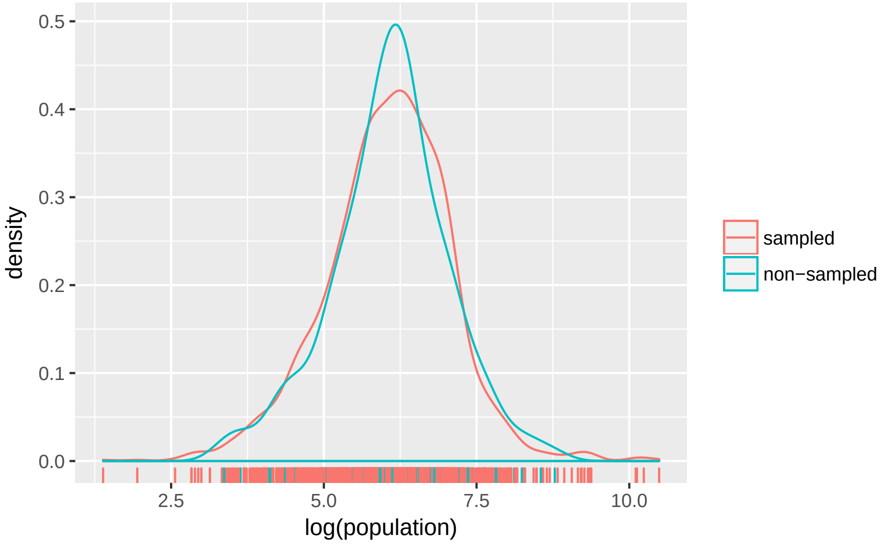
Box plots log-population values of sampled and non-sampled

```
ggplot(afghan.village, aes(x = factor(village.surveyed,
                                      labels = c("sampled", "non-sampled")),
                           y = log(population))) +
  geom_boxplot() +
  labs(y = "log(population)", x = "") +
  coord_flip()
```



You can also compare these distributions by plotting their densities:

```
ggplot(afghan.village, aes(colour = factor(village.surveyed,
                                           labels = c("sampled", "non-sampled")),
                               x = log(population))) +
  geom_density() +
  geom_rug() +
  labs(x = "log(population)", colour = "")
```



3.4.2 Non-response and other sources of bias

Calculate the rates of item non-response by province to the question about civilian victimization by ISAF and Taliban forces (`violent.exp.ISAF` and `violent.exp.taliban`):

```
afghan %>%
  group_by(province) %>%
  summarise(ISAF = mean(is.na(violent.exp.ISAF)),
            taliban = mean(is.na(violent.exp.taliban))) %>%
  arrange(-ISAF)
```

```
#> # A tibble: 5 x 3
#>   province    ISAF taliban
#>   <chr>      <dbl>   <dbl>
#> 1 Uruzgan  0.0207  0.0620
#> 2 Helmand  0.0164  0.0304
#> 3 Khost    0.00476 0.00635
#> 4 Kunar    0.      0.
#> 5 Logar    0.      0.
```

Calculate the proportion who support the ISAF using the difference in means between the ISAF and control groups:

```
(mean(filter(afghan, list.group == "ISAF")$list.response) -
  mean(filter(afghan, list.group == "control")$list.response))
#> [1] 0.049
```

To calculate the table responses to the list experiment in the control, ISAF, and Taliban groups:

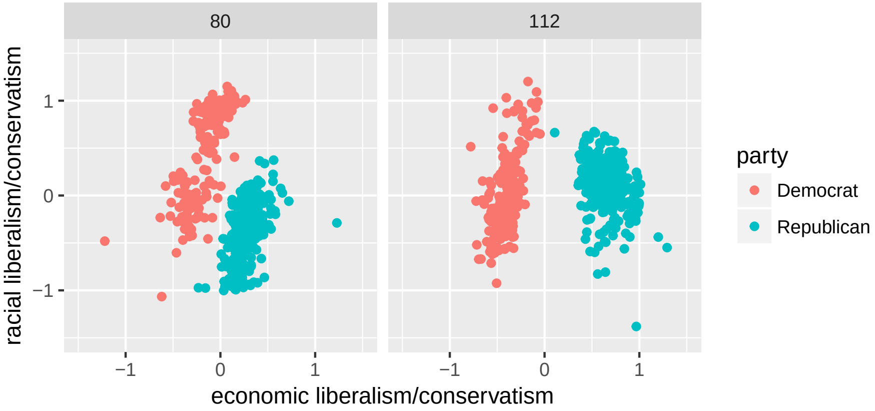
```
afghan %>%
  group_by(list.response, list.group) %>%
  count() %>%
  glimpse() %>%
  spread(list.group, n, fill = 0)
#> Observations: 12
#> Variables: 3
#> $ list.response <int> 0, 0, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4
#> $ list.group    <chr> "control", "ISAF", "control", "ISAF", "taliban",...
#> $ n             <int> 188, 174, 265, 278, 433, 265, 260, 287, 200, 182...
#> # A tibble: 5 x 4
#> # Groups:   list.response [5]
#>   list.response control  ISAF taliban
#>           <int>   <dbl> <dbl>   <dbl>
#> 1             0    188.  174.      0.
#> 2             1    265.  278.    433.
#> 3             2    265.  260.    287.
#> 4             3    200.  182.    198.
#> 5             4      0.   24.      0.
```

3.5 Measuring Political Polarization

```
data("congress", package = "qss")
```

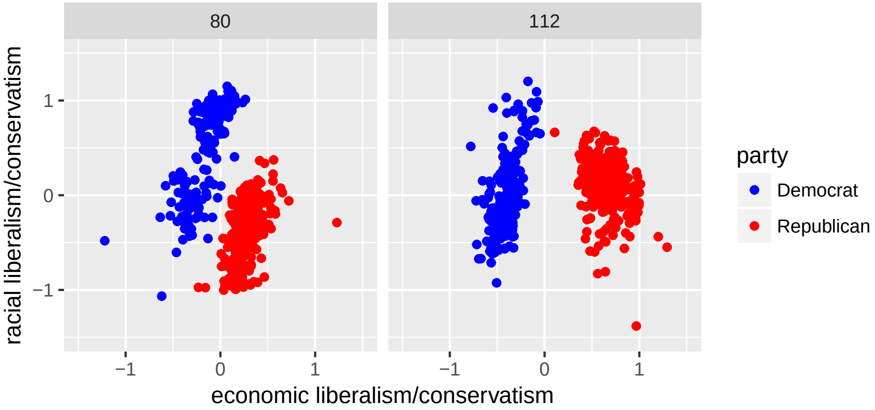
```
glimpse(congress)
#> Observations: 14,552
#> Variables: 7
#> $ congress <int> 80, 80, 80, 80, 80, 80, 80, 80, 80, 80, 80, 80, 80, 8...
#> $ district <int> 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 98, 98, 1, 2, 3, 4, 5, ...
#> $ state    <chr> "USA", "ALABAMA", "ALABAMA", "ALABAMA", "ALABAMA", "A...
#> $ party    <chr> "Democrat", "Democrat", "Democrat", "Democrat", "Demo...
#> $ name     <chr> "TRUMAN", "BOYKIN  F.", "GRANT  G.", "ANDREWS  G.", "...
#> $ dwnom1   <dbl> -0.276, -0.026, -0.042, -0.008, -0.082, -0.170, -0.12...
#> $ dwnom2   <dbl> 0.016, 0.796, 0.999, 1.005, 1.066, 0.870, 0.990, 0.89...
```

```r
q <-
  congress %>%
  filter(congress %in% c(80, 112),
         party %in% c("Democrat", "Republican")) %>%
  ggplot(aes(x = dwnom1, y = dwnom2, colour = party)) +
  geom_point() +
  facet_wrap(~ congress) +
  coord_fixed() +
  scale_y_continuous("racial liberalism/conservatism",
                     limits = c(-1.5, 1.5)) +
  scale_x_continuous("economic liberalism/conservatism",
                     limits = c(-1.5, 1.5))
q
```

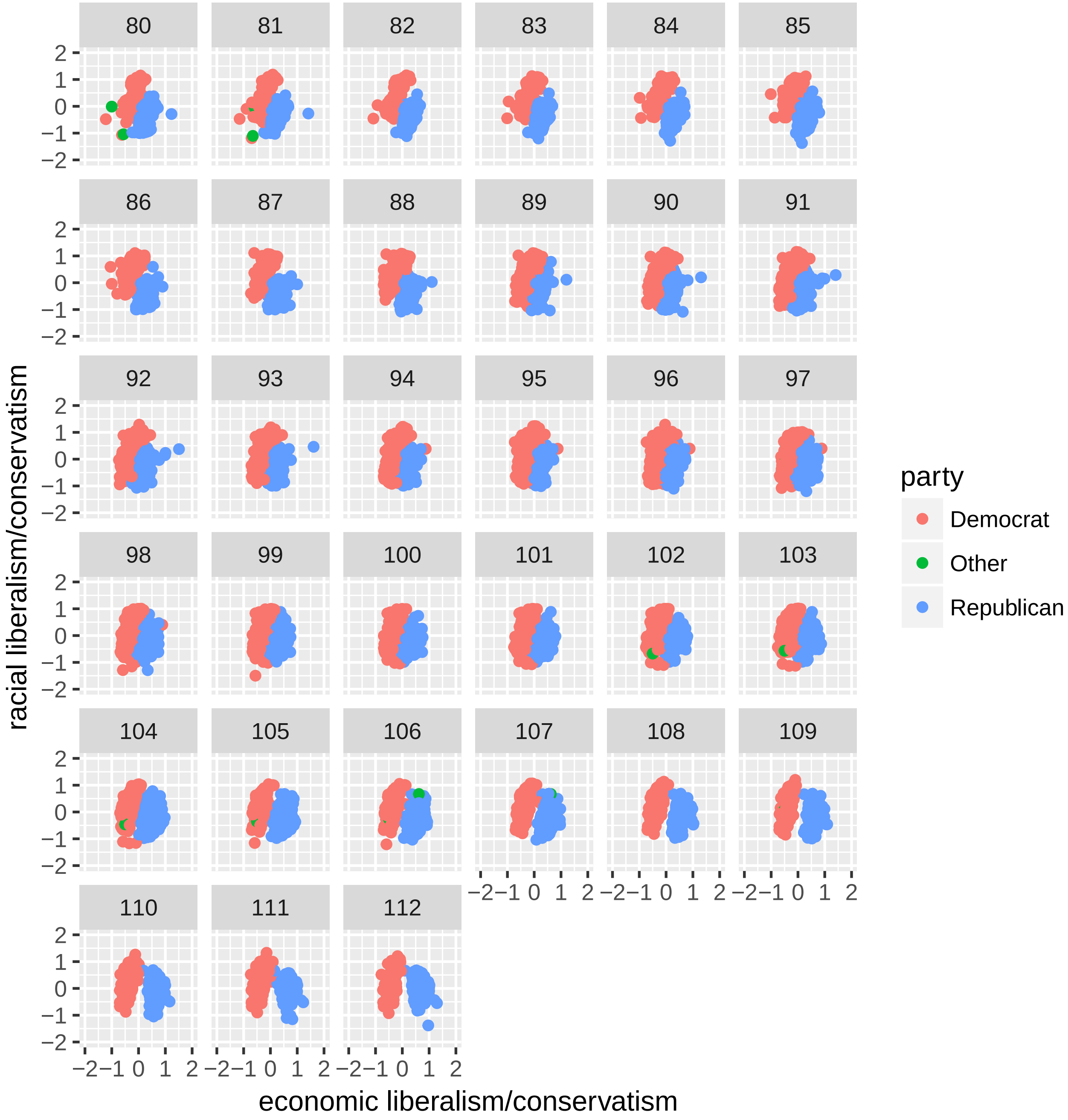


However, since there are colors associated with Democrats (blue) and Republicans (blue), we should use them rather than the defaults. There's some evidence that using semantically-resonant colors can help decoding data visualizations (See Lin, et al. 2013). Since I'll reuse the scale several times, I'll save it in a variable.

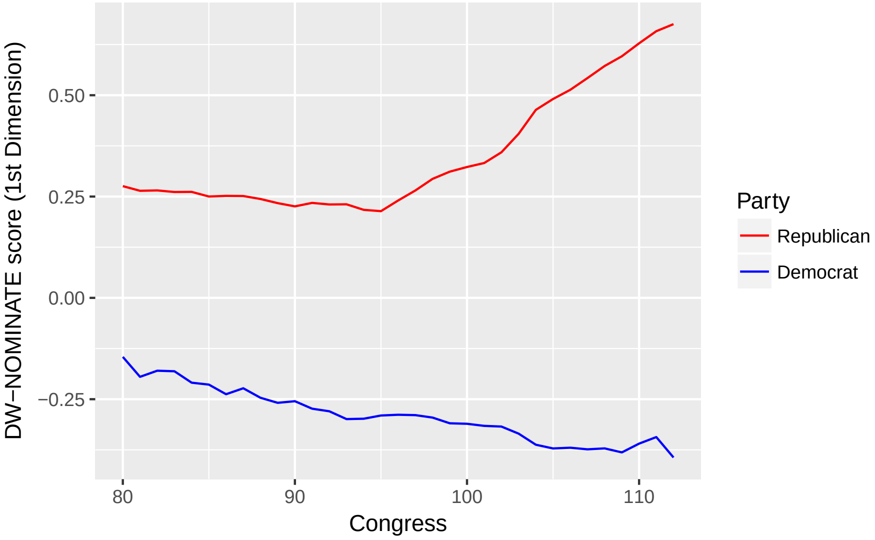
```r
scale_colour_parties <-
  scale_colour_manual(values = c(Democrat = "blue",
                                 Republican = "red",
                                 Other = "green"))
q + scale_colour_parties
```



```r
congress %>%
  ggplot(aes(x = dwnom1, y = dwnom2, colour = party)) +
  geom_point() +
  facet_wrap(~ congress) +
  coord_fixed() +
  scale_y_continuous("racial liberalism/conservatism",
                     limits = c(-2, 2)) +
  scale_x_continuous("economic liberalism/conservatism",
                     limits = c(-2, 2))
  #scale_colour_parties
```

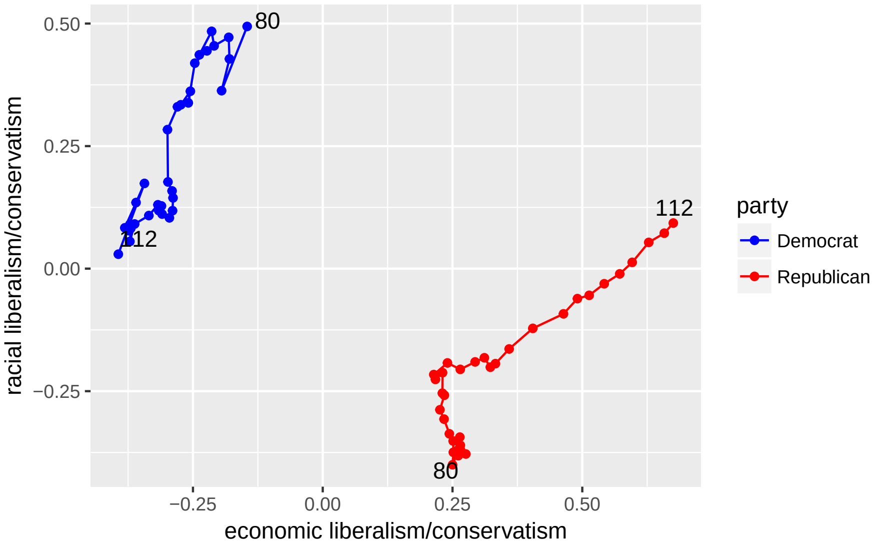


```
congress %>%
  group_by(congress, party) %>%
  summarise(dwnom1 = mean(dwnom1)) %>%
  filter(party %in% c("Democrat", "Republican")) %>%
  ggplot(aes(x = congress, y = dwnom1,
            colour = fct_reorder2(party, congress, dwnom1))) +
  geom_line() +
  scale_colour_parties +
  labs(y = "DW-NOMINATE score (1st Dimension)", x = "Congress",
       colour = "Party")
```



Alternatively, you can plot the mean DW-Nominate scores for each party and congress over time. This plot uses color for parties and lets the points and labels for the first and last congresses (80 and 112) to convey progress through time.

```
party_means <-
  congress %>%
  filter(party %in% c("Democrat", "Republican")) %>%
  group_by(party, congress) %>%
  summarise(dwnom1 = mean(dwnom1),
            dwnom2 = mean(dwnom2))

party_endpoints <-
  party_means %>%
  filter(congress %in% c(min(congress), max(congress))) %>%
  mutate(label = str_c(party, congress, sep = " - "))

ggplot(party_means,
         aes(x = dwnom1, y = dwnom2, color = party,
             group = party)) +
  geom_point() +
  geom_path() +
  ggrepel::geom_text_repel(data = party_endpoints,
                           mapping = aes(label = congress),
                           color = "black") +
  scale_y_continuous("racial liberalism/conservatism") +
  scale_x_continuous("economic liberalism/conservatism") +
  scale_colour_parties
```

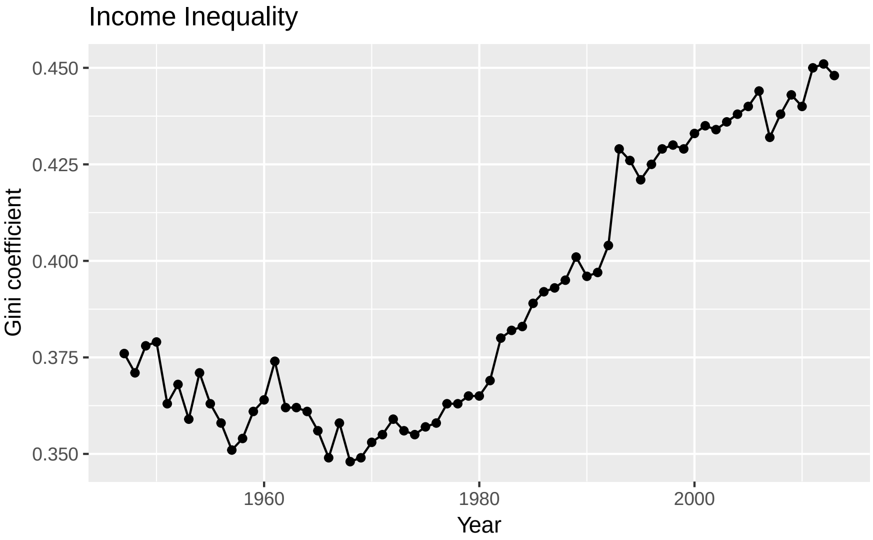


3.5.1 Correlation

Let's plot the Gini coefficient

```
data("USGini", package = "qss")
```

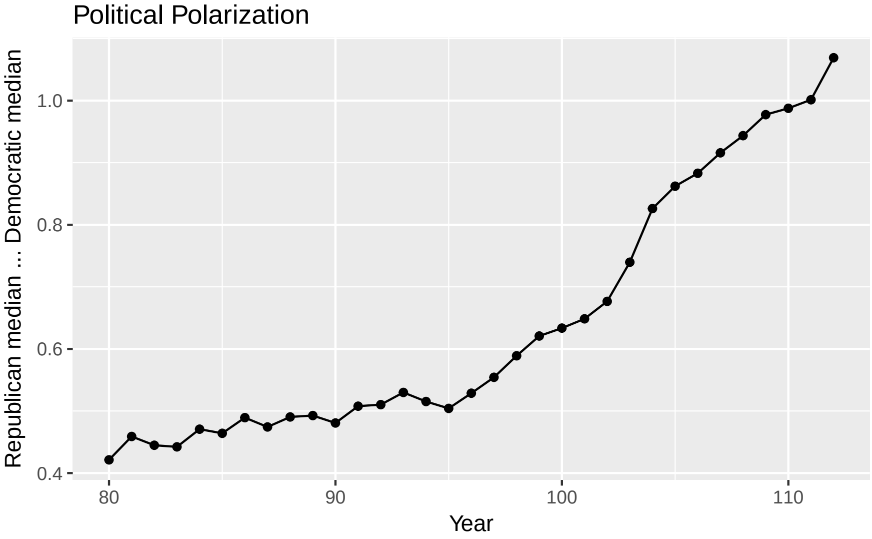
```
ggplot(USGini, aes(x = year, y = gini)) +
  geom_point() +
  geom_line() +
  labs(x = "Year", y = "Gini coefficient") +
  ggtitle("Income Inequality")
```



To calculate a measure of party polarization take the code used in the plot of Republican and Democratic party median ideal points and adapt it to calculate the difference in the party medians:

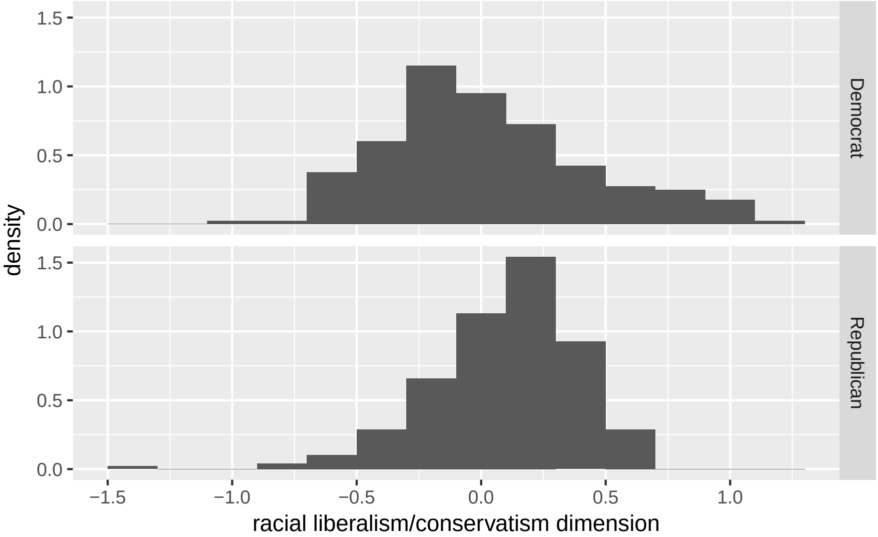
```
party_polarization <-
  congress %>%
  group_by(congress, party) %>%
  summarise(dwnom1 = mean(dwnom1)) %>%
  filter(party %in% c("Democrat", "Republican")) %>%
  spread(party, dwnom1) %>%
  mutate(polarization = Republican - Democrat)
party_polarization
#> # A tibble: 33 x 4
#> # Groups:   congress [33]
#>   congress Democrat Republican polarization
#>      <int>    <dbl>      <dbl>        <dbl>
#> 1       80   -0.146      0.276        0.421
#> 2       81   -0.195      0.264        0.459
#> 3       82   -0.180      0.265        0.445
#> 4       83   -0.181      0.261        0.442
#> 5       84   -0.209      0.261        0.471
#> 6       85   -0.214      0.250        0.464
#> # ... with 27 more rows
```

```
ggplot(party_polarization, aes(x = congress, y = polarization)) +
  geom_point() +
  geom_line() +
  ggtitle("Political Polarization") +
  labs(x = "Year", y = "Republican median - Democratic median")
#> Warning in grid.Call(C_stringMetric, as.graphicsAnnot(x$label)): font
#> metrics unknown for Unicode character U+2212

#> Warning in grid.Call(C_stringMetric, as.graphicsAnnot(x$label)): font
#> metrics unknown for Unicode character U+2212
#> Warning in grid.Call(C_stringMetric, as.graphicsAnnot(x$label)): conversion
#> failure on 'Republican median - Democratic median' in 'mbcsToSbcs': dot
#> substituted for <e2>
#> Warning in grid.Call(C_stringMetric, as.graphicsAnnot(x$label)): conversion
#> failure on 'Republican median - Democratic median' in 'mbcsToSbcs': dot
#> substituted for <88>
#> Warning in grid.Call(C_stringMetric, as.graphicsAnnot(x$label)): conversion
#> failure on 'Republican median - Democratic median' in 'mbcsToSbcs': dot
#> substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
#> Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <e2>
#> Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <88>
#> Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x
#> $y, : conversion failure on 'Republican median - Democratic median' in
#> 'mbcsToSbcs': dot substituted for <92>
```



3.5.2 Quantile-Quantile Plot

```
congress %>%
  filter(congress == 112, party %in% c("Republican", "Democrat")) %>%
  ggplot(aes(x = dwnom2, y = ..density..)) +
  geom_histogram(binwidth = .2) +
  facet_grid(party ~ .) +
  labs(x = "racial liberalism/conservatism dimension")
```

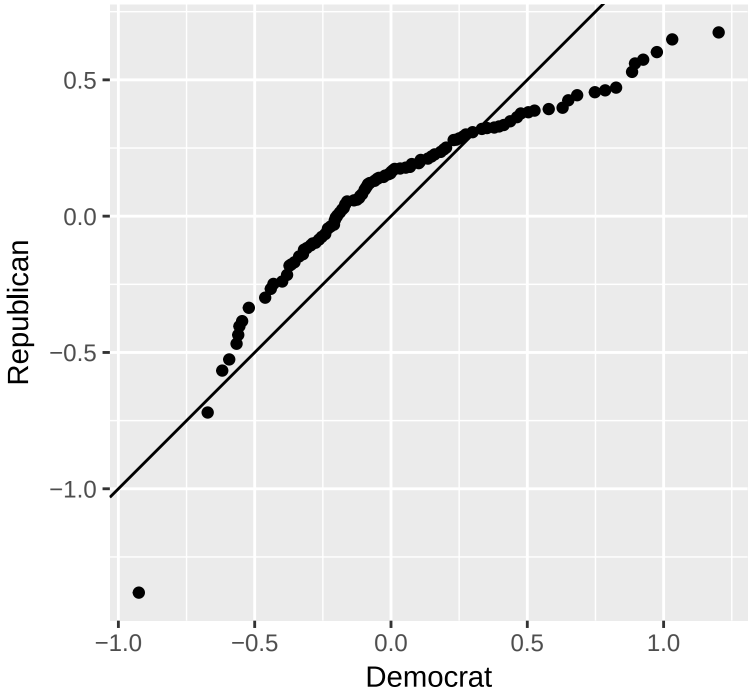


The package *ggplot2* includes a function `stat_qq` which can be used to create qq-plots but it is more suited to comparing a sample distribution with a theoretical distribution, usually the normal one. However, we can calculate one by hand, which may give more insight into exactly what the qq-plot is doing.

```
party_qtiles <- tibble(
  probs = seq(0, 1, by = 0.01),
  Democrat = quantile(filter(congress, congress == 112,
                             party == "Democrat")$dwnom2,
         probs = probs),
  Republican = quantile(filter(congress, congress == 112,
                               party == "Republican")$dwnom2,
         probs = probs)
)
party_qtiles
#> # A tibble: 101 x 3
#>    probs Democrat Republican
#>    <dbl>    <dbl>      <dbl>
#> 1 0.       -0.925     -1.38
#> 2 0.0100   -0.672     -0.720
#> 3 0.0200   -0.619     -0.566
#> 4 0.0300   -0.593     -0.526
#> 5 0.0400   -0.567     -0.468
#> 6 0.0500   -0.560     -0.436
#> # ... with 95 more rows
```

The plot looks different than the one in the text since the x- and y-scales are in the original values instead of z-scores (see the next section).

```
party_qtiles %>%
  ggplot(aes(x = Democrat, y = Republican)) +
  geom_point() +
  geom_abline() +
  coord_fixed()
```



3.6 Clustering

3.6.1 Matrices

While matrices are great for numerical computations, such as when you are implementing algorithms, generally keeping data in data frames is more convenient for data wrangling.

See R for Data Science chapter Vectors.

3.6.2 Lists

See R for Data Science chapters Vectors and Iteration, as well as the purrr package for more powerful methods of computing on lists.

3.6.3 k-means algorithms

Calculate the clusters by the 80th and 112th congresses:

```
k80two.out <-
  kmeans(select(filter(congress, congress == 80),
                     dwnom1, dwnom2),
              centers = 2, nstart = 5)
```

Add the cluster ids to data sets:

```
congress80 <-
  congress %>%
  filter(congress == 80) %>%
  mutate(cluster2 = factor(k80two.out$cluster))
```

We will also create a data sets with the cluster centroids. These are in the `centers` element of the cluster object.

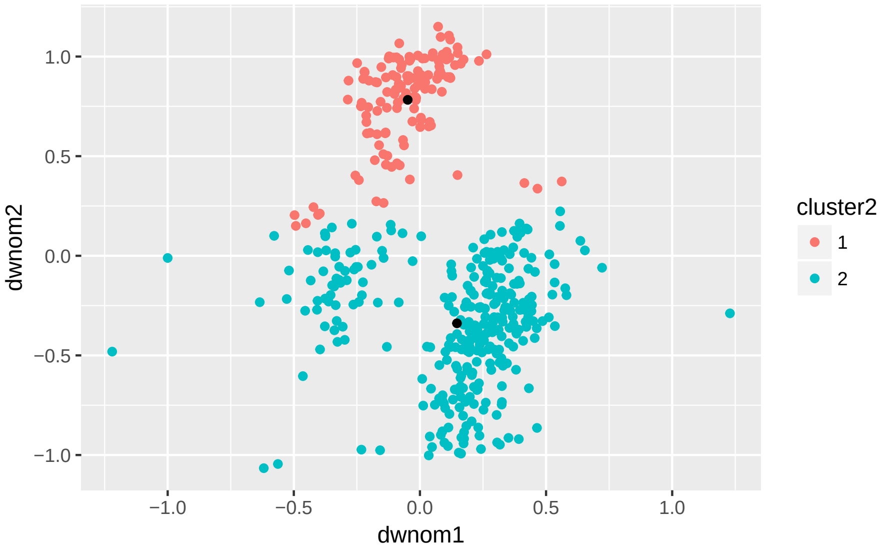
```
k80two.out$centers
#>    dwnom1 dwnom2
#> 1 -0.0484  0.783
#> 2  0.1468 -0.339
```

To make it easier to use with ggplot2, we need to convert this to a data frame. The tidy function from the broom package:

```
k80two.clusters <- tidy(k80two.out)
k80two.clusters
#>        x1     x2 size withinss cluster
#> 1 -0.0484  0.783  135     10.9       1
#> 2  0.1468 -0.339  311     54.9       2
```

Plot the ideal points and clusters:

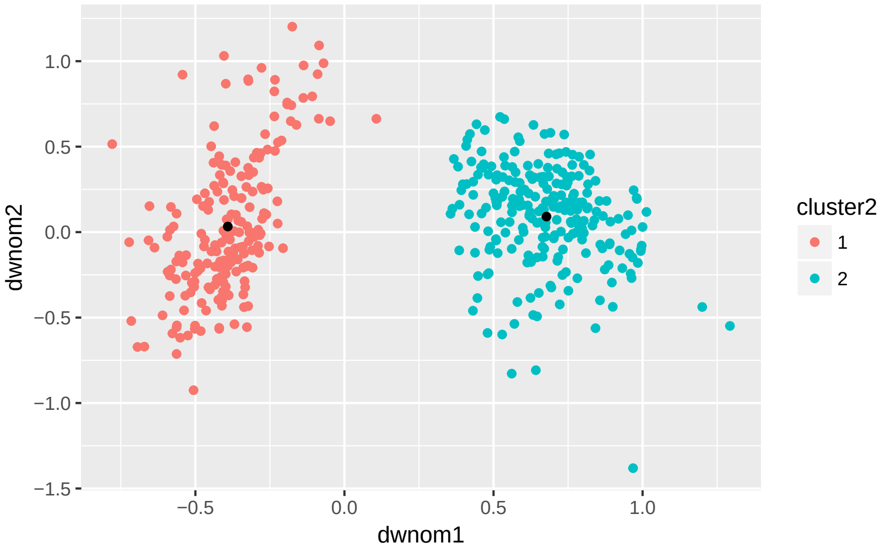
```
ggplot() +
  geom_point(data = congress80,
             aes(x = dwnom1, y = dwnom2, colour = cluster2)) +
  geom_point(data = k80two.clusters, mapping = aes(x = x1, y = x2))
```



```
congress80 %>%
  group_by(party, cluster2) %>%
  count()
#> # A tibble: 5 x 3
#> # Groups:   party, cluster2 [5]
#>   party      cluster2     n
#>   <chr>      <fct>    <int>
#> 1 Democrat   1          132
#> 2 Democrat   2           62
#> 3 Other      2            2
#> 4 Republican 1            3
#> 5 Republican 2          247
```

And now we can repeat these steps for the 112th congress:

```
k112two.out <-
  kmeans(select(filter(congress, congress == 112),
                dwnom1, dwnom2),
         centers = 2, nstart = 5)
congress112 <-
  filter(congress, congress == 112) %>%
  mutate(cluster2 = factor(k112two.out$cluster))
k112two.clusters <- tidy(k112two.out)
ggplot() +
  geom_point(data = congress112,
             mapping = aes(x = dwnom1, y = dwnom2, colour = cluster2)) +
  geom_point(data = k112two.clusters,
             mapping = aes(x = x1, y = x2))
```

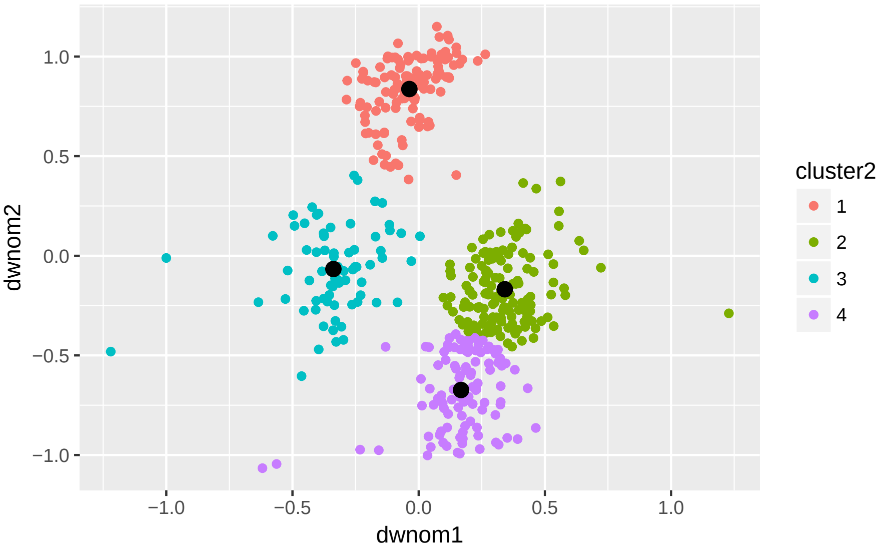


Number of observations from each party in each cluster:

```
congress112 %>%
  group_by(party, cluster2) %>%
  count()
#> # A tibble: 3 x 3
#> # Groups:   party, cluster2 [3]
#>   party      cluster2     n
#>   <chr>      <fct>    <int>
#> 1 Democrat   1          200
#> 2 Republican 1            1
#> 3 Republican 2          242
```

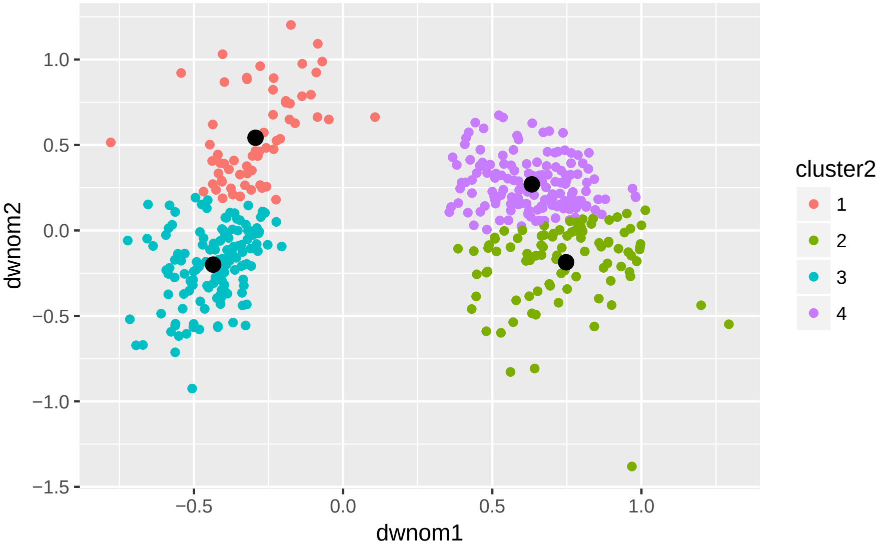
Now repeat the same with four clusters on the 80th congress:

```
k80four.out <-
  kmeans(select(filter(congress, congress == 80),
                dwnom1, dwnom2),
         centers = 4, nstart = 5)
congress80 <-
  filter(congress, congress == 80) %>%
  mutate(cluster2 = factor(k80four.out$cluster))
k80four.clusters <- tidy(k80four.out)
ggplot() +
  geom_point(data = congress80,
             mapping = aes(x = dwnom1, y = dwnom2, colour = cluster2)) +
  geom_point(data = k80four.clusters,
             mapping = aes(x = x1, y = x2), size = 3)
```



and on the 112th congress:

```
k112four.out <-
  kmeans(select(filter(congress, congress == 112),
                dwnom1, dwnom2),
         centers = 4, nstart = 5)
congress112 <-
  filter(congress, congress == 112) %>%
  mutate(cluster2 = factor(k112four.out$cluster))
k112four.clusters <- tidy(k112four.out)
ggplot() +
  geom_point(data = congress112,
             mapping = aes(x = dwnom1, y = dwnom2, colour = cluster2)) +
  geom_point(data = k112four.clusters,
             mapping = aes(x = x1, y = x2), size = 3)
```



Chapter 4

Prediction

Prerequisites

```r
library("tidyverse")
library("lubridate")
library("stringr")
library("forcats")
```

The packages modelr and broom are used to wrangle the results of linear regressions,

```r
library("broom")
library("modelr")
```

4.1 Predicting Election Outcomes

4.1.1 Loops in R

RStudio provides many features to help debugging, which will be useful in for loops and function: see this article for an example.

```r
values <- c(2, 3, 6)
n <- length(values)
results <- rep(NA, n)
for (i in 1:n) {
  results[i] <- values[i] * 2
  cat(values[i], "times 2 is equal to", results[i], "\n")
}
#> 2 times 2 is equal to 4
#> 3 times 2 is equal to 6
#> 6 times 2 is equal to 12
```

Note that the above code uses the for loop for pedagogical purposes only, this could have simply been written

```r
results <- values * 2
results
#> [1]  4  6 12
```

In general, avoid using for loops when there is a *vectorized* function.

But sticking with the for loop, there are several things that could be improved.

Avoid using the idiom `1:n` in for loops. To see why, look what happens when values are empty:

```r
values <- c()
n <- length(values)
results <- rep(NA, n)
for (i in 1:n) {
  cat("i = ", i, "\n")
  results[i] <- values[i] * 2
  cat(values[i], "times 2 is equal to", results[i], "\n")
}
#> i =  1
#>  times 2 is equal to NA
#> i =  0
#>  times 2 is equal to
```

Instead of not running a loop, as you would expect, it runs two loops, where `i = 1`, then `i = 0`. This edge case occurs more than you may think, especially if you are writing functions where you don't know the length of the vector is *ex ante*.

The way to avoid this is to use either `rdoc("base", "seq_len")` or `rdoc("base", "seq_along")`, which will handle 0-length vectors correctly.

```r
values <- c()
n <- length(values)
results <- rep(NA, n)
for (i in seq_along(values)) {
  results[i] <- values[i] * 2
}
print(results)
#> logical(0)
```

or

```r
values <- c()
n <- length(values)
results <- rep(NA, n)
for (i in seq_len(n)) {
  results[i] <- values[i] * 2
}
print(results)
#> logical(0)
```

Also, note that the the result is `logical(0)`. That's because the `NA` missing value has class logical, and thus `rep(NA, ...)` returns a logical vector. It is better style to initialize the vector with the same data type that you will be using,

```r
results <- rep(NA_real_, length(values))
results
#> numeric(0)
class(results)
#> [1] "numeric"
```

Often loops can be rewritten to use a map function. Read the R for Data Science chapter Iteration before proceeding.

To do so, we first write a function that will be applied to each element of the vector. When converting from a `for` loop to a function, this is usually simply the body of the `for` loop, though you may need to add arguments for any variables defined outside the body of the for loop. In this case,

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

We can now test that this function works on different values:

```r
mult_by_two(0)
#> [1] 0
mult_by_two(2.5)
#> [1] 5
mult_by_two(-3)
#> [1] -6
```

At this point, we could replace the body of the `for` loop with this function:

```r
values <- c(2, 4, 6)
n <- length(values)
results <- rep(NA, n)
for (i in seq_len(n)) {
  results[i] <- mult_by_two(values[i])
}
print(results)
#> [1]  4  8 12
```

This can be useful if the body of a for loop is many lines long.

However, this loop is still unwieldy code. We have to remember to define an empty vector `results` that is the same size as `values` to hold the results, and then correctly loop over all the values. We already saw how these steps have possibilities for errors. Functionals like `map`, apply a function to each element of a vector.

```r
results <- map(values, mult_by_two)
results
#> [[1]]
#> [1] 4
#> 
#> [[2]]
#> [1] 8
#> 
#> [[3]]
#> [1] 12
```

The values of each element are correct, but `map` returns a list vector, not a numeric vector like we may have been expecting. If we want a numeric vector, use `map_dbl`,

```r
results <- map_dbl(values, mult_by_two)
results
#> [1]  4  8 12
```

Also, instead of explicitly defining a function, like `mult_by_two`, we could have instead used an *anonymous function* with the functional. An anonymous function is a function that is not assigned to a name.

```r
results <- map_dbl(values, function(x) x * 2)
results
#> [1]  4  8 12
```

The various purrr functions also will interpret formulas as functions where `.x` and `.y` are interpreted as (up to) two arguments.

```
results <- map_dbl(values, ~ .x * 2)
results
#> [1]  4  8 12
```

This is for parsimony and convenience; in the background, these functions are creating anonymous functions from the given formula.

QSS discusses several debugging strategies. The functional approach lends itself to easier debugging because the function can be tested with input values independently of the loop.

4.1.2 General Conditional Statements in R

See the *R for Data Science* section Conditional Execution for a more complete discussion of conditional execution.

If you are using conditional statements to assign values for data frame, see the **dplyr** functions if_else, recode, and case_when

The following code which uses a for loop,

```
values <- 1:5
n <- length(values)
results <- rep(NA_real_, n)
for (i in seq_len(n)) {
  x <- values[i]
  r <- x %% 2
  if (r == 0) {
    cat(x, "is even and I will perform addition", x, " + ", x, "\n")
    results[i] <- x + x
  } else {
    cat(x, "is even and I will perform multiplication", x, " * ", x, "\n")
    results[i] <- x * x
  }
}
#> 1 is even and I will perform multiplication 1  *  1
#> 2 is even and I will perform addition 2  +  2
#> 3 is even and I will perform multiplication 3  *  3
#> 4 is even and I will perform addition 4  +  4
#> 5 is even and I will perform multiplication 5  *  5
results
#> [1]  1  4  9  8 25
```

could be rewritten to use `if_else`,

```
if_else(values %% 2 == 0, values + values, values * values)
#> [1]  1  4  9  8 25
```

or using the `map_dbl` functional with a named function,

```
myfunc <- function(x) {
  if (x %% 2 == 0) {
    x + x
  } else {
    x * x
  }
}
```

```
map_dbl(values, myfunc)
#> [1]  1  4  9  8 25
```

or `map_dbl` with an anonymous function,

```
map_dbl(values, function(x) {
  if (x %% 2 == 0) {
    x + x
  } else {
    x * x
  }
})
#> [1]  1  4  9  8 25
```

4.1.3 Poll Predictions

Load the election polls by state for the 2008 US Presidential election,

```
data("polls08", package = "qss")
glimpse(polls08)
#> Observations: 1,332
#> Variables: 5
#> $ state    <chr> "AL", "AL", "AL", "AL", "AL", "AL", "AL", "AL", "AL",...
#> $ Pollster <chr> "SurveyUSA-2", "Capital Survey-2", "SurveyUSA-2", "Ca...
#> $ Obama    <int> 36, 34, 35, 35, 39, 34, 36, 25, 35, 34, 37, 36, 36, 3...
#> $ McCain   <int> 61, 54, 62, 55, 60, 64, 58, 52, 55, 47, 55, 51, 49, 5...
#> $ middate  <date> 2008-10-27, 2008-10-15, 2008-10-08, 2008-10-06, 2008...
```

and the election results,

```
data("pres08", package = "qss")
glimpse(pres08)
#> Observations: 51
#> Variables: 5
#> $ state.name <chr> "Alabama", "Alaska", "Arizona", "Arkansas", "Califo...
#> $ state      <chr> "AL", "AK", "AZ", "AR", "CA", "CO", "CT", "DC", "DE...
#> $ Obama      <int> 39, 38, 45, 39, 61, 54, 61, 92, 62, 51, 47, 72, 36,...
#> $ McCain     <int> 60, 59, 54, 59, 37, 45, 38, 7, 37, 48, 52, 27, 62, ...
#> $ EV         <int> 9, 3, 10, 6, 55, 9, 7, 3, 3, 27, 15, 4, 4, 21, 11, ...
```

Compute Obama's margin in polls and final election

```
polls08 <-
  polls08 %>% mutate(margin = Obama - McCain)
pres08 <-
  pres08 %>% mutate(margin = Obama - McCain)
```

To work with dates, the R package lubridate makes wrangling them much easier. See the R for Data Science chapter Dates and Times.

The function ymd will convert character strings like `year-month-day` and more into dates, as long as the order is (year, month, day). See dmy, mdy, and others for other ways to convert strings to dates.

```
x <- ymd("2008-11-04")
y <- ymd("2008/9/1")
x - y
#> Time difference of 64 days
```

However, note that in `polls08`, the date `middate` is *already* a `date` object,

```
class(polls08$middate)
#> [1] "Date"
```

The function read_csv by default will check character vectors to see if they have patterns that appear to be dates, and if so, will parse those columns as dates.

We'll create a variable for election day

```
ELECTION_DAY <- ymd("2008-11-04")
```

and add a new column to `poll08` with the days to the election

```
polls08 <- mutate(polls08, ELECTION_DAY - middate)
```

Although the code in the chapter uses a `for` loop, there is no reason to do so. We can accomplish the same task by merging the election results data to the polling data by `state`.

```
polls_w_results <- left_join(polls08,
                             select(pres08, state, elec_margin = margin),
                             by = "state") %>%
  mutate(error = elec_margin - margin)
glimpse(polls_w_results)
#> Observations: 1,332
#> Variables: 9
#> $ state                     <chr> "AL", "AL", "AL", "AL", "AL", "AL", "...
#> $ Pollster                  <chr> "SurveyUSA-2", "Capital Survey-2", "S...
#> $ Obama                     <int> 36, 34, 35, 35, 39, 34, 36, 25, 35, 3...
#> $ McCain                    <int> 61, 54, 62, 55, 60, 64, 58, 52, 55, 4...
#> $ middate                   <date> 2008-10-27, 2008-10-15, 2008-10-08, ...
#> $ margin                    <int> -25, -20, -27, -20, -21, -30, -22, -2...
#> $ `ELECTION_DAY - middate` <time> 8 days, 20 days, 27 days, 29 days, 4...
#> $ elec_margin               <int> -21, -21, -21, -21, -21, -21, -21, -2...
#> $ error                     <int> 4, -1, 6, -1, 0, 9, 1, 6, -1, -8, -3,...
```

To get the last poll in each state, arrange and filter on `middate`

```
last_polls <-
  polls_w_results %>%
  arrange(state, desc(middate)) %>%
  group_by(state) %>%
  slice(1)
last_polls
#> # A tibble: 51 x 9
#> # Groups:   state [51]
#>   state Pollster      Obama McCain middate    margin `ELECTION_DAY - midd~
#>   <chr> <chr>         <int>  <int> <date>      <int> <time>
#> 1 AK    Research 200~    39     58 2008-10-29    -19 6
#> 2 AL    SurveyUSA-2      36     61 2008-10-27    -25 8
#> 3 AR    ARG-4            44     51 2008-10-29     -7 6
#> 4 AZ    ARG-3            46     50 2008-10-29     -4 6
#> 5 CA    SurveyUSA-3      60     36 2008-10-30     24 5
#> 6 CO    ARG-3            52     45 2008-10-29      7 6
#> # ... with 45 more rows, and 2 more variables: elec_margin <int>,
#> #   error <int>
```

Challenge: Instead of using the last poll, use the average of polls in the last week? Last month? How do the margins on the polls change over the election period?

To simplify things for later, let's define a function `rmse` which calculates the root mean squared error, as defined in the book. See the R for Data Science chapter Functions for more on writing functions.

```
rmse <- function(actual, pred) {
  sqrt(mean( (actual - pred) ^ 2))
}
```

Now we can use `rmse()` to calculate the RMSE for all the final polls:

```
rmse(last_polls$margin, last_polls$elec_margin)
#> [1] 5.88
```

Or since we already have a variable `error`,

```
sqrt(mean(last_polls$error ^ 2))
#> [1] 5.88
```

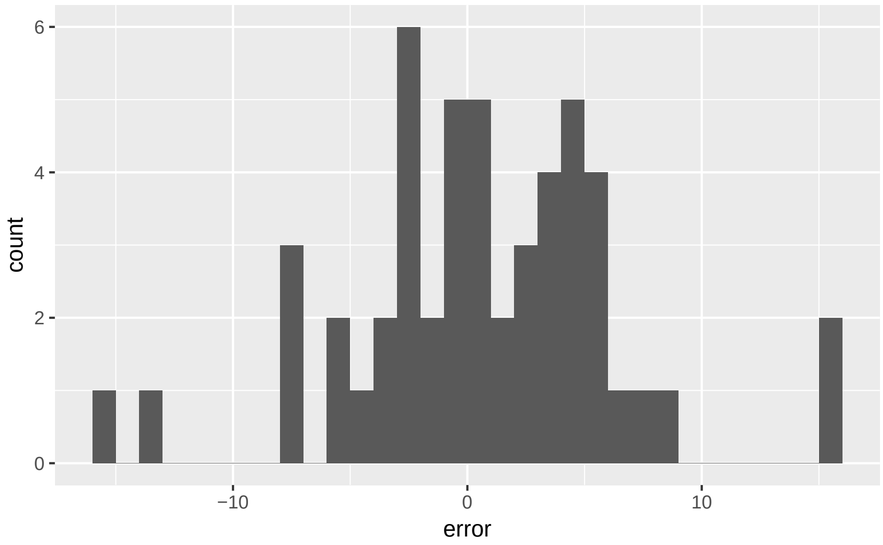
The mean prediction error is

```
mean(last_polls$error)
#> [1] 1.08
```

This is slightly different than what is in the book due to the difference in the poll used as the final poll; many states have many polls on the last day.

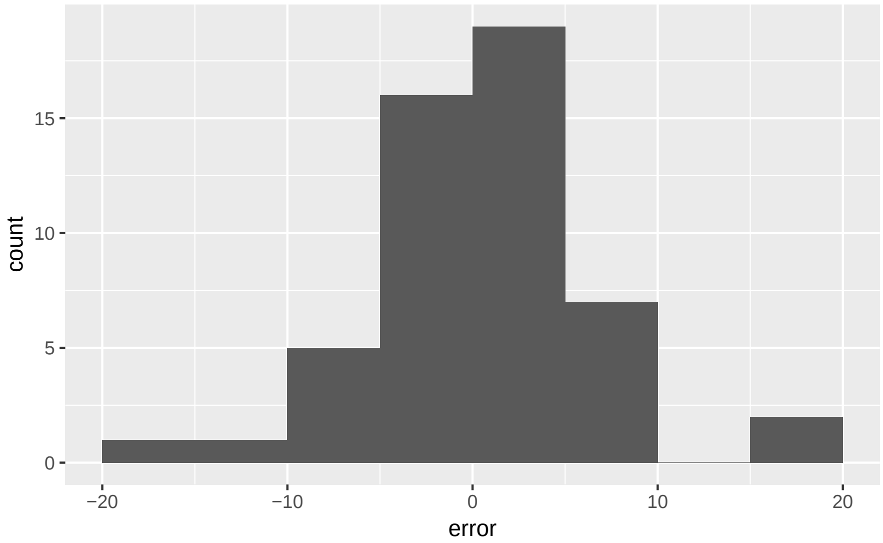
I'll choose bin widths of 1%, since that is fairly interpretable:

```
ggplot(last_polls, aes(x = error)) +
  geom_histogram(binwidth = 1, boundary = 0)
```



The text uses bin widths of 5%:

```
ggplot(last_polls, aes(x = error)) +
  geom_histogram(binwidth = 5, boundary = 0)
```

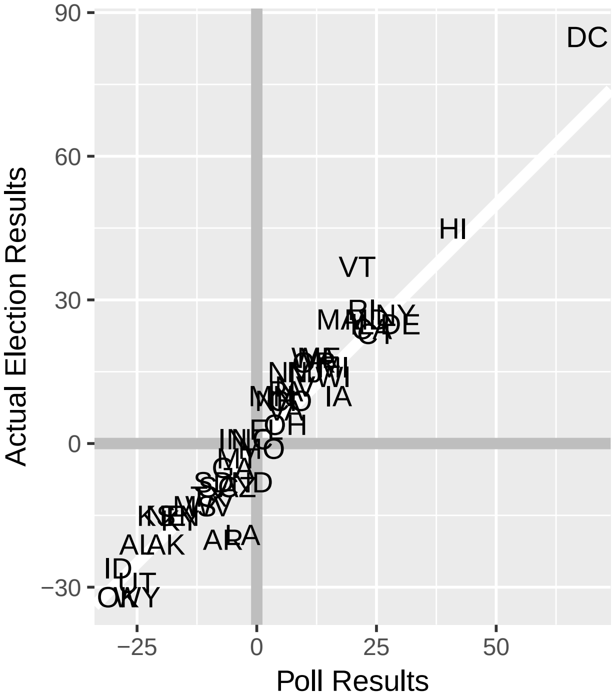


Challenge: What other ways could you visualize the results? How would you show all states? What about plotting the absolute or squared errors instead of the errors?

Challenge: What happens to prediction error if you average polls? Consider averaging back over time? What happens if you take the averages of the state poll average and average of **all** polls - does that improve prediction?

To create a scatter plots using the state abbreviations instead of points use geom_text instead of geom_point.

```r
ggplot(last_polls, aes(x = margin, y = elec_margin, label = state)) +
  geom_abline(color = "white", size = 2) +
  geom_hline(yintercept = 0, color = "gray", size = 2) +
  geom_vline(xintercept = 0, color = "gray", size = 2) +
  geom_text() +
  coord_fixed() +
  labs(x = "Poll Results", y = "Actual Election Results")
```



We can create a confusion matrix as follows. Create a new column `classification` which shows how the poll's classification was related to the actual election outcome ("true positive", "false positive", "true negative", "false negative"). If there were two outcomes, then we would use the function. But with more than two outcomes, it is easier to use the dplyr function .

```
last_polls <-
  last_polls %>%
  ungroup() %>%
  mutate(classification =
           case_when(
             (.$margin > 0 & .$elec_margin > 0) ~ "true positive",
             (.$margin > 0 & .$elec_margin < 0) ~ "false positive",
             (.$margin < 0 & .$elec_margin < 0) ~ "true negative",
             (.$margin < 0 & .$elec_margin > 0) ~ "false negative"
           ))
```

You need to use `.` to refer to the data frame when using `case_when()` within `mutate()`. Also, we needed to first use in order to remove the grouping variable so `mutate()` will work.

Now simply count the number of polls in each category of `classification`:

```
last_polls %>%
  group_by(classification) %>%
  count()
#> # A tibble: 4 x 2
#> # Groups:   classification [4]
#>   classification     n
#>   <chr>          <int>
#> 1 false negative     2
#> 2 false positive     1
#> 3 true negative     21
#> 4 true positive     27
```

Which states were incorrectly predicted by the polls, and what was their margins?

```
last_polls %>%
  filter(classification %in% c("false positive", "false negative")) %>%
  select(state, margin, elec_margin, classification) %>%
  arrange(desc(elec_margin))
#> # A tibble: 3 x 4
#>   state margin elec_margin classification
#>   <chr>  <int>       <int> <chr>
#> 1 IN        -5           1 false negative
#> 2 NC        -1           1 false negative
#> 3 MO         1          -1 false positive
```

What was the difference in the poll prediction of electoral votes and actual electoral votes? We hadn't included the variable `EV` when we first merged, but that's no problem, we'll just merge again in order to grab that variable:

```
last_polls %>%
  left_join(select(pres08, state, EV), by = "state") %>%
  summarise(EV_pred = sum( (margin > 0) * EV),
            EV_actual = sum( (elec_margin > 0) * EV))
#> # A tibble: 1 x 2
#>   EV_pred EV_actual
#>     <int>     <int>
#> 1     349       364
```

```
data("pollsUS08", package = "qss")
```

```
pollsUS08 <- mutate(pollsUS08, DaysToElection = ELECTION_DAY - middate)
```

We'll produce the seven-day averages slightly differently than the method used in the text. For all dates in the data, we'll calculate the moving average. The code presented in *QSS* uses a for loop similar to the following:

```
all_dates <- seq(min(polls08$middate), ELECTION_DAY, by = "days")

# Number of poll days to use
POLL_DAYS <- 7

pop_vote_avg <- vector(length(all_dates), mode = "list")
for (i in seq_along(all_dates)) {
  date <- all_dates[i]
  # summarise the seven day
  week_data <-
     filter(polls08,
            as.integer(middate - date) <= 0,
            as.integer(middate - date) > - POLL_DAYS) %>%
     summarise(Obama = mean(Obama, na.rm = TRUE),
               McCain = mean(McCain, na.rm = TRUE))
  # add date for the observation
  week_data$date <- date
  pop_vote_avg[[i]] <- week_data
}

pop_vote_avg <- bind_rows(pop_vote_avg)
```

Write a function which takes a `date`, and calculates the `days` (set the default to 7 days) moving average using the dataset `.data`:

```
poll_ma <- function(date, .data, days = 7) {
  filter(.data,
        as.integer(middate - date) <= 0,
        as.integer(middate - date) > - !!days) %>%
  summarise(Obama = mean(Obama, na.rm = TRUE),
           McCain = mean(McCain, na.rm = TRUE)) %>%
  mutate(date = !!date)
}
```

The code above uses `!!`. This tells `filter` that `days` refers to a variable `days` in the calling environment, and not a column named `days` in the data frame. In this case, there wouldn't be any ambiguities since there is not a column named `days`, but in general there can be ambiguities in the dplyr functions as to whether the names refer to columns in the data frame or variables in the environment calling the function. Read Programming with dplyr for an in-depth discussion of this.

This returns a one row data frame with the moving average for McCain and Obama on Nov 1, 2008.

```
poll_ma(as.Date("2008-11-01"), polls08)
#>   Obama McCain       date
#> 1  49.1   45.4 2008-11-01
```

Since we made `days` an argument to the function we could easily change the code to calculate other moving averages,

```r
poll_ma(as.Date("2008-11-01"), polls08, days = 3)
#>   Obama McCain       date
#> 1  50.6   45.4 2008-11-01
```

Now use a functional to execute that function with all dates for which we want moving averages. The function `poll_ma` returns a data frame, and our ideal output is a data frame that stacks those data frames row-wise. So we will use the `map_df` function,

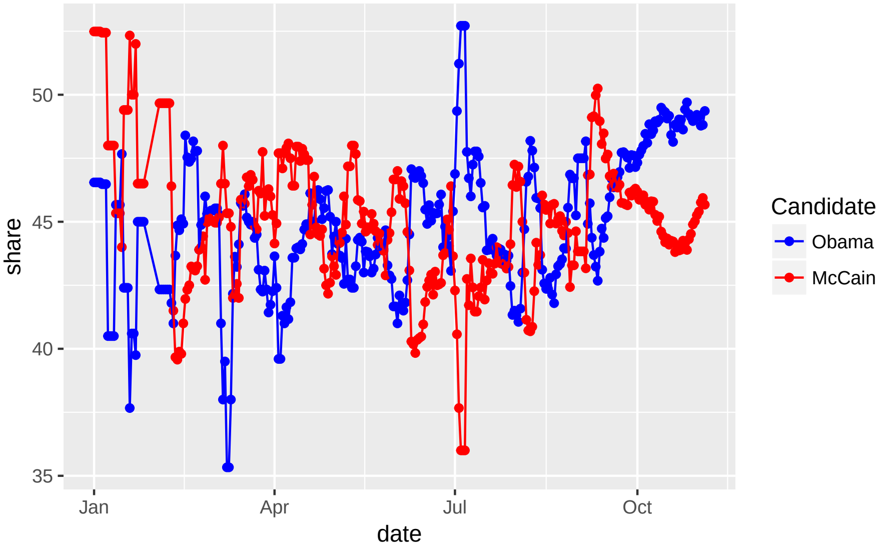
```r
map_df(all_dates, poll_ma, polls08)
```

Note that the other arguments for `poll_ma` are placed after the name of the function as additional arguments to `map_df`.

It is easier to plot this if the data are tidy, with `Obama` and `McCain` as categories of a column `candidate`.

```r
pop_vote_avg_tidy <-
  pop_vote_avg %>%
  gather(candidate, share, -date, na.rm = TRUE)
head(pop_vote_avg_tidy)
#>         date candidate share
#> 1 2008-01-01     Obama  46.5
#> 2 2008-01-02     Obama  46.5
#> 3 2008-01-03     Obama  46.5
#> 4 2008-01-04     Obama  46.5
#> 5 2008-01-05     Obama  46.5
#> 6 2008-01-06     Obama  46.5
```

```r
ggplot(pop_vote_avg_tidy, aes(x = date, y = share,
                              colour = fct_reorder2(candidate, date, share))) +
  geom_point() +
  geom_line() +
  scale_colour_manual("Candidate",
                      values = c(Obama = "blue", McCain = "red"))
```



Challenge read R for Data Science chapter Iteration and use the function map_df to create the object `poll_vote_avg` as above instead of a for loop.

The 7-day average is similar to the simple method used by Real Clear Politics. The RCP average is simply the average of all polls in their data for the last seven days. Sites like 538 and the Huffpost Pollster, on the other hand, also use what amounts to averaging polls, but using more sophisticated statistical methods to assign different weights to different polls.

Challenge Why do we need to use different polls for the popular vote data? Why not simply average all the state polls? What would you have to do? Would the overall popular vote be useful in predicting state-level polling, or vice-versa? How would you use them?

4.2 Linear Regression

4.2.1 Facial Appearance and Election Outcomes

Load the `face` dataset:

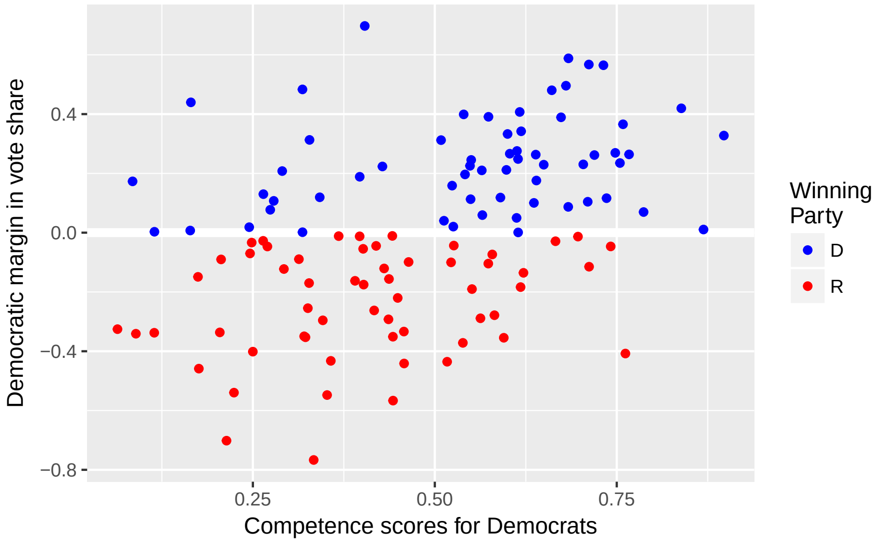
```
data("face", package = "qss")
```

Add Democrat and Republican vote shares, and the difference in shares:

```
face <- mutate(face,
               d.share = d.votes / (d.votes + r.votes),
               r.share = r.votes / (d.votes + r.votes),
               diff.share = d.share - r.share)
```

Plot facial competence vs. vote share:

```
ggplot(face, aes(x = d.comp, y = diff.share, colour = w.party)) +
  geom_ref_line(h = 0) +
  geom_point() +
  scale_colour_manual("Winning\nParty",
                      values = c(D = "blue", R = "red")) +
  labs(x = "Competence scores for Democrats",
       y = "Democratic margin in vote share")
```



4.2.2 Correlation and Scatter Plots

```
cor(face$d.comp, face$diff.share)
#> [1] 0.433
```

4.2.3 Least Squares

Run the linear regression

```
fit <- lm(diff.share ~ d.comp, data = face)
fit
#>
#> Call:
#> lm(formula = diff.share ~ d.comp, data = face)
#>
#> Coefficients:
#> (Intercept)       d.comp
#>      -0.312        0.660
```

There are many functions to get data out of the `lm` model.

In addition to these, the broom package provides three functions: `glance`, `tidy`, and `augment` that always return data frames.

The function glance returns a one-row data-frame summary of the model,

```
glance(fit)
#>   r.squared adj.r.squared sigma statistic  p.value df logLik AIC  BIC
#> 1     0.187          0.18 0.266        27 8.85e-07  2  -10.5  27 35.3
#>   deviance df.residual
#> 1     8.31         117
```

The function tidy returns a data frame in which each row is a coefficient,

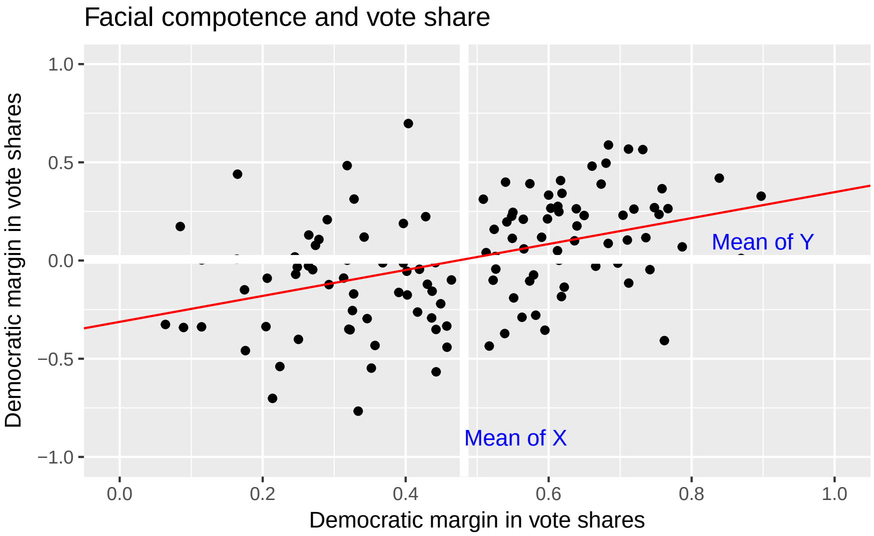
```
tidy(fit)
#>          term estimate std.error statistic  p.value
#> 1 (Intercept)   -0.312     0.066     -4.73 6.24e-06
#> 2      d.comp    0.660     0.127      5.19 8.85e-07
```

The function augment returns the original data with fitted values, residuals, and other observation level stats from the model appended to it.

```
augment(fit) %>% head()
#>   diff.share d.comp .fitted .se.fit  .resid    .hat .sigma  .cooksd
#> 1     0.2101  0.565  0.0606  0.0266  0.1495 0.00996  0.267 0.001600
#> 2     0.1194  0.342 -0.0864  0.0302  0.2059 0.01286  0.267 0.003938
#> 3     0.0499  0.612  0.0922  0.0295 -0.0423 0.01229  0.268 0.000158
#> 4     0.1965  0.542  0.0454  0.0256  0.1511 0.00922  0.267 0.001510
#> 5     0.4958  0.680  0.1370  0.0351  0.3588 0.01737  0.266 0.016307
#> 6    -0.3495  0.321 -0.1006  0.0319 -0.2490 0.01433  0.267 0.006436
#>   .std.resid
#> 1      0.564
#> 2      0.778
#> 3     -0.160
#> 4      0.570
#> 5      1.358
#> 6     -0.941
```

We can plot the results of the bivariate linear regression as follows:

```
ggplot() +
  geom_point(data = face, mapping = aes(x = d.comp, y = diff.share)) +
  geom_ref_line(v = mean(face$d.comp)) +
  geom_ref_line(h = mean(face$diff.share)) +
  geom_abline(slope = coef(fit)["d.comp"],
              intercept = coef(fit)["(Intercept)"],
              colour = "red") +
  annotate("text", x = 0.9, y = mean(face$diff.share) + 0.05,
           label = "Mean of Y", color = "blue", vjust = 0) +
  annotate("text", y = -0.9, x = mean(face$d.comp), label = "Mean of X",
           color = "blue", hjust = 0) +
  scale_y_continuous("Democratic margin in vote shares",
                     breaks = seq(-1, 1, by = 0.5), limits = c(-1, 1)) +
  scale_x_continuous("Democratic margin in vote shares",
                     breaks = seq(0, 1, by = 0.2), limits = c(0, 1)) +
  ggtitle("Facial compotence and vote share")
```

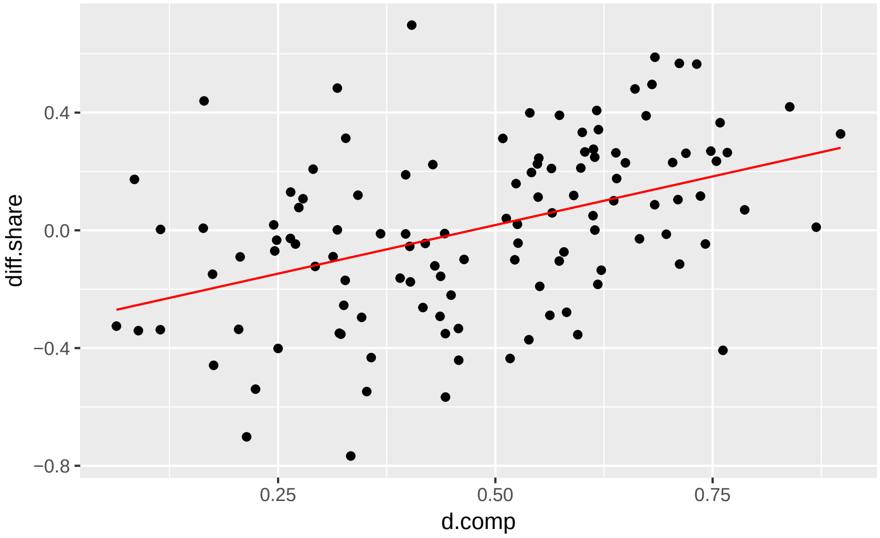


A more general way to plot the predictions of the model against the data is to use the methods described in Ch 23.3.3 of R4DS. Create an evenly spaced grid of values of `d.comp`, and add predictions of the model to it.

```
grid <- face %>%
  data_grid(d.comp) %>%
  add_predictions(fit)
head(grid)
#> # A tibble: 6 x 2
#>   d.comp   pred
#>    <dbl>  <dbl>
#> 1 0.0640 -0.270
#> 2 0.0847 -0.256
#> 3 0.0893 -0.253
#> 4 0.115  -0.237
#> 5 0.115  -0.236
#> 6 0.164  -0.204
```

Now we can plot the regression line and the original data just like any other plot.

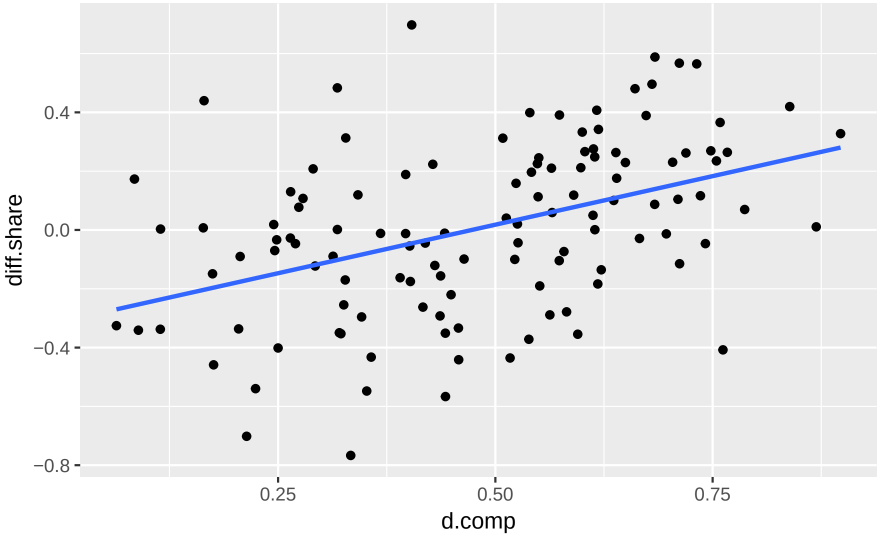
```
ggplot() +
  geom_point(data = face, mapping = aes(x = d.comp, y = diff.share)) +
  geom_line(data = grid, mapping = aes(x = d.comp, y = pred),
            colour = "red")
```



This method is more complicated than the `geom_abline` method for a bivariate regression, but will work for more complicated models, while the `geom_abline` method won't.

Note that geom_smooth can be used to add a regression line to a data-set.

```r
ggplot(data = face, mapping = aes(x = d.comp, y = diff.share)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



The argument `method = "lm"` specifies that the function `lm` is to be used to generate fitted values. It is equivalent to running the regression `lm(y ~ x)` and plotting the regression line, where `y` and `x` are the aesthetics specified by the mappings. The argument `se = FALSE` tells the function not to plot the confidence interval of the regression (discussed later).

4.2.4 Regression towards the mean

4.2.5 Merging Data Sets in R

See the R for Data Science chapter Relational data.

```
data("pres12", package = "qss")
```

To join both data frames

```
full_join(pres08, pres12, by = "state")
```

However, since there are duplicate names, `.x` and `.y` are appended.

Challenge What would happen if `by = "state"` was dropped?

To avoid the duplicate names, or change them, you can rename before merging,

```
full_join(select(pres08, state, Obama_08 = Obama, McCain_08 = McCain,
                 EV_08 = EV),
          select(pres12, state, Obama_12 = Obama, Romney_12 = Romney,
                 EV_12 = EV),
          by = "state")
```

or use the `suffix` argument to `full_join`

```
pres <- full_join(pres08, pres12, by = "state", suffix = c("_08", "_12"))
head(pres)
#>   state.name state Obama_08 McCain EV_08 margin Obama_12 Romney EV_12
#> 1    Alabama    AL       39     60     9    -21       38     61     9
#> 2     Alaska    AK       38     59     3    -21       41     55     3
#> 3    Arizona    AZ       45     54    10     -9       45     54    11
#> 4   Arkansas    AR       39     59     6    -20       37     61     6
#> 5 California    CA       61     37    55     24       60     37    55
#> 6   Colorado    CO       54     45     9      9       51     46     9
```

Challenge Would you consider this data tidy? How would you make it tidy?

The **dplyr** equivalent functions for cbind is bind_cols.

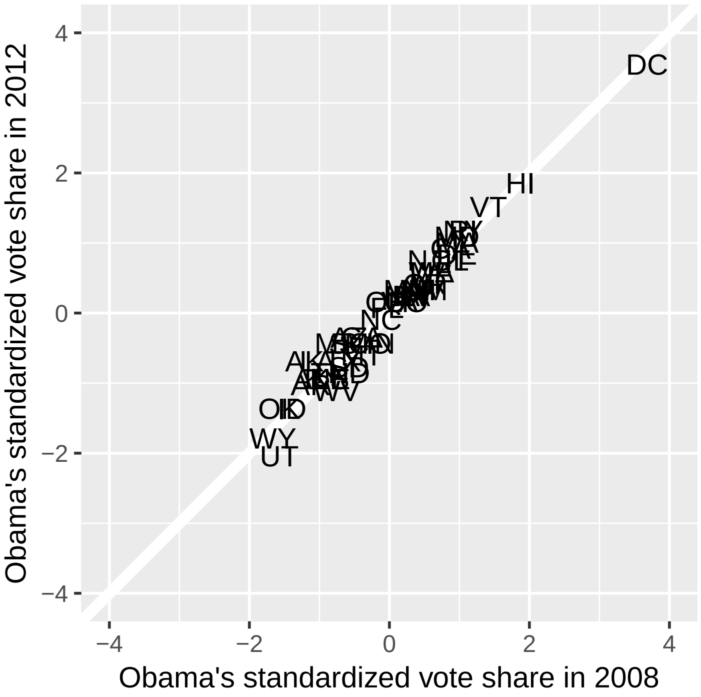
```
pres <- pres %>%
  mutate(Obama2008_z = as.numeric(scale(Obama_08)),
         Obama2012_z = as.numeric(scale(Obama_12)))
```

Likewise, bind_cols concatenates data frames by row.

We need to use the `as.numeric` function because `scale()` always returns a matrix. Omitting `as.numeric()` would not produce an error in the code chunk above, since the columns of a data frame can be matrices, but it would produce errors in some of the following code if it were omitted.

Scatter plot of states with vote shares in 2008 and 2012

```
ggplot(pres, aes(x = Obama2008_z, y = Obama2012_z, label = state)) +
  geom_abline(colour = "white", size = 2) +
  geom_text() +
  coord_fixed() +
  scale_x_continuous("Obama's standardized vote share in 2008",
                     limits = c(-4, 4)) +
  scale_y_continuous("Obama's standardized vote share in 2012",
                     limits = c(-4, 4))
```



To calculate the bottom and top quartiles

```
pres %>%
  filter(Obama2008_z < quantile(Obama2008_z, 0.25)) %>%
  summarise(improve = mean(Obama2012_z > Obama2008_z))
#>   improve
#> 1   0.583

pres %>%
  filter(Obama2008_z < quantile(Obama2008_z, 0.75)) %>%
  summarise(improve = mean(Obama2012_z > Obama2008_z))
#>   improve
#> 1     0.5
```

Challenge: Why is it important to standardize the vote shares?

4.2.6 Model Fit

```
data("florida", package = "qss")
fit2 <- lm(Buchanan00 ~ Perot96, data = florida)
fit2
#> 
#> Call:
#> lm(formula = Buchanan00 ~ Perot96, data = florida)
#> 
#> Coefficients:
#> (Intercept)      Perot96  
#>      1.3458       0.0359
```

Extract R^2 from the results of `summary`,

```
summary(fit2)$r.squared
#> [1] 0.513
```

Alternatively, can get the R squared value from the data frame glance returns:

```
glance(fit2)
#>   r.squared adj.r.squared sigma statistic  p.value df logLik AIC BIC
#> 1     0.513         0.506   316      68.5 9.47e-12  2   -480 966 972
#>   deviance df.residual
#> 1  6506118          65
```

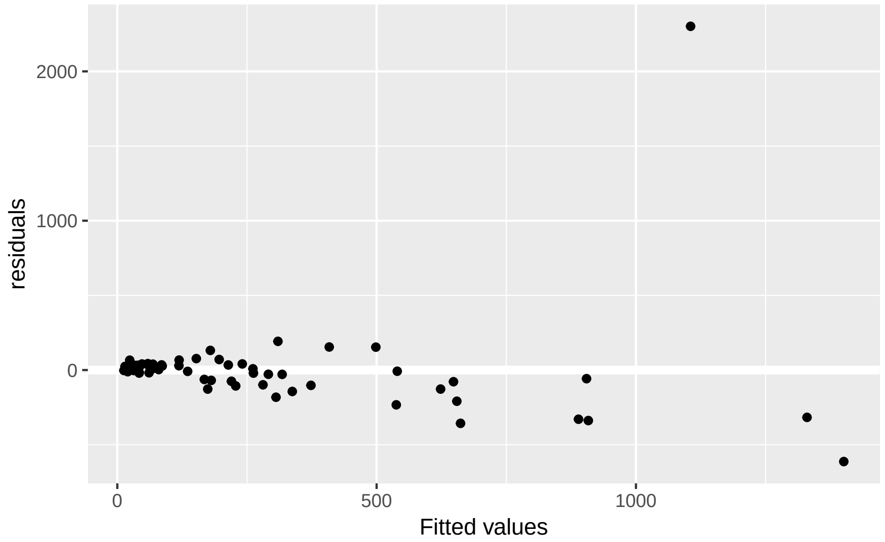
We can add predictions and residuals to the original data frame using the modelr functions add_residuals and add_predictions

```
florida <-
  florida %>%
  add_predictions(fit2) %>%
  add_residuals(fit2)
glimpse(florida)
#> Observations: 67
#> Variables: 9
#> $ county     <chr> "Alachua", "Baker", "Bay", "Bradford", "Brevard", "...
#> $ Clinton96  <int> 40144, 2273, 17020, 3356, 80416, 320736, 1794, 2712...
#> $ Dole96     <int> 25303, 3684, 28290, 4038, 87980, 142834, 1717, 2783...
#> $ Perot96    <int> 8072, 667, 5922, 819, 25249, 38964, 630, 7783, 7244...
#> $ Bush00     <int> 34124, 5610, 38637, 5414, 115185, 177323, 2873, 354...
#> $ Gore00     <int> 47365, 2392, 18850, 3075, 97318, 386561, 2155, 2964...
#> $ Buchanan00 <int> 263, 73, 248, 65, 570, 788, 90, 182, 270, 186, 122,...
#> $ pred       <dbl> 291.3, 25.3, 214.0, 30.8, 908.2, 1400.7, 24.0, 280....
#> $ resid      <dbl> -2.83e+01, 4.77e+01, 3.40e+01, 3.42e+01, -3.38e+02,...
```

There are now two new columns in `florida`, `pred` with the fitted values (predictions), and `resid` with the residuals.

Use `fit2_augment` to create a residual plot:

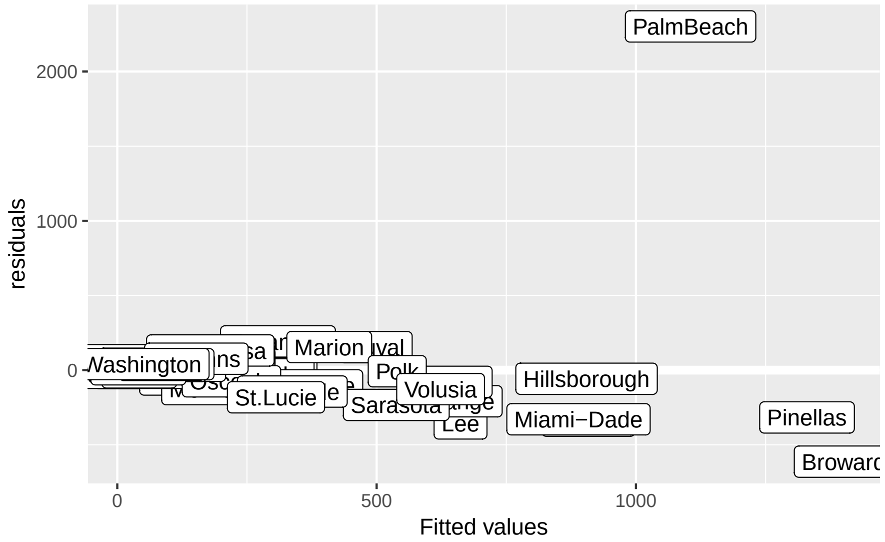
```
fit2_resid_plot <-
  ggplot(florida, aes(x = pred, y = resid)) +
  geom_ref_line(h = 0) +
  geom_point() +
  labs(x = "Fitted values", y = "residuals")
fit2_resid_plot
```



Note, we use the function geom_refline to add a reference line at 0.

Let's add some labels to points, who is that outlier?

```
fit2_resid_plot +
  geom_label(aes(label = county))
```



The outlier county is "Palm Beach"

```
arrange(florida) %>%
  arrange(desc(abs(resid))) %>%
  select(county, resid) %>%
  head()
#>       county resid
#> 1  PalmBeach  2302
#> 2    Broward  -613
#> 3        Lee  -357
#> 4    Brevard  -338
#> 5 Miami-Dade  -329
#> 6   Pinellas  -317
```

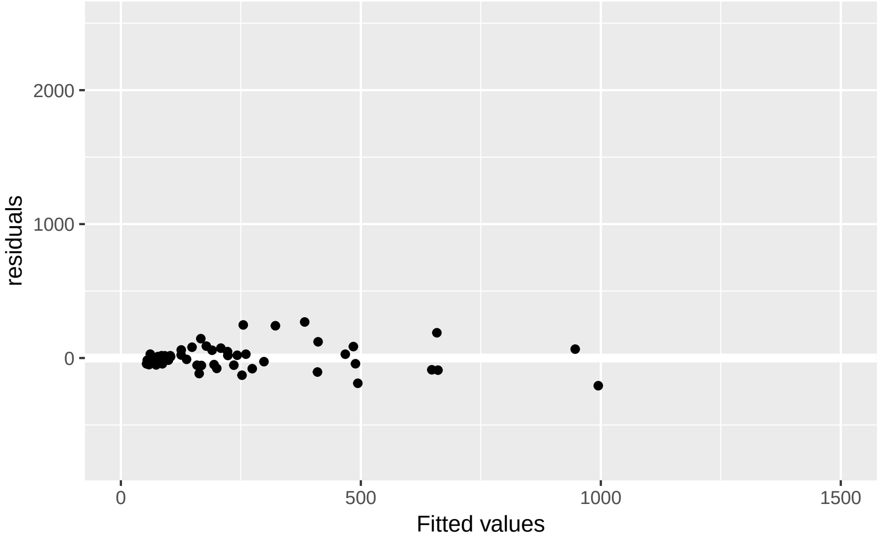
Data without Palm Beach

```
florida_pb <- filter(florida, county != "PalmBeach")
fit3 <- lm(Buchanan00 ~ Perot96, data = florida_pb)
fit3
#> 
#> Call:
#> lm(formula = Buchanan00 ~ Perot96, data = florida_pb)
#> 
#> Coefficients:
#> (Intercept)      Perot96  
#>     45.8419       0.0244
```

R^2 or coefficient of determination

```
glance(fit3)
#>   r.squared adj.r.squared sigma statistic  p.value df logLik AIC BIC
#> 1     0.851         0.849  87.7       366 3.61e-28  2   -388 782 788
#>   deviance df.residual
#> 1   492803          64
```

```
florida_pb %>%
  add_residuals(fit3) %>%
  add_predictions(fit3) %>%
  ggplot(aes(x = pred, y = resid)) +
  geom_ref_line(h = 0) +
  geom_point() +
  ylim(-750, 2500) +
  xlim(0, 1500) +
  labs(x = "Fitted values", y = "residuals")
```

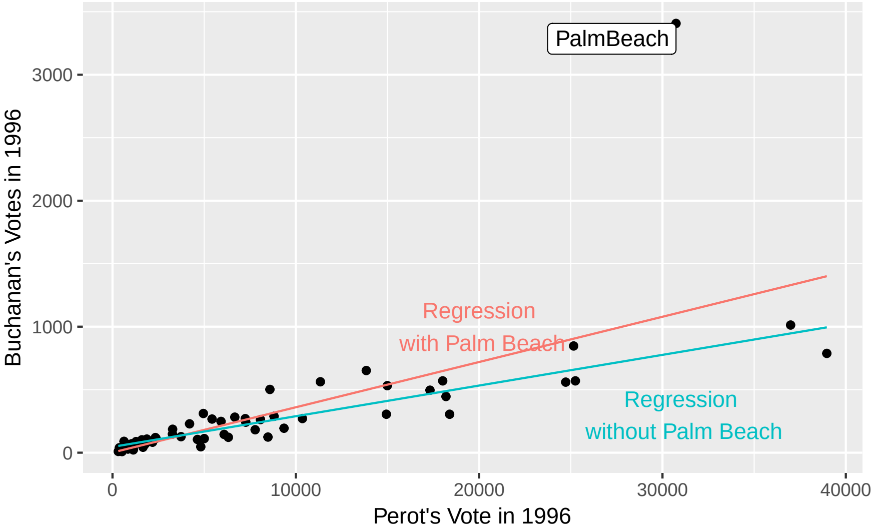


Create predictions for both models using data_grid and gather_predictions:

```
florida_grid <-
  florida %>%
  data_grid(Perot96) %>%
  gather_predictions(fit2, fit3) %>%
  mutate(model =
           fct_recode(model,
                      "Regression\n with Palm Beach" = "fit2",
                      "Regression\n without Palm Beach" = "fit3"))
```

Note this is an example of using non-syntactic column names in a tibble, as discussed in Chapter 10 of R for data science.

```
ggplot() +
  geom_point(data = florida, mapping = aes(x = Perot96, y = Buchanan00)) +
  geom_line(data = florida_grid,
             mapping = aes(x = Perot96, y = pred,
                           colour = model)) +
  geom_label(data = filter(florida, county == "PalmBeach"),
             mapping = aes(x = Perot96, y = Buchanan00, label = county),
                           vjust = "top", hjust = "right") +
  geom_text(data = tibble(label = unique(florida_grid$model),
                           x = c(20000, 31000),
                           y = c(1000, 300)),
             mapping = aes(x = x, y = y, label = label, colour = label)) +
  labs(x = "Perot's Vote in 1996", y = "Buchanan's Votes in 1996") +
  theme(legend.position = "none")
```



See Graphics for communication in *R for Data Science* on labels and annotations in plots.

4.3 Regression and Causation

4.3.1 Randomized Experiments

Load data

```
data("women", package = "qss")
```

Proportion of female politicians in reserved GP vs. unreserved GP

```
women %>%
  group_by(reserved) %>%
  summarise(prop_female = mean(female))
#> # A tibble: 2 x 2
#>   reserved prop_female
#>      <int>       <dbl>
#> 1        0      0.0748
#> 2        1      1.00
```

The diff in means estimator:

```
# drinking water facilities

# irrigation facilities
mean(women$irrigation[women$reserved == 1]) -
    mean(women$irrigation[women$reserved == 0])
#> [1] -0.369
```

Mean values of `irrigation` and `water` in reserved and non-reserved districts.

```
women %>%
  group_by(reserved) %>%
  summarise(irrigation = mean(irrigation),
            water = mean(water))
#> # A tibble: 2 x 3
#>   reserved irrigation water
#>      <int>      <dbl> <dbl>
#> 1        0       3.39  14.7
#> 2        1       3.02  24.0
```

The difference between the two groups can be calculated with the function diff, which calculates the difference between subsequent observations. This works as long as we are careful about which group is first or second.

```
women %>%
  group_by(reserved) %>%
  summarise(irrigation = mean(irrigation),
            water = mean(water)) %>%
  summarise(diff_irrigation = diff(irrigation),
            diff_water = diff(water))
#> # A tibble: 1 x 2
#>   diff_irrigation diff_water
#>             <dbl>      <dbl>
#> 1          -0.369       9.25
```

The other way uses **tidyr** spread and gather,

```
women %>%
  group_by(reserved) %>%
  summarise(irrigation = mean(irrigation),
            water = mean(water)) %>%
  gather(variable, value, -reserved) %>%
  spread(reserved, value) %>%
  mutate(diff = `1` - `0`)
#> # A tibble: 2 x 4
#>   variable     `0`   `1`   diff
#>   <chr>      <dbl> <dbl>  <dbl>
#> 1 irrigation  3.39  3.02 -0.369
#> 2 water      14.7  24.0   9.25
```

Now each row is an outcome variable of interest, and there are columns for the treatment (`1`) and control (`0`) groups, and the difference (`diff`).

```
lm(water ~ reserved, data = women)
#>
#> Call:
#> lm(formula = water ~ reserved, data = women)
#>
#> Coefficients:
#> (Intercept)     reserved
#>       14.74         9.25
```

```
lm(irrigation ~ reserved, data = women)
#>
#> Call:
#> lm(formula = irrigation ~ reserved, data = women)
#>
#> Coefficients:
#> (Intercept)     reserved
#>       3.388       -0.369
```

4.3.2 Regression with multiple predictors

```
data("social", package = "qss")
glimpse(social)
#> Observations: 305,866
#> Variables: 6
#> $ sex         <chr> "male", "female", "male", "female", "female", "mal...
#> $ yearofbirth <int> 1941, 1947, 1951, 1950, 1982, 1981, 1959, 1956, 19...
#> $ primary2004 <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0,...
#> $ messages    <chr> "Civic Duty", "Civic Duty", "Hawthorne", "Hawthorn...
#> $ primary2006 <int> 0, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1,...
#> $ hhsize      <int> 2, 2, 3, 3, 3, 3, 3, 3, 2, 2, 1, 2, 2, 1, 2, 2, 1,...
levels(social$messages)
#> NULL
fit <- lm(primary2006 ~ messages, data = social)
fit
#>
#> Call:
#> lm(formula = primary2006 ~ messages, data = social)
#>
#> Coefficients:
#>       (Intercept)    messagesControl  messagesHawthorne
#>           0.31454           -0.01790            0.00784
#> messagesNeighbors
#>           0.06341
```

Create indicator variables for each message:

```
social <-
  social %>%
  mutate(Control = as.integer(messages == "Control"),
         Hawthorne = as.integer(messages == "Hawthorne"),
         Neighbors = as.integer(messages == "Neighbors"))
```

alternatively, create these using a for loop. This is easier to understand and less prone to typos:

```
for (i in unique(social$messages)) {
  social[[i]] <- as.integer(social[["messages"]] == i)
}
```

We created a variable for each level of `messages` even though we will exclude one of them.

```
lm(primary2006 ~ Control + Hawthorne + Neighbors, data = social)
#> 
#> Call:
#> lm(formula = primary2006 ~ Control + Hawthorne + Neighbors, data = social)
#> 
#> Coefficients:
#> (Intercept)      Control    Hawthorne    Neighbors  
#>     0.31454     -0.01790      0.00784      0.06341
```

Create predictions for each unique value of `messages`

```
unique_messages <-
  data_grid(social, messages) %>%
  add_predictions(fit)
unique_messages
#> # A tibble: 4 x 2
#>   messages    pred
#>   <chr>      <dbl>
#> 1 Civic Duty 0.315
#> 2 Control    0.297
#> 3 Hawthorne  0.322
#> 4 Neighbors  0.378
```

Compare to the sample averages

```
social %>%
  group_by(messages) %>%
  summarise(mean(primary2006))
#> # A tibble: 4 x 2
#>   messages   `mean(primary2006)`
#>   <chr>                    <dbl>
#> 1 Civic Duty               0.315
#> 2 Control                  0.297
#> 3 Hawthorne                0.322
#> 4 Neighbors                0.378
```

Linear regression without intercept.

```
fit_noint <- lm(primary2006 ~ -1 + messages, data = social)
fit_noint
#> 
#> Call:
#> lm(formula = primary2006 ~ -1 + messages, data = social)
#> 
#> Coefficients:
#> messagesCivic Duty     messagesControl   messagesHawthorne  
#>              0.315               0.297               0.322  
#>  messagesNeighbors  
#>              0.378
```

Calculating the regression average effect is also easier if we make the control group the first level so all regression coefficients are comparisons to it. Use fct_relevel to make "Control"

```
fit_control <-
  mutate(social, messages = fct_relevel(messages, "Control")) %>%
  lm(primary2006 ~ messages, data = .)
fit_control
#> 
#> Call:
#> lm(formula = primary2006 ~ messages, data = .)
#> 
#> Coefficients:
#>       (Intercept)  messagesCivic Duty   messagesHawthorne  
#>            0.2966              0.0179              0.0257  
#>  messagesNeighbors  
#>            0.0813
```

Difference in means

```
social %>%
  group_by(messages) %>%
  summarise(primary2006 = mean(primary2006)) %>%
  mutate(Control = primary2006[messages == "Control"],
         diff = primary2006 - Control)
#> # A tibble: 4 x 4
#>   messages   primary2006 Control   diff
#>   <chr>            <dbl>   <dbl>  <dbl>
#> 1 Civic Duty       0.315   0.297 0.0179
#> 2 Control          0.297   0.297 0.
#> 3 Hawthorne        0.322   0.297 0.0257
#> 4 Neighbors        0.378   0.297 0.0813
```

Adjusted R-squared is included in the output of `broom::glance()`

```
glance(fit)
#>   r.squared adj.r.squared sigma statistic   p.value df  logLik    AIC
#> 1   0.00328       0.00327 0.463       336 1.06e-217  4 -198247 396504
#>      BIC deviance df.residual
#> 1 396557    65468      305862
glance(fit)[["adj.r.squared"]]
#> [1] 0.00327
```

4.3.3 Heterogeneous Treatment Effects

Average treatment effect (ate) among those who voted in 2004 primary

```
ate <-
  social %>%
  group_by(primary2004, messages) %>%
  summarise(primary2006 = mean(primary2006)) %>%
  spread(messages, primary2006) %>%
  mutate(ate_Neighbors = Neighbors - Control) %>%
  select(primary2004, Neighbors, Control, ate_Neighbors)
ate
#> # A tibble: 2 x 4
#> # Groups:   primary2004 [2]
#>   primary2004 Neighbors Control ate_Neighbors
#>         <int>     <dbl>   <dbl>         <dbl>
#> 1           0     0.306   0.237        0.0693
#> 2           1     0.482   0.386        0.0965
```

Difference in ATE in 2004 voters and non-voters

```
diff(ate$ate_Neighbors)
#> [1] 0.0272
```

```
social_neighbor <- social %>%
  filter( (messages == "Control") | (messages == "Neighbors"))

fit_int <- lm(primary2006 ~ primary2004 + messages + primary2004:messages,
              data = social_neighbor)
fit_int
#>
#> Call:
#> lm(formula = primary2006 ~ primary2004 + messages + primary2004:messages,
#>     data = social_neighbor)
#>
#> Coefficients:
#>                    (Intercept)                     primary2004
#>                         0.2371                          0.1487
#>              messagesNeighbors  primary2004:messagesNeighbors
#>                         0.0693                          0.0272
```

```
lm(primary2006 ~ primary2004 * messages, data = social_neighbor)
#>
#> Call:
#> lm(formula = primary2006 ~ primary2004 * messages, data = social_neighbor)
#>
#> Coefficients:
#>                    (Intercept)                     primary2004
#>                         0.2371                          0.1487
#>              messagesNeighbors  primary2004:messagesNeighbors
#>                         0.0693                          0.0272
```

```
social_neighbor <-
  social_neighbor %>%
  mutate(age = 2008 - yearofbirth)

summary(social_neighbor$age)
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#>    22.0    43.0    52.0    51.8    61.0   108.0

fit.age <- lm(primary2006 ~ age * messages, data = social_neighbor)
fit.age
#>
#> Call:
#> lm(formula = primary2006 ~ age * messages, data = social_neighbor)
#>
#> Coefficients:
#>            (Intercept)                      age      messagesNeighbors
#>               0.089477                 0.003998               0.048573
#> age:messagesNeighbors
#>               0.000628
```

Calculate average treatment effects

```
ate.age <-
  crossing(age = seq(from = 25, to = 85, by = 20),
         messages = c("Neighbors", "Control")) %>%
  add_predictions(fit.age) %>%
  spread(messages, pred) %>%
  mutate(diff = Neighbors - Control)
ate.age
#> # A tibble: 4 x 4
#>     age Control Neighbors   diff
#>   <dbl>   <dbl>     <dbl>  <dbl>
#> 1   25.   0.189     0.254 0.0643
#> 2   45.   0.269     0.346 0.0768
#> 3   65.   0.349     0.439 0.0894
#> 4   85.   0.429     0.531 0.102
```

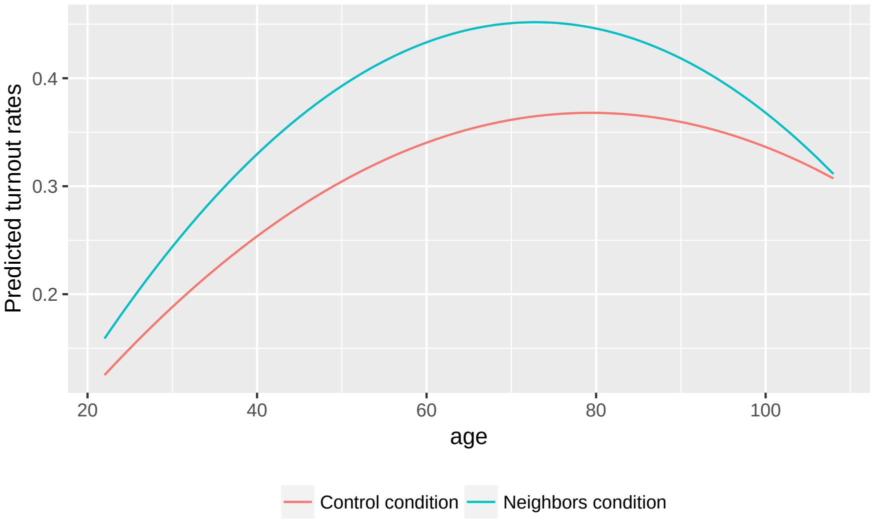
You can use poly function to calculate polynomials instead of adding each term, `age + I(age ^ 2)`. Though note that the coefficients will be be different since by default `poly` calculates orthogonal polynomials instead of the natural (raw) polynomials. However, you really shouldn't interpret the coefficients directly anyways, so this should matter.

```
fit.age2 <- lm(primary2006 ~ poly(age, 2) * messages,
               data = social_neighbor)
fit.age2
#>
#> Call:
#> lm(formula = primary2006 ~ poly(age, 2) * messages, data = social_neighbor)
#>
#> Coefficients:
#>                      (Intercept)                     poly(age, 2)1
#>                           0.2966                           27.6665
#>                    poly(age, 2)2                 messagesNeighbors
#>                         -10.2832                            0.0816
#> poly(age, 2)1:messagesNeighbors  poly(age, 2)2:messagesNeighbors
#>                           4.5820                           -5.5124
```

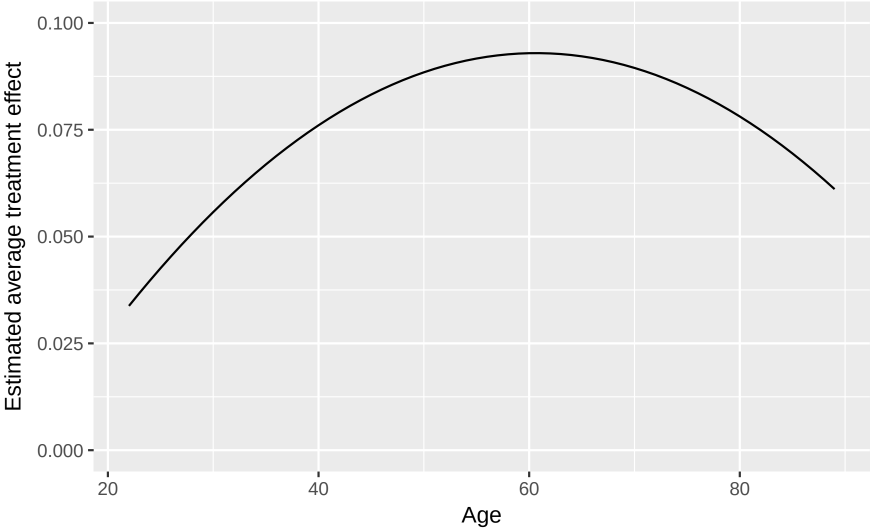
Create a data frame of combinations of ages and messages using data_grid, which means that we only need to specify the variables, and not the specific values,

```
y.hat <-
  data_grid(social_neighbor, age, messages) %>%
  add_predictions(fit.age2)
```

```
ggplot(y.hat, aes(x = age, y = pred,
                  colour = str_c(messages, " condition"))) +
  geom_line() +
  labs(colour = "", y = "Predicted turnout rates") +
  theme(legend.position = "bottom")
```



```r
y.hat %>%
  spread(messages, pred) %>%
  mutate(ate = Neighbors - Control) %>%
  filter(age > 20, age < 90) %>%
  ggplot(aes(x = age, y = ate)) +
  geom_line() +
  labs(y = "Estimated average treatment effect",
       x = "Age") +
  ylim(0, 0.1)
```



4.3.4 Regression Discontinuity Design

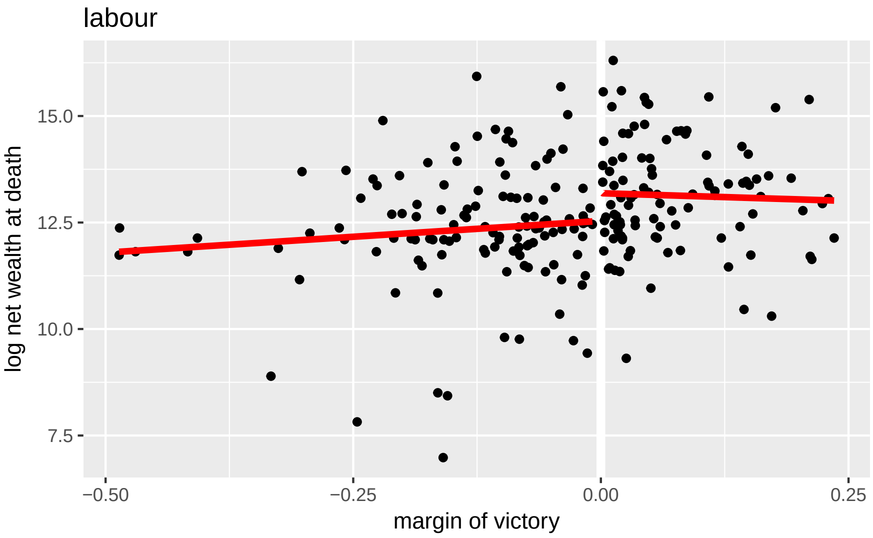
```r
data("MPs", package = "qss")

MPs_labour <- filter(MPs, party == "labour")
MPs_tory <- filter(MPs, party == "tory")

labour_fit1 <- lm(ln.net ~ margin,
                 data = filter(MPs_labour, margin < 0))
labour_fit2 <- lm(ln.net ~ margin, MPs_labour, margin > 0)

tory_fit1 <- lm(ln.net ~ margin,
                data = filter(MPs_tory, margin < 0))
tory_fit2 <- lm(ln.net ~ margin, data = filter(MPs_tory, margin > 0))
```

Use to generate a grid for predictions.

```
y1_labour <-
  filter(MPs_labour, margin < 0) %>%
  data_grid(margin) %>%
  add_predictions(labour_fit1)
y2_labour <-
  filter(MPs_labour, margin > 0) %>%
  data_grid(margin) %>%
  add_predictions(labour_fit2)

y1_tory <-
  filter(MPs_tory, margin < 0) %>%
  data_grid(margin) %>%
  add_predictions(tory_fit1)

y2_tory <-
  filter(MPs_tory, margin > 0) %>%
  data_grid(margin) %>%
  add_predictions(tory_fit2)
```

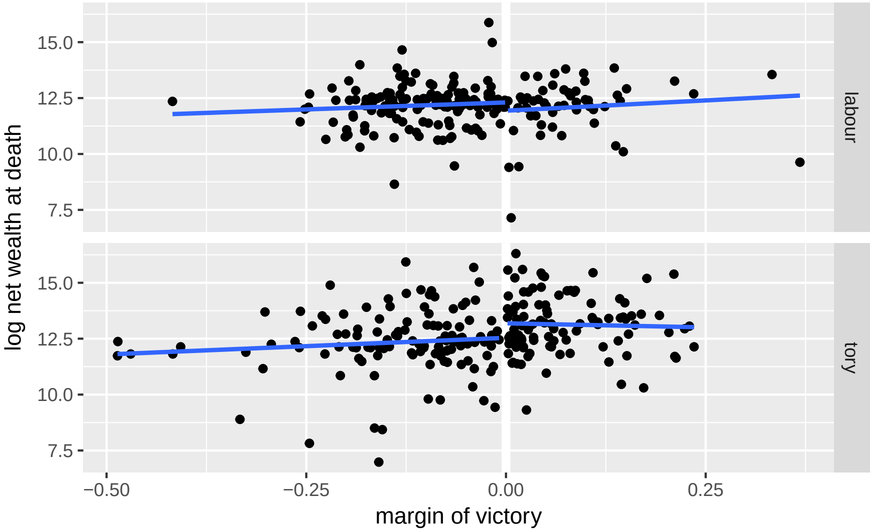
Tory politicians

```
ggplot() +
  geom_ref_line(v = 0) +
  geom_point(data = MPs_tory,
             mapping = aes(x = margin, y = ln.net)) +
  geom_line(data = y1_tory,
            mapping = aes(x = margin, y = pred), colour = "red", size = 1.5) +
  geom_line(data = y2_tory,
            mapping = aes(x = margin, y = pred), colour = "red", size = 1.5) +
  labs(x = "margin of victory", y = "log net wealth at death",
       title = "labour")
```



We can actually produce this plot easily without running the regressions, by using `geom_smooth`:

```
ggplot(mutate(MPs, winner = (margin > 0)),
       aes(x = margin, y = ln.net)) +
  geom_ref_line(v = 0) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE, mapping = aes(group = winner)) +
  facet_grid(party ~ .) +
  labs(x = "margin of victory", y = "log net wealth at death")
```



In the previous code, I didn't directly compute the the average net wealth at 0, so I'll need to do that here. I'll use gather_predictions to add predictions for multiple models:

```
spread_predictions(data_frame(margin = 0),
                   tory_fit1, tory_fit2) %>%
  mutate(rd_est = tory_fit2 - tory_fit1)
#> # A tibble: 1 x 4
#>   margin tory_fit1 tory_fit2 rd_est
#>    <dbl>     <dbl>     <dbl>  <dbl>
#> 1     0.      12.5      13.2  0.650
```

```
tory_fit3 <- lm(margin.pre ~ margin, data = filter(MPs_tory, margin < 0))
tory_fit4 <- lm(margin.pre ~ margin, data = filter(MPs_tory, margin > 0))

(filter(tidy(tory_fit4), term == "(Intercept)")[["estimate"]] -
 filter(tidy(tory_fit3), term == "(Intercept)")[["estimate"]])
#> [1] -0.0173
```

Chapter 5

Discovery

The idea of tidy data and the common feature of tidyverse packages is that data should be stored in data frames with certain conventions. This works well with naturally tabular data, the type which has been common in social science applications. But there are other domains in which other data structures are more appropriate because they more naturally model the data or processes, or for computational reasons. The three applications in this chapter: text, networks, and spatial data are examples where the tidy data structure is less of an advantage. I will still rely on **ggplot2** for plotting, and use tidy verse compatible packages where appropriate.

- Textual data: tidytext
- Network data: igraph for network computation, as in the chapter. But several **ggplot2**2 extension packages for plotting the networks.
- Spatial data: ggplot2 has some built-in support for maps. The map package provides map data.

See the R for Data Science section 12.7 Non-tidy data and this post on Non-tidy data by Jeff Leek for more on non-tidy data.

5.1 Textual data

Prerequisites

```r
library("tidyverse")
library("lubridate")
library("stringr")
library("forcats")
library("modelr")
library("tm")
library("SnowballC")
library("tidytext")
library("wordcloud")
```

This section will primarily use the tidytext package. It is a relatively new package. The tm and quanteda (by Ken Benoit) packages are more established and use the document-term matrix format as described in the QSS chapter. The **tidytext** package stores everything in a data frame; this may be less efficient than the other packages, but has the benefit of being able to easily take advantage of the tidyverse ecosystem. If your corpus is not too large, this shouldn't be an issue.

See Tidy Text Mining with R for a full introduction to using **tidytext**.

In tidy data, each row is an observation and each column is a variable. In the **tidytext** package, documents are stored as data frames with **one-term-per-row**.

We can cast data into the **tidytext** format either from the `Corpus` object, or, after processing, from the document-term matrix object.

```
DIR_SOURCE <- system.file("extdata/federalist", package = "qss")
corpus_raw <- VCorpus(DirSource(directory = DIR_SOURCE, pattern = "fp"))
corpus_raw
#> <<VCorpus>>
#> Metadata:  corpus specific: 0, document level (indexed): 0
#> Content:  documents: 85
```

Use the function tidy to convert the to a data frame with one row per document.

```
corpus_tidy <- tidy(corpus_raw, "corpus")
corpus_tidy
#> # A tibble: 85 x 8
#>   author datetimestamp       description heading id       language origin
#>   <lgl>  <dttm>              <lgl>       <lgl>   <chr>    <chr>    <lgl>
#> 1 NA     2018-02-26 22:22:03 NA          NA      fp01.txt en       NA
#> 2 NA     2018-02-26 22:22:03 NA          NA      fp02.txt en       NA
#> 3 NA     2018-02-26 22:22:03 NA          NA      fp03.txt en       NA
#> 4 NA     2018-02-26 22:22:03 NA          NA      fp04.txt en       NA
#> 5 NA     2018-02-26 22:22:03 NA          NA      fp05.txt en       NA
#> 6 NA     2018-02-26 22:22:03 NA          NA      fp06.txt en       NA
#> # ... with 79 more rows, and 1 more variable: text <chr>
```

The `text` column contains the text of the documents themselves. Since most of the metadata columns are either missings or irrelevant for our purposes, we'll delete those columns, keeping only the document (`id`) and `text` columns.

```
corpus_tidy <- select(corpus_tidy, id, text)
```

Also, we want to extract the essay number and use that as the document id rather than its file name.

```
corpus_tidy <-
  mutate(corpus_tidy, document = as.integer(str_extract(id, "\\d+"))) %>%
  select(-id)
```

The function tokenizes the document texts:

```
tokens <- corpus_tidy %>%
  # tokenizes into words and stems them
  unnest_tokens(word, text, token = "word_stems") %>%
  # remove any numbers in the strings
  mutate(word = str_replace_all(word, "\\d+", "")) %>%
  # drop any empty strings
  filter(word != "")
tokens
#> # A tibble: 202,089 x 2
#>   document word
#>      <int> <chr>
#> 1        1 after
#> 2        1 an
#> 3        1 unequivoc
#> 4        1 experi
#> 5        1 of
#> 6        1 the
#> # ... with 2.021e+05 more rows
```

The `unnest_tokens` function uses the tokenizers package to tokenize the text. By default, it uses the function which removes punctuation, and lowercases the words. I set the tokenizer to to stem the word, using the SnowballC package.

We can remove stop-words with an anti_join on the dataset stop_words

```
data("stop_words", package = "tidytext")
tokens <- anti_join(tokens, stop_words, by = "word")
```

5.1.1 Document-Term Matrix

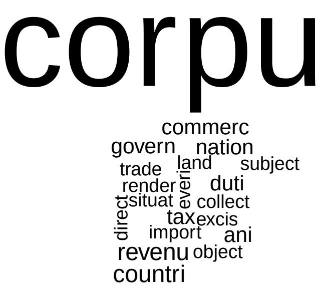
In `tokens` there is one observation for each token (word) in the each document. This is almost equivalent to a document-term matrix. For a document-term matrix we need documents, and terms as the keys for the data and a column with the number of times the term appeared in the document.

```
dtm <- count(tokens, document, word)
head(dtm)
#> # A tibble: 6 x 3
#>   document word           n
#>      <int> <chr>      <int>
#> 1        1 abl            1
#> 2        1 absurd         1
#> 3        1 accid          1
#> 4        1 accord         1
#> 5        1 acknowledg     1
#> 6        1 act            1
```

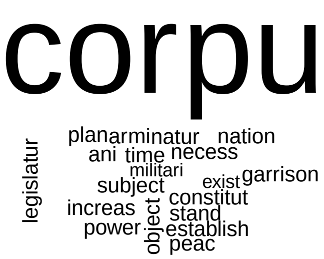
5.1.2 Topic Discovery

Plot the word-clouds for essays 12 and 24:

```
filter(dtm, document == 12) %>% {
    wordcloud(.$word, .$n, max.words = 20)
  }
```



```
filter(dtm, document == 24) %>% {
    wordcloud(.$word, .$n, max.words = 20)
  }
```



Use the function bind_tf_idf to add a column with the tf-idf to the data frame.

```
dtm <- bind_tf_idf(dtm, word, document, n)
dtm
#> # A tibble: 38,847 x 6
#>   document word              n      tf   idf   tf_idf
#>      <int> <chr>         <int>   <dbl> <dbl>    <dbl>
#> 1        1 abl               1 0.00145 0.705 0.00102
#> 2        1 absurd            1 0.00145 1.73  0.00251
#> 3        1 accid             1 0.00145 3.75  0.00543
#> 4        1 accord            1 0.00145 0.754 0.00109
#> 5        1 acknowledg        1 0.00145 1.55  0.00225
#> 6        1 act               1 0.00145 0.400 0.000579
#> # ... with 3.884e+04 more rows
```

The 10 most important words for Paper No. 12 are

```
dtm %>%
  filter(document == 12) %>%
  top_n(10, tf_idf)
#> # A tibble: 10 x 6
#>   document word              n      tf   idf  tf_idf
#>      <int> <chr>         <int>   <dbl> <dbl>   <dbl>
#> 1       12 cent              2 0.00199  4.44 0.00884
#> 2       12 coast             3 0.00299  3.75 0.0112
#> 3       12 commerc           8 0.00796  1.11 0.00884
#> 4       12 contraband        3 0.00299  4.44 0.0133
#> 5       12 excis             5 0.00498  2.65 0.0132
#> 6       12 gallon            2 0.00199  4.44 0.00884
#> # ... with 4 more rows
```

and for Paper No. 24,

```
dtm %>%
  filter(document == 24) %>%
  top_n(10, tf_idf)
#> # A tibble: 10 x 6
#>   document word          n      tf   idf  tf_idf
#>      <int> <chr>     <int>   <dbl> <dbl>   <dbl>
#> 1       24 armi          7 0.00858  1.26 0.0108
#> 2       24 arsenal       2 0.00245  3.75 0.00919
#> 3       24 dock          3 0.00368  4.44 0.0163
#> 4       24 frontier      3 0.00368  2.83 0.0104
#> 5       24 garrison      6 0.00735  2.83 0.0208
#> 6       24 nearer        2 0.00245  3.34 0.00820
#> # ... with 4 more rows
```

The slightly different results from the book are due to tokenization differences.

Subset those documents known to have been written by Hamilton.

```
HAMILTON_ESSAYS <- c(1, 6:9, 11:13, 15:17, 21:36, 59:61, 65:85)
dtm_hamilton <- filter(dtm, document %in% HAMILTON_ESSAYS)
```

The kmeans function expects the input to be rows for observations and columns for each variable: in our case that would be documents as rows, and words as columns, with the tf-idf as the cell values. We could use `spread` to do this, but that would be a large matrix.

```
CLUSTERS <- 4
km_out <-
  kmeans(cast_dtm(dtm_hamilton, document, word, tf_idf), centers = CLUSTERS,
         nstart = 10)
km_out$iter
#> [1] 3
```

Data frame with the unique terms used by Hamilton. I extract these from the column names of the DTM after `cast_dtm` to ensure that the order is the same as the k-means results.

```
hamilton_words <-
  tibble(word = colnames(cast_dtm(dtm_hamilton, document, word, tf_idf)))
```

The centers of the clusters is a cluster x word matrix. We want to transpose it and then append columns to `hamilton_words` so the location of each word in the cluster is listed.

```
dim(km_out$centers)
#> [1]    4 3850
```

```
hamilton_words <- bind_cols(hamilton_words, as_tibble(t(km_out$centers)))
hamilton_words
#> # A tibble: 3,850 x 5
#>   word              `1`      `2`     `3`      `4`
#>   <chr>           <dbl>    <dbl>   <dbl>    <dbl>
#> 1 abl          0.000939 0.000743 0.      0.
#> 2 absurd       0.       0.000517 0.      0.000882
#> 3 accid        0.       0.000202 0.      0.
#> 4 accord       0.       0.000399 0.      0.000852
#> 5 acknowledg 0.       0.000388 0.      0.000473
#> 6 act          0.       0.000560 0.00176 0.000631
#> # ... with 3,844 more rows
```

To find the top 10 words in each centroid, we use `top_n` with `group_by`:

```
top_words_cluster <-
  gather(hamilton_words, cluster, value, -word) %>%
  group_by(cluster) %>%
  top_n(10, value)
```

We can print them out using a for loop

```
for (i in 1:CLUSTERS) {
  cat("CLUSTER ", i, ": ",
      str_c(filter(top_words_cluster, cluster == i)$word, collapse = ", "),
      "\n\n")
}
#> CLUSTER  1 :  presid, appoint, senat, claus, expir, fill, recess, session, unfound, vacanc
#>
#> CLUSTER  2 :  offic, presid, tax, land, revenu, armi, militia, senat, taxat, claus
#>
```

```
#> CLUSTER  3 :  sedit, guilt, chief, clemenc, impun, plead, crime, pardon, treason, conniv
#>
#> CLUSTER  4 :  court, jurisdict, inferior, suprem, trial, tribun, cogniz, juri, impeach, appel
```

This is alternative code that prints out a table:

```
gather(hamilton_words, cluster, value, -word) %>%
  group_by(cluster) %>%
  top_n(10, value) %>%
  summarise(top_words = str_c(word, collapse = ", ")) %>%
  knitr::kable()
```

cluster	top_words
1	presid, appoint, senat, claus, expir, fill, recess, session, unfound, vacanc
2	offic, presid, tax, land, revenu, armi, militia, senat, taxat, claus
3	sedit, guilt, chief, clemenc, impun, plead, crime, pardon, treason, conniv
4	court, jurisdict, inferior, suprem, trial, tribun, cogniz, juri, impeach, appel

Or to print out the documents in each cluster,

```
enframe(km_out$cluster, "document", "cluster") %>%
  group_by(cluster) %>%
  summarise(documents = str_c(document, collapse = ", ")) %>%
  knitr::kable()
```

cluster	documents
1	67
2	1, 6, 7, 8, 9, 11, 12, 13, 15, 16, 17, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 59, 60, 61, 66, 68, 6
3	74
4	65, 81, 82, 83

5.1.3 Authorship Prediction

We'll create a data-frame with the known

```
MADISON_ESSAYS <- c(10, 14, 37:48, 58)
JAY_ESSAYS <- c(2:5, 64)
known_essays <- bind_rows(tibble(document = MADISON_ESSAYS,
                                 author = "Madison"),
                          tibble(document = HAMILTON_ESSAYS,
                                 author = "Hamilton"),
                          tibble(document = JAY_ESSAYS,
                                 author = "Jay"))
```

```
STYLE_WORDS <-
  tibble(word = c("although", "always", "commonly", "consequently",
                  "considerable", "enough", "there", "upon", "while", "whilst"))

hm_tfm <-
  unnest_tokens(corpus_tidy, word, text) %>%
  count(document, word) %>%
  # term freq per 1000 words
  group_by(document) %>%
  mutate(count = n / sum(n) * 1000) %>%
  select(-n) %>%
  inner_join(STYLE_WORDS, by = "word") %>%
  # merge known essays
  left_join(known_essays, by = "document") %>%
  # make wide with each word a column
  # fill empty values with 0
  spread(word, count, fill = 0)
```

Calculate average usage by each author of each word

```
hm_tfm %>%
  # remove docs with no author
  filter(!is.na(author)) %>%
  # convert back to long (tidy) format to make it easier to summarize
  gather(word, count, -document, -author) %>%
  # calculate averge document word usage by author
  group_by(author, word) %>%
  summarise(avg_count = mean(count)) %>%
  spread(author, avg_count) %>%
  knitr::kable()
```

word	Hamilton	Jay	Madison
although	0.012	0.543	0.206
always	0.522	0.929	0.154
commonly	0.184	0.129	0.000
consequently	0.018	0.469	0.344
considerable	0.377	0.081	0.123
enough	0.274	0.000	0.000
there	3.065	0.954	0.849
upon	3.054	0.112	0.152
while	0.255	0.192	0.000
whilst	0.005	0.000	0.292

```
author_data <-
  hm_tfm %>%
  ungroup() %>%
  filter(is.na(author) | author != "Jay") %>%
  mutate(author2 = case_when(.$author == "Hamilton" ~ 1,
                             .$author == "Madison" ~ -1,
                             TRUE ~ NA_real_))

hm_fit <- lm(author2 ~ upon + there + consequently + whilst,
             data = author_data)
hm_fit
#>
#> Call:
#> lm(formula = author2 ~ upon + there + consequently + whilst,
#>     data = author_data)
#>
#> Coefficients:
#>  (Intercept)          upon         there  consequently        whilst
#>       -0.195         0.229         0.127        -0.644        -0.984

author_data <- author_data %>%
  add_predictions(hm_fit) %>%
  mutate(pred_author = if_else(pred >= 0, "Hamilton", "Madison"))
```

```
sd(author_data$pred)
#> [1] 0.79
```

These coefficients are a little different, probably due to differences in the tokenization procedure, and in particular, the document size normalization.

5.1.4 Cross-Validation

tidyverse: For cross-validation, I rely on the modelr package function `RDoc("modelr::crossv_kfold")`. See the tutorial Cross validation of linear regression with modelr for more on using **modelr** for cross validation or k-fold cross-validation with modelr and broom.

In sample, this regression perfectly predicts the authorship of the documents with known authors.

```
author_data %>%
  filter(!is.na(author)) %>%
  group_by(author) %>%
  summarise(`Proportion Correct` = mean(author == pred_author))
#> # A tibble: 2 x 2
#>   author   `Proportion Correct`
#>   <chr>                   <dbl>
#> 1 Hamilton                   1.
#> 2 Madison                    1.
```

Create the cross-validation data-sets using . As in the chapter, I will use a leave-one-out cross-validation, which is a k-fold cross-validation where k is the number of observations. To simplify this, I define the `crossv_loo` function that runs `crossv_kfold` with `k = nrow(data)`.

```
crossv_loo <- function(data, id = ".id") {
  modelr::crossv_kfold(data, k = nrow(data), id = id)
}

# leave one out cross-validation object
cv <- author_data %>%
  filter(!is.na(author)) %>%
  crossv_loo()
```

Now estimate the model for each training dataset

```
models <- purrr::map(cv$train, ~ lm(author2 ~ upon + there + consequently + whilst,
                                    data = ., model = FALSE))
```

Note that I use `purrr::map` to ensure that the correct `map()` function is used since the **maps** package also defines a `map`.

Now calculate the test performance on the held out observation,

```
test <- map2_df(models, cv$test,
                function(mod, test) {
                  add_predictions(as.data.frame(test), mod) %>%
                    mutate(pred_author =
                             if_else(pred >= 0, "Hamilton", "Madison"),
                           correct = (pred_author == author))
                })
test %>%
  group_by(author) %>%
  summarise(mean(correct))
```

```
#> # A tibble: 2 x 2
#>   author   `mean(correct)`
#>   <chr>              <dbl>
#> 1 Hamilton           1.00
#> 2 Madison            0.786
```

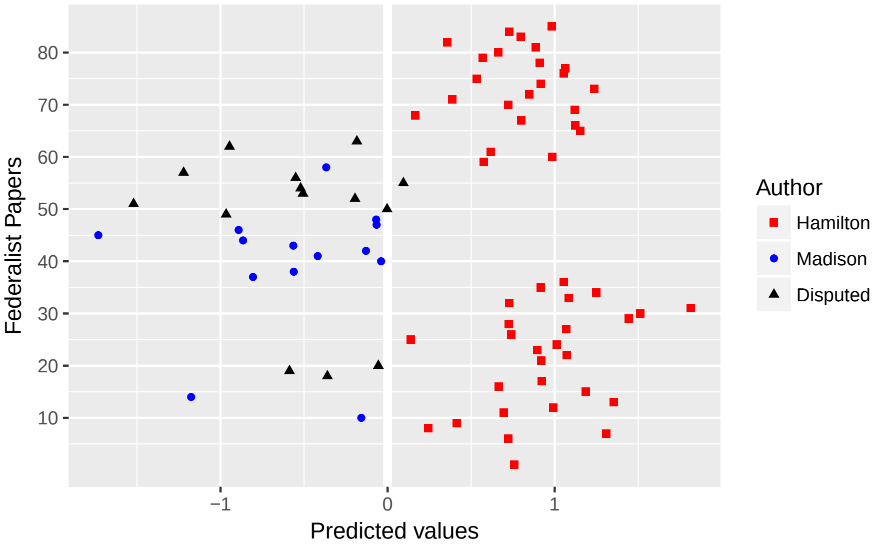
When adding prediction with `add_predictions` it added predictions for missing values as well.

Table of authorship of disputed papers

```
author_data %>%
  filter(is.na(author)) %>%
  select(document, pred, pred_author) %>%
  knitr::kable()
```

document	pred	pred_author
18	-0.360	Madison
19	-0.587	Madison
20	-0.055	Madison
49	-0.966	Madison
50	-0.003	Madison
51	-1.520	Madison
52	-0.195	Madison
53	-0.506	Madison
54	-0.521	Madison
55	0.094	Hamilton
56	-0.550	Madison
57	-1.221	Madison
62	-0.946	Madison
63	-0.184	Madison

```
disputed_essays <- filter(author_data, is.na(author))$document

ggplot(mutate(author_data,
              author = fct_explicit_na(factor(author), "Disputed")),
       aes(y = document, x = pred, colour = author, shape = author)) +
  geom_ref_line(v = 0) +
  geom_point() +
  scale_y_continuous(breaks = seq(10, 80, by = 10),
                     minor_breaks = seq(5, 80, by = 5)) +
  scale_color_manual(values = c("Madison" = "blue",
                                "Hamilton" = "red",
                                "Disputed" = "black")) +
  scale_shape_manual(values = c("Madison" = 16, "Hamilton" = 15,
                                 "Disputed" = 17)) +
  labs(colour = "Author", shape = "Author",
       y = "Federalist Papers", x = "Predicted values")
```



5.2 Network data

The igraph, sna, and network packages are the best in class. See the Social Network Analysis section of the Social Sciences Task View. See this tutorial by Katherin Ognyanova, Static and dynamic network visualization with R, for a good overview of network visualization with those packages in R.

There are several packages that plot networks in ggplot2.

- ggnetwork
- ggraph
- geomnet
- GGally functions ggnet, `ggnet2`, and `ggnetworkmap`.
- ggCompNet compares the speed of various network plotting packages in R.

See this presentation for an overview of some of those packages for data visualization.

Examples: Network Visualization Examples with the ggplot2 Package

Prerequisites

```
library("tidyverse")
library("lubridate")
library("stringr")
library("forcats")
library("igraph")
library("intergraph")
library("GGally")
```

5.2.1 Twitter Following Network

```
data("twitter.following", package = "qss")
```

```
data("twitter.senator", package = "qss")
```

Since the names `twitter.following` and `twitter.senator` are verbose, we'll simplify future code by copying their values to variables named `twitter` and `senator`, respectively.

```
twitter <- twitter.following
senator <- twitter.senator
```

Simply use the function since `twitter` consists of edges (a link from a senator to another). Since `graph_from_edgelist` expects a matrix, convert the data frame to a matrix using .

```
twitter_adj <- graph_from_edgelist(as.matrix(twitter))
```

Add in- and out-degree variables to the `senator` data frame:

```
senator <-
  mutate(senator,
         indegree = igraph::degree(twitter_adj, mode = "in"),
         outdegree = igraph::degree(twitter_adj, mode = "out"))
```

Now find the senators with the 3 greatest in-degrees

```
arrange(senator, desc(indegree)) %>%
  slice(1:3) %>%
  select(name, party, state, indegree, outdegree)
#> # A tibble: 3 x 5
#>   name               party state indegree outdegree
#>   <chr>              <chr> <chr>    <dbl>     <dbl>
#> 1 Tom Cotton         R     AR         64.       15.
#> 2 Richard J. Durbin D     IL         60.       87.
#> 3 John Barrasso      R     WY         58.       79.
```

or using the function:

```
top_n(senator, 3, indegree) %>%
  arrange(desc(indegree)) %>%
  select(name, party, state, indegree, outdegree)
#>                name party state indegree outdegree
#> 1        Tom Cotton     R    AR       64        15
#> 2 Richard J. Durbin     D    IL       60        87
#> 3     John Barrasso     R    WY       58        79
#> 4       Joe Donnelly     D    IN       58         9
#> 5     Orrin G. Hatch     R    UT       58        50
```

The `top_n` function catches that three senators are tied for 3rd highest outdegree, whereas the simply sorting and slicing cannot.

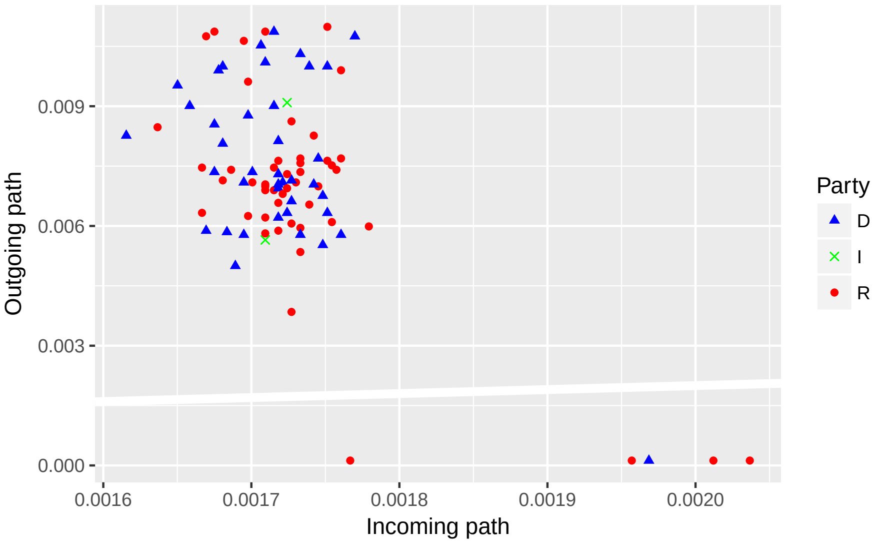
And we can find the senators with the three highest out-degrees similarly,

```
top_n(senator, 3, outdegree) %>%
  arrange(desc(outdegree)) %>%
  select(name, party, state, indegree, outdegree)
#>               name party state indegree outdegree
#> 1     Thad Cochran     R    MS       55        89
#> 2     Steve Daines     R    MT       30        88
#> 3      John McCain     R    AZ       41        88
#> 4 Joe Manchin, III     D    WV       43        88
```

```
# Define scales to reuse for the plots
scale_colour_parties <- scale_colour_manual("Party", values = c(R = "red",
                                                                 D = "blue",
                                                                 I = "green"))
```

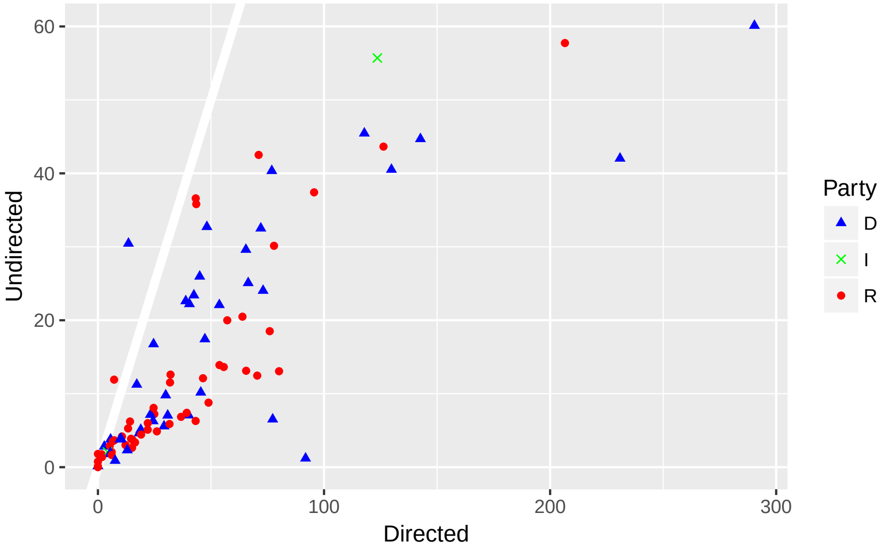
```
scale_shape_parties <- scale_shape_manual("Party", values = c(R = 16,
                                                              D = 17,
                                                              I = 4))
```

```
senator %>%
  mutate(closeness_in = igraph::closeness(twitter_adj, mode = "in"),
         closeness_out = igraph::closeness(twitter_adj, mode = "out")) %>%
  ggplot(aes(x = closeness_in, y = closeness_out,
             colour = party, shape = party)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_point() +
  scale_colour_parties +
  scale_shape_parties +
  labs(main = "Closeness", x = "Incoming path", y = "Outgoing path")
```



What does the reference line indicate? What does that say about senators twitter networks?

```
senator %>%
  mutate(betweenness_dir = igraph::betweenness(twitter_adj, directed = TRUE),
         betweenness_undir = igraph::betweenness(twitter_adj,
                                                 directed = FALSE)) %>%
  ggplot(aes(x = betweenness_dir, y = betweenness_undir, colour = party,
             shape = party)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_point() +
  scale_colour_parties +
  scale_shape_parties +
  labs(main = "Betweenness", x = "Directed", y = "Undirected")
```

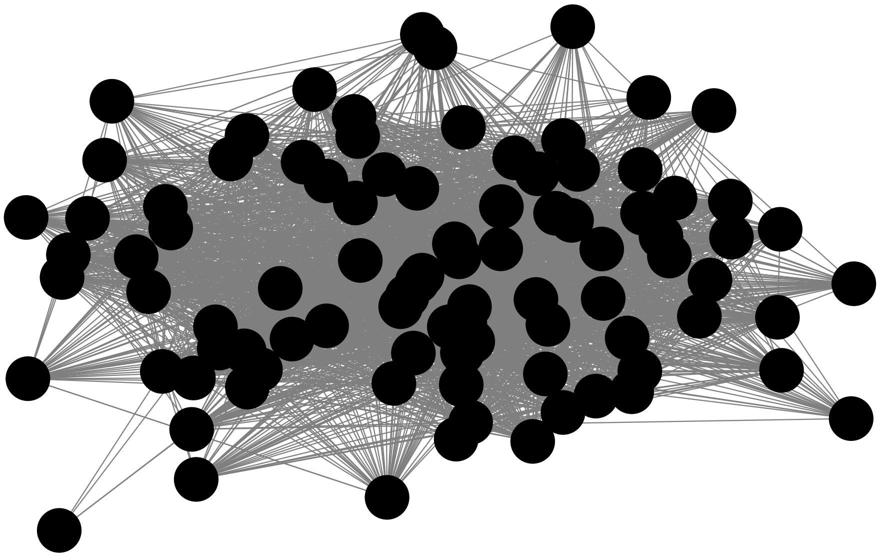


We've covered three different methods of calculating the importance of a node in a network: degree, closeness, and centrality. But what do they mean? What's the "best" measure of importance? The answer to the the former is "it depends on the question". There are probably other papers out there on this, but Borgatti (2005) is a good discussion:

> Borgatti, Stephen. 2005. "Centrality and Network Flow". *Social Networks.* DOI

Add and plot page-rank:

```r
senator <- mutate(senator, page_rank = page_rank(twitter_adj)[["vector"]])
ggnet(twitter_adj, mode = "target")
```



5.3 Spatial Data

Some resources on plotting spatial data in R:

- ggplot2 has several map-related functions
  - borders
  - fortify.map

    - map_data

- ggmap allows ggplot to us a map from Google Maps, OpenStreet Maps or similar as a background for the plot.
    - David Kahle and Hadley Wickham. 2013. ggmap: Spatial Visualization with ggplot2. *Journal of Statistical Software*
    - Github dkahle/ggmamp
- tmap is not built on ggplot2 but uses a ggplot2-like API for network data.
- leaflet is an R interface to a popular javascript mapping library.

Here are few tutorials on plotting spatial data in ggplot2:

- Making Maps with R
- Plotting Data on a World Map
- Introduction to Spatial Data and ggplot2

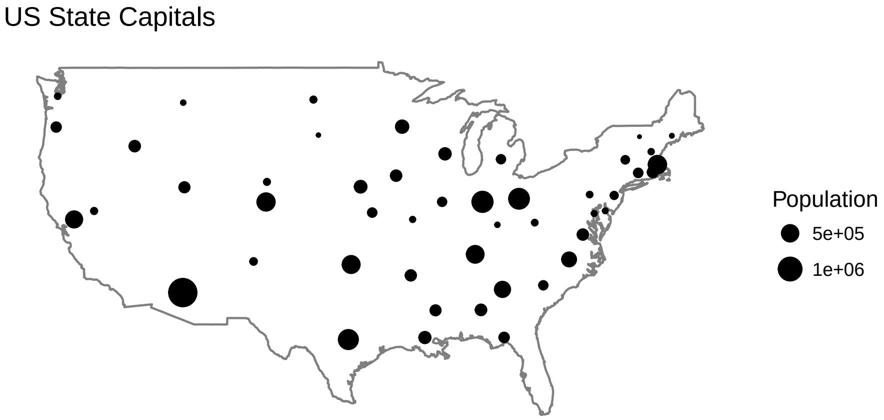
Prerequisites

```r
library("tidyverse")
library("lubridate")
library("stringr")
library("forcats")
library("modelr")
library("ggrepel")
```

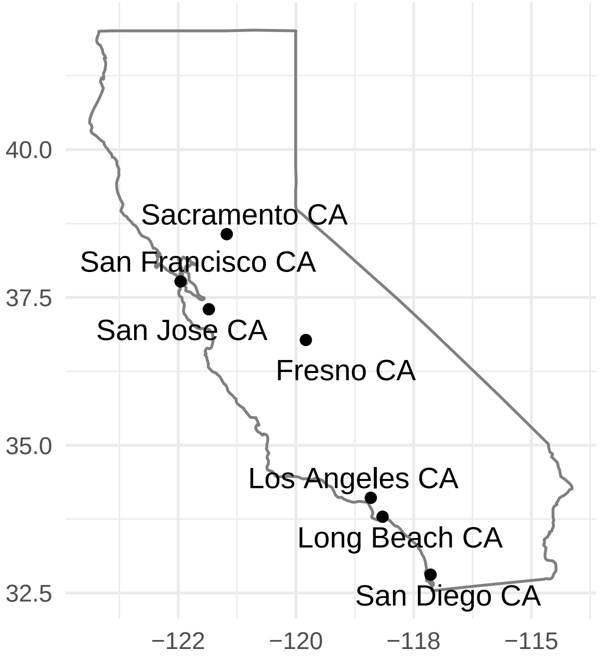
5.3.1 Spatial Data in R

```r
data("us.cities", package = "maps")
glimpse(us.cities)
#> Observations: 1,005
#> Variables: 6
#> $ name        <chr> "Abilene TX", "Akron OH", "Alameda CA", "Albany GA...
#> $ country.etc <chr> "TX", "OH", "CA", "GA", "NY", "OR", "NM", "LA", "V...
#> $ pop         <int> 113888, 206634, 70069, 75510, 93576, 45535, 494962...
#> $ lat         <dbl> 32.5, 41.1, 37.8, 31.6, 42.7, 44.6, 35.1, 31.3, 38...
#> $ long        <dbl> -99.7, -81.5, -122.3, -84.2, -73.8, -123.1, -106.6...
#> $ capital     <int> 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
```

```r
usa_map <- map_data("usa")
#>
#> Attaching package: 'maps'
#> The following object is masked from 'package:purrr':
#>
#>     map
capitals <- filter(us.cities,
                   capital == 2,
                   !country.etc %in% c("HI", "AK"))
ggplot() +
  geom_map(map = usa_map) +
  borders(database = "usa") +
  geom_point(aes(x = long, y = lat, size = pop),
             data = capitals) +
  # scale size area ensures: 0 = no area
  scale_size_area() +
  coord_quickmap() +
  theme_void() +
  labs(x = "", y = "", title = "US State Capitals",
       size = "Population")
```



```
cal_cities <- filter(us.cities, country.etc == "CA") %>%
  top_n(7, pop)

ggplot() +
  borders(database = "state", regions = "California") +
  geom_point(aes(x = long, y = lat), data = cal_cities) +
  geom_text_repel(aes(x = long, y = lat, label = name), data = cal_cities) +
  coord_quickmap() +
  theme_minimal() +
  labs(x = "", y = "")
```



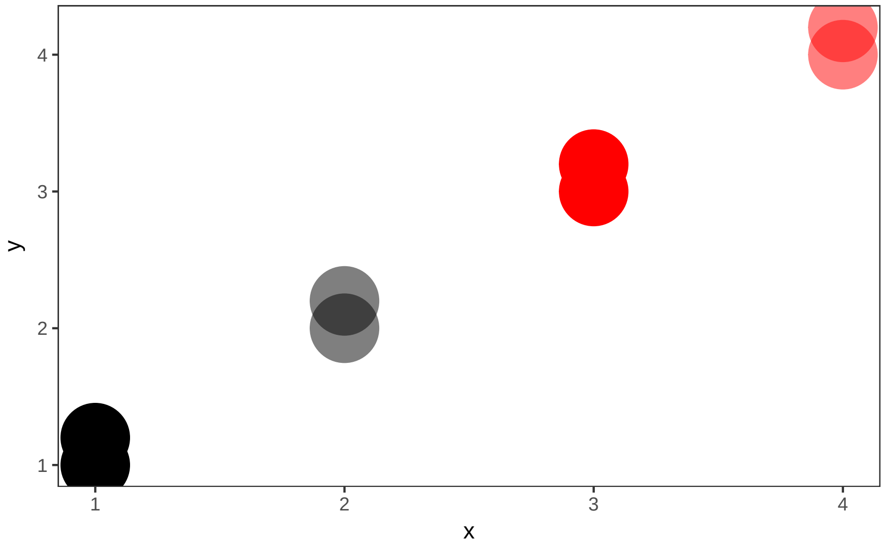
5.3.2 Colors in R

For more resources on using colors in R

- R4DS chapter Graphics for Communication
- ggplot2 book Chapter "Scales"
- Jenny Bryan Using colors in R
- Achim Zeileis, Kurt Hornik, Paul Murrell (2009). Escaping RGBland: Selecting Colors for Statistical Graphics. Computational Statistics & Data Analysis DOI
- colorspace vignette
- Maureen Stone Choosing Colors for Data Visualization
- ColorBrewer A website with a variety of palettes, primarily designed for maps, but also useful in data viz.
- Stephen Few Practical Rules for Using Color in Charts
- Why Should Engineers and Scientists by Worried About Color?
- A Better Default Colormap for Matplotlib A SciPy 2015 talk that describes how the viridis was created.
- Evaluation of Artery Visualizations for Heart Disease Diagnosis Using the wrong color scale can be deadly … literally.
- The python package matplotlib has a good discussion of colormaps.
- Peter Kovesi Good Color Maps: How to Design Them.
- See the viridis, ggthemes, dichromat, and pals packages for color palettes.

Use scale_identity for the color and alpha scales since the values of the variables are the values of the scale itself (the color names, and the alpha values).

```r
ggplot(tibble(x = rep(1:4, each = 2),
              y = x + rep(c(0, 0.2), times = 2),
              colour = rep(c("black", "red"), each = 4),
              alpha = c(1, 1, 0.5, 0.5, 1, 1, 0.5, 0.5)),
  aes(x = x, y = y, colour = colour, alpha = alpha)) +
  geom_point(size = 15) +
  scale_color_identity() +
  scale_alpha_identity() +
  theme_bw() +
  theme(panel.grid = element_blank())
```



5.3.3 United States Presidential Elections

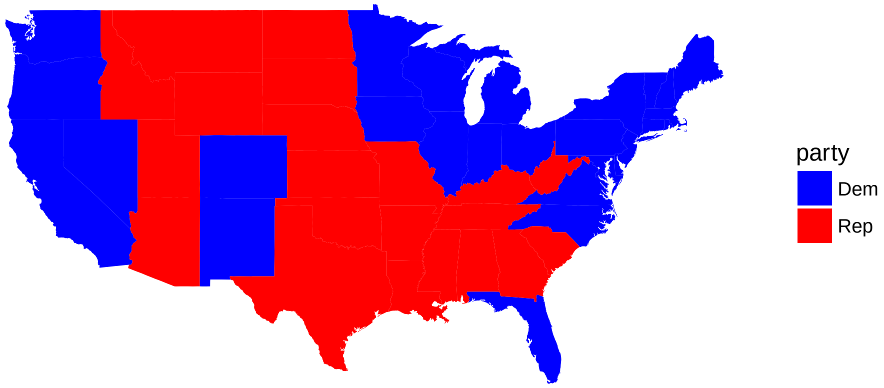
```
data("pres08", package = "qss")

pres08 <- pres08 %>%
  mutate(Dem = Obama / (Obama + McCain),
         Rep = McCain / (Obama + McCain))
```

```
ggplot() +
  borders(database = "state", regions = "California", fill = "blue") +
  coord_quickmap() +
  theme_void()
```

```
cal_color <- filter(pres08, state == "CA") %>% {
    rgb(red = .$Rep, green = 0, blue = .$Dem)
  }

ggplot() +
  borders(database = "state", regions = "California", fill = cal_color) +
  coord_quickmap() +
  theme_void()
```

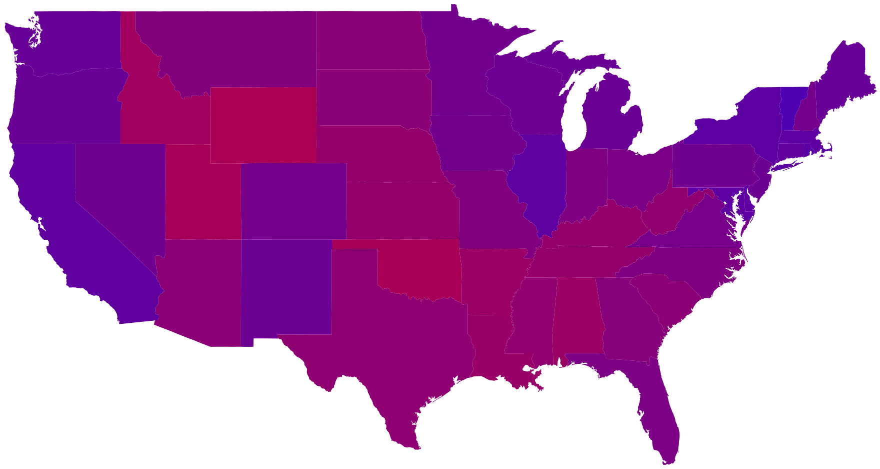
```r
# America as red and blue states
map(database = "state") # create a map
for (i  in 1:nrow(pres08)) {
    if ( (pres08$state[i] != "HI") & (pres08$state[i] != "AK") &
        (pres08$state[i] != "DC")) {
        map(database = "state", regions = pres08$state.name[i],
            col = ifelse(pres08$Rep[i] > pres08$Dem[i], "red", "blue"),
            fill = TRUE, add = TRUE)
    }
}

## America as purple states
map(database = "state") # create a map
for (i in 1:nrow(pres08)) {
    if ( (pres08$state[i] != "HI") & (pres08$state[i] != "AK") &
        (pres08$state[i] != "DC")) {
        map(database = "state", regions = pres08$state.name[i],
            col = rgb(red = pres08$Rep[i], blue = pres08$Dem[i],
               green = 0), fill = TRUE, add = TRUE)
    }
}
```

```r
states <- map_data("state") %>%
  left_join(mutate(pres08, state.name = str_to_lower(state.name)),
            by = c("region" = "state.name")) %>%
  # drops DC
  filter(!is.na(EV)) %>%
  mutate(party = if_else(Dem > Rep, "Dem", "Rep"),
         color = map2_chr(Dem, Rep, ~ rgb(blue = .x, red = .y, green = 0)))

ggplot(states) +
  geom_polygon(aes(group = group, x = long, y = lat,
                   fill = party)) +
  coord_quickmap() +
  scale_fill_manual(values = c("Rep" = "red", "Dem" = "blue")) +
  theme_void() +
  labs(x = "", y = "")
```



For plotting the purple states, I use since the `color` column contains the RGB values to use in the plot:

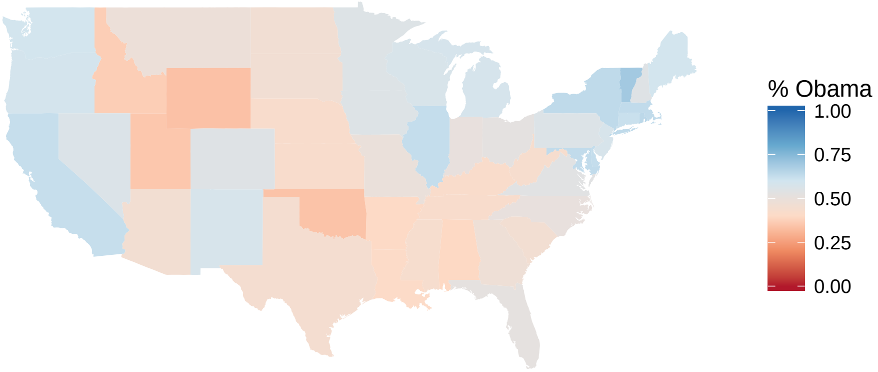
```
ggplot(states) +
  geom_polygon(aes(group = group, x = long, y = lat,
                   fill = color)) +
  coord_quickmap() +
  scale_fill_identity() +
  theme_void() +
  labs(x = "", y = "")
```



However, plotting purple states is not a good data visualization. Even though the colors are a proportional mixture of red and blue, human visual perception doesn't work that way.

The proportion of the democratic vote is best thought of a diverging scale with 0.5 is midpoint. And since the Democratic Party is associated with the color blue and the Republican Party is associated with the color red. The Color Brewer palette RdBu is an example:

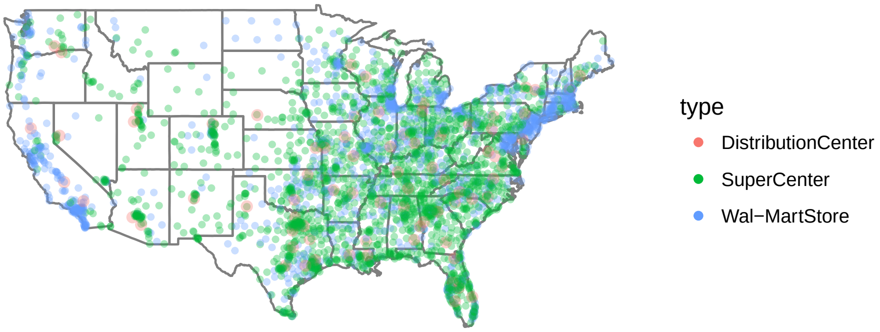
```
ggplot(states) +
  geom_polygon(aes(group = group, x = long, y = lat, fill = Dem)) +
  scale_fill_distiller("% Obama", direction = 1, limits = c(0, 1), type = "div",
                       palette = "RdBu") +
  coord_quickmap() +
  theme_void() +
  labs(x = "", y = "")
```



5.3.4 Expansion of Walmart

We don't need to do the direct mapping since

```
data("walmart", package = "qss")

ggplot() +
  borders(database = "state") +
  geom_point(aes(x = long, y = lat, colour = type, size = size),
             data = mutate(walmart,
                           size = if_else(type == "DistributionCenter", 2, 1)),
             alpha = 1 / 3) +
  coord_quickmap() +
  scale_size_identity() +
  guides(color = guide_legend(override.aes = list(alpha = 1))) +
  theme_void()
```

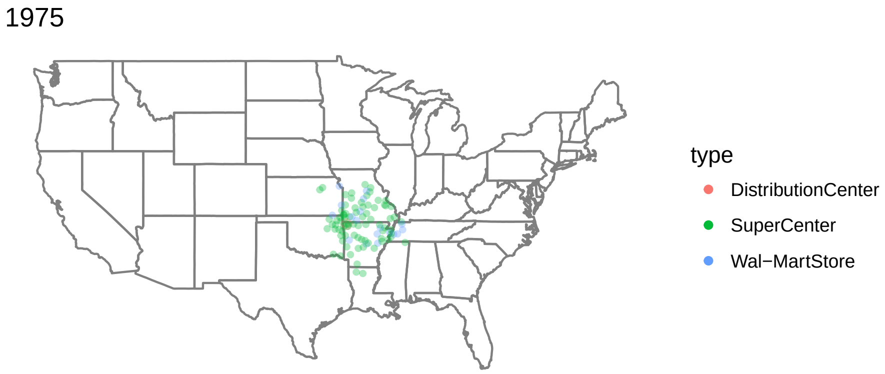


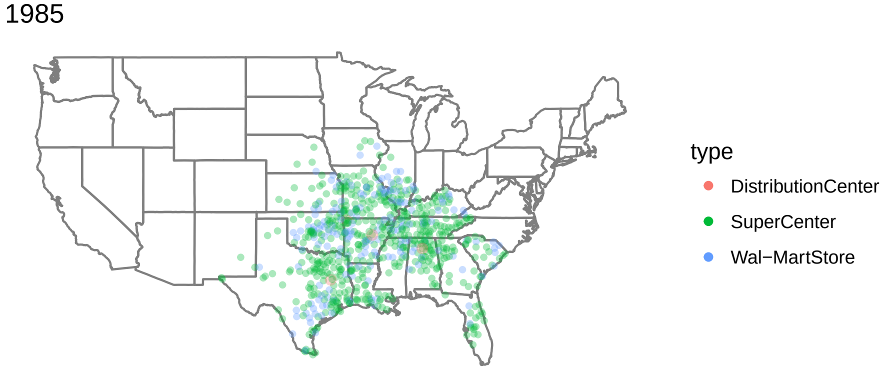
We don't need to worry about colors since `ggplot` handles that. I use guides to so that the colors or not transparent in the legend (see *R for Data Science* chapterGraphics for communication).

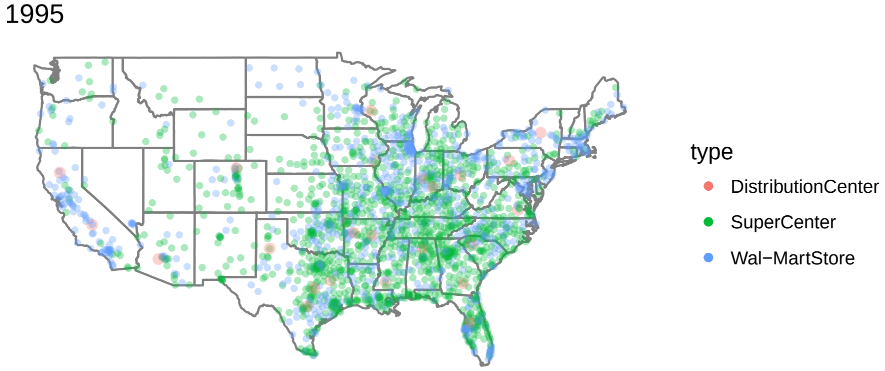
To make a plot showing all Walmart stores opened up through that year, I write a function, that takes the year and dataset as parameters.

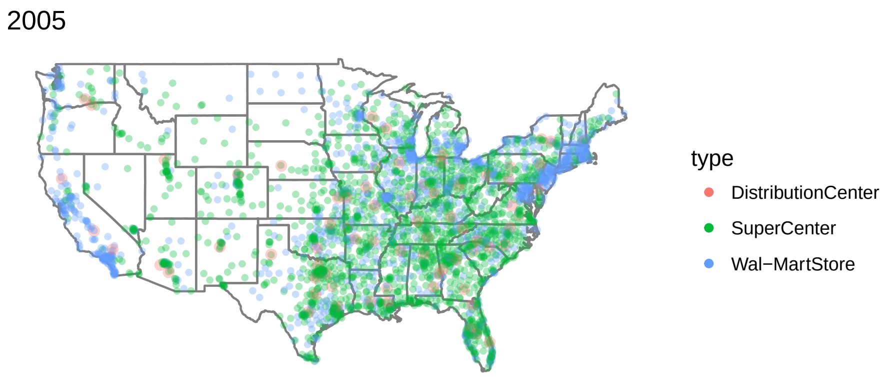
Since I am calling the function for its side effect (printing the plot) rather than the value it returns, I use the walk function rather than map. See R for Data Science, Chapter 21.8: Walk for more information.

```
map_walmart <- function(year, .data) {
  .data <- filter(.data, opendate < make_date(year, 1, 1)) %>%
    mutate(size = if_else(type == "DistributionCenter", 2, 1))
  ggplot() +
    borders(database = "state") +
    geom_point(aes(x = long, y = lat, colour = type, size = size),
               data = .data, alpha = 1 / 3) +
    coord_quickmap() +
    scale_size_identity() +
    guides(color = guide_legend(override.aes = list(alpha = 1))) +
    theme_void() +
    ggtitle(year)
}

years <- c(1975, 1985, 1995, 2005)
walk(years, ~ print(map_walmart(.x, walmart)))
```









5.3.5 Animation in R

For easy animation with ggplot2, use the gganimate package. Note that the **gganimate** package is not on CRAN, so you have to install it with the devtools package:

```
install.packages("cowplot")
devtools::install_github("dgrtwo/animate")
```

```
library("gganimate")
```

An animation is a series of frames. The gganimate package works by adding a `frame` aesthetic to ggplots, and function will animate the plot.

I use `frame = year(opendate)` to have the animation use each year as a frame, and `cumulative = TRUE` so that the previous years are shown.

```
walmart_animated <-
  ggplot() +
    borders(database = "state") +
    geom_point(aes(x = long, y = lat,
                   colour = type,
                   fill = type,
                   frame = year(opendate),
                   cumulative = TRUE),
               data = walmart) +
    coord_quickmap() +
    theme_void()
gganimate(walmart_animated)
```

Chapter 6

Probability

Prerequisites

```
library("tidyverse")
library("forcats")
library("stringr")
library("broom")
```

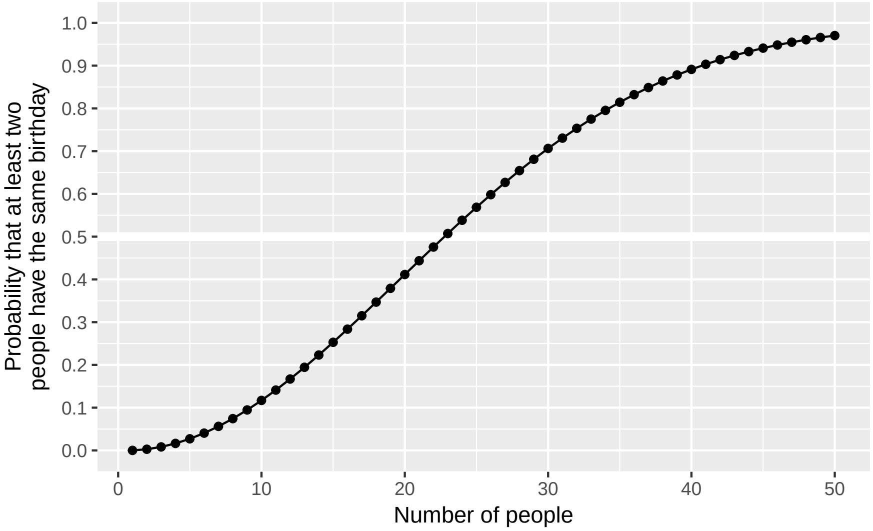
6.1 Probability

6.1.1 Frequentist vs. Bayesian

6.1.2 Definition and Axioms

6.1.3 Permutations

```
birthday <- function(k) {
  logdenom <- k * log(365) + lfactorial(365 - k)
  lognumer <- lfactorial(365)
  pr <- 1 -   exp(lognumer - logdenom)
  pr
}

bday <- tibble(k = 1:50, pr = birthday(k))

ggplot(bday, aes(x = k, y = pr)) +
  geom_hline(yintercept = 0.5, colour = "white", size = 2) +
  geom_line() +
  geom_point() +
  scale_y_continuous(str_c("Probability that at least two",
                           "people have the same birthday", sep = "\n"),
                     limits = c(0, 1), breaks = seq(0, 1, by = 0.1)) +
  labs(x = "Number of people")
```



Note: The logarithm is used for numerical stability. Basically, "floating-point" numbers are approximations of numbers. If you perform arithmetic with numbers that are very large, very small, or vary differently in magnitudes, you could have problems. Logarithms help with some of those issues. See "Falling Into the Floating Point Trap" in The R Inferno for a summary of floating point numbers. See these John Fox posts 1 2 for an example of numerical stability gone wrong. Also see: http://andrewgelman.com/2016/06/11/log-sum-of-exponentials/.

6.1.4 Sampling without replacement

Instead of using a `for` loop, we could do the simulations using a functional as described in R for Data Science chapter "Iterations".

Define the function `sim_bdays` which randomly samples `k` birthdays, and returns `TRUE` if there are any duplicate birthdays, and `FALSE` if there are none.

```
sim_bdays <- function(k) {
  days <- sample(1:365, k, replace = TRUE)
  length(unique(days)) < k
}
```

We can test the code for `k = 10` birthdays.

```
sim_bdays(10)
#> [1] FALSE
```

Since the function is randomly sampling birthdays, running it multiple times will produce different answers.

One helpful feature of a functional style of writing code vs. a `for` loop is that the function encapsulates the code and allows you to test that it works for different inputs before repeating it for many inputs. It is more difficult to debug functions that produce random outputs, but some sanity checks are that the function:

- returns a logical vector of length one (`TRUE` or `FALSE`)
- always returns `FALSE` when `k = 1` since there can never be a duplicates with one person
- always returns `TRUE` when `k > 365` by the pidgeonhole principle.

```
sim_bdays(1)
#> [1] FALSE
sim_bdays(366)
#> [1] TRUE
```

Set the parameters for 1,000 simulations, and 23 individuals. We use `map_lgl` since `sim_bdays` returns a logical value (`TRUE`, `FALSE`):

```
sims <- 1000
k <- 23
map_lgl(seq_len(sims), ~ sim_bdays(k)) %>%
  mean()
#> [1] 0.489
```

An alternative way of running this is using the rerun and using `flatten` to turn the output to a numeric vector:

```
rerun(sims, sim_bdays(k)) %>%
  flatten_dbl() %>%
  mean()
#> [1] 0.477
```

6.1.5 Combinations

The function for $\binom{84}{6}$ is:

```
choose(84, 6)
#> [1] 4.06e+08
```

However, due to the the larges values that the binomial coefficient, it is almost always better to use the log of the binomial coefficient, $\log \binom{84}{6}$,

```
lchoose(84, 6)
#> [1] 19.8
```

6.2 Conditional Probability

6.2.1 Conditional, Marginal, and Joint Probabilities

Load Florida voting data from the **qss** package:

```
data(FLVoters, package = "qss")
dim(FLVoters)
#> [1] 10000     6
glimpse(FLVoters)
#> Observations: 10,000
#> Variables: 6
#> $ surname <chr> "PIEDRA", "LYNCH", "CHESTER", "LATHROP", "HUMMEL", "CH...
#> $ county  <int> 115, 115, 115, 115, 115, 115, 115, 115, 1, 1, 115, 115...
#> $ VTD     <int> 66, 13, 103, 80, 8, 55, 84, 48, 41, 39, 26, 45, 11, 48...
#> $ age     <int> 58, 51, 63, 54, 77, 49, 77, 34, 56, 60, 44, 45, 80, 83...
#> $ gender  <chr> "f", "m", "m", "m", "f", "m", "f", "f", "f", "m", "m",...
#> $ race    <chr> "white", "white", NA, "white", "white", "white", "whit...
FLVoters <- FLVoters %>%
  na.omit()
dim(FLVoters)
#> [1] 9113    6
```

Note the difference between `glimpse()` and `dim()` - what is different in how they handle NA observations?

Instead of using prop.base, we calculate the probabilities with a data frame. Calculate the marginal probabilities of each race:

```
margin_race <-
  FLVoters %>%
  count(race) %>%
  mutate(prop = n / sum(n))
margin_race
#> # A tibble: 6 x 3
#>   race         n    prop
#>   <chr>    <int>   <dbl>
#> 1 asian      175 0.0192
#> 2 black     1194 0.131
#> 3 hispanic  1192 0.131
#> 4 native      29 0.00318
#> 5 other      310 0.0340
#> 6 white     6213 0.682
```

Calculate the marginal probabilities of each gender:

```
margin_gender <-
  FLVoters %>%
  count(gender) %>%
  mutate(prop = n / sum(n))
margin_gender
#> # A tibble: 2 x 3
#>   gender     n  prop
#>   <chr>  <int> <dbl>
#> 1 f       4883 0.536
#> 2 m       4230 0.464
```

```
FLVoters %>%
  filter(gender == "f") %>%
  count(race) %>%
  mutate(prop = n / sum(n))
#> # A tibble: 6 x 3
#>   race         n    prop
#>   <chr>    <int>   <dbl>
#> 1 asian       83 0.0170
#> 2 black      678 0.139
#> 3 hispanic   666 0.136
#> 4 native      17 0.00348
#> 5 other      158 0.0324
#> 6 white     3281 0.672
```

```
joint_p <-
  FLVoters %>%
  count(gender, race) %>%
  mutate(prop = n / sum(n))
joint_p
#> # A tibble: 12 x 4
#>   gender race         n    prop
#>   <chr>  <chr>    <int>   <dbl>
#> 1 f      asian       83 0.00911
#> 2 f      black      678 0.0744
#> 3 f      hispanic   666 0.0731
#> 4 f      native      17 0.00187
#> 5 f      other      158 0.0173
#> 6 f      white     3281 0.360
#> # ... with 6 more rows
```

We can convert the data frame to have gender as columns:

```
joint_p %>%
  select(-n) %>%
  spread(gender, prop)
#> # A tibble: 6 x 3
#>   race           f       m
#>   <chr>      <dbl>   <dbl>
#> 1 asian    0.00911 0.0101
#> 2 black    0.0744  0.0566
#> 3 hispanic 0.0731  0.0577
#> 4 native   0.00187 0.00132
#> 5 other    0.0173  0.0167
#> 6 white    0.360   0.322
```

Sum over race:

```
joint_p %>%
  group_by(race) %>%
  summarise(prop = sum(prop))
#> # A tibble: 6 x 2
#>   race        prop
#>   <chr>      <dbl>
#> 1 asian    0.0192
#> 2 black    0.131
#> 3 hispanic 0.131
#> 4 native   0.00318
#> 5 other    0.0340
#> 6 white    0.682
```

Sum over gender:

```
joint_p %>%
  group_by(gender) %>%
  summarise(prop = sum(prop))
#> # A tibble: 2 x 2
#>   gender  prop
#>   <chr>  <dbl>
#> 1 f      0.536
#> 2 m      0.464
```

```
FLVoters <-
  FLVoters %>%
  mutate(age_group = cut(age, c(0, 20, 40, 60, Inf), right = TRUE,
                       labels = c("<= 20", "20-40", "40-60", "> 60")))
```

```
joint3 <-
  FLVoters %>%
  count(race, age_group, gender) %>%
  ungroup() %>%
  mutate(prop = n / sum(n))
joint3
```

```
#> # A tibble: 47 x 5
#>   race  age_group gender     n     prop
#>   <chr> <fct>     <chr>  <int>    <dbl>
#> 1 asian <= 20     f          1 0.000110
#> 2 asian <= 20     m          2 0.000219
#> 3 asian 20-40     f         24 0.00263
#> 4 asian 20-40     m         26 0.00285
#> 5 asian 40-60     f         38 0.00417
#> 6 asian 40-60     m         47 0.00516
#> # ... with 41 more rows
```

Marginal probabilities by age groups

```
margin_age <-
  FLVoters %>%
  count(age_group) %>%
  mutate(prop = n / sum(n))
margin_age
#> # A tibble: 4 x 3
#>   age_group     n   prop
#>   <fct>     <int>  <dbl>
#> 1 <= 20       161 0.0177
#> 2 20-40      2469 0.271
#> 3 40-60      3285 0.360
#> 4 > 60       3198 0.351
```

Calculate the probabilities that each group is in a given age group, and show $P(\text{black} \wedge \text{female} \wedge \text{age} > 60)$: (*Note: the symbol* $\wedge$ *is the logical symbol for 'and', implying the joint probability.*)

```
left_join(joint3,
          select(margin_age, age_group, margin_age = prop),
          by = "age_group") %>%
  mutate(prob_age_group = prop / margin_age) %>%
  filter(race == "black", gender == "f", age_group == "> 60") %>%
  select(race, age_group, gender, prob_age_group)
#> # A tibble: 1 x 4
#>   race  age_group gender prob_age_group
#>   <chr> <fct>     <chr>           <dbl>
#> 1 black > 60      f              0.0538
```

Two-way joint probability table for age group and gender

```
joint2 <- FLVoters %>%
  count(age_group, gender) %>%
  ungroup() %>%
  mutate(prob_age_gender = n / sum(n))
joint2
#> # A tibble: 8 x 4
#>   age_group gender     n prob_age_gender
#>   <fct>     <chr>  <int>           <dbl>
#> 1 <= 20     f         88         0.00966
#> 2 <= 20     m         73         0.00801
#> 3 20-40     f       1304         0.143
#> 4 20-40     m       1165         0.128
#> 5 40-60     f       1730         0.190
#> 6 40-60     m       1555         0.171
#> # ... with 2 more rows
```

The joint probability $P(\text{age} > 60 \wedge \text{female})$,

```
joint2 %>%
  filter(age_group == "> 60", gender == "f")
#> # A tibble: 1 x 4
#>   age_group gender     n prob_age_gender
#>   <fct>     <chr>  <int>           <dbl>
#> 1 > 60      f       1761           0.193
```

The conditional probabilities $P(\text{race} \mid \text{gender, age})$,

```
condprob_race <-
  left_join(joint3, select(joint2, -n), by = c("age_group", "gender")) %>%
  mutate(prob_race = prop / prob_age_gender) %>%
  arrange(age_group, gender) %>%
  select(age_group, gender, race, prob_race)
```

Each row is the $P(\text{race} \mid \text{age group} \wedge \text{gender})$, so $P(\text{black} \mid \text{female} \wedge \text{age} > 60)$,

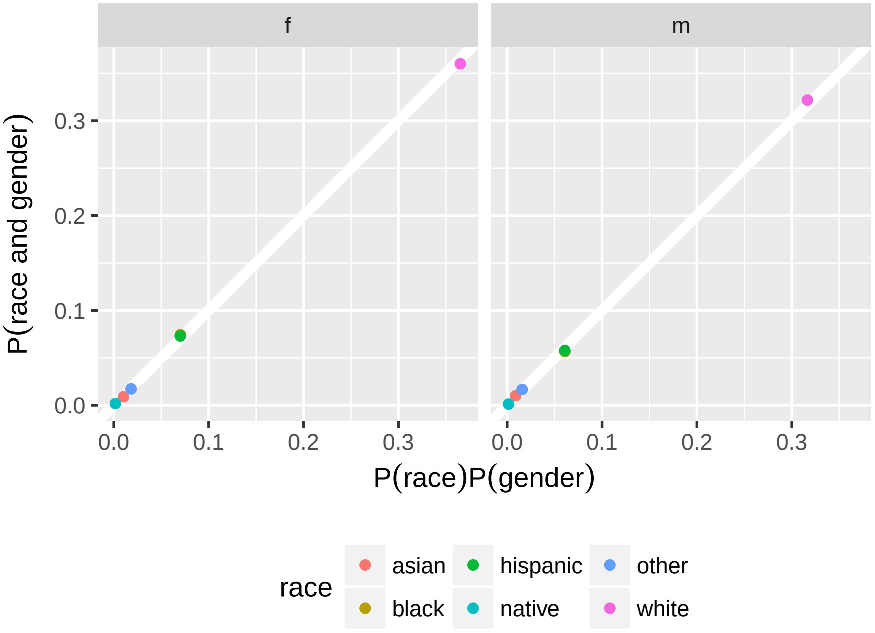
```
filter(condprob_race, gender == "f", age_group == "> 60", race == "black")
#> # A tibble: 1 x 4
#>   age_group gender race  prob_race
#>   <fct>     <chr>  <chr>     <dbl>
#> 1 > 60      f      black    0.0977
```

6.2.2 Independence

Create a table with the products of margins of race and age. Using the function crossing to create a tibble with all combinations of race and gender and the independent prob.

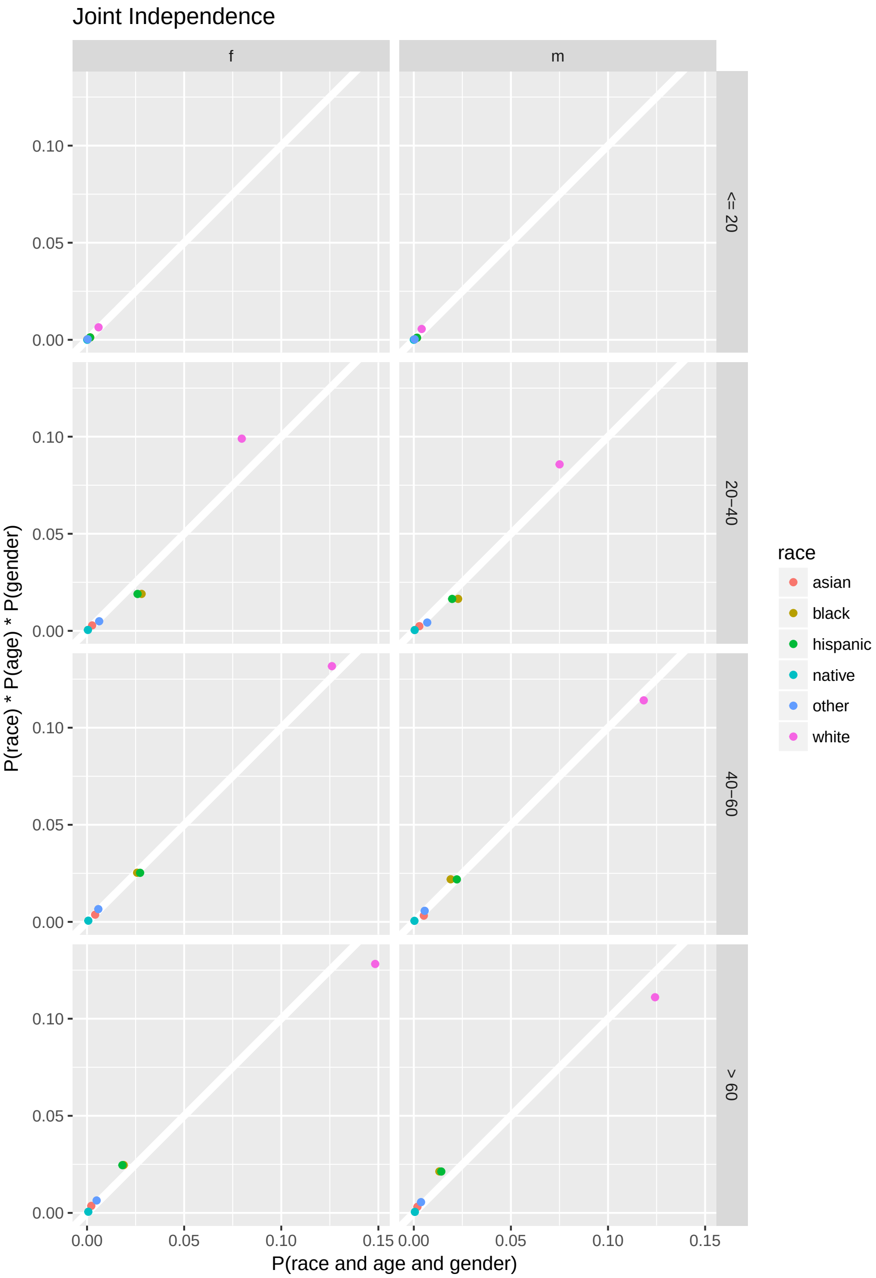
```
race_gender_indep <-
  crossing(select(margin_race, race, prob_race = prop),
           select(margin_gender, gender, prob_gender = prop)) %>%
  mutate(prob_indep = prob_race * prob_gender) %>%
  left_join(select(joint_p, gender, race, prob = prop),
            by = c("gender", "race")) %>%
  select(race, gender, everything())
race_gender_indep
#> # A tibble: 12 x 6
#>   race     gender prob_race prob_gender prob_indep    prob
#>   <chr>    <chr>      <dbl>       <dbl>      <dbl>   <dbl>
#> 1 asian    f         0.0192       0.536    0.0103  0.00911
#> 2 asian    m         0.0192       0.464    0.00891 0.0101
#> 3 black    f         0.131        0.536    0.0702  0.0744
#> 4 black    m         0.131        0.464    0.0608  0.0566
#> 5 hispanic f         0.131        0.536    0.0701  0.0731
#> 6 hispanic m         0.131        0.464    0.0607  0.0577
#> # ... with 6 more rows
```

```
ggplot(race_gender_indep,
       aes(x = prob_indep, y = prob, colour = race)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_point() +
  facet_grid(. ~ gender) +
  coord_fixed() +
  theme(legend.position = "bottom") +
  labs(x = expression(P("race") * P("gender")),
       y = expression(P("race and gender")))
```



While the original code only calculates joint-independence value for values of age > 60, and female, this calculates the joint probabilities for all combinations of the three variables, and facets by age and gender.

```
joint_indep <-
  crossing(select(margin_race, race, prob_race = prop),
           select(margin_age, age_group, prob_age = prop),
           select(margin_gender, gender, prob_gender = prop)) %>%
  mutate(indep_prob = prob_race * prob_age * prob_gender) %>%
  left_join(select(joint3, race, age_group, gender, prob = prop),
            by = c("gender", "age_group", "race")) %>%
  replace_na(list(prob = 0))

ggplot(joint_indep, aes(x = prob, y = indep_prob, colour = race)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_point() +
  facet_grid(age_group ~ gender) +
  coord_fixed() +
  labs(x = "P(race and age and gender)",
       y = "P(race) * P(age) * P(gender)",
       title = "Joint Independence")
```



While code in *QSS* only calculates the conditional independence given female, the following code calculates conditional independence for all values of `gender`:

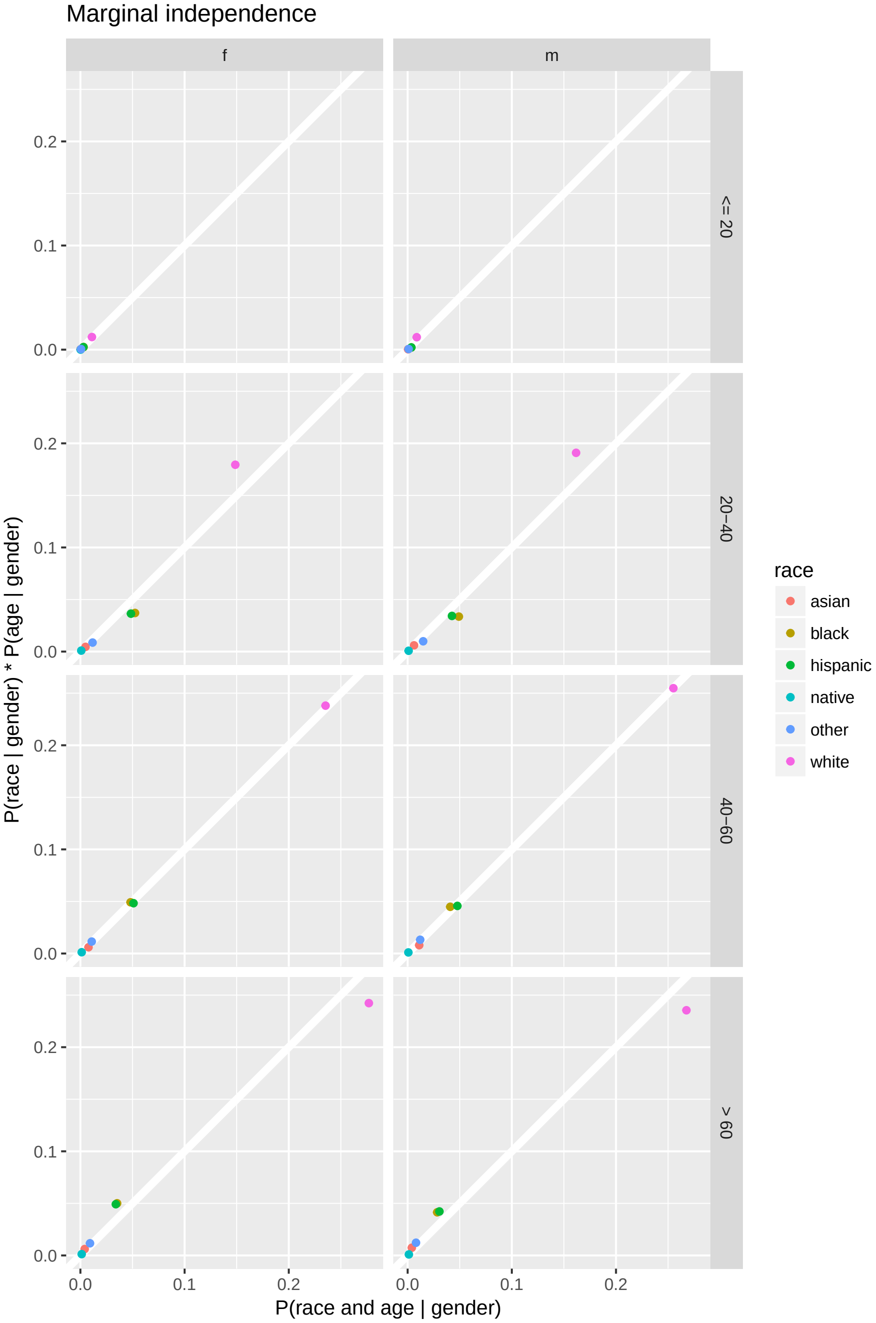
```
cond_gender <-
  left_join(select(joint3, race, age_group, gender, joint_prob = prop),
            select(margin_gender, gender, prob_gender = prop),
            by = c("gender")) %>%
  mutate(cond_prob = joint_prob / prob_gender)
```

Calculate the conditional distribution Pr(race|gender):

```
prob_race_gender <-
  left_join(select(joint_p, race, gender, prob_race_gender = prop),
            select(margin_gender, gender, prob_gender = prop),
            by = "gender") %>%
  mutate(prob_race = prob_race_gender / prob_gender)
```

Calculate the conditional distribution Pr(age|gender):

```
prob_age_gender <-
  left_join(select(joint2, age_group, gender, prob_age_gender),
            select(margin_gender, gender, prob_gender = prop),
            by = "gender") %>%
  mutate(prob_age = prob_age_gender / prob_gender)

# indep prob of race and age
indep_cond_gender <-
  full_join(select(prob_race_gender, race, gender, prob_race),
            select(prob_age_gender, age_group, gender, prob_age),
            by = "gender") %>%
  mutate(indep_prob = prob_race * prob_age)

inner_join(select(indep_cond_gender, race, age_group, gender, indep_prob),
           select(cond_gender, race, age_group, gender, cond_prob),
           by = c("gender", "age_group", "race")) %>%
  ggplot(aes(x = cond_prob, y = indep_prob, colour = race)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_point() +
  facet_grid(age_group ~ gender) +
  coord_fixed() +
  labs(x = "P(race and age | gender)",
       y = "P(race | gender) * P(age | gender)",
       title = "Marginal independence")
```



Monty-hall problem

The `for` loop approach in *QSS* is valid code, but here we provide a more functional approach to solving the problem. We will define a function to choose a door, repeat the function multiple times while storing the results in a data frame, and then summarize that data frame.

First, create a function for a single iteration. This returns a single logical value:

```
choose_door <- function(.iter) {
  # what's behind each door door:
  # Why is it okay that this is fixed?
  doors <- c("goat", "goat", "car")

  # User randomly chooses a door
  first <- sample(1:3, 1)

  # randomly choose the door that Monty Hall reveals
  remain <- doors[-first]
  monty <- sample( (1:2)[remain == "goat"], size = 1)
  # did the contestant win?
  tibble(.iter = .iter,
         result = remain[-monty] == "car")
}
```

Now use map_df to run `choose_door` multiple times, and then summarize the results:

```
sims <- 1000
map_df(seq_len(sims), choose_door) %>%
  summarise(win_pct = mean(result))
#> # A tibble: 1 x 1
#>   win_pct
#>     <dbl>
#> 1   0.649
```

6.2.3 Bayes' Rule

6.2.4 Predicting Race Using Surname and Residence Location

Start with the Census names files:

```
data("cnames", package = "qss")
glimpse(cnames)
#> Observations: 151,671
#> Variables: 7
#> $ surname      <chr> "SMITH", "JOHNSON", "WILLIAMS", "BROWN", "JONES", ...
#> $ count        <int> 2376206, 1857160, 1534042, 1380145, 1362755, 11278...
#> $ pctwhite     <dbl> 73.34, 61.55, 48.52, 60.72, 57.69, 85.80, 64.73, 6...
#> $ pctblack     <dbl> 22.22, 33.80, 46.72, 34.54, 37.73, 10.41, 30.77, 0...
#> $ pctapi       <dbl> 0.40, 0.42, 0.37, 0.41, 0.35, 0.42, 0.40, 1.43, 0....
#> $ pcthispanic <dbl> 1.56, 1.50, 1.60, 1.64, 1.44, 1.43, 1.58, 90.82, 9...
#> $ pctothers    <dbl> 2.48, 2.73, 2.79, 2.69, 2.79, 1.94, 2.52, 1.09, 0....
```

For each surname, `cnames` contains variables with the probability that it belongs to an individual of a given race (`pctwhite`, `pctblack`, …). We want to find the most-likely race for a given surname, by finding the race with the maximum proportion. Instead of dealing with multiple variables, it is easier to use `max` on a single variable, so we will rearrange the data to in order to use a grouped summarize, and then merge the new variable back to the original data sets. We will also remove the 'pct' prefix from each of the variable names.

Calculate the most likely race for each name:

```
most_likely_race <-
  cnames %>%
  select(-count) %>%
  gather(race_pred, pct, -surname) %>%
  # remove pct_ prefix from variable names
  mutate(race_pred = str_replace(race_pred, "^pct", "")) %>%
  # # group by surname
  group_by(surname) %>%
  # select obs with the largest percentage
  filter(row_number(desc(pct)) == 1L) %>%
  # Ungroup to avoid errors later
  ungroup %>%
  # # don't need pct anymore
  select(-pct) %>%
  mutate(race_pred = recode(race_pred, asian = "api", other = "others"))
```

Merge the data frame with the most likely race for each surname to the the original `cnames` data frame:

```
cnames <-
  cnames %>%
  left_join(most_likely_race, by = "surname")
```

Instead of using `match`, use `inner_join` to merge the surnames to `FLVoters`:

```
FLVoters <-
  FLVoters %>%
  inner_join(cnames, by = "surname")
dim(FLVoters)
#> [1] 8022   14
```

`FLVoters` also includes a "native" category that the surname dataset does not.

```
FLVoters <-
  FLVoters %>%
  mutate(race2 = fct_recode(race, other = "native"))
```

Check that the levels of `race` and `race_pred` are the same:

```
FLVoters %>%
  count(race2)
#> # A tibble: 5 x 2
#>   race2        n
#>   <fct>    <int>
#> 1 asian      140
#> 2 black     1078
#> 3 hispanic  1023
#> 4 other      277
#> 5 white     5504
FLVoters %>%
  count(race_pred)
#> # A tibble: 5 x 2
#>   race_pred     n
#>   <chr>     <int>
#> 1 api         120
#> 2 black       258
#> 3 hispanic   1121
#> 4 others        7
#> 5 white      6516
```

Now we can calculate *True positive rate* for *all* races

```
FLVoters %>%
  group_by(race2) %>%
  summarise(tp = mean(race2 == race_pred)) %>%
  arrange(desc(tp))
#> # A tibble: 5 x 2
#>   race2       tp
#>   <fct>    <dbl>
#> 1 white    0.950
#> 2 hispanic 0.847
#> 3 black    0.160
#> 4 asian    0.
#> 5 other    0.
```

and the *False discovery rate* for *all* races,

```
FLVoters %>%
  group_by(race_pred) %>%
  summarise(fp = mean(race2 != race_pred)) %>%
  arrange(desc(fp))
#> # A tibble: 5 x 2
#>   race_pred    fp
#>   <chr>     <dbl>
#> 1 api       1.00
#> 2 others    1.00
#> 3 black     0.329
#> 4 hispanic  0.227
#> 5 white     0.197
```

Now add residence data using the `FLCensus` data included in the

```
data("FLCensus", package = "qss")
```

$P(\text{race})$ in Florida:

```
race.prop <-
  FLCensus %>%
  select(total.pop, white, black, api, hispanic, others) %>%
  gather(race, pct, -total.pop) %>%
  group_by(race) %>%
  summarise(mean = weighted.mean(pct, weights = total.pop)) %>%
  arrange(desc(mean))
race.prop
#> # A tibble: 5 x 2
#>   race       mean
#>   <chr>     <dbl>
#> 1 white    0.605
#> 2 hispanic 0.213
#> 3 black    0.139
#> 4 api      0.0219
#> 5 others   0.0214
```

6.2.5 Predicting Election Outcomes with Uncertainty

Load the `pres08` data from the **qss** package.

```
data("pres08", package = "qss")
```

Add a column `p` which contains Obama's vote share of the major parties:

```
pres08 <- pres08 %>%
  mutate(p = Obama / (Obama + McCain))
```

Write a function to simulate the elections. df is the data frame (pres08) with the state, EV, and p columns. n_draws is the size of the binomial distribution to draw from. .id is the simulation number.

```
sim_election <- function(.id, df, n_draws = 1000) {
  # For each state randomly sample
  mutate(df,
         draws = rbinom(n(), n_draws, p)) %>%
  filter(draws > (n_draws / 2)) %>%
  summarise(EV = sum(EV),
            .id = .id)
}
```

Now simulate the election 10,000 times:

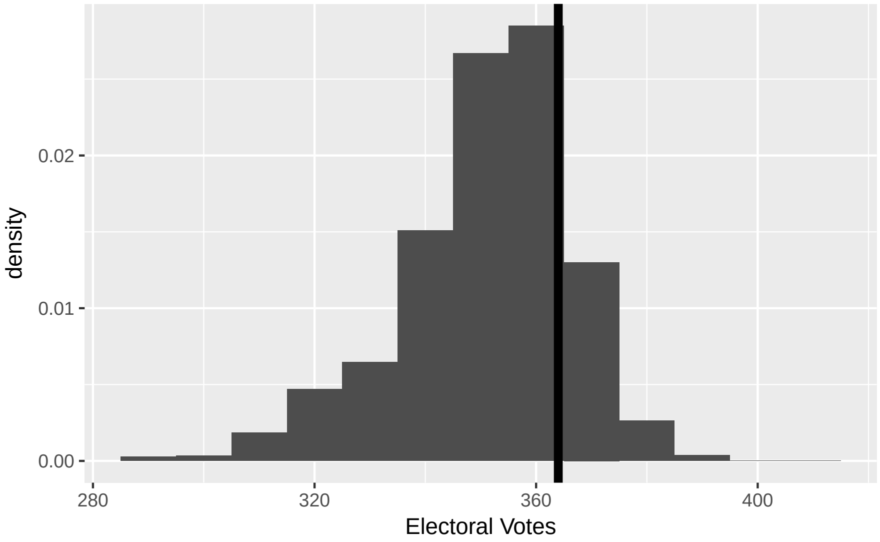
```
sims <- 10000
sim_results <- map_df(seq_len(sims), ~ sim_election(.x, pres08, n_draws = 1000))
```

In the 2008 election, Obama received 364 electoral votes

```
ELECTION_EV <- 364
```

And plot them,

```
ggplot(sim_results, aes(x = EV, y = ..density..)) +
  geom_histogram(binwidth = 10, fill = "gray30") +
  geom_vline(xintercept = ELECTION_EV, colour = "black", size = 2) +
  labs(x = "Electoral Votes", y = "density")
```



Simulation mean, variance, and standard deviations:

```
sim_results %>%
  select(EV) %>%
  summarise_all(funs(mean, var, sd))
#>   mean var   sd
#> 1  352 270 16.4
```

Theoretical probabilities from a binomial distribution:

```
# we cannot use n, because mutate will look for n() first.
n_draws <- 1000
pres08 %>%
  mutate(pb = pbinom(n_draws / 2, size = n_draws, prob = p,
                     lower.tail  = FALSE)) %>%
  summarise(mean = sum(pb * EV),
            V = sum(pb * (1 - pb) * EV ^ 2),
            sd = sqrt(V))
#>   mean   V   sd
#> 1  352 269 16.4
```

6.3 Random Variables and Probability Distributions

6.3.1 Bernoulli and Uniform Distributions

Uniform distribution functions:

```
dunif(0.5, min = 0, max = 1)
#> [1] 1
punif(1, min = -2, max = 2)
#> [1] 0.75
```

Sample from a uniform distribution, and convert to a probability:

```
sims <- 1000
p <- 0.5
```

A Bernoulli distribution is a discrete distribution which randomly samples from 0 and 1. A random variable X with a Bernoulli distribution with probability parameter p has the distribution,

$$
\begin{aligned}
P(X = 1 | p) &= p \\
P(X = 0 | p) &= 1 - p
\end{aligned}
$$

R does not have a `rbernoulli` for the Bernoulli distribution (because as we will see it is a special case of the Binomial distribution, and there are several other ways to sample from it): Here are three ways to sample from a Bernoulli distribution.

First, we can use the `sample` from values `c(0, 1)` with replacement. By default it will set sample 0 and 1 with equal probability ($p = 0.5$), but using the `prob` argument we can sample 0 and 1 with difference probabilities. Take 50 samples from a Bernoulli distribution with `p = 0.6`,

```
p <- 0.6
n <- 100
y <- sample(c(0, 1), n, prob = c(1 - p, p), replace = TRUE)
head(y)
#> [1] 0 1 1 0 0 0
mean(y)
#> [1] 0.46
```

A second method to sample n values from a Bernoulli distribution that has a probability parameter p is,

1. Take a sample of n values from a uniform distribution. Call this vector x.
2. To generate a sample y taking values of 0 and 1 from this vector x, set $y_i = 1$ if $x_i >= p$, and $y_i = 0$ if $x_i < p$.

Note how this method works. Given a value p between 0 and 1, in a sample from Uniform distribution, in expectation a fraction of p values will be less than p, and in expectation a fraction of $1 - p$ values will be greater than p. These are exactly the probabilities of sampling 1 and 0 in the probability mass of the Uniform distribution:

```
y <- as.integer(runif(n, min = 0, max = 1) <= p)
head(y)
#> [1] 1 1 1 1 1 1
mean(y)
#> [1] 0.58
```

Third, note that the Bernoulli distribution is a special case of the binomial distribution (discussed in the next section), where $size = 1$. Thus, we can use the `rbinom` function to sample from a binomial distribution.

```
y <- rbinom(n, size = 1, prob = p)
head(y)
#> [1] 1 1 1 1 1 1
mean(y)
#> [1] 0.63
```

Since the R functions for the Binomial distribution don't exist here are examples of how you would write them as examples of writing functions to sample and calculate the PDF or PMF, CDF, and quantile functions of a distribution. Sample from the distribution:

```
rbernoulli <- function(n, prob = 0.5) {
  sample(c(1L, 0L), n, replace = FALSE, prob = c(prob, 1 - prob))
}
```

Probability mass function (PMF):

```
dbernoulli <- function(x, prob = 0.5) {
  d <- rep(NA_real_, length(x))
  d[x == 1] <- prob
  d[x == 0] <- 1 - prob
  d
}
```

Cumulative density function (CDF):

$$
P(X \leq x|p) = \begin{cases} 0 & \text{if } x < 0, \\ 1 - p & \text{if } 0 \leq x < 1, \\ 1 & \text{if } x \geq 1. \end{cases}
$$

```
pbernoulli <- function(q, prob = 0.5) {
  p <- rep(NA_real_, length(q))
  p[q < 0] <- 0
  p[q >= 0 & q < 1] <- 1 - prob
  p[q >= 1] <- 1
  p
}
```

The inverse cumulative density function or quantile function,

$$
q = \begin{cases} \emptyset & \text{if } x \leq 1 - p, \\ 0 & \text{if } 1 - p \leq x < 1, \\ 1 & \text{if } x \geq 1. \end{cases}
$$

where,

$$
q \text{ such that } P(X \leq q|p) = x.
$$

```
qbernoulli <- function(p, prob = 0.5) {
  q <- rep(NA_integer_, length(p))
  q[prob >= 1 - p & prob < 1] <- 0L
  q[prob >= 1] <- 1L
  q
}
```

Alternatively, since the Bernoulli distribution is a special case of the Binomial distribution, write `*bernoulli` functions that wrap calls to to `*binom` functions for the special case where `size = 1`:

```
rbernoulli <- function(n, prob = 0.5, ...) {
  rbinom(n, size = 1, prob = prob, ...)
}
pbernoulli <- function(q, prob = 0.5, ...) {
  rbinom(q, size = 1, prob = prob, ...)
}
pbernoulli <- function(q, prob = 0.5, ...) {
  rbinom(q, size = 1, prob = prob, ...)
}
dbernoulli <- function(x, prob = 0.5, ...) {
  rbinom(x, size = 1, prob = prob, ...)
}
```

6.3.2 Binomial distribution

```
dbinom(2, size = 3, prob = 0.5)
#> [1] 0.375
pbinom(1, 3, 0.5)
#> [1] 0.5
```

```
voters <- c(1000, 10000, 100000)
dbinom(voters / 2, size = voters, prob = 0.5)
#> [1] 0.02523 0.00798 0.00252
```

6.3.3 Normal distribution

```
pnorm(1) - pnorm(-1)
#> [1] 0.683
pnorm(2) - pnorm(-2)
#> [1] 0.954
```

Write a function to calculate the area of a normal distribution $\pm\sigma$

```
normal_pm_sigma <- function(x, mu = 0, sd = 1) {
  (pnorm(mu + sd * x, mean = mu, sd = sd) -
     pnorm(mu - sd * x, mean = mu, sd = sd))
}
normal_pm_sigma(1)
#> [1] 0.683
normal_pm_sigma(2)
#> [1] 0.954
normal_pm_sigma(1, mu = 5, sd = 2)
#> [1] 0.683
```

```
normal_pm_sigma(2, mu = 5, sd = 2)
#> [1] 0.954
```

```
data("pres08", package = "qss")
data("pres12", package = "qss")
```

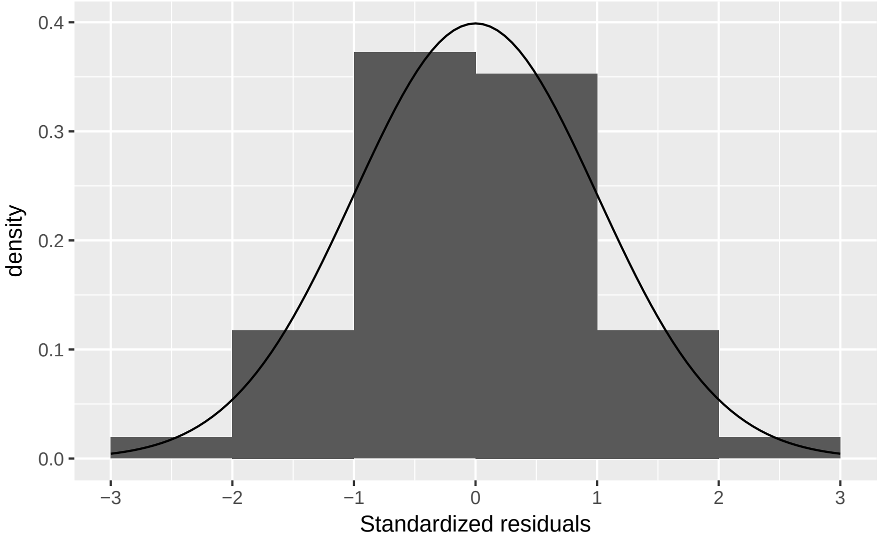
To join both data frames

```
pres <-
  full_join(select(pres08, state, Obama_2008 = Obama, McCain_2008 = McCain,
                   EV_2008 = EV),
            select(pres12, state, Obama_2012 = Obama, Romney_2012 = Romney,
                   EV_2012 = EV),
            by = "state") %>%
  mutate(Obama_2008_z = as.numeric(scale(Obama_2008)),
         Obama_2012_z = as.numeric(scale(Obama_2012)))
```

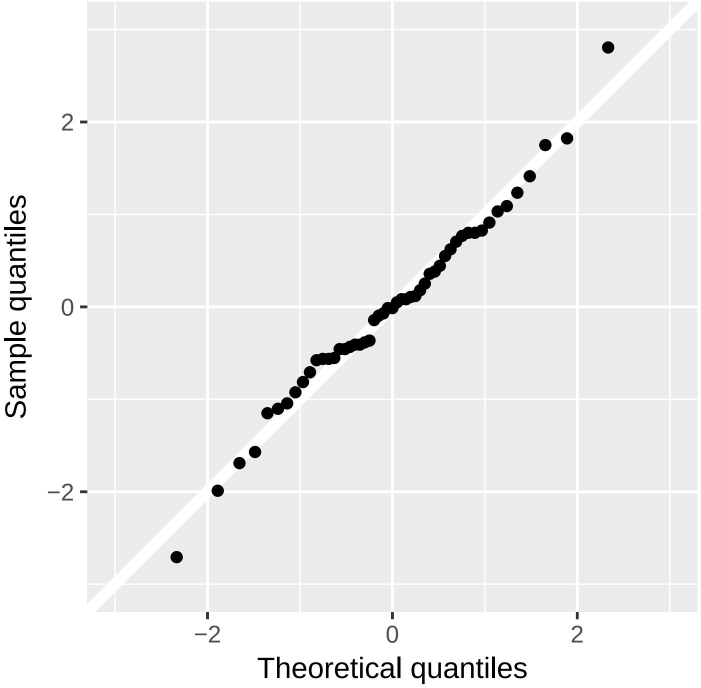
```
fit1 <- lm(Obama_2012_z ~ -1 + Obama_2008_z, data = pres)
```

Plot the residuals and compare them to a normal distribution:

```
err <- tibble(err = resid(fit1)) %>%
  # z-score of residuals
  mutate(err_std = err / sd(err))

ggplot(err, aes(x = err_std)) +
  geom_histogram(mapping = aes(y = ..density..),
                 binwidth = 1, boundary = 0) +
  stat_function(geom = "line", fun = dnorm) +
  scale_x_continuous("Standardized residuals",
                     breaks = -3:3, limits = c(-3, 3))
```

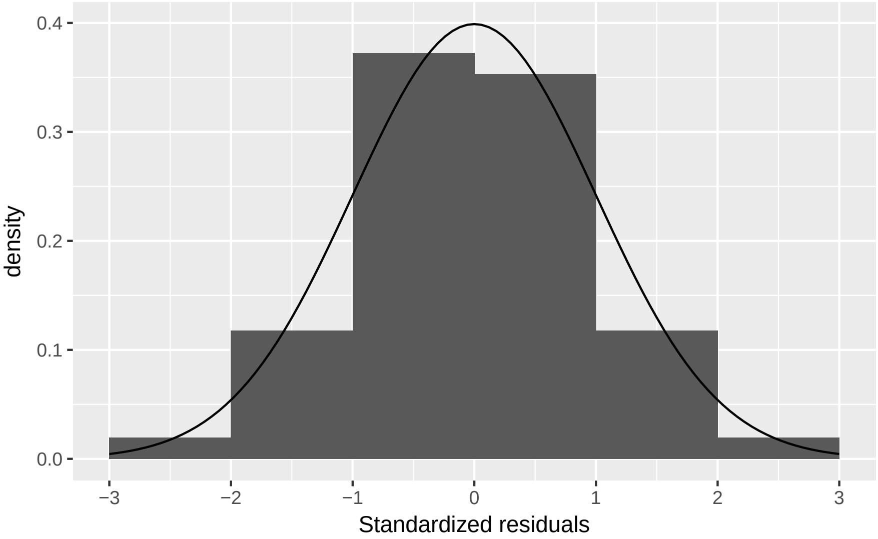


```
ggplot(err, aes(sample = err_std)) +
  geom_abline(intercept = 0, slope = 1, color = "white", size = 2) +
  geom_qq() +
  coord_fixed(ratio = 1) +
  scale_y_continuous("Sample quantiles", limits = c(-3, 3)) +
  scale_x_continuous("Theoretical quantiles", limits = c(-3, 3))
```



Alternatively, you can use the `augment` function from **broom** which returns the residuals for each observation in the `.resid` column.

```r
augment(fit1) %>%
  mutate(.resid_z = .resid / sd(.resid)) %>%
  ggplot(aes(x = .resid_z)) +
  geom_histogram(mapping = aes(y = ..density..),
                 binwidth = 1, boundary = 0) +
  stat_function(geom = "line", fun = dnorm) +
  scale_x_continuous("Standardized residuals",
                     breaks = -3:3, limits = c(-3, 3))
```



Obama's vote shares in 2008 and 2012.

Standard deviation of errors:

```r
err_sd <- sd(resid(fit1))
```

Probability of having a larger vote in California in 2012 than in 2008?

```r
CA_2008 <- filter(pres, state == "CA")$Obama_2008_z
```

The predicted value of 2012 vote share can be calculated manually with $\hat{beta} \times x$,

```r
CA_mean_2012 <- CA_2008 * coef(fit1)["Obama_2008_z"]
CA_mean_2012
#> Obama_2008_z
#>        0.858
```

or calculated using the predict function with the `newdata` argument providing any specific values to calculate?

```r
predict(fit1, newdata = tibble(Obama_2008_z = CA_2008))
#>     1
#> 0.858
```

Now calculate

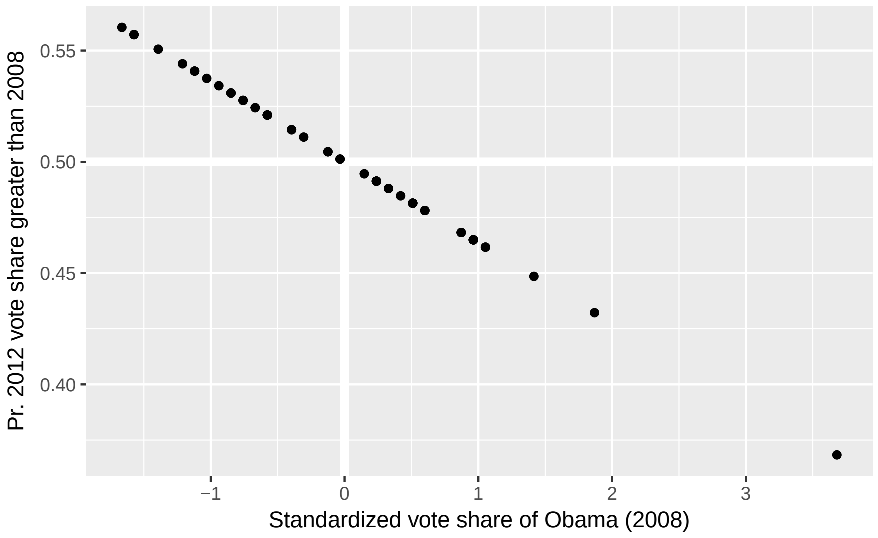
```r
pnorm(CA_2008, mean = CA_mean_2012, sd = err_sd,
      lower.tail = FALSE)
#> [1] 0.468
```

We can generalize the previous code to calculate the probability that Obama would exceed his 2008 vote to all states:

```r
pres_gt_2008 <- augment(fit1) %>%
  mutate(p_greater = pnorm(Obama_2008_z, mean = .fitted, sd = err_sd,
                           lower.tail = FALSE))
```

Plotting these results, we can observe regression to the mean. States with larger (smaller) 2008 vote shares had a lower (higher) probability that the 2012 vote share will exceed them.

```r
ggplot(pres_gt_2008, aes(x = Obama_2008_z, y = p_greater)) +
  modelr::geom_ref_line(h = 0.5) +
  modelr::geom_ref_line(v = 0) +
  geom_point() +
  labs(x = "Standardized vote share of Obama (2008)",
       y = "Pr. 2012 vote share greater than 2008")
```



6.3.4 Expectation and Variance

Theoretical and actual sample variable of a set of Bernoulli draws:

```
p <- 0.5
# theretical variance
p * (1 - p)
#> [1] 0.25
# a sample
y <- sample(c(0, 1), size = 1000, replace = TRUE, prob = c(p, 1 - p))
# the sample variance of that sample
var(y)
#> [1] 0.249
```

6.3.5 Predicting Election Outcomes with Uncertainty

Load 2008 Presidential Election data:

```
data("pres08", package = "qss")
pres08 <- mutate(pres08, p = Obama / (Obama + McCain))
```

```
sim_election <- function(x, n = 1000) {
  n_states <- nrow(x)
  # samples the number of votes for Obama
  mutate(x,
         draws = rbinom(n_states, size = !!n, prob = p),
         obama_EV = EV * (draws > (!!n / 2))) %>%
    pluck("obama_EV") %>%
    sum()
}
```

This function returns the electoral votes for Obama for a single simulation:

```
sim_election(pres08)
#> [1] 338
```

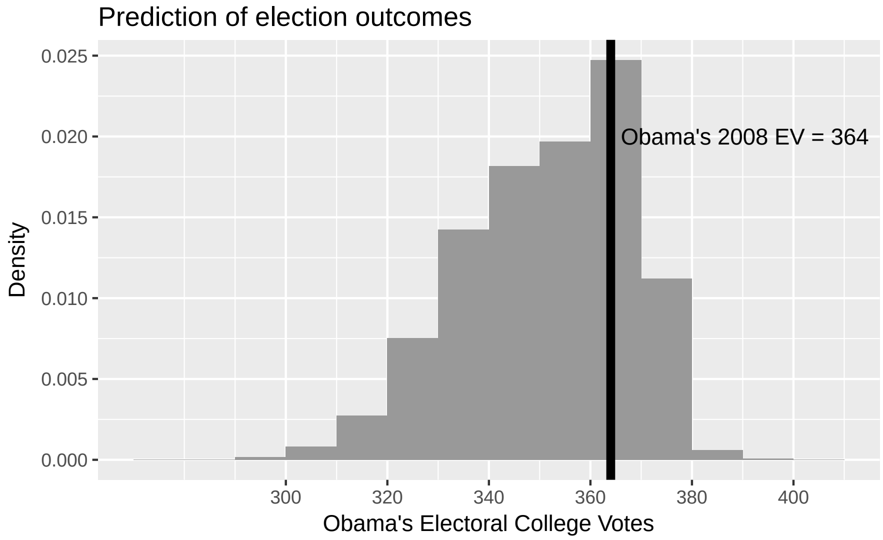
Run this simulation `sims` times, saving the electoral votes of Obama in each simulation:

```
sims <- 10000
Obama_EV_sims <- map_dbl(seq_len(sims), ~ sim_election(pres08))
```

Obama's actual electoral value

```
OBAMA_EV <- 364
```

```
library("glue")
#>
#> Attaching package: 'glue'
#> The following object is masked from 'package:dplyr':
#>
#>     collapse
ggplot(tibble(Obama_EV = Obama_EV_sims),
       aes(x = Obama_EV, y = ..density..)) +
  geom_histogram(binwidth = 10, boundary = 0, fill = "gray60") +
  geom_vline(xintercept = OBAMA_EV, colour = "black", size = 2) +
  annotate("text", x = OBAMA_EV + 2, y = 0.02,
           label = glue("Obama's 2008 EV = {OBAMA_EV}"), hjust = 0) +
  scale_x_continuous("Obama's Electoral College Votes",
                     breaks = seq(300, 400, by = 20)) +
  scale_y_continuous("Density") +
  labs(title = "Prediction of election outcomes")
```



Summarize the simulations:

```
summary(Obama_EV_sims)
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#>     278     340     353     352     364     401
```

Compare theoretical and simulation means:

```
# simulation EV
mean(Obama_EV_sims)
#> [1] 352
# theoretical
n <- 1000
pres08 %>%
  mutate(Obama_EV = EV * pbinom(n / 2, size = n, prob = p,
                                lower.tail = FALSE)) %>%
  summarise(Obama_EV = sum(Obama_EV))
#>   Obama_EV
#> 1      352
```

Compare theoretical and simulation variances:

```
# simulation variance
var(Obama_EV_sims)
#> [1] 272
# theoretical variance
Obama_EV_var <- pres08 %>%
  mutate(pb = pbinom(n / 2, size = n, prob = p, lower.tail = FALSE),
         EV_var = pb * (1 - pb) * EV ^ 2) %>%
  summarise(EV_var = sum(EV_var)) %>%
  pluck("EV_var")
Obama_EV_var
#> [1] 269
```

and standard deviations

```
# sim
sd(Obama_EV_sims)
#> [1] 16.5
# theoretical
sqrt(Obama_EV_var)
#> [1] 16.4
```

6.4 Large Sample Theorems

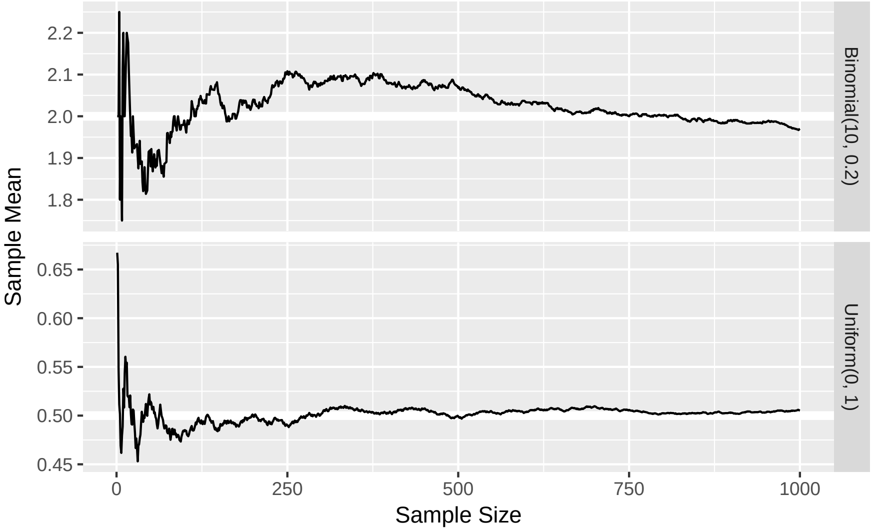
6.4.1 Law of Large Numbers

Put the simulation number, `x` and `mean` in a tibble:

```
sims <- 1000
p <- 0.2
size <- 10
lln_binom <- tibble(
  n = seq_len(sims),
  x = rbinom(sims, prob = p, size = size),
  mean = cumsum(x) / n,
  distrib = str_c("Binomial(", size, ", ", p, ")"))
```

```
lln_unif <-
 tibble(n = seq_len(sims),
        x = runif(sims),
        mean = cumsum(x) / n,
        distrib = str_c("Uniform(0, 1)"))
```

```
true_means <-
  tribble(~distrib, ~mean,
          "Uniform(0, 1)", 0.5,
          str_c("Binomial(", size, ", ", p, ")"), size * p)

ggplot() +
  geom_hline(aes(yintercept = mean), data = true_means,
             colour = "white", size = 2) +
  geom_line(aes(x = n, y = mean),
            data = bind_rows(lln_binom, lln_unif)) +
  facet_grid(distrib ~ ., scales = "free_y") +
  labs(x = "Sample Size", y = "Sample Mean")
```



6.4.2 Central Limit Theorem

The population mean of the binomial distribution is $\mu = pn$ and the variance is $\sigma^2 = p(1-p)n$.

```
sims <- 1000
n_samp <- 1000
```

Write functions to calculate the mean of a binomial distribution with size, `size`, and probability, `p`,

```
binom_mean <- function(size, p) {
  size * p
}
```

variance of a binomial distribution,

```
binom_var <- function(size, p) {
  size * p * (1 - p)
}
```

Write a function that takes `n_samp` samples from a binomial distribution with size, `size`, and probability of success, `p`, and returns a data frame with the z-score of the sample distribution:

```
sim_binom_clt <- function(n_samp, size, p) {
  x <- rbinom(n_samp, prob = p, size = size)
  z <- (mean(x) - binom_mean(size, p)) /
    sqrt(binom_var(size, p) / n_samp)
  tibble(distrib = str_c("Binomial(", p, ", ", size, ")"),
         z = z)
}
```

For the uniform distribution, we need a function to calculate the mean of a uniform distribution,

```
unif_mean <- function(min, max) {
  0.5 * (min + max)
}
```

variance of a uniform distribution,

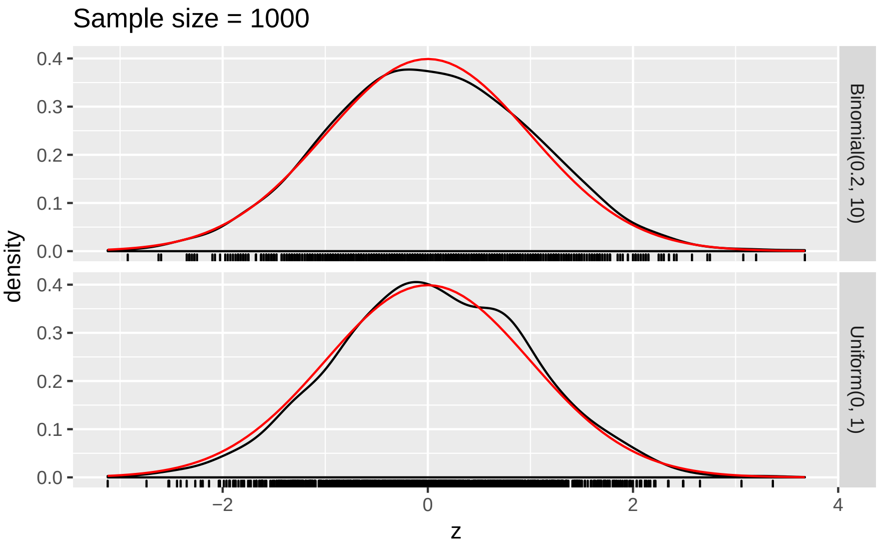
```
unif_var <- function(min, max) {
  (1 / 12) * (max - min) ^ 2
}
```

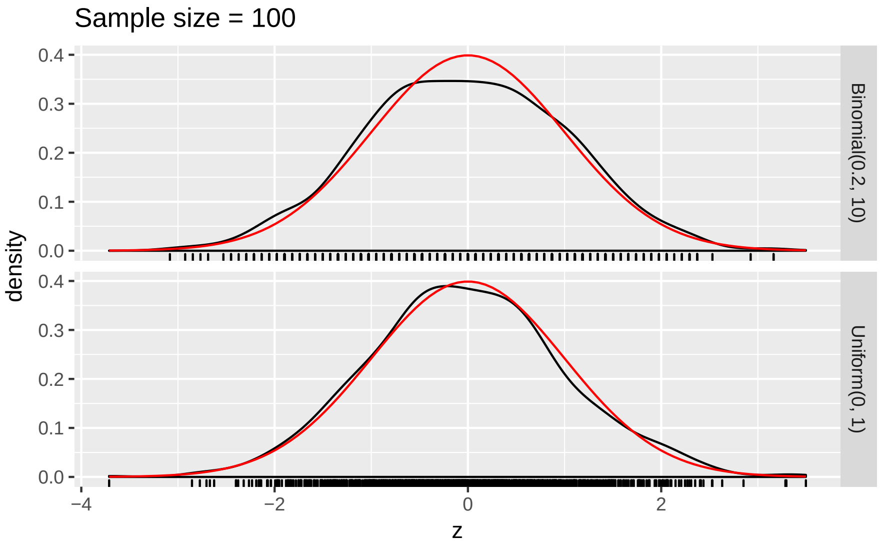
and a function to perform the CLT simulation,

```
sim_unif_clt <- function(n_samp, min = 0, max = 1) {
  x <- runif(n_samp, min = min, max = max)
  z <- (mean(x) - unif_mean(min, max)) /
    sqrt(unif_var(min, max) / n_samp)
  tibble(distrib = str_c("Uniform(", min, ", ", max, ")"),
         z = z)
}
```

Since we will calculate this for `n_samp = 1000` and `n_samp`, we might as well write a function for it.

```
clt_plot <- function(n_samp) {
  bind_rows(map_df(seq_len(sims), ~ sim_binom_clt(n_samp, size, p)),
            map_df(seq_len(sims), ~ sim_unif_clt(n_samp))) %>%
    ggplot(aes(x = z)) +
    geom_density() +
    geom_rug() +
    stat_function(fun = dnorm, colour = "red") +
    facet_grid(distrib ~ .) +
    ggtitle(str_c("Sample size = ", n_samp))
}
clt_plot(1000)
clt_plot(100)
```




Sample size = 100
density
0.4
0.3
0.2
0.1
0.0
Binomial(0.2, 10)
Uniform(0, 1)
−4
−2
0
2
z

Chapter 7

Uncertainty

Prerequisites

We will use these package in this chapter:

```r
library("tidyverse")
library("forcats")
library("lubridate")
library("stringr")
library("modelr")
library("broom")
library("purrr")
```

7.1 Estimation

7.1.1 Unbiasedness and Consistency

In these simulations, we draw a sample of size `n` from normal distributions with means `mu0` and `mu1` and standard deviations `sd0` and `sd1` respectively,

```r
n <- 100
mu0 <- 0
sd0 <- 1
mu1 <- 1
sd1 <- 1
smpl <- tibble(id = seq_len(n),
               # Y if not treated
               Y0 = rnorm(n, mean = mu0, sd = sd0),
               # Y if treated
               Y1 = rnorm(n, mean = mu1, sd = sd1),
               # individual treatment effects
               tau = Y1 - Y0)
```

The SATE is:

```r
SATE <- mean(smpl[["tau"]])
SATE
#> [1] 0.952
```

Simulations of RCTs. Write a function that takes the sample as an input `smpl`, then randomly assigns the treatment to each individual:

```r
sim_treat <- function(smpl) {
  n <- nrow(smpl)
  SATE <- mean(smpl[["tau"]])
  # indexes of obs receiving treatment
  idx <- sample(seq_len(n), floor(nrow(smpl) / 2), replace = FALSE)
  # treat variable are those receiving treatment, else 0
  smpl[["treat"]] <- as.integer(seq_len(nrow(smpl)) %in% idx)
  smpl %>%
    mutate(Y_obs = if_else(treat == 1L, Y1, Y0)) %>%
    group_by(treat) %>%
    summarise(Y_obs = mean(Y_obs)) %>%
    spread(treat, Y_obs) %>%
    rename(Y1_mean = `1`, Y0_mean = `0`) %>%
    mutate(diff_mean = Y1_mean - Y0_mean,
           est_error = diff_mean - SATE)
}
```

This returns a data frame with columns: `Y0_mean` (mean Y for observations not receiving the treatment), `Y1_mean` (mean Y for observations receiving the treatment), `diff` (difference in mean values between the two groups), and `est_error` (difference between the estimated difference and the known SATE):

```r
sim_treat(smpl)
#> # A tibble: 1 x 4
#>   Y0_mean Y1_mean diff_mean est_error
#>     <dbl>   <dbl>     <dbl>     <dbl>
#> 1 -0.0570   0.875     0.932   -0.0207
```

Rerun this function `sims` times:

```r
sims <- 5000
sate_sims <- map_df(seq_len(sims), ~ sim_treat(smpl))
summary(sate_sims[["est_error"]])
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
#>  -0.484  -0.087  -0.002  -0.001   0.085   0.414
```

Simulate the PATE:

```r
PATE <- mu1 - mu0
```

```r
sim_pate <- function(n, mu0, mu1, sd0, sd1) {
  smpl <- tibble(Y0 = rnorm(n, mean = mu0, sd = sd0),
                 Y1 = rnorm(n, mean = mu1, sd = sd1),
                 tau = Y1 - Y0)
  # indexes of obs receiving treatment
  idx <- sample(seq_len(n), floor(nrow(smpl) / 2), replace = FALSE)
  # treat variable are those receiving treatment, else 0
  smpl[["treat"]] <- as.integer(seq_len(nrow(smpl)) %in% idx)
  smpl %>%
    mutate(Y_obs = if_else(treat == 1L, Y1, Y0)) %>%
    group_by(treat) %>%
    summarise(Y_obs = mean(Y_obs)) %>%
    spread(treat, Y_obs) %>%
    rename(Y1_mean = `1`, Y0_mean = `0`) %>%
    mutate(diff_mean = Y1_mean - Y0_mean,
           est_error = diff_mean - PATE)
}
```

Example of one simulation

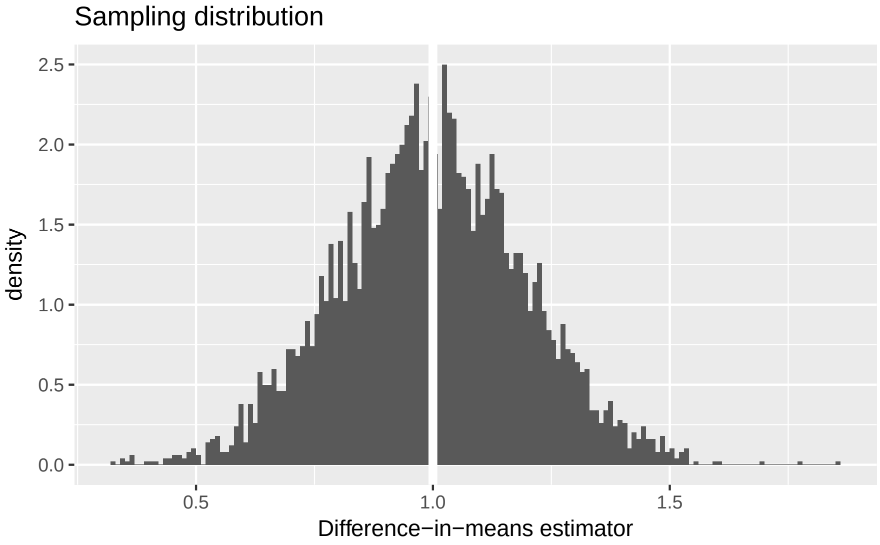
```
sim_pate(n, mu0, mu1, sd0, sd1)
#> # A tibble: 1 x 4
#>   Y0_mean Y1_mean diff_mean est_error
#>     <dbl>   <dbl>     <dbl>     <dbl>
#> 1  -0.109   0.925      1.03    0.0338
```

```
pate_sims <-
  map_df(seq_len(sims), ~ sim_pate(n, mu0, mu1, sd0, sd1))
summary(pate_sims[["est_error"]])
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#>  -0.677  -0.135  -0.004  -0.003   0.129   0.853
```

7.1.2 Standard Error

Plot of the sampling distribution of the difference-in-means estimator:

```
ggplot(pate_sims, aes(x = diff_mean, y = ..density..)) +
  geom_histogram(binwidth = 0.01, boundary = 1) +
  geom_vline(xintercept = PATE, colour = "white", size = 2) +
  ggtitle("Sampling distribution") +
  labs(x = "Difference-in-means estimator")
```



```
sd(pate_sims[["diff_mean"]])
#> [1] 0.196
```

Simulate PATE with a standard error:

```
sim_pate_se <- function(n, mu0, mu1, sd0, sd1) {
  # PATE - difference in means
  PATE <- mu1 - mu0
  # sample
  smpl <- tibble(Y0 = rnorm(n, mean = mu0, sd = sd0),
                 Y1 = rnorm(n, mean = mu1, sd = sd1),
                 tau = Y1 - Y0)
  # indexes of obs receiving treatment
  idx <- sample(seq_len(n), floor(nrow(smpl) / 2), replace = FALSE)
  # treat variable are those receiving treatment, else 0
  smpl[["treat"]] <- as.integer(seq_len(nrow(smpl)) %in% idx)
  # sample
  smpl %>%
    mutate(Y_obs = if_else(treat == 1L, Y1, Y0)) %>%
    group_by(treat) %>%
    summarise(mean = mean(Y_obs),
              var = var(Y_obs),
              nobs = n()) %>%
    summarise(diff_mean = diff(mean),
              se = sqrt(sum(var / nobs)),
              est_error = diff_mean - PATE)
}
```

Run a single simulation:

```
sim_pate_se(n, mu0, mu1, sd0, sd1)
#> # A tibble: 1 x 3
#>   diff_mean    se est_error
#>       <dbl> <dbl>     <dbl>
#> 1      1.05 0.190    0.0539
```

Run `sims` simulations:

```
sims <- 5000
pate_sims_se <-
  map_df(seq_len(sims), ~ sim_pate_se(n, mu0, mu1, sd0, sd1))
```

Standard deviation of difference-in-means

```
sd(pate_sims_se[["diff_mean"]])
#> [1] 0.199
```

Mean of standard errors,

```
mean(pate_sims_se[["se"]])
#> [1] 0.2
```

7.1.3 Confidence Intervals

Calculate a $p\%$ confidence interval for the binomial distribution:

```
# Sample size
n <- 1000
# point estimate
x_bar <- 0.6
# standard error
se <- sqrt(x_bar * (1 - x_bar) / n)
# Desired Confidence levels
levels <- c(0.99, 0.95, 0.90)
```

```
tibble(level = levels) %>%
  mutate(
    ci_lower = x_bar - qnorm(1 - (1 - level) / 2) * se,
    ci_upper = x_bar + qnorm(1 - (1 - level) / 2) * se
  )
#> # A tibble: 3 x 3
#>   level ci_lower ci_upper
#>   <dbl>    <dbl>    <dbl>
#> 1 0.990    0.560    0.640
#> 2 0.950    0.570    0.630
#> 3 0.900    0.575    0.625
```

Calculate the coverage ratio of the 95% confidence interval in the PATE simulations.

```
level <- 0.95
pate_sims_se %>%
  mutate(ci_lower = diff_mean - qnorm(1 - (1 - level) / 2) * se,
         ci_upper = diff_mean + qnorm(1 - (1 - level) / 2) * se,
         includes_pate = PATE > ci_lower & PATE < ci_upper) %>%
  summarise(coverage = mean(includes_pate))
#> # A tibble: 1 x 1
#>   coverage
#>      <dbl>
#> 1    0.948
```

To do this for multiple levels encapsulate the above code in a function with arguments `.data` (the data frame) and the confidence level, `level`:

```
pate_sims_coverage <- function(.data, level = 0.95) {
  mutate(.data,
         ci_lower = diff_mean - qnorm(1 - (1 - level) / 2) * se,
         ci_upper = diff_mean + qnorm(1 - (1 - level) / 2) * se,
         includes_pate = PATE > ci_lower & PATE < ci_upper) %>%
    summarise(coverage = mean(includes_pate))
}

pate_sims_coverage(pate_sims_se, 0.95)
#> # A tibble: 1 x 1
#>   coverage
#>      <dbl>
#> 1    0.948
pate_sims_coverage(pate_sims_se, 0.99)
#> # A tibble: 1 x 1
#>   coverage
#>      <dbl>
#> 1    0.989
pate_sims_coverage(pate_sims_se, 0.90)
#> # A tibble: 1 x 1
#>   coverage
#>      <dbl>
#> 1    0.898
```

```
p <- 0.6
n <- 10
alpha <- 0.05
sims <- 5000
```

Define a function that samples from a Bernoulli distribution, calculates its standard error, and returns a logical value as to whether it contains the true value:

```r
binom_ci_contains <- function(n, p, alpha = 0.05) {
  x <- rbinom(n, size = 1, prob = p)
  x_bar <- mean(x)
  se <- sqrt(x_bar * (1 - x_bar) / n)
  ci_lower <- x_bar - qnorm(1 - alpha / 2) * se
  ci_upper <- x_bar + qnorm(1 - alpha / 2) * se
  (ci_lower <= p) & (p <= ci_upper)
}
```

We can run this once for given sample size:

```r
n <- 10
binom_ci_contains(n, p)
#> [1] FALSE
```

Using `map_df` we can rerun it `sims` times and calculate the coverage proportion:

```r
mean(map_lgl(seq_len(sims), ~ binom_ci_contains(n, p)))
#> [1] 0.905
```

Encapsulate the above code in a function that calculates the coverage of a confidence interval with size, `n`, and success probability, `p`:

```r
binom_ci_coverage <- function(n, p, sims) {
  mean(map_lgl(seq_len(sims), ~ binom_ci_contains(n, p)))
}
```

Use `binom_ci_coverage` to calculate CI coverage for multiple values of the sample size:

```r
tibble(n = c(10L, 100L, 1000L)) %>%
  mutate(coverage = map_dbl(n, binom_ci_coverage, p = !!p, sims = !!sims))
#> # A tibble: 3 x 2
#>       n coverage
#>   <int>    <dbl>
#> 1    10    0.900
#> 2   100    0.943
#> 3  1000    0.948
```

7.1.4 Margin of Error and Sample Size Calculation in Polls

Write a function to calculate the sample size needed for a given proportion.

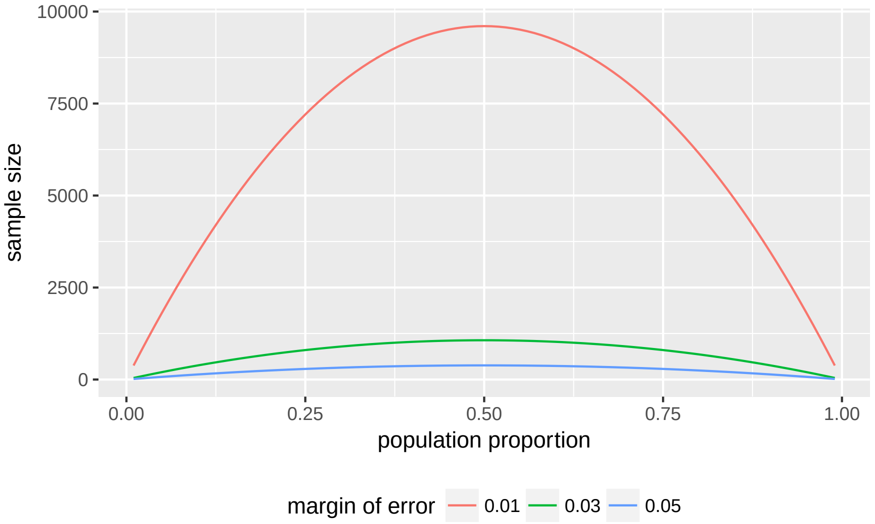
```r
moe_pop_prop <- function(MoE) {
  tibble(p = seq(from = 0.01, to = 0.99, by = 0.01),
         n = 1.96 ^ 2 * p * (1 - p) / MoE ^ 2,
         MoE = MoE)
}
moe_pop_prop(0.01)
#> # A tibble: 99 x 3
#>        p     n    MoE
#>    <dbl> <dbl>  <dbl>
#> 1 0.0100  380. 0.0100
#> 2 0.0200  753. 0.0100
#> 3 0.0300 1118. 0.0100
#> 4 0.0400 1475. 0.0100
#> 5 0.0500 1825. 0.0100
#> 6 0.0600 2167. 0.0100
#> # ... with 93 more rows
```

Then use map_df to call this function for different margins of error, and return the entire thing as a data frame with columns: `n`, `p`, and `MoE`.

```
MoE <- c(0.01, 0.03, 0.05)
props <- map_df(MoE, moe_pop_prop)
```

Since its a data frame, its easy to plot with ggplot:

```
ggplot(props, aes(x = p, y = n, colour = factor(MoE))) +
  geom_line() +
  labs(colour = "margin of error",
       x = "population proportion",
       y = "sample size") +
  theme(legend.position = "bottom")
```



read_csv already recognizes the date columns, so we don't need to convert them. The 2008 election was on Nov 11, 2008, so we'll store that in a variable.

```
ELECTION_DATE <- ymd(20081104)
```

Load the final vote shares,

```
data("pres08", package = "qss")
```

and polling data

```
data("polls08", package = "qss")
```

We need to add an additional column to the `polls08` data frame which contains the number of days until the election:

```
polls08 <- polls08 %>%
  mutate(DaysToElection = as.integer(ELECTION_DATE - middate))
```

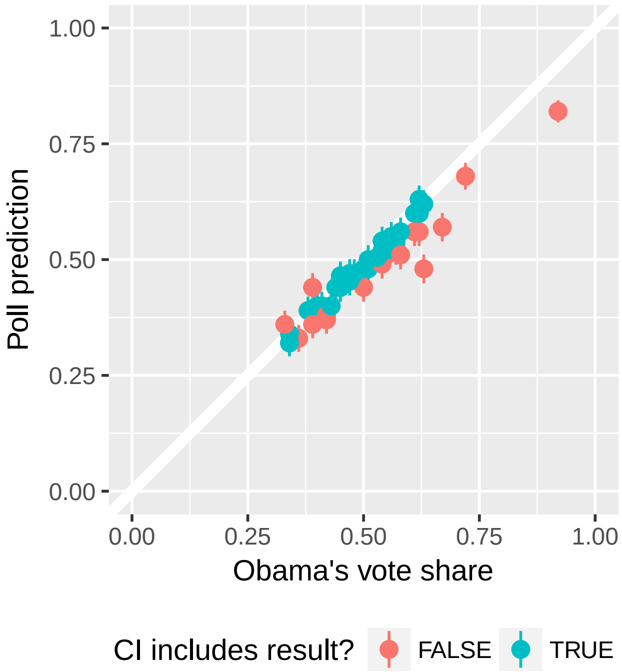
For each state calculate the mean of the latest polls,

```
poll_pred <-
  polls08 %>%
  group_by(state) %>%
  # latest polls in the state
```

```r
  filter(DaysToElection == min(DaysToElection)) %>%
  # take mean of latest polls and convert from 0-100 to 0-1
  summarise(Obama = mean(Obama) / 100)
# Add confidence itervals
# sample size
sample_size <- 1000
# confidence level
alpha <- 0.05
poll_pred <-
  poll_pred %>%
  mutate(se = sqrt(Obama * (1 - Obama) / sample_size),
         ci_lwr = Obama + qnorm(alpha / 2) * se,
         ci_upr = Obama + qnorm(1 - alpha / 2) * se)
# Add actual outcome
poll_pred <-
  left_join(poll_pred,
            select(pres08, state, actual = Obama),
            by = "state") %>%
  mutate(actual = actual / 100,
         covers = (ci_lwr <= actual) & (actual <= ci_upr))
poll_pred
#> # A tibble: 51 x 7
#>   state Obama     se ci_lwr ci_upr actual covers
#>   <chr> <dbl>  <dbl>  <dbl>  <dbl>  <dbl> <lgl>
#> 1 AK    0.390 0.0154  0.360  0.420  0.380 TRUE
#> 2 AL    0.360 0.0152  0.330  0.390  0.390 FALSE
#> 3 AR    0.440 0.0157  0.409  0.471  0.390 FALSE
#> 4 AZ    0.465 0.0158  0.434  0.496  0.450 TRUE
#> 5 CA    0.600 0.0155  0.570  0.630  0.610 TRUE
#> 6 CO    0.520 0.0158  0.489  0.551  0.540 TRUE
#> # ... with 45 more rows
```

In the plot, color the point ranges by whether they include the election day outcome.

```r
ggplot(poll_pred, aes(x = actual, y = Obama,
                      ymin = ci_lwr, ymax = ci_upr,
                      colour = covers)) +
  geom_abline(intercept = 0, slope = 1, colour = "white", size = 2) +
  geom_pointrange() +
  scale_y_continuous("Poll prediction", limits = c(0, 1)) +
  scale_x_continuous("Obama's vote share", limits = c(0, 1)) +
  scale_colour_discrete("CI includes result?") +
  coord_fixed() +
  theme(legend.position = "bottom")
```



Proportion of polls with confidence intervals that include the election outcome?

```
poll_pred %>%
  summarise(mean(covers))
#> # A tibble: 1 x 1
#>   `mean(covers)`
#>            <dbl>
#> 1          0.588
```

```
poll_pred <-
  poll_pred %>%
  # calc bias
  mutate(bias = Obama - actual) %>%
  # bias corrected prediction, se, and CI
  mutate(Obama_bc = Obama - mean(bias),
         se_bc = sqrt(Obama_bc * (1 - Obama_bc) / sample_size),
         ci_lwr_bc = Obama_bc + qnorm(alpha / 2) * se_bc,
         ci_upr_bc = Obama_bc + qnorm(1 - alpha / 2) * se_bc,
         covers_bc = (ci_lwr_bc <= actual) & (actual <= ci_upr_bc))
poll_pred %>%
  summarise(mean(covers_bc))
#> # A tibble: 1 x 1
#>   `mean(covers_bc)`
#>               <dbl>
#> 1             0.765
```

7.1.5 Analysis of Randomized Controlled Trials

Load the STAR data from the **qss** package,

```
data("STAR", package = "qss")
```

Add meaningful labels to the classtype variable:

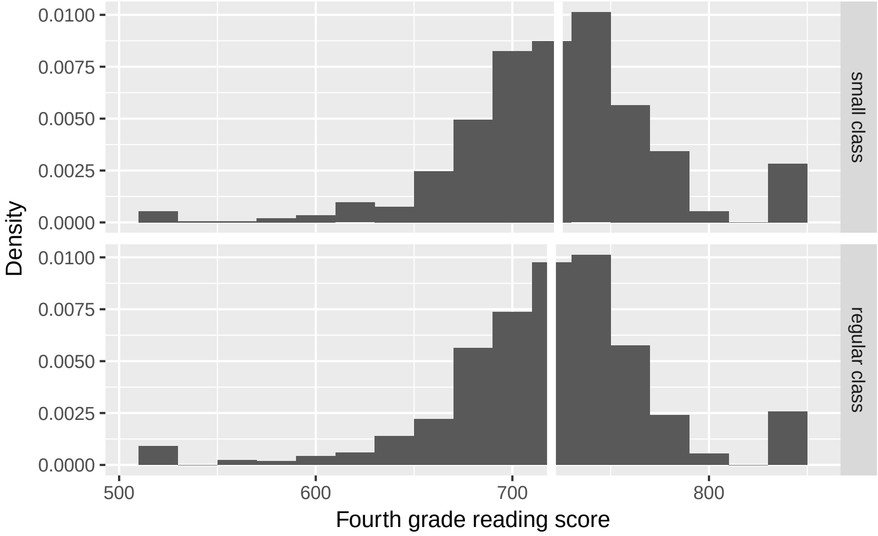
```
STAR <- STAR %>%
  mutate(classtype = factor(classtype,
                            labels = c("small class", "regular class",
                                       "regular class with aid")))
```

Summarize scores by classroom type:

```
classtype_means <-
  STAR %>%
  group_by(classtype) %>%
  summarise(g4reading = mean(g4reading, na.rm = TRUE))
```

Plot the distribution of scores by classroom type:

```
classtypes_used <- c("small class", "regular class")
ggplot(filter(STAR,
              classtype %in% classtypes_used,
              !is.na(g4reading)),
       aes(x = g4reading, y = ..density..)) +
  geom_histogram(binwidth = 20) +
  geom_vline(data = filter(classtype_means, classtype %in% classtypes_used),
             mapping = aes(xintercept = g4reading),
             colour = "white", size = 2) +
  facet_grid(classtype ~ .) +
  labs(x = "Fourth grade reading score", y = "Density")

alpha <- 0.05
star_estimates <-
  STAR %>%
  filter(!is.na(g4reading)) %>%
  group_by(classtype) %>%
  summarise(n = n(),
            est = mean(g4reading),
            se = sd(g4reading) / sqrt(n)) %>%
  mutate(lwr = est + qnorm(alpha / 2) * se,
         upr = est + qnorm(1 - alpha / 2) * se)
star_estimates
#> # A tibble: 3 x 6
#>   classtype                  n   est    se   lwr   upr
#>   <fct>                  <int> <dbl> <dbl> <dbl> <dbl>
#> 1 small class              726  723.  1.91  720.  727.
#> 2 regular class            836  720.  1.84  716.  723.
#> 3 regular class with aid   791  721.  1.86  717.  724.

star_estimates %>%
  filter(classtype %in% c("small class", "regular class")) %>%
  # ensure that it is ordered small then regular
  arrange(desc(classtype)) %>%
  summarise(
    se = sqrt(sum(se ^ 2)),
    est = diff(est)
  ) %>%
  mutate(ci_lwr = est + qnorm(alpha / 2) * se,
         ci_up = est + qnorm(1 - alpha / 2) * se)
#> # A tibble: 1 x 4
#>      se   est ci_lwr ci_up
#>   <dbl> <dbl>  <dbl> <dbl>
#> 1  2.65  3.50  -1.70  8.70
```



Use we could use spread and gather:

```
star_ate <-
  star_estimates %>%
  filter(classtype %in% c("small class", "regular class")) %>%
  mutate(classtype = fct_recode(factor(classtype),
                                "small" = "small class",
                                "regular" = "regular class")) %>%
  select(classtype, est, se) %>%
  gather(stat, value, -classtype) %>%
  unite(variable, stat, classtype)  %>%
  spread(variable, value) %>%
  mutate(ate_est = est_small - est_regular,
         ate_se = sqrt(se_small ^ 2 + se_regular ^ 2),
         ci_lwr = ate_est + qnorm(alpha / 2) * ate_se,
         ci_upr = ate_est + qnorm(1 - alpha / 2) * ate_se)
star_ate
#> # A tibble: 1 x 8
#>   est_regular est_small se_regular se_small ate_est ate_se ci_lwr ci_upr
#>         <dbl>     <dbl>      <dbl>    <dbl>   <dbl>  <dbl>  <dbl>  <dbl>
#> 1        720.      723.       1.84     1.91    3.50   2.65  -1.70   8.70
```

7.1.6 Analysis Based on Student's t-Distribution

Use filter to subset.

```
t.test(filter(STAR, classtype == "small class")$g4reading,
       filter(STAR, classtype == "regular class")$g4reading)
#>
#>  Welch Two Sample t-test
#>
#> data:  filter(STAR, classtype == "small class")$g4reading and filter(STAR, classtype == "regular cla
#> t = 1, df = 2000, p-value = 0.2
#> alternative hypothesis: true difference in means is not equal to 0
#> 95 percent confidence interval:
#>  -1.70  8.71
#> sample estimates:
#> mean of x mean of y
#>       723       720
```

The function t.test can also take a formula as its first parameter.

```
t.test(g4reading ~ classtype,
       data = filter(STAR, classtype %in% c("small class", "regular class")))
#>
#>  Welch Two Sample t-test
#>
#> data:  g4reading by classtype
#> t = 1, df = 2000, p-value = 0.2
#> alternative hypothesis: true difference in means is not equal to 0
#> 95 percent confidence interval:
#>  -1.70  8.71
#> sample estimates:
#>   mean in group small class mean in group regular class
#>                         723                         720
```

7.2 Hypothesis Testing

7.2.1 Tea-Testing Experiment

```
# Number of cups of tea
cups <- 4
# Number guessed correctly
k <- c(0, seq_len(cups))
true <-  tibble(correct = k * 2,
                n = choose(cups, k) * choose(cups, cups - k)) %>%
  mutate(prob = n / sum(n))
true
#> # A tibble: 5 x 3
#>   correct     n   prob
#>     <dbl> <dbl>  <dbl>
#> 1      0.    1. 0.0143
#> 2      2.   16. 0.229
#> 3      4.   36. 0.514
#> 4      6.   16. 0.229
#> 5      8.    1. 0.0143

sims <- 1000
guess <- tibble(guess = c("M", "T", "T", "M", "M", "T", "T", "M"))
randomize_tea <- function(df) {
  # randomize the order of teas
  assignment <- sample_frac(df, 1) %>%
    rename(actual = guess)
  bind_cols(df, assignment) %>%
    summarise(correct = sum(guess == actual))
}
approx <-
  map_df(seq_len(sims), ~ randomize_tea(guess)) %>%
  count(correct) %>%
  mutate(prob = n / sum(n))
left_join(select(approx, correct, prob_sim = prob),
          select(true, correct, prob_exact = prob),
          by = "correct") %>%
  mutate(diff = prob_sim - prob_exact)
#> # A tibble: 5 x 4
#>   correct prob_sim prob_exact     diff
#>     <dbl>    <dbl>      <dbl>    <dbl>
#> 1      0.   0.0110     0.0143 -0.00329
#> 2      2.   0.234      0.229   0.00543
#> 3      4.   0.486      0.514  -0.0283
#> 4      6.   0.253      0.229   0.0244
#> 5      8.   0.0160     0.0143  0.00171
```

7.2.2 The General Framework

The test functions like fisher.test do not work particularly well with data frames, and expect vectors or matrices as input, so tidyverse functions are less directly applicable

```
# all guesses correct
x <- tribble(~Guess, ~Truth, ~Number,
             "Milk", "Milk", 4L,
             "Milk", "Tea", 0L,
             "Tea", "Milk", 0L,
             "Tea", "Tea", 4L)
x
#> # A tibble: 4 x 3
#>   Guess Truth Number
#>   <chr> <chr>  <int>
#> 1 Milk  Milk       4
#> 2 Milk  Tea        0
#> 3 Tea   Milk       0
#> 4 Tea   Tea        4
# 6 correct guesses
y <- x %>%
  mutate(Number = c(3L, 1L, 1L, 3L))
y
#> # A tibble: 4 x 3
#>   Guess Truth Number
#>   <chr> <chr>  <int>
#> 1 Milk  Milk       3
#> 2 Milk  Tea        1
#> 3 Tea   Milk       1
#> 4 Tea   Tea        3
# Turn into a 2x2 table for fisher.test
select(spread(x, Truth, Number), -Guess)
#> # A tibble: 2 x 2
#>    Milk   Tea
#>   <int> <int>
#> 1     4     0
#> 2     0     4
# Use spread to make it a 2 x 2 table
fisher.test(select(spread(x, Truth, Number), -Guess),
            alternative = "greater")
#> 
#>  Fisher's Exact Test for Count Data
#> 
#> data:  select(spread(x, Truth, Number), -Guess)
#> p-value = 0.01
#> alternative hypothesis: true odds ratio is greater than 1
#> 95 percent confidence interval:
#>    2 Inf
#> sample estimates:
#> odds ratio 
#>        Inf
fisher.test(select(spread(y, Truth, Number), -Guess))
#> 
#>  Fisher's Exact Test for Count Data
#> 
#> data:  select(spread(y, Truth, Number), -Guess)
#> p-value = 0.5
#> alternative hypothesis: true odds ratio is not equal to 1
#> 95 percent confidence interval:
#>    0.212 621.934
#> sample estimates:
#> odds ratio 
#>       6.41
```

7.2.3 One-Sample Tests

```
n <- 1018
x_bar <- 550 / n
se <- sqrt(0.5 * 0.5 / n) # standard deviation of sampling distribution
# upper red area in the figure
upper <- pnorm(x_bar, mean = 0.5, sd = se, lower.tail = FALSE)
# lower red area in the figure; identical to the upper area
lower <- pnorm(0.5 - (x_bar - 0.5), mean = 0.5, sd = se)
# two side p value
upper + lower
#> [1] 0.0102
2 * upper
#> [1] 0.0102
# one sided p value
upper
#> [1] 0.00508
z_score <- (x_bar - 0.5) / se
z_score
#> [1] 2.57
pnorm(z_score, lower.tail = FALSE) # one-sided p-value
#> [1] 0.00508
2 * pnorm(z_score, lower.tail = FALSE) # two-sided p-value
```

```
#> [1] 0.0102
# 99% confidence interval contains 0.5
c(x_bar - qnorm(0.995) * se, x_bar + qnorm(0.995) * se)
#> [1] 0.500 0.581
# 95% confidence interval does not contain 0.5
c(x_bar - qnorm(0.975) * se, x_bar + qnorm(0.975) * se)
#> [1] 0.510 0.571
# no continuity correction to get the same p-value as above
prop.test(550, n = n, p = 0.5, correct = FALSE)
#>
#>  1-sample proportions test without continuity correction
#>
#> data:  550 out of n, null probability 0.5
#> X-squared = 7, df = 1, p-value = 0.01
#> alternative hypothesis: true p is not equal to 0.5
#> 95 percent confidence interval:
#>  0.510 0.571
#> sample estimates:
#>    p
#> 0.54
# with continuity correction
prop.test(550, n = n, p = 0.5)
#>
#>  1-sample proportions test with continuity correction
#>
#> data:  550 out of n, null probability 0.5
#> X-squared = 6, df = 1, p-value = 0.01
#> alternative hypothesis: true p is not equal to 0.5
#> 95 percent confidence interval:
#>  0.509 0.571
#> sample estimates:
#>    p
#> 0.54
prop.test(550, n = n, p = 0.5, conf.level = 0.99)
#>
#>  1-sample proportions test with continuity correction
#>
#> data:  550 out of n, null probability 0.5
#> X-squared = 6, df = 1, p-value = 0.01
#> alternative hypothesis: true p is not equal to 0.5
#> 99 percent confidence interval:
#>  0.499 0.581
#> sample estimates:
#>    p
#> 0.54
```

```
# two-sided one-sample t-test
t.test(STAR$g4reading, mu = 710)
#>
#>  One Sample t-test
#>
#> data:  STAR$g4reading
#> t = 10, df = 2000, p-value <2e-16
#> alternative hypothesis: true mean is not equal to 710
#> 95 percent confidence interval:
#>  719 723
#> sample estimates:
#> mean of x 
#>       721
```

7.2.4 Two-sample tests

The ATE estimates are stored in a data frame, `star_ate`. Note that the dplyr function transmute is like `mutate`, but only returns the variables specified in the function.

```
star_ate %>%
  transmute(p_value_1sided = pnorm(-abs(ate_est),
                                   mean = 0, sd = ate_se),
            p_value_2sided = 2 * pnorm(-abs(ate_est), mean = 0,
                                   sd = ate_se))
#> # A tibble: 1 x 2
#>   p_value_1sided p_value_2sided
#>            <dbl>          <dbl>
#> 1         0.0935          0.187

t.test(g4reading ~ classtype,
  data = filter(STAR, classtype %in% c("small class", "regular class")))
#> 
#>  Welch Two Sample t-test
#> 
#> data:  g4reading by classtype
#> t = 1, df = 2000, p-value = 0.2
#> alternative hypothesis: true difference in means is not equal to 0
#> 95 percent confidence interval:
#>  -1.70  8.71
#> sample estimates:
#>   mean in group small class mean in group regular class 
#>                         723                         720
```

or

```
t.test(filter(STAR, classtype == "small class")$g4reading,
       filter(STAR, classtype == "regular class")$g4reading)
#> 
#>  Welch Two Sample t-test
#> 
#> data:  filter(STAR, classtype == "small class")$g4reading and filter(STAR, classtype == "regular cla
#> t = 1, df = 2000, p-value = 0.2
#> alternative hypothesis: true difference in means is not equal to 0
#> 95 percent confidence interval:
#>  -1.70  8.71
#> sample estimates:
#> mean of x mean of y 
#>       723       720
```

```
data("resume", package = "qss")
x <- resume %>%
  count(race, call) %>%
  spread(call, n) %>%
  ungroup()
x
#> # A tibble: 2 x 3
#>   race    `0`   `1`
#>   <chr> <int> <int>
#> 1 black  2278   157
#> 2 white  2200   235
prop.test(as.matrix(select(x, -race)), alternative = "greater")
#> 
#>  2-sample test for equality of proportions with continuity
#>  correction
#> 
#> data:  as.matrix(select(x, -race))
#> X-squared = 20, df = 1, p-value = 2e-05
#> alternative hypothesis: greater
#> 95 percent confidence interval:
#>  0.0188 1.0000
#> sample estimates:
#> prop 1 prop 2 
#>  0.936  0.903
```

Assign sample sizes and proportions, then calculate point estimates, standard error, z-statistic and one-sided p-value.

```
n0 <- sum(resume$race == "black")
n1 <- sum(resume$race == "white")

p <- mean(resume$call)
p0 <- mean(filter(resume, race == "black")$call)
p1 <- mean(filter(resume, race == "white")$call)

est <- p1 - p0
est
#> [1] 0.032

se <- sqrt(p * (1 - p) * (1 / n0 + 1 / n1))
se
#> [1] 0.0078

zstat <- est / se
zstat
#> [1] 4.11

pnorm(-abs(zstat))
#> [1] 1.99e-05
```

The only thing that changed is using filter for selecting the groups.

7.2.5 Power Analysis

Set the parameters: the sample size,

```
n <- 250
```

the population proportional under the alternative data generating process,

```
p_star <- 0.48
```

the null hypothesis,

```
p <- 0.5
```

the p-value,

```
alpha <- 0.05
```

and

```
cr_value <- qnorm(1 - alpha / 2)
```

The standard errors under the hypothetical data generating process is

```
se_star <- sqrt(p_star * (1 - p_star) / n)
```

and the standard error under the null is

```
se <- sqrt(p * (1 - p) / n)
```

The power for this test is

```
pnorm(p - cr_value * se, mean = p_star, sd = se_star) +
    pnorm(p + cr_value * se, mean = p_star, sd = se_star,
          lower.tail = FALSE)
#> [1] 0.0967
```

The parameters (sample sizes and proportions) are

```
n1 <- 500
n0 <- 500
p1_star <- 0.05
p0_star <- 0.1
```

Calculate the overall call back rate as a weighted average,

```
p <- (n1 * p1_star + n0 * p0_star) / (n1 + n0)
```

the standard error under the null,

```
se <- sqrt(p * (1 - p) * (1 / n1 + 1 / n0))
```

the standard error under the hypothetical data generating process,

```
se.star <- sqrt(p1_star * (1 - p1_star) / n1 + p0_star * (1 - p0_star) / n0)
```

```
pnorm(-cr_value * se, mean = p1_star - p0_star, sd = se.star) +
    pnorm(cr_value * se, mean = p1_star - p0_star, sd = se.star,
          lower.tail = FALSE)
#> [1] 0.852
```

```
power.prop.test(n = 500, p1 = 0.05, p2 = 0.1, sig.level = 0.05)
#>
#>      Two-sample comparison of proportions power calculation
#>
#>               n = 500
#>              p1 = 0.05
#>              p2 = 0.1
#>       sig.level = 0.05
#>           power = 0.852
#>     alternative = two.sided
#>
#> NOTE: n is number in *each* group
```

```
power.prop.test(p1 = 0.05, p2 = 0.1, sig.level = 0.05, power = 0.9)
#>
#>      Two-sample comparison of proportions power calculation
#>
#>               n = 581
#>              p1 = 0.05
#>              p2 = 0.1
#>       sig.level = 0.05
#>           power = 0.9
#>     alternative = two.sided
#>
#> NOTE: n is number in *each* group
```

```
power.t.test(n = 100, delta = 0.25, sd = 1, type = "one.sample")
#>
#>      One-sample t test power calculation
#>
#>               n = 100
#>           delta = 0.25
#>              sd = 1
#>       sig.level = 0.05
#>           power = 0.697
#>     alternative = two.sided
```

```
power.t.test(power = 0.9, delta = 0.25, sd = 1, type = "one.sample")
#>
#>      One-sample t test power calculation
#>
#>               n = 170
#>           delta = 0.25
#>              sd = 1
#>       sig.level = 0.05
#>           power = 0.9
#>     alternative = two.sided
```

```
power.t.test(delta = 0.25, sd = 1, type = "two.sample",
             alternative = "one.sided", power = 0.9)
#>
#>      Two-sample t test power calculation
#>
#>               n = 275
#>           delta = 0.25
#>              sd = 1
#>       sig.level = 0.05
#>           power = 0.9
#>     alternative = one.sided
#>
#> NOTE: n is number in *each* group
```

7.3 Linear Regression Model with Uncertainty

7.3.1 Linear Regression as a Generative Model

Load the minimum wage date included with the **qss** package:

```
data("minwage", package = "qss")
```

```
minwage <- mutate(minwage,
                  fullPropBefore = fullBefore / (fullBefore + partBefore),
                  fullPropAfter = fullAfter / (fullAfter + partAfter),
                  NJ = as.integer(location == "PA"))
```

```
fit_minwage <- lm(fullPropAfter ~ -1 + NJ + fullPropBefore +
                    wageBefore + chain, data = minwage)
fit_minwage
#>
#> Call:
#> lm(formula = fullPropAfter ~ -1 + NJ + fullPropBefore + wageBefore +
#>     chain, data = minwage)
#>
#> Coefficients:
#>             NJ  fullPropBefore      wageBefore  chainburgerking
#>        -0.0542          0.1688          0.0813          -0.0614
#>       chainkfc       chainroys      chainwendys
#>        -0.0966         -0.1522         -0.1659
fit_minwage1 <- lm(fullPropAfter ~ NJ + fullPropBefore +
                     wageBefore + chain, data = minwage)
fit_minwage1
#>
#> Call:
#> lm(formula = fullPropAfter ~ NJ + fullPropBefore + wageBefore +
#>     chain, data = minwage)
#>
#> Coefficients:
#>    (Intercept)              NJ  fullPropBefore      wageBefore
#>        -0.0614         -0.0542          0.1688          0.0813
#>       chainkfc       chainroys     chainwendys
#>        -0.0352         -0.0908         -0.1045
gather_predictions(slice(minwage, 1), fit_minwage, fit_minwage1) %>%
  select(model, pred)
#> # A tibble: 2 x 2
#>   model         pred
#>   <chr>        <dbl>
#> 1 fit_minwage  0.271
#> 2 fit_minwage1 0.271
```

7.3.2 Inference about coefficients

Use the tidy function to return the coefficients, including confidence intervals, as a data frame:

```
data("women", package = "qss")
fit_women <- lm(water ~ reserved, data = women)
summary(fit_women)
```

```
#>
#> Call:
#> lm(formula = water ~ reserved, data = women)
#>
#> Residuals:
#>    Min     1Q Median     3Q    Max
#> -23.99 -14.74  -7.86   2.26 316.01
#>
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)    14.74       2.29    6.45  4.2e-10 ***
#> reserved        9.25       3.95    2.34     0.02 *
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 33.4 on 320 degrees of freedom
#> Multiple R-squared:  0.0169, Adjusted R-squared:  0.0138
#> F-statistic: 5.49 on 1 and 320 DF,  p-value: 0.0197
tidy(fit_women)
#>          term estimate std.error statistic  p.value
#> 1 (Intercept)    14.74      2.29      6.45 4.22e-10
#> 2    reserved     9.25      3.95      2.34 1.97e-02
```

You need to set `conf.int = TRUE` for tidy to include the confidence interval:

```
summary(fit_minwage)
#>
#> Call:
#> lm(formula = fullPropAfter ~ -1 + NJ + fullPropBefore + wageBefore +
#>     chain, data = minwage)
#>
#> Residuals:
#>     Min      1Q  Median      3Q     Max
#> -0.4862 -0.1813 -0.0281  0.1513  0.7509
#>
#> Coefficients:
#>                 Estimate Std. Error t value Pr(>|t|)
#> NJ               -0.0542     0.0332   -1.63   0.1034
#> fullPropBefore    0.1688     0.0566    2.98   0.0031 **
#> wageBefore        0.0813     0.0389    2.09   0.0374 *
#> chainburgerking  -0.0614     0.1755   -0.35   0.7266
#> chainkfc         -0.0966     0.1793   -0.54   0.5904
#> chainroys        -0.1522     0.1832   -0.83   0.4066
#> chainwendys      -0.1659     0.1853   -0.90   0.3711
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 0.244 on 351 degrees of freedom
#> Multiple R-squared:  0.635,  Adjusted R-squared:  0.628
#> F-statistic: 87.2 on 7 and 351 DF,  p-value: <2e-16
tidy(fit_minwage, conf.int = TRUE)
#>              term estimate std.error statistic p.value conf.low conf.high
#> 1              NJ  -0.0542    0.0332    -1.633 0.10343 -0.11953    0.0111
#> 2  fullPropBefore   0.1688    0.0566     2.981 0.00307  0.05744    0.2801
#> 3      wageBefore   0.0813    0.0389     2.090 0.03737  0.00478    0.1579
#> 4 chainburgerking  -0.0614    0.1755    -0.350 0.72657 -0.40648    0.2837
#> 5         chainkfc  -0.0966    0.1793    -0.539 0.59044 -0.44919    0.2560
#> 6        chainroys  -0.1522    0.1832    -0.831 0.40664 -0.51238    0.2080
#> 7      chainwendys  -0.1659    0.1853    -0.895 0.37115 -0.53031    0.1985
```

7.3.3 Inference about predictions

```
data("MPs", package = "qss")
MPs_labour <- filter(MPs, party == "labour")
MPs_tory <- filter(MPs, party == "tory")
labour_fit1 <- lm(ln.net ~ margin, data = filter(MPs_labour, margin < 0))
labour_fit2 <- lm(ln.net ~ margin, data = filter(MPs_labour, margin > 0))
tory_fit1 <- lm(ln.net ~ margin, data = filter(MPs_tory, margin < 0))
tory_fit2 <- lm(ln.net ~ margin, data = filter(MPs_tory, margin > 0))
```

Predictions at the threshold. The broom function augment will return prediction fitted values and standard errors for each value, but not the confidence intervals themselves (we'd have to multiply the correct t-distribution with degrees of freedom.) So instead, we'll directly use the predict function:

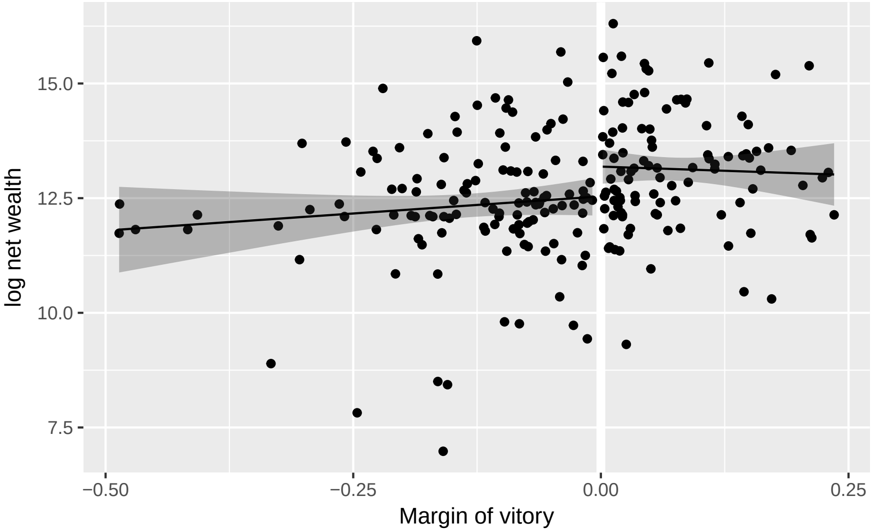
```
tory_y0 <-
  predict(tory_fit1, interval = "confidence",
          newdata = tibble(margin = 0)) %>% as_tibble()
tory_y0
#> # A tibble: 1 x 3
#>     fit   lwr   upr
#>   <dbl> <dbl> <dbl>
#> 1  12.5  12.1  13.0
tory_y1 <-
  predict(tory_fit2, interval = "confidence",
          newdata = tibble(margin = 0)) %>% as_tibble()
tory_y1
#> # A tibble: 1 x 3
#>     fit   lwr   upr
#>   <dbl> <dbl> <dbl>
#> 1  13.2  12.8  13.6
```

Alternatively, using `augment` (and assuming a normal distribution since the number of observations is so large its not worth worrying about the t-distribution):

```
tory_y0 <-
  augment(tory_fit1, newdata = tibble(margin = 0)) %>%
  mutate(lwr = .fitted + qnorm(0.025) * .se.fit,
         upr = .fitted + qnorm(0.975) * .se.fit)
tory_y0
#>   margin .fitted .se.fit  lwr upr
#> 1      0    12.5   0.214 12.1  13
tory_y1 <-
  augment(tory_fit2, newdata = tibble(margin = 0)) %>%
  mutate(lwr = .fitted + qnorm(0.025) * .se.fit,
         upr = .fitted + qnorm(0.975) * .se.fit)
tory_y1
#>   margin .fitted .se.fit  lwr  upr
#> 1      0    13.2   0.192 12.8 13.6
```

```r
y1_range <- data_grid(filter(MPs_tory, margin <= 0), margin)
tory_y0 <- augment(tory_fit1, newdata = y1_range)
y2_range <- data_grid(filter(MPs_tory, margin >= 0), margin)
tory_y1 <- augment(tory_fit2, newdata = y2_range)
```

```r
ggplot() +
  geom_ref_line(v = 0) +
  geom_point(aes(y = ln.net, x = margin), data = MPs_tory) +
  # plot losers
  geom_ribbon(aes(x = margin,
                  ymin = .fitted + qnorm(0.025) * .se.fit,
                  ymax = .fitted + qnorm(0.975) * .se.fit),
              data = tory_y0, alpha = 0.3) +
  geom_line(aes(x = margin, y = .fitted), data = tory_y0) +
  # plot winners
  geom_ribbon(aes(x = margin,
                  ymin = .fitted + qnorm(0.025) * .se.fit,
                  ymax = .fitted + qnorm(0.975) * .se.fit),
              data = tory_y1, alpha = 0.3) +
  geom_line(aes(x = margin, y = .fitted), data = tory_y1) +
  labs(x = "Margin of vitory", y = "log net wealth")
```



```r
tory_y1 <- augment(tory_fit1, newdata = tibble(margin = 0))
tory_y1
#>   margin .fitted .se.fit
#> 1      0    12.5   0.214
tory_y0 <- augment(tory_fit2, newdata = tibble(margin = 0))
tory_y0
#>   margin .fitted .se.fit
#> 1      0    13.2   0.192
summary(tory_fit1)
#> 
#> Call:
#> lm(formula = ln.net ~ margin, data = filter(MPs_tory, margin <
#>     0))
#> 
#> Residuals:
```

```
#>    Min     1Q Median     3Q    Max 
#> -5.320 -0.472 -0.035  0.663  3.580 
#> 
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)    
#> (Intercept)   12.538      0.214   58.54   <2e-16 ***
#> margin         1.491      1.291    1.15     0.25    
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#> 
#> Residual standard error: 1.43 on 119 degrees of freedom
#> Multiple R-squared:  0.0111, Adjusted R-squared:  0.00277 
#> F-statistic: 1.33 on 1 and 119 DF,  p-value: 0.251
summary(tory_fit2)
#> 
#> Call:
#> lm(formula = ln.net ~ margin, data = filter(MPs_tory, margin > 
#>     0))
#> 
#> Residuals:
#>    Min     1Q Median     3Q    Max 
#> -3.858 -0.877  0.001  0.830  3.126 
#> 
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)    
#> (Intercept)   13.188      0.192   68.69   <2e-16 ***
#> margin        -0.728      1.982   -0.37     0.71    
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#> 
#> Residual standard error: 1.29 on 100 degrees of freedom
#> Multiple R-squared:  0.00135,    Adjusted R-squared:  -0.00864 
#> F-statistic: 0.135 on 1 and 100 DF,  p-value: 0.714
```

Since we aren't doing anything more with these values, there isn't much benefit in keeping them in data frames.

```
# standard error
se_diff <- sqrt(tory_y0$.se.fit ^ 2 + tory_y1$.se.fit ^ 2)
se_diff
#> [1] 0.288
# point estimate
diff_est <- tory_y1$.fitted - tory_y0$.fitted
diff_est
#> [1] -0.65
# confidence interval
CI <- c(diff_est - se_diff * qnorm(0.975),
        diff_est + se_diff * qnorm(0.975))
CI
#> [1] -1.2134 -0.0859
# hypothesis test
z_score <- diff_est / se_diff
# two sided p value
p_value <- 2 * pnorm(abs(z_score), lower.tail = FALSE)
```

```
p_value
#> [1] 0.0239
```