

Advanced R - Data Simulation and Advanced Data Visualisation

Andrew Stewart

Andrew.Stewart@manchester.ac.uk



@ajstewart_lang



<https://github.com/ajstewartlang>

Workshop	Topic
1	Mixed Models (Andrew)
2	Bayesian Statistics (Johan)
3	Advanced R (Andrew)
4	Hackathon (Andrew)
5	Matlab (Bo)

Assignment hand in:

Mixed Models - Feb 28th

Hackathon - May 1st

Today

- You're going to learn how to simulate 100s (or even 100,000s) of repeats of the same experiment to determine what pattern of *p*-values and effect size estimates you'll get (assuming there is a medium size effect to be found).
- We're also going to look at more advanced data visualisation tools including animated plots using the `ggridge` package, the `ggforce` package visualisations of text data, sentiment analysis using `tidytext`, how to create BBC-style visualisations using `ggplot2` and the BBC R Cookbook.

Writing clear, human readable, and consistent code.

- I've seen a variety of different types of approaches to coding - while most code works fine, it can vary quite a lot in terms of clarity and consistency.
- Code needs to be both computer readable and human readable.
- A good resource for mastering writing clear and human readable code can be found in the Tidyverse style guide:

https://style.tidyverse.org/_main.pdf

Simulating Data in R

- So far we've looked at wrangling, visualising, and modelling data using R.
- Now we're going to look at creating or simulating data using R and looking at some programming in R.

Why?

- Data simulation allows you to do a number of things:
 - Determine whether your design supports the kinds of analyses you are planning to do (especially important if you pre-registered your analysis plan on OSF).
 - Determine whether the sample size and number of observations you are collecting is sufficient for you to detect the magnitude of the effect you are predicting with a reasonable level of precision.
 - Write your analysis script before you've even collected your data thus making everything more efficient.

The `rnorm()` function

- The `rnorm()` function allows us to sample n times from the normal distribution where we can specify both the mean and the standard deviation of the distribution we want to sample from. The function takes three parameters - the number of samples, the mean and the standard deviation of the distribution to sample from.

```
> rnorm(5, 0, 1)
```

```
[1] 0.24751016 1.12242126 2.13538261 -0.04670306  
0.32518029
```

```
> rnorm(5, 0, 1)
```

```
[1] 0.1661151 0.1937463 -0.7434664 1.0375703 2.2625231
```

- Notice that the two times we call the `rnorm()` function we get different random samples...

- We want to make sure we can replicate our sample - we can use the `set.seed()` function to specify the seed of the randomisation (so we can rerun the code and get the same result).

```
> set.seed(1234)

> rnorm(5, 0, 1)

[1] -1.2070657  0.2774292  1.0844412 -2.3456977  0.4291247

> set.seed(1234)

> rnorm(5, 0, 1)

[1] -1.2070657  0.2774292  1.0844412 -2.3456977  0.4291247
```

- Now the two samples are identical.

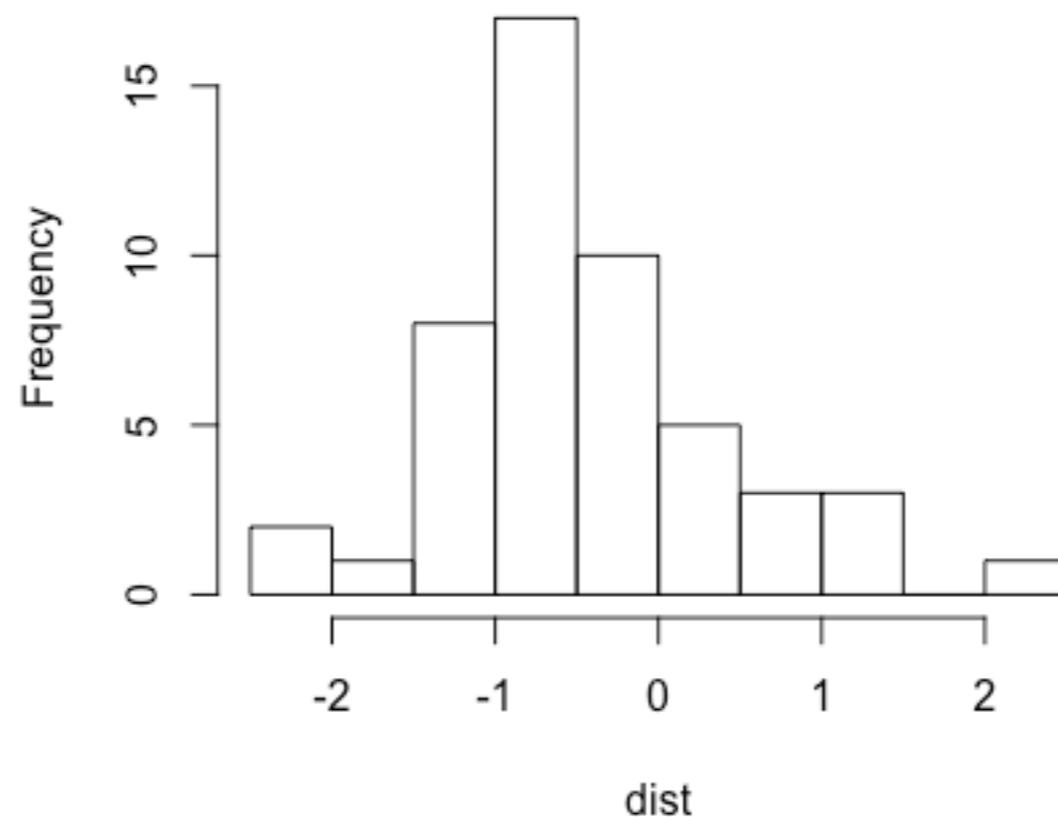
- We can map our random sample onto a new variable I'm calling `dist` and then plot a histogram of the values. Here is a $N = 50$ sample.

```
> set.seed(1234)
```

```
> dist <- rnorm(50, 0, 1)
```

```
> hist(dist)
```

Histogram of dist

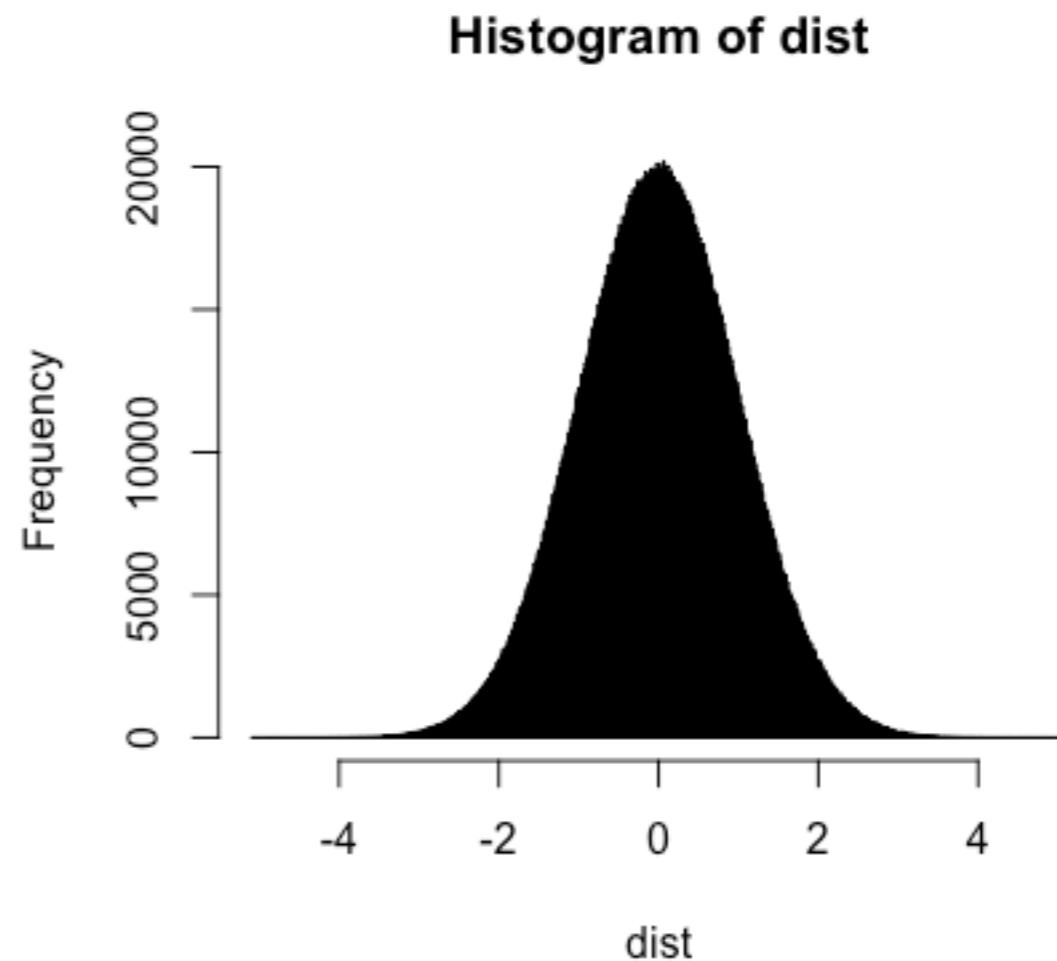


- The larger the sample the more representative it is of the population it is drawn from. Here is a $N = 5$ million sample from the standard normal distribution.

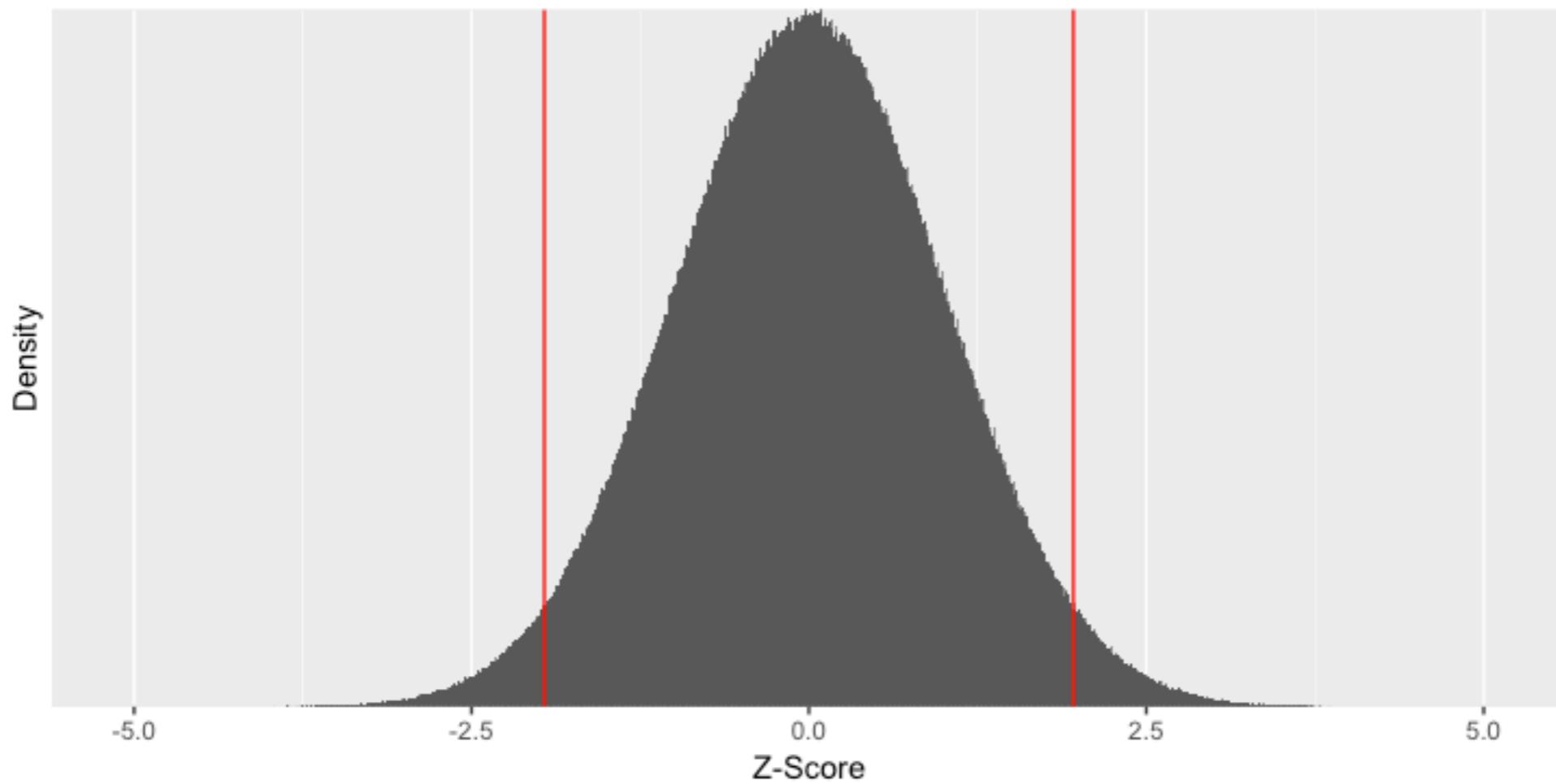
```
> set.seed(1234)
```

```
> dist <- rnorm(5000000, 0, 1)
```

```
> hist(dist, breaks = 1000)
```



- In the standard normal distribution, 95% of the data is contained within 1.96 standard deviations either side of the mean.



- We can use the `pnorm()` function to give us the area under the curve of the normal distribution.
- To work out the area bounded by 1.96 standard deviations from the mean in the standard normal distribution:

```
> pnorm(1.96, mean = 0, sd = 1) - pnorm(-1.96, mean = 0, sd = 1)
```

```
[1] 0.9500042
```



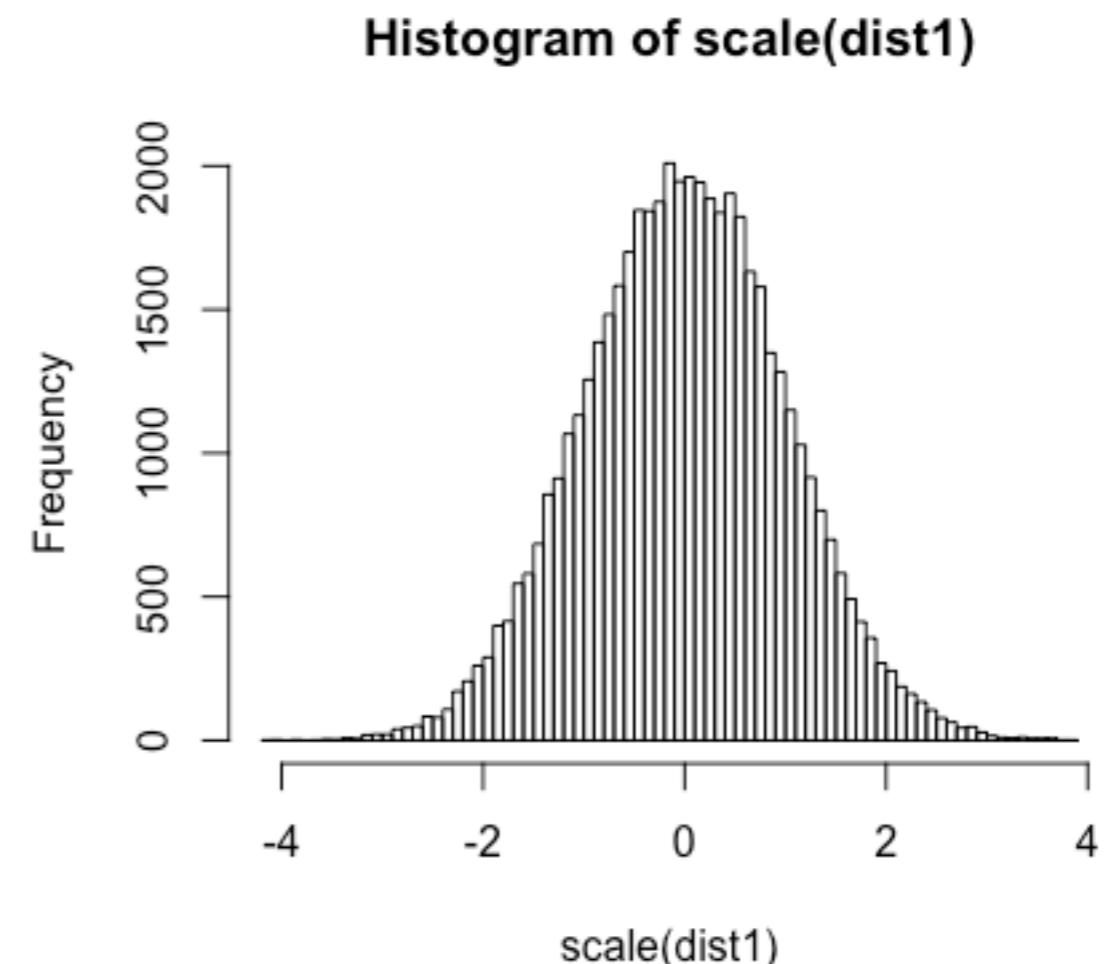
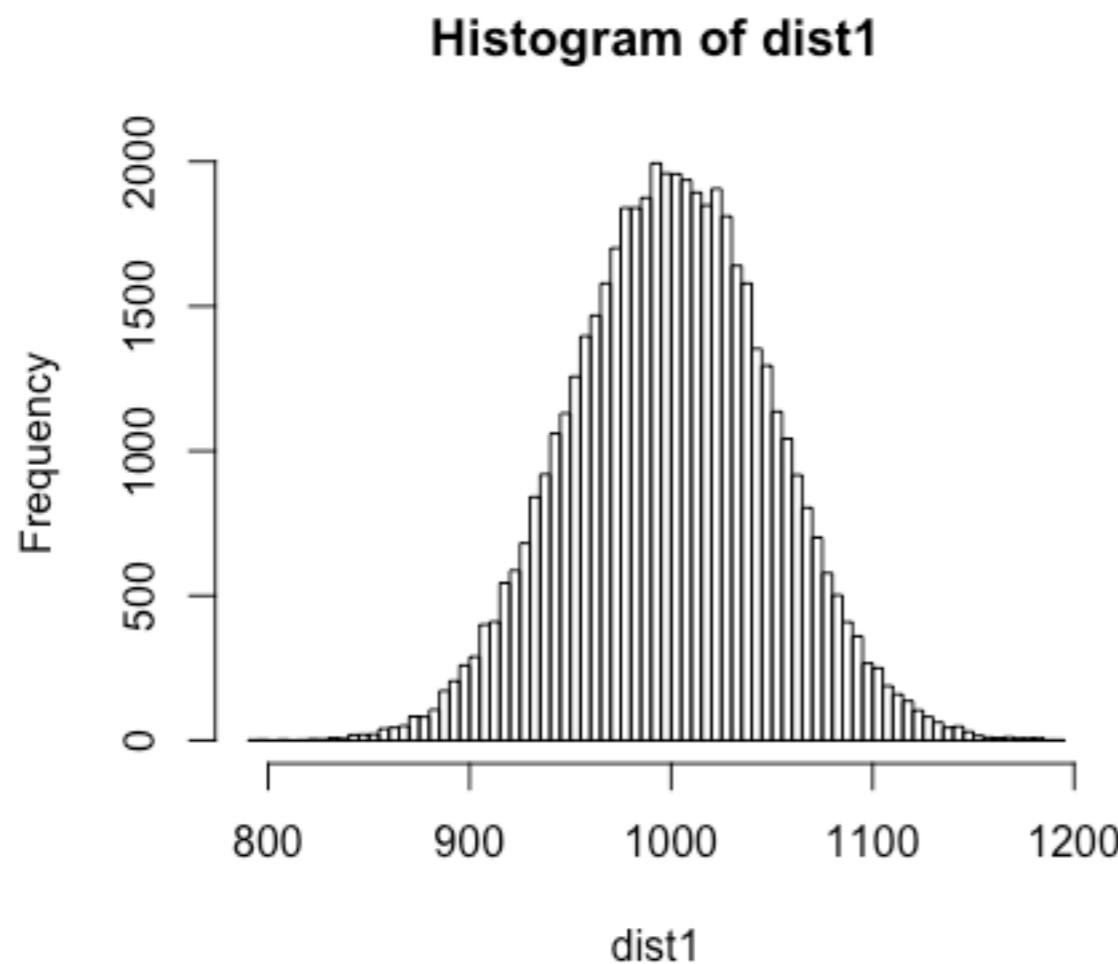
- We can convert any normally distributed data to the standard normal (i.e., Z) distribution by using the `scale()` function. This will centre it so the mean is 0 and scale it so that the standard deviation is 1.

```
> set.seed(1234)
```

```
> dist1 <- rnorm(50000, 1000, 50)
```

```
> hist(dist1, breaks = 100)
```

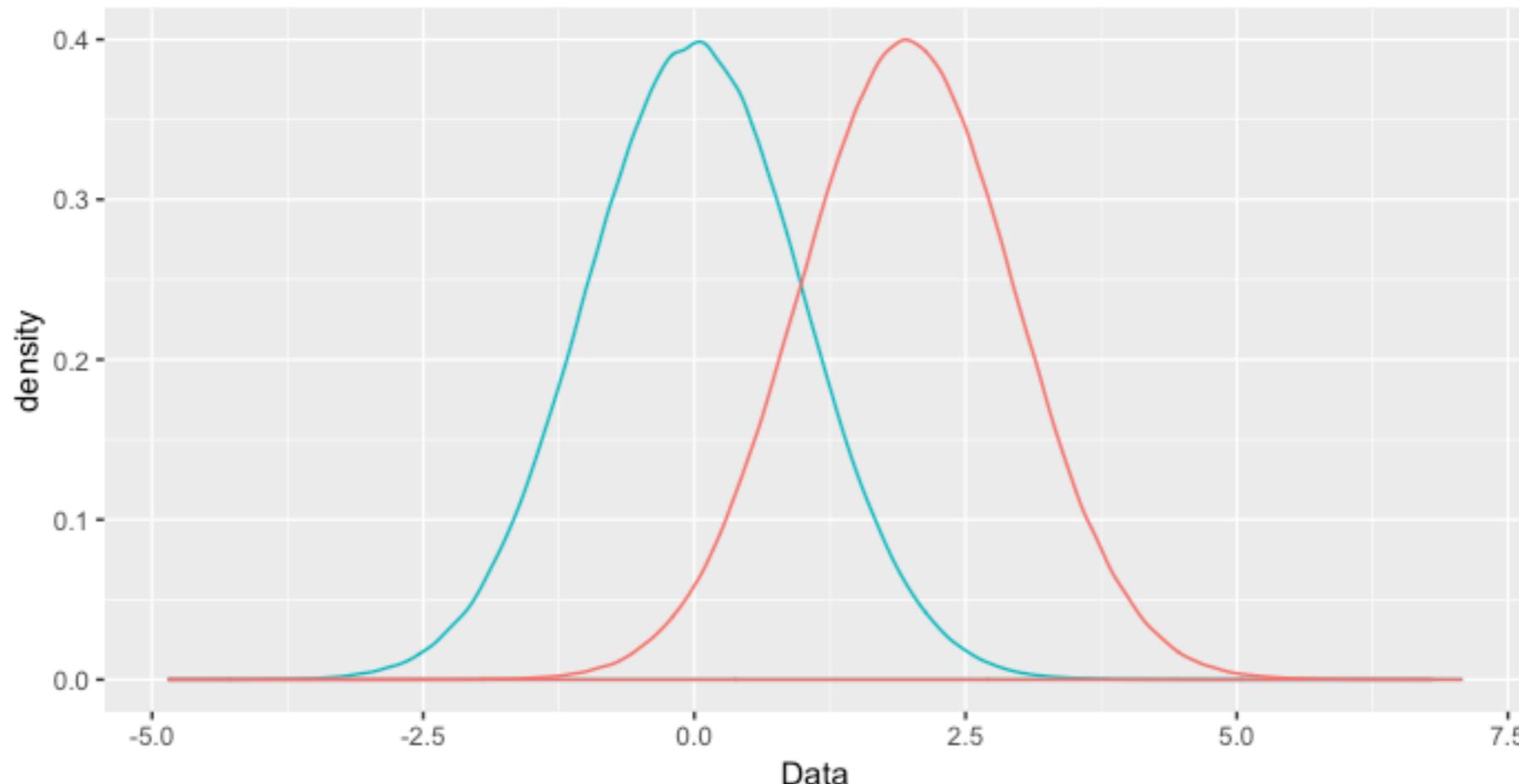
```
> hist(scale(dist1), breaks = 100)
```



- Simulating data sampled from 2 distributions and plotting them on the same graph:

```
> set.seed(1234)
> cond1 <- rnorm(1000000, 0, 1)
> cond2 <- rnorm(1000000, 1.96, 1)
> my_data <- as.tibble(cbind(cond1, cond2))

> ggplot(my_data) +
  geom_density(aes(x = cond1, y = ..density.., colour = "red")) +
  geom_density(aes(x = cond2, y = ..density.., colour = "green")) +
  xlab("Data") +
  guides(colour = FALSE)
```



Some useful functions

- Previously we have used a function `c()` which combines elements into one vector.
- On the previous slide you might have spotted the function `cbind()` which combines vectors by column.

```
> a <- c(1, 2, 3)
> b <- c(4, 5, 6)
> cbind(a,b)
      a  b
[1, ] 1  4
[2, ] 2  5
[3, ] 3  6
```

Some useful functions

- Related to `cbind()` there is `rbind()` which combines vectors by row:

```
> a <- c(1, 2, 3)
> b <- c(4, 5, 6)
> rbind(a, b)
 [,1] [,2] [,3]
a     1     2     3
b     4     5     6
```

Some useful functions

- There are a few other functions we'll use when we simulate data - there include `seq()` and `rep()`
- `seq()` will generate a sequence from one number to another - you can also specify the number to increment the sequence by. You can map this onto a new variable...

```
> seq(from = 1, to = 10, by = 1)
```

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

```
> seq(from = 1, to = 10, by = 2)
```

```
[1] 1 3 5 7 9
```

- `rep()` stands for replicate and allows you to replicate elements in a vector a certain number of times:

```
> rep(1:5, times = 2)
```

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

- You can also embed one function within another:

```
> rep(seq(from = 1, to = 10, by = 2), times = 2)
```

```
[1] 1 3 5 7 9 1 3 5 7 9
```

- the vector you're replicating doesn't have to just be numbers:

```
> rep("fast", times = 12)
```

- and you can use the combine function `c()` within the `rep()` function:

```
> c(rep("fast", times = 12), rep("slow", times = 12))
```

- We can start using what we know so far to simulate a data set. Let's simulate data from an independent samples experiment with one factor with two levels.
- Each of the 24 participants will have a measure - participants 1-12 are in the 'fast' condition and 13-24 in the 'slow' condition.
- First let's create a vector for our participant ID number. It will range from 1 to 24

```
> participant <- seq(1:24)
```

```
> participant
```

```
[1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14  
15 16 17 18 19 20 21 22 23 24
```

- Now we need to create the conditions - Condition 1 we will label 'fast' and Condition 2 we will label 'slow'.
- We use the `c()` function to combine the arguments that follow it (i.e., "fast" and "slow") into a vector.

```
> condition <- c(rep("fast", times = 12), rep("slow",  
times = 12))  
  
> condition  
  
[1] "fast" "fast" "fast" "fast" "fast" "fast" "fast"  
"fast" "fast" "fast" "fast" "fast"  
  
[13] "slow" "slow" "slow" "slow" "slow" "slow" "slow"  
"slow" "slow" "slow" "slow" "slow"
```

- Now we need to simulate our data - we will sample from the normal distribution so will use the `rnorm()` function.
- We want to simulate the data for our "fast" condition as coming from a distribution with a `mean = 1000` and `sd = 50`, and the data for our "slow" condition from a distribution with a `mean = 1020` and `sd = 50`.
- We need to make sure we set up the order of our `rnorm()` function in the same way as we did for specifying the condition variable (i.e., sampling 12 times for the 'fast' condition and then 12 for the 'slow').

- To make sure we can reproduce these random samples in future, we can use the function `set.seed()` to specify the start of the random number generation.

```
> set.seed(1234)
> dv <- c(rnorm(12, 1000, 50), rnorm(12, 1020, 50))
> dv
[1] 939.6467 1013.8715 1054.2221 882.7151 1021.4562
1025.3028 971.2630 972.6684 971.7774
[10] 955.4981 976.1404 950.0807 981.1873 1023.2229
1067.9747 1014.4857 994.4495 974.4402
[19] 978.1414 1140.7918 1026.7044 995.4657 997.9726
1042.9795
```

- We now need to combine our 3 columns (participant, condition, dv) into a tibble. We use the `cbind()` function to first bind the three variables together as columns, and then `as.tibble()` to convert these three combined columns to a tibble I'm calling `data`.
- A tibble is really just a supercharged dataframe.

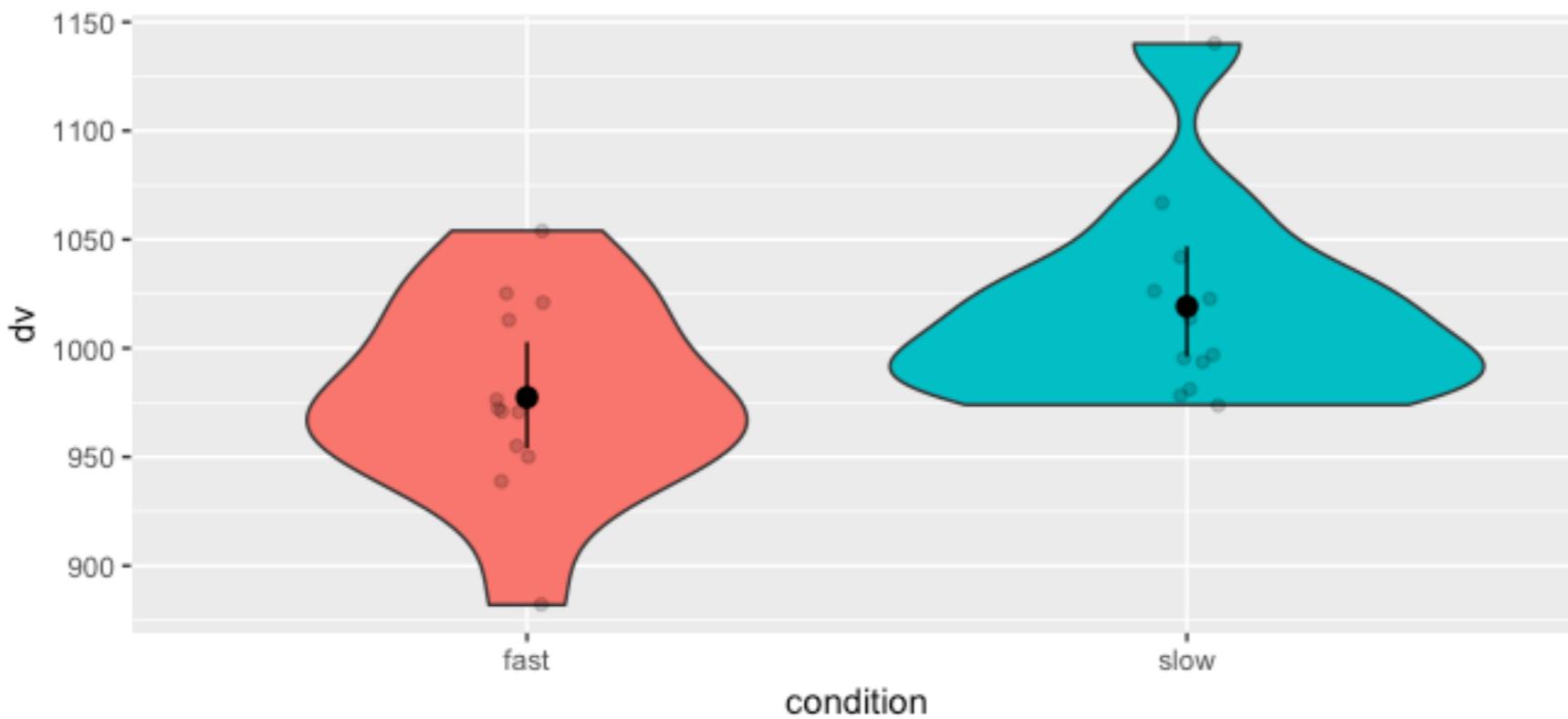
```
> my_data <- as.tibble(cbind(participant, condition, dv))
> my_data
# A tibble: 24 x 3
  participant condition    dv
  <chr>        <chr>     <chr>
1 1             fast      939.646712530729
2 2             fast      1013.87146210553
3 3             fast      1054.22205883415
4 4             fast      882.715114868533
5 5             fast      1021.45623444055
6 6             fast      1025.30279460788
7 7             fast      971.263001993268
8 8             fast      972.668407210791
9 9             fast      971.777400045336
10 10            fast      955.498108547795
# ... with 14 more rows
```

- As our three columns are all listed as character type, we need to change condition to a factor and dv to an integer.

```
> my_data$condition <- as.factor(my_data$condition)
> my_data$dv <- as.integer(my_data$dv)
> my_data
# A tibble: 24 x 3
  participant condition     dv
  <chr>        <fct>    <int>
1 1            fast      939
2 2            fast      1013
3 3            fast      1054
4 4            fast      882
5 5            fast      1021
6 6            fast      1025
7 7            fast      971
8 8            fast      972
9 9            fast      971
10 10          fast      955
# ... with 14 more rows
```

- So the tibble structure looks like what we expect, but do the data look like what we expect?
- Remember, we sampled the ‘fast’ group from a distribution with a mean of 1000, and the ‘slow’ group from a distribution with a mean of 1020 - both with a standard deviation of 50.

```
ggplot(my_data, aes(x = condition, y = dv, fill = condition)) +  
  geom_violin() +  
  stat_summary(fun.data = "mean_cl_boot", colour = "black") +  
  geom_jitter(alpha = .2, width = .05) +  
  guides(fill = FALSE)
```



```
my_data %>%
  group_by(condition) %>%
  summarise(Mean = mean(dv), SD = sd(dv))
```

```
# A tibble: 2 x 3
  condition      Mean       SD
  <fct>        <dbl>     <dbl>
1 fast          977.      46.0
2 slow         1019.      47.1
```

- Looks pretty much like what we'd expect to me given a bit sampling error...

- We can now perform an independent samples t-test to see if the conditions differ:

```
> t.test(filter(my_data, condition == "fast")$dv, filter(my_data, condition == "slow")$dv, paired = FALSE)
```

Welch Two Sample t-test

```
data: filter(my_data, condition == "fast")$dv and filter(my_data, condition == "slow")$dv
t = -2.202, df = 21.987, p-value = 0.03845
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-81.233786 -2.432881
sample estimates:
mean of x mean of y
 977.4167 1019.2500
```

- The important stuff is a bit buried in the text - wouldn't it be great if we could somehow extract it and save it?
- Note the default t-test in R is Welch's t-test (rather than Student's) - do you know why?

- We can save the result of this t-test using the `broom::tidy()` function. This converts the output of the t-test into a tidy tibble.

```
> result <- tidy(t.test(filter(my_data, condition == "fast")$dv, filter(my_data, condition == "slow")$dv, paired = FALSE))
> result
# A tibble: 1 x 10
  estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high method
    <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <dbl> <chr>
1    -41.8      977.    1019.     -2.20    0.0385     22.0    -81.2    -2.43 Welch...
# ... with 1 more variable: alternative <chr>
```

- We can reference columns in this tibble - for example, just to get the p-value we can type:

```
> result$p.value
[1] 0.03845285
```

- Wouldn't it be amazing if we could run t-tests on 100 simulations and save the result of each in a tibble that ends up containing the p-values for all the results?
- We can, but first we need to learn about loops...

Loops



- Loops involve repeating a command or a set of commands surrounded by { } a certain number of times - popular with kids in the 1980s...unpopular with many computer scientists because they can be inefficient...but liked by me because they are relatively easy to understand!
 - Printing something i times:

```
> for (i in 1:10){  
>   print("Hello world")  
> }
```

- Our variable `i` increments one by one from the start of the sequence `1:10` to the end.
- We can also use `i` in our code embedded within the loop:

```
> for (i in 1:10) {  
>   print(i)  
> }  
[1] 1  
[1] 2  
[1] 3  
[1] 4  
[1] 5  
[1] 6  
[1] 7  
[1] 8  
[1] 9  
[1] 10
```

- We can also add `i` as part of a string:

```
> for (i in 1:10) {  
>   print(paste("This is the number", i, sep = " "))  
> }  
[1] "This is the number 1"  
[1] "This is the number 2"  
[1] "This is the number 3"  
[1] "This is the number 4"  
[1] "This is the number 5"  
[1] "This is the number 6"  
[1] "This is the number 7"  
[1] "This is the number 8"  
[1] "This is the number 9"  
[1] "This is the number 10"
```

- We can use `i` to index a column in a tibble - here is the tibble `my_data`:

```
> my_data
# A tibble: 24 x 3
  participant condition     dv
  <chr>        <fct>    <int>
1 1            fast      939
2 2            fast      1013
3 3            fast      1054
4 4            fast      882
5 5            fast      1021
6 6            fast      1025
7 7            fast      971
8 8            fast      972
9 9            fast      971
10 10          fast      955
# ... with 14 more rows
```

- And here we use `i` to index the column `dv` in the tibble called `my_data`:

```
> for (i in 1:10) {  
>   print(my_data$dv[i])  
> }  
[1] 939  
[1] 1013  
[1] 1054  
[1] 882  
[1] 1021  
[1] 1025  
[1] 971  
[1] 972  
[1] 971  
[1] 955
```

- We can put together all we know so far to simulate data from 10 experiments:

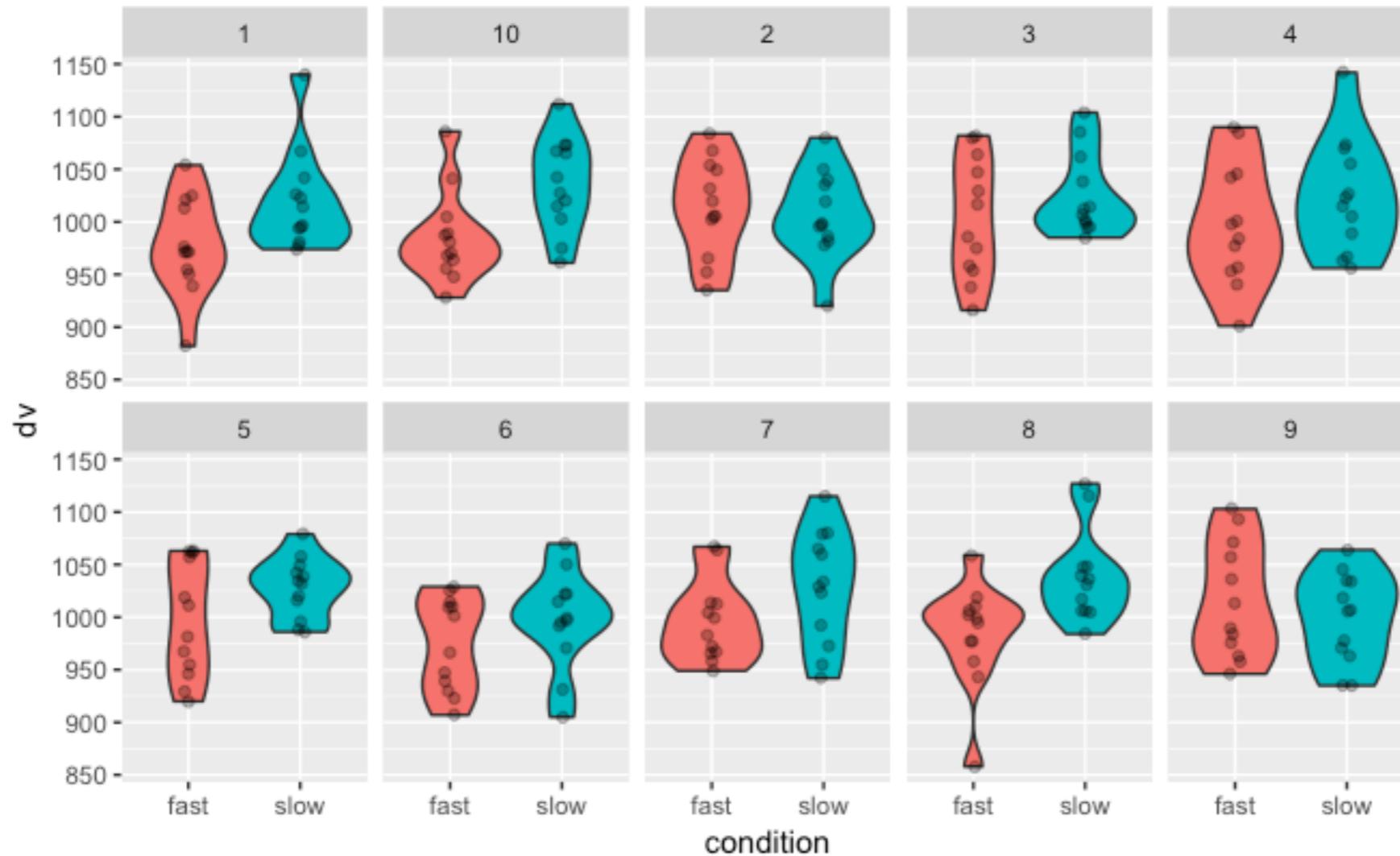
```
total_samples <- 10
sample_size <- 24
participant <- rep(1:sample_size)
condition <- c(rep("fast", times = sample_size/2), rep("slow", times = sample_size/2))
all_data <- NULL

for (i in 1:total_samples) {
  sample <- i
  set.seed(1233 + i)
  dv <- c(rnorm(sample_size/2, 1000, 50), rnorm(sample_size/2, 1020, 50))
  my_data <- as.tibble(cbind(participant, condition, dv, sample))
  all_data <- rbind(my_data, all_data)
}

all_data$condition <- as.factor(all_data$condition)

all_data$dv <- as.integer(all_data$dv)
```

```
ggplot(all_data, aes(x = condition, y = dv, fill = condition)) +
  geom_violin() + geom_jitter(alpha = .3, width = .05) +
  guides(fill = FALSE) + facet_wrap(~sample, ncol = 5, nrow = 2)
```



```
> str(all_data)
Classes 'tbl_df', 'tbl' and 'data.frame': 240 obs. of 4 variables:
$ participant: chr "1" "2" "3" "4" ...
$ condition   : Factor w/ 2 levels "fast","slow": 1 1 1 1 1 1 1 1 1 ...
$ dv          : int 981 948 964 1041 989 970 956 968 1086 928 ...
$ sample      : chr "10" "10" "10" "10" ...
```

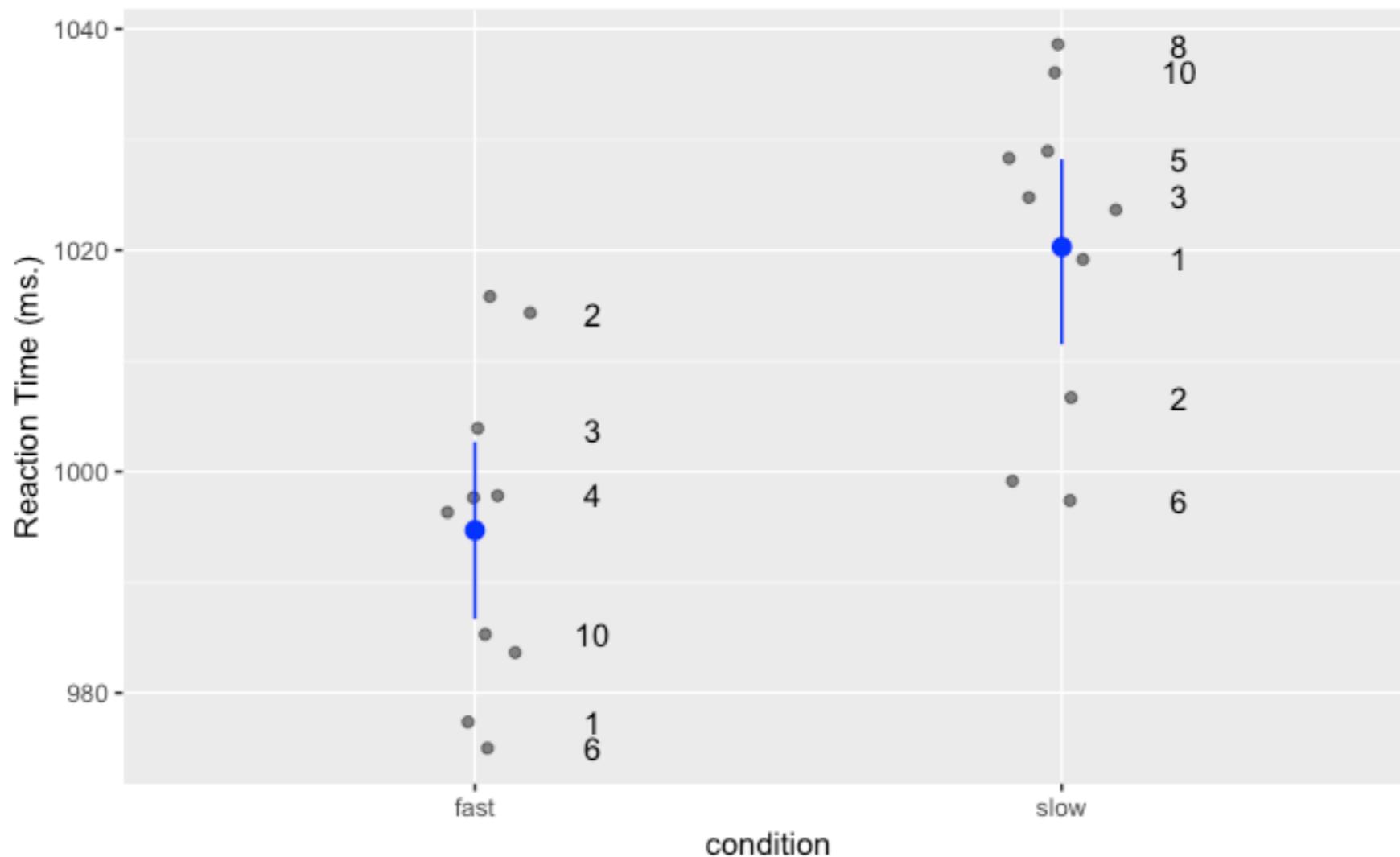
```
> all_data %>% group_by(condition, sample) %>% summarise(mean(dv), sd(dv))

# A tibble: 20 x 4
# Groups:   condition [?]
  condition sample `mean(dv)` `sd(dv)`
  <fct>     <chr>      <dbl>     <dbl>
1 fast       1           977.      46.0
2 fast       10          985.      42.8
3 fast       2           1014.     46.5
4 fast       3           1004.     57.2
5 fast       4           998.      58.2
6 fast       5           998.      54.9
7 fast       6           975       44.2
8 fast       7           996.      38.7
9 fast       8           984.      49.6
10 fast      9           1016.     54.8
11 slow      1           1019.     47.1
12 slow      10          1036.     44.3
13 slow      2           1007.     41.5
14 slow      3           1025.     38.8
15 slow      4           1024.     54.5
16 slow      5           1028.     28.5
17 slow      6           997.      46.0
18 slow      7           1029.     54.2
19 slow      8           1038.     43.3
20 slow      9           999.      42.7
```

```

all_data %>%
  group_by(condition, sample) %>%
  summarise(average = mean(dv), sd(dv)) %>%
  ggplot(aes(x = condition, y = average, group = condition,
  label = sample)) +
  geom_jitter(width = .1, alpha = .5) +
  stat_summary(fun.data = "mean_cl_boot", colour = "blue") +
  geom_text(check_overlap = TRUE, nudge_x = .2, nudge_y = 0, colour =
  "black")

```

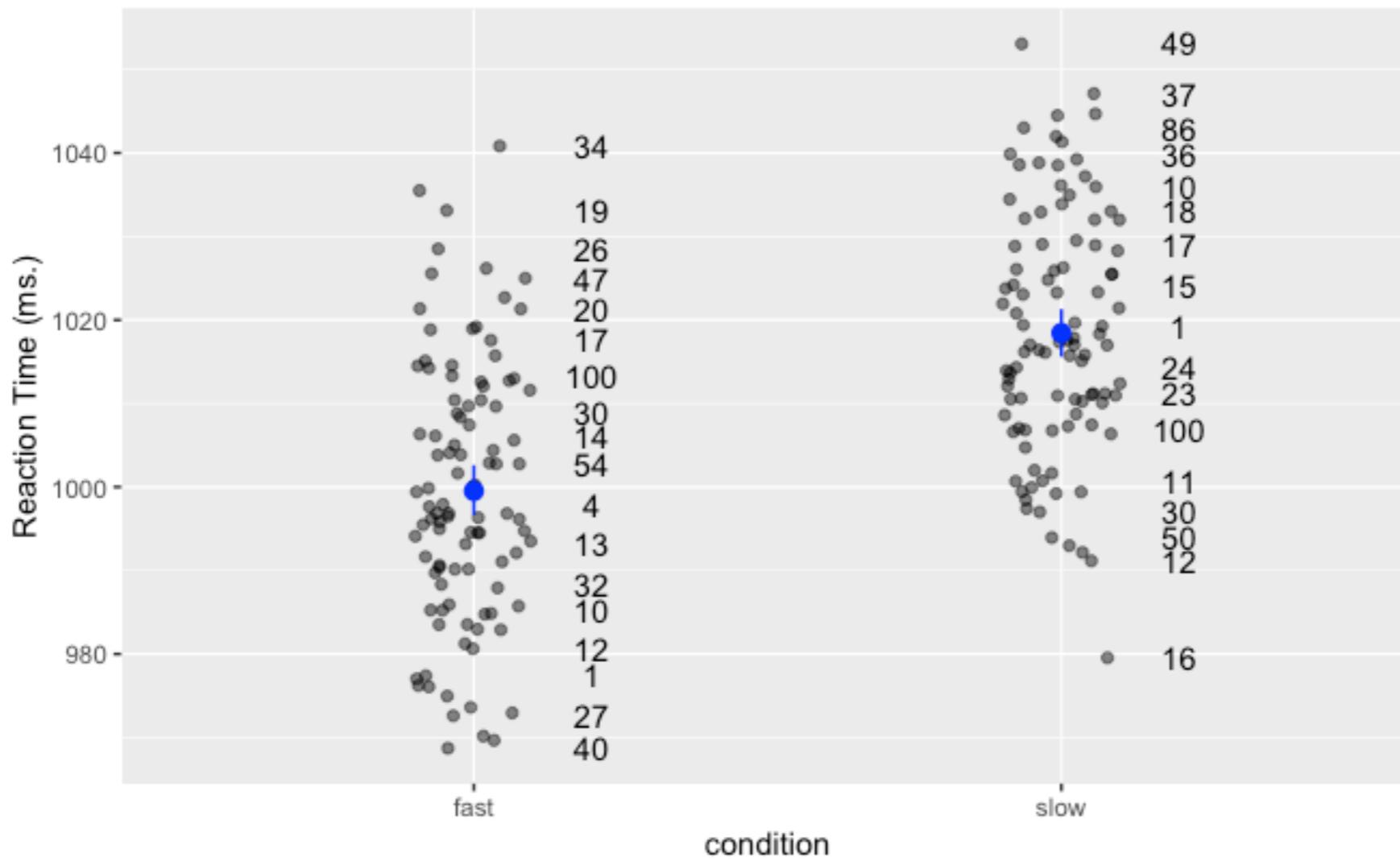




The mean for our ‘fast’ condition is a bit away but quite close to the population mean (1000), while the mean for our ‘slow’ condition is very close to the population mean (1020). Sample 2 has an extreme mean for the ‘slow’ condition which is having an adverse effect on the overall mean for this condition - indeed, numerically the ‘slow’ condition is faster than the ‘fast’ condition in Sample 2. This is sampling error in practice and further highlights the problem with small sample sizes...

Comparing conditions

- Now imagine a case where we're simulating data from 100 experiments - each with one repeated measures factor with two levels - 'Fast' vs. 'Slow'
- After we have created our 100 simulations, we can carry out 100 t-tests to determine how many of the simulations produce a significant difference between our two conditions.



Overall the “Slow” condition RTs are higher than the “Fast” Condition RTs - but we can spot some simulations where the difference is negligible or even goes the wrong way (e.g., Simulation 100). The blue circles corresponds to the overall means and are pretty much bang on 1000 and 1020.

- We can use another loop to run `i` number of independent sample t-tests and to save the results of each test to a new data frame we are calling `result`

```

result <- NULL

for (i in 1:total_samples) {
  result <- rbind(tidy(t.test(filter(all_data, condition == "fast" & sample == i)$dv,
                            filter(all_data, condition == "slow" & sample == i)$dv,
                            paired = FALSE)), result)
}

> result
# A tibble: 100 x 10
   estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high method
   <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <dbl>     <chr> 
1      6.5    1013.    1007.     0.364     0.720    20.2    -30.7    43.7  Welch Two Sample t-test two.sided
2     -15     1000.    1015.    -0.695     0.494    22.0    -59.7    29.7  Welch Two Sample t-test two.sided
3      7.92   1019.    1011.     0.445     0.661    21.0    -29.1    44.9  Welch Two Sample t-test two.sided
4     -16.4    984.    1000.    -0.697     0.493    22.0    -65.3    32.5  Welch Two Sample t-test two.sided
5     -10.8   1002.    1012.    -0.517     0.612    16.9    -54.7    33.2  Welch Two Sample t-test two.sided
6      7.25   1000.     993     0.359     0.723    20.4    -34.8    49.3  Welch Two Sample t-test two.sided
7     -35      994.    1030.    -1.66     0.113    20.6    -79.0     8.99 Welch Two Sample t-test two.sided
8     -27.5    983     1010.    -1.40     0.175    21.8    -68.2    13.2  Welch Two Sample t-test two.sided
9      4.83   1026.    1021.     0.246     0.808    18.3    -36.3    46.0  Welch Two Sample t-test two.sided
10    -35.8    996.    1032     -1.58     0.130    18.9    -83.2    11.5  Welch Two Sample t-test two.sided
# ... with 90 more rows

```

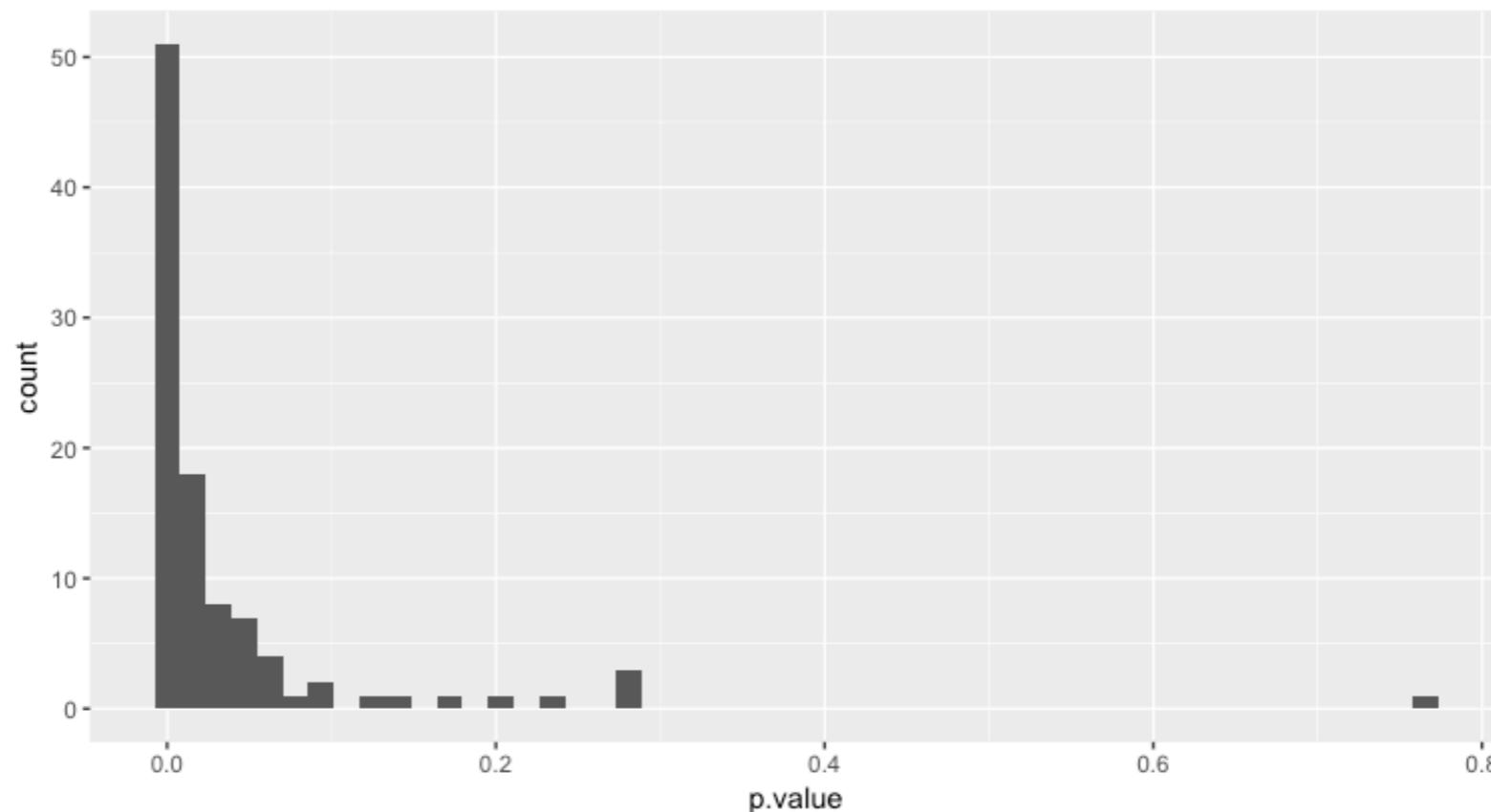
- We can work out for how many of the 100 tests we have found a significant difference at $< .05$ - and remember, there is actually a real difference (of 20 ms.) in the two population distributions we sampled from!

```
> count(filter(result, p.value < .05))  
# A tibble: 1 × 1  
      n  
  <int>  
1     17
```

- So, less than a fifth of the time are we finding a significant difference even though one exists in the distributions we sampled from. So with a sample size of 24 (12 per group) power to detect the effect we are looking for is .17

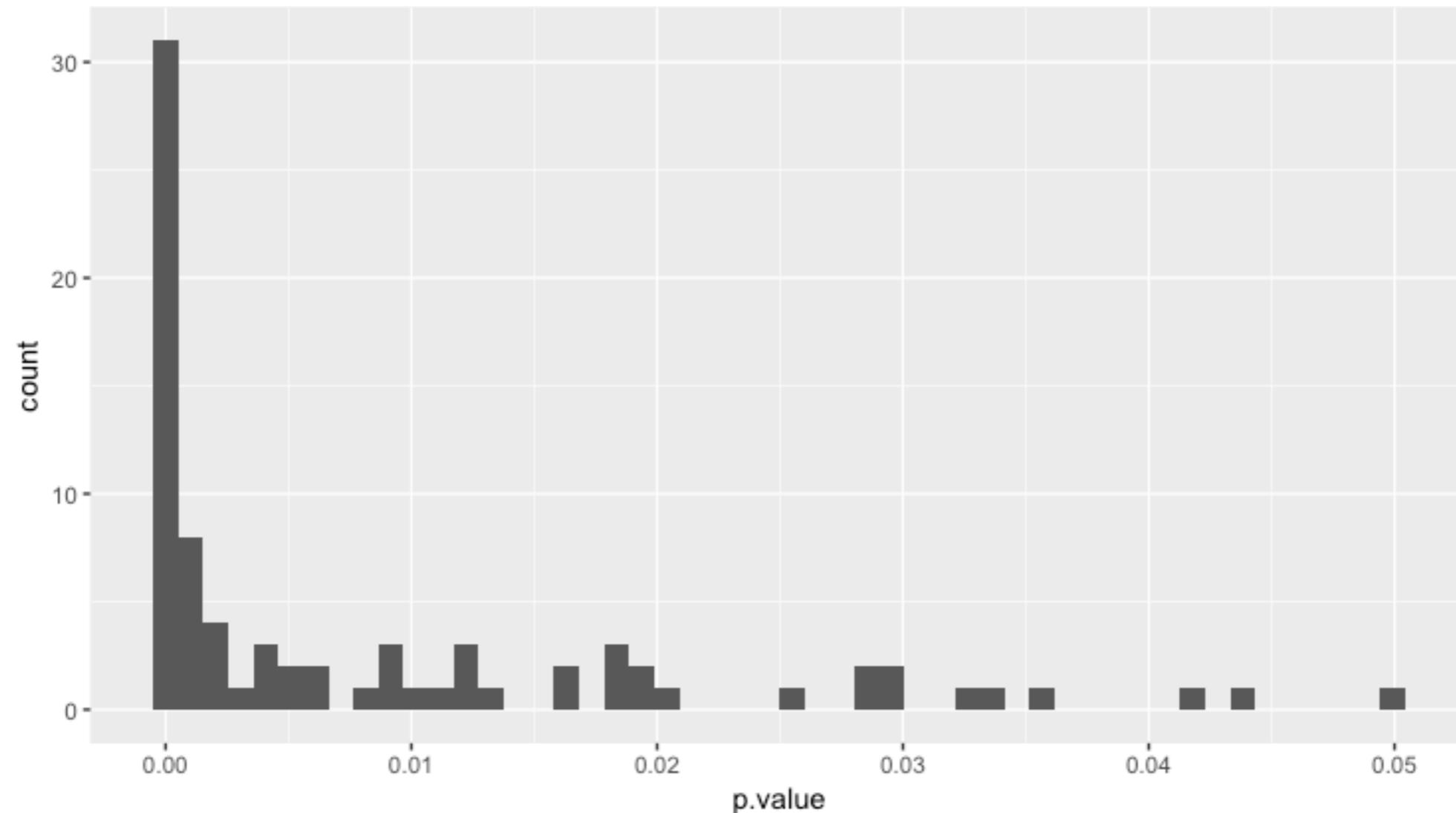
- So let's work out Cohen's d as a measure of our effect size - we can do this precisely because we know what the real effect size is comparing the two populations.
- The “classic” Cohen's d calculation is the mean of one sample minus the mean of the other divided by the pooled standard deviation.
- In our case, it's $(1020 - 1000) / 50$ which gives a Cohen's d of 0.4 (which is a small to medium effect size) - standard in many areas of psychology.

- We actually need 200(!) participants to give us 80% power for a Cohen's $d = .4$
- Let's run the 100 simulations again but this time we'll set sample size to 200 - here's the histogram of the p-values - 80 of the t-tests are now significant at $< .05$:



```
> count(filter(result, p.value < .05))
# A tibble: 1 x 1
  n
  <int>
1 80
```

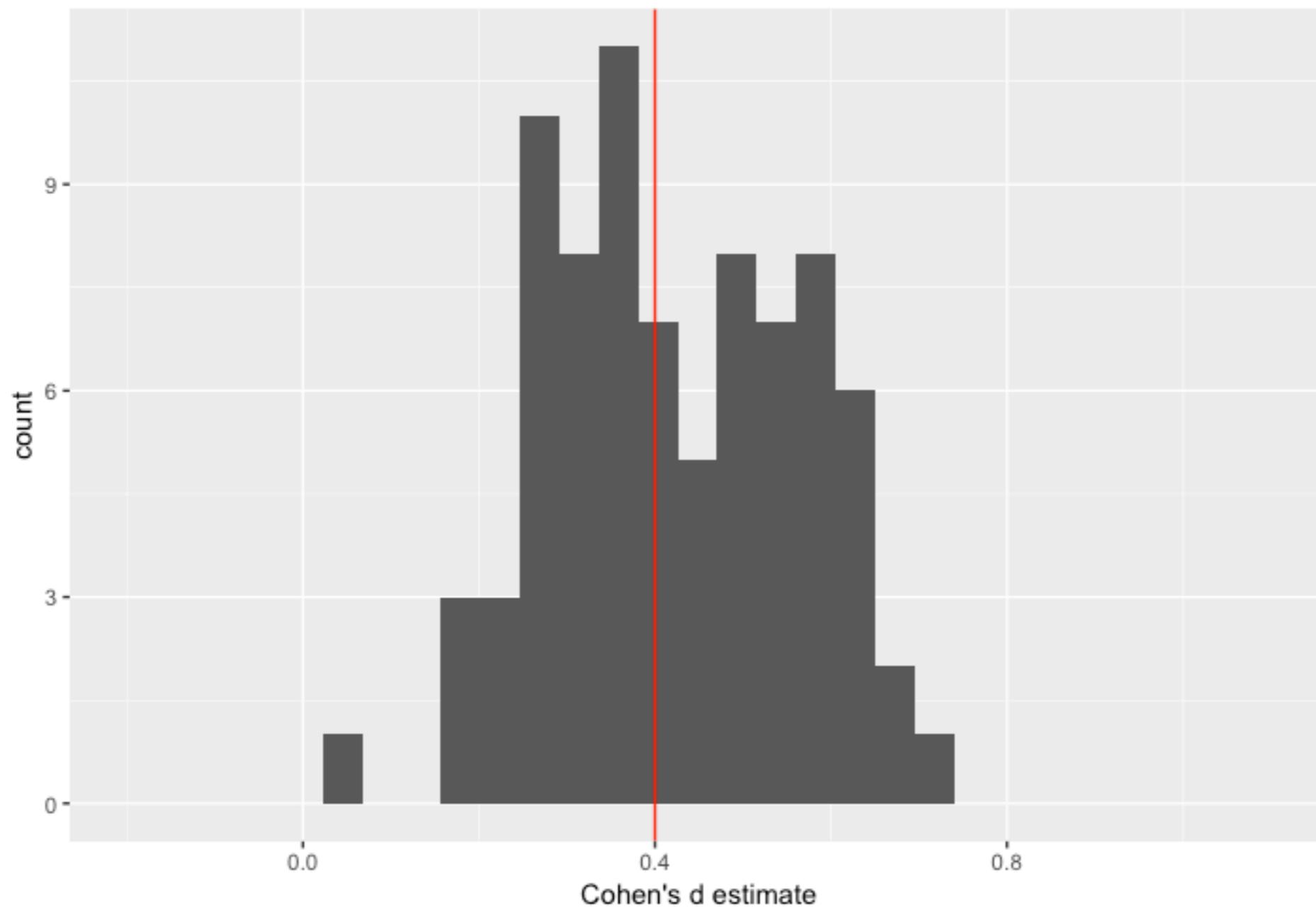
- If we zoom in and look at p-values $< .05$ we'll see lots of tiny ones - this is what we would expect to see in the literature but instead analysis has shown more p-values at the threshold of significance (i.e, just below $.05$) than we would expect - suggests possible p-hacking and other QRPs.
- Nathan C. Leggett, Nicole A. Thomas, Tobias Loetscher & Michael E. R. Nicholls (2013). The life of p: “Just significant” results are on the rise. *The Quarterly Journal of Experimental Psychology*, 66, 2303-2309. <http://dx.doi.org/10.1080/17470218.2013.863371>



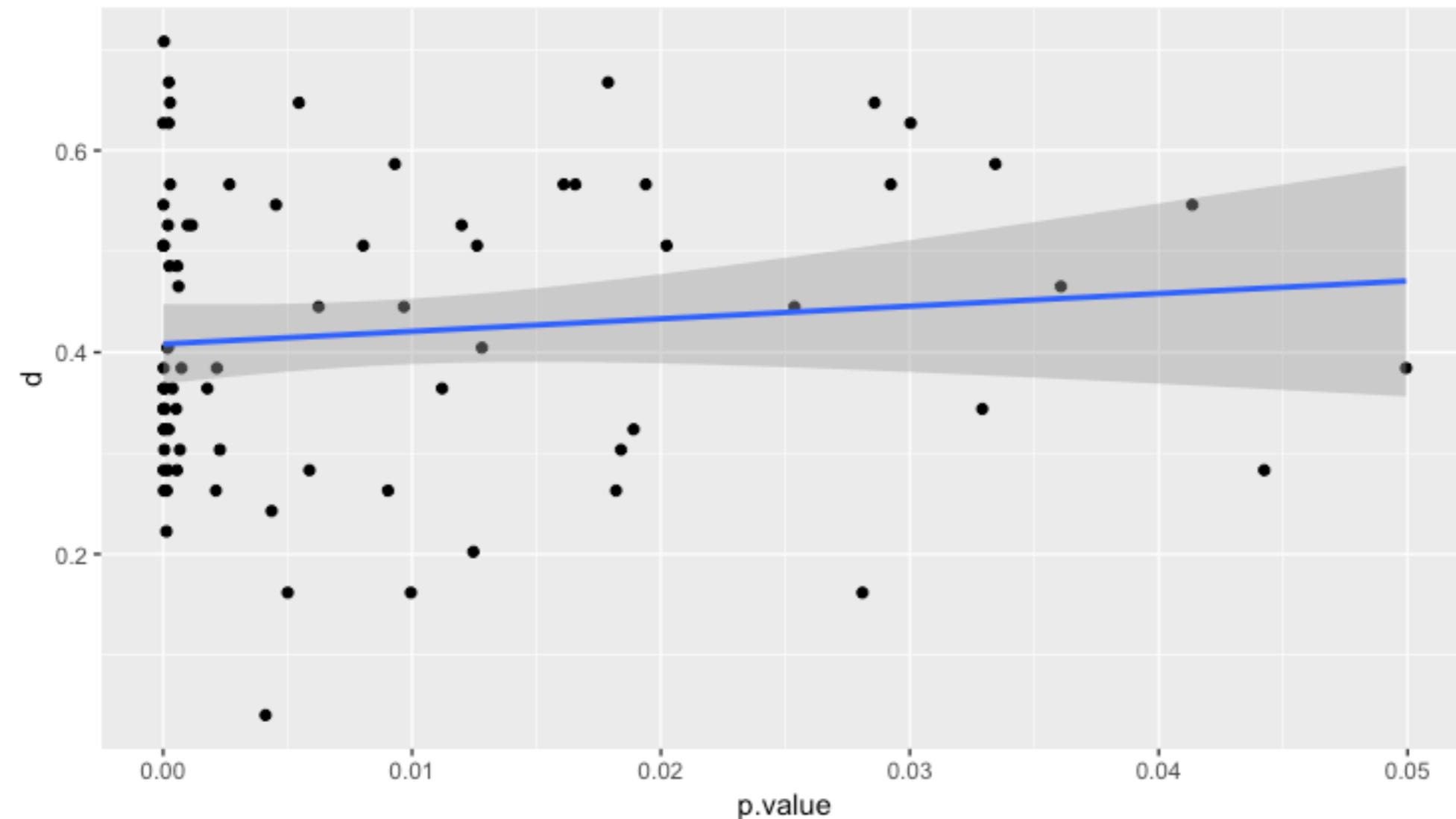
- Another problem with small sample studies is not just that they fail to find an effect, but they also provide quite wide estimates of the effect size - here is the histogram of Cohen's d values for the 17 significant results when we have a sample size = 24 with the red vertical line being the true effect size in the population.



- When we increase the sample size to 200 (for .8 power) we get a much more accurate (and less variable) view of the effect size - but each effect size estimate is still just one point drawn from a distribution of effect sizes.



- It's worth noting, there's no clear relationship between the p-value of a t-test and Cohen's d (i.e., smaller p-values don't mean bigger effect size estimates). Pearson's r in this case = 0.11



The Advantage of Simulation

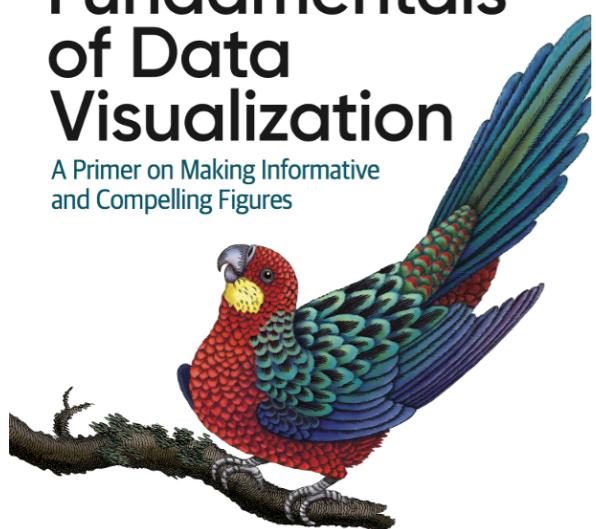
- You can specify the kind of effect size you're interested in looking for - think about what magnitude might be of theoretical importance - and then model different sample sizes to determine (roughly) how many observations you might need to have a reasonable chance of detecting the effect (assuming it is there).
- Data simulation can be used to motivate pre-registered analysis plans (e.g., on OSF).

Advanced Data Viz

O'REILLY®

Fundamentals of Data Visualization

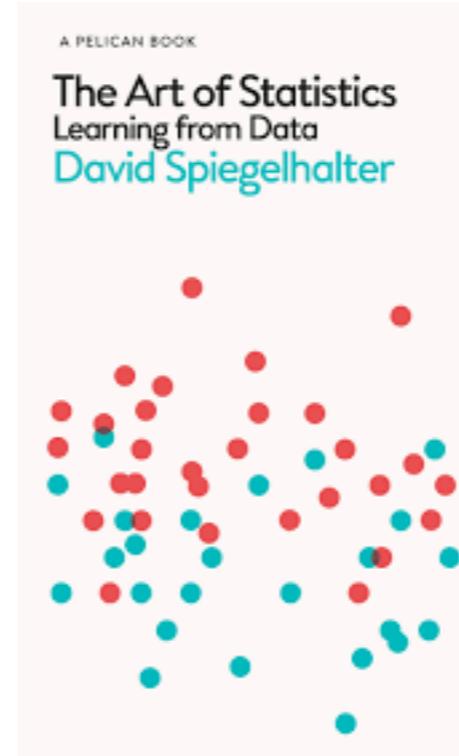
A Primer on Making Informative
and Compelling Figures



Claus O. Wilke



EDWARD R. TUFTÉ



A PELICAN BOOK

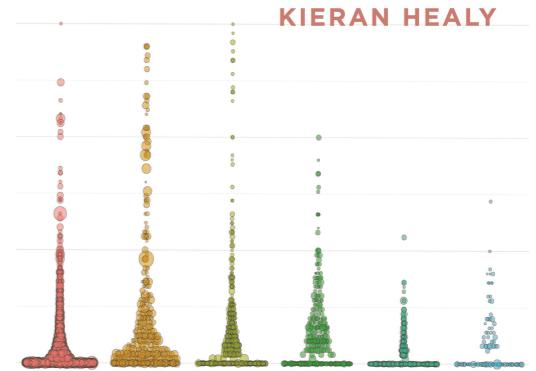
The Art of Statistics Learning from Data

David Spiegelhalter

DATA VISUALIZATION

A PRACTICAL INTRODUCTION

KIERAN HEALY



Make it reproducible...

↪ Claus Wilke Retweeted

 **Kara Woo** @kara_woo · Jun 1

Good case for reproducibility from [@ClausWilke](#): he had to **redo** all 305 figures in his book in 5 days before the *corrected proofs* were due. If they hadn't been created in a reproducible way it would have been impossible. [#SDSS2019](#)

3 21 118

"(visualizations) should be autogenerated as part of the data analysis pipeline (which should also be automated), and they should come out of the pipeline ready to be sent to the printer..."

...the moment you manually edit a figure, your final figure becomes irreproducible. A third party cannot generate the exact same figure you did."

ggforce

- The aim of `ggplot2` is to aid in visual data investigations. This focus has led to a lack of facilities for composing specialised plots.
- `ggforce` aims to be a collection of mainly new stats and geoms that fills this gap.

<https://cran.r-project.org/web/packages/ggforce/index.html>

Spatial plotting

Using the package `nycflights13`.

```
> library(nycflights13)
> head(airports)
# A tibble: 6 x 8
  faa    name                      lat   lon   alt   tz dst tzone
  <chr> <chr>                  <dbl> <dbl> <int> <dbl> <chr> <chr>
1 04G  Lansdowne Airport          41.1 -80.6 1044  -5  A America/New_York
2 06A  Moton Field Municipal Airport 32.5 -85.7  264  -6  A America/Chicago
3 06C  Schaumburg Regional        42.0 -88.1  801  -6  A America/Chicago
4 06N  Randall Airport            41.4 -74.4  523  -5  A America/New_York
5 09J  Jekyll Island Airport      31.1 -81.4   11  -5  A America/New_York
6 0A9  Elizabethton Municipal Airport 36.4 -82.2 1593  -5  A America/New_York
>
```

Simply plotting the latitude and longitude values for each row...

```
my_plot <- airports %>%
  filter(lon < 0, lat > 23, tzone != "\\"N") %>%
  ggplot(aes(x = lon, y = lat, color = tzone)) +
  geom_point(show.legend = FALSE)
```



Using geom_mark_rect()

```
my_plot +  
  geom_mark_rect(aes(label = tzone, fill = tzone), show.legend = FALSE) +  
  labs(title = "Plot of continental US airports grouped by IANA time zone") +  
  theme_void()
```



Using geom_mark_hull()

```
my_plot +  
  geom_mark_hull(aes(label = tzone, fill = tzone), show.legend = FALSE) +  
  labs(title = "Plot of continental US airports grouped by IANA time zone") +  
  theme_void()
```

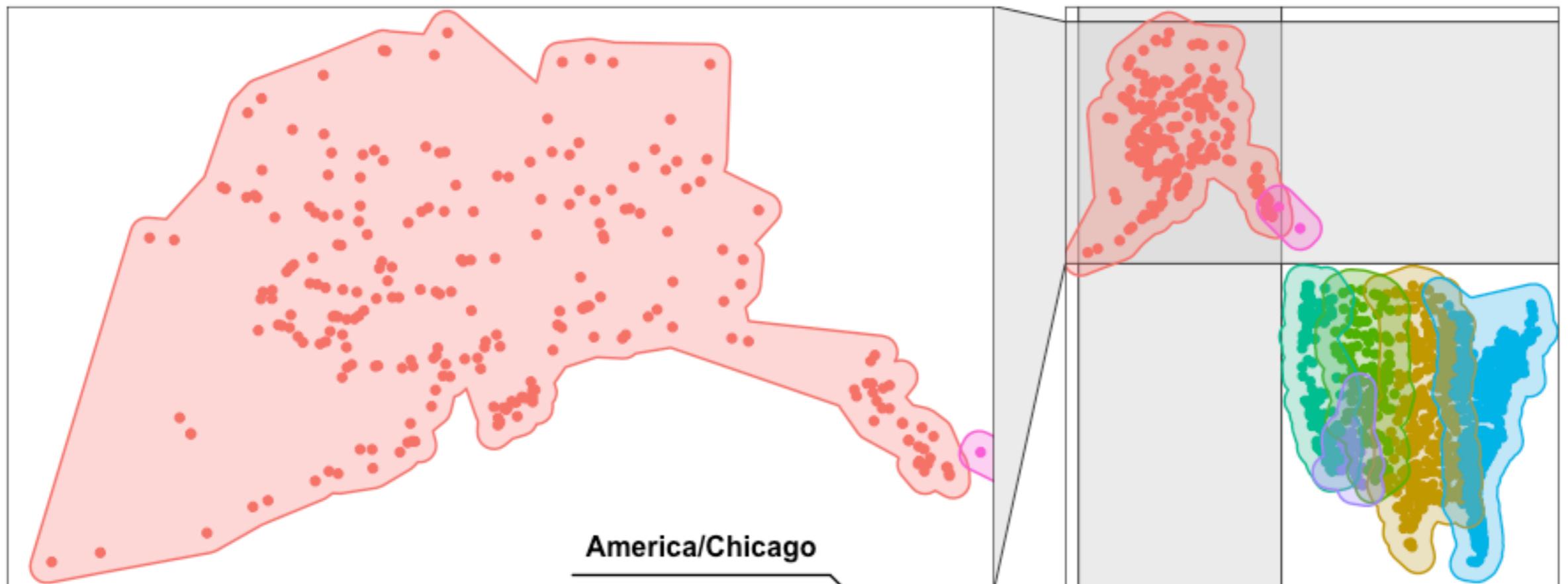
Plot of continental US airports grouped by IANA time zone



Using facet_zoom()

```
my_plot +  
  geom_mark_hull(aes(label = tzone, fill = tzone), show.legend = FALSE, expand =  
unit(3, "mm")) +  
  labs(title = "Plot of continental US airports grouped by IANA time zone") +  
  facet_zoom(xy = (tzone == "America/Anchorage")) +  
  theme_no_axes()
```

Plot of continental US airports grouped by IANA time zone



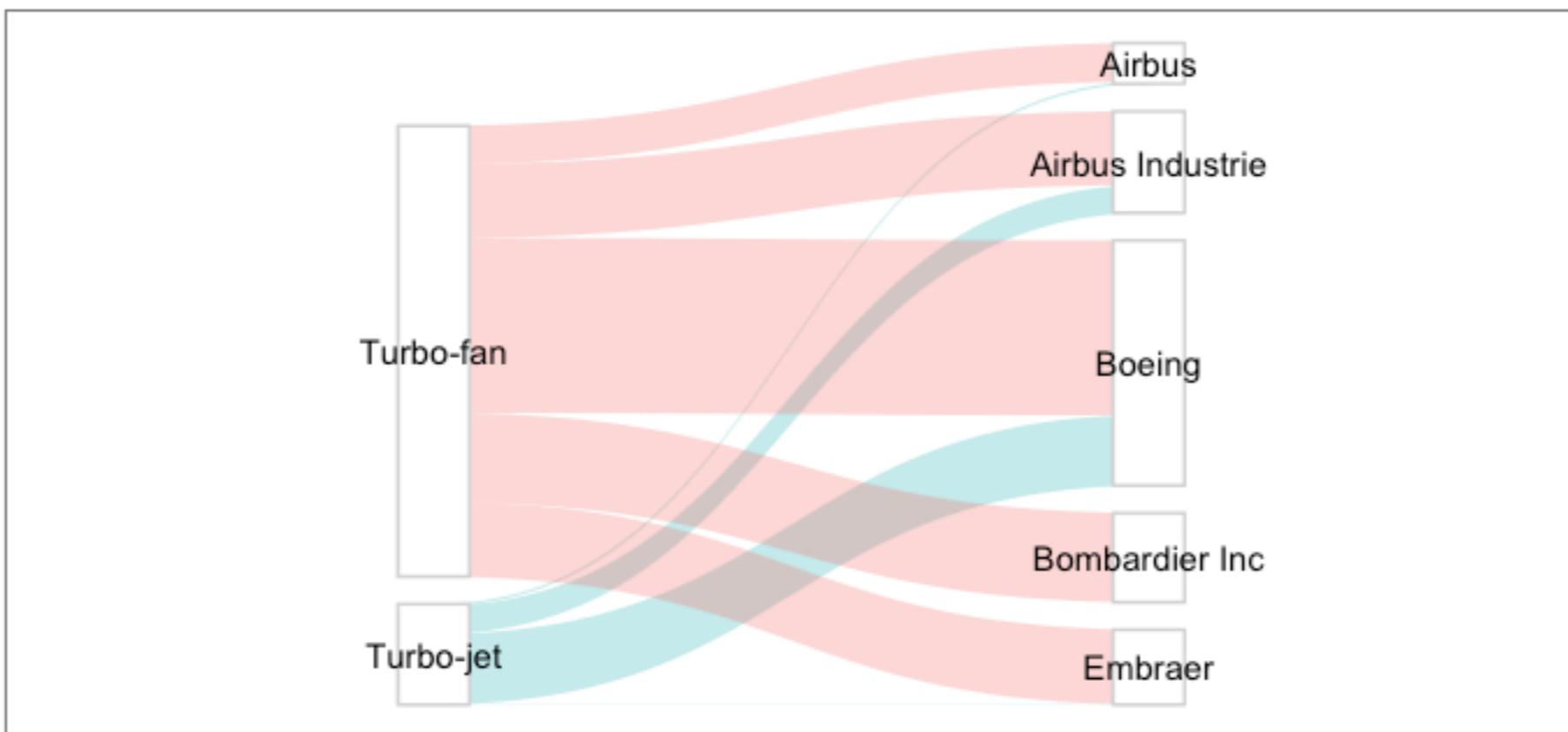
Alluvial Diagram

Alluvial diagrams can be used to visualise the relationship between categorical variables.

```
> prep_planes
# A tibble: 1,287 x 2
  manufacturer      engine
  <chr>              <chr>
  1 Embraer           Turbo-fan
  2 Airbus Industrie Turbo-fan
  3 Airbus Industrie Turbo-fan
  4 Embraer           Turbo-fan
  5 Airbus Industrie Turbo-fan
  6 Airbus Industrie Turbo-fan
  7 Airbus Industrie Turbo-fan
  8 Airbus Industrie Turbo-fan
  9 Airbus Industrie Turbo-fan
 10 Embraer           Turbo-fan
# ... with 1,277 more rows
```

Alluvial Diagram

```
prep_planes %>%
  gather_set_data(1:2) %>%
  ggplot(aes(x = x, id = id, split = y, value = 1)) +
  geom_parallel_sets(aes(fill = engine), show.legend = FALSE, alpha = 0.3) +
  geom_parallel_sets_axes(axis.width = 0.1, color = "lightgrey", fill =
"white") +
  geom_parallel_sets_labels(angle = 0) +
  theme_no_axes()
```

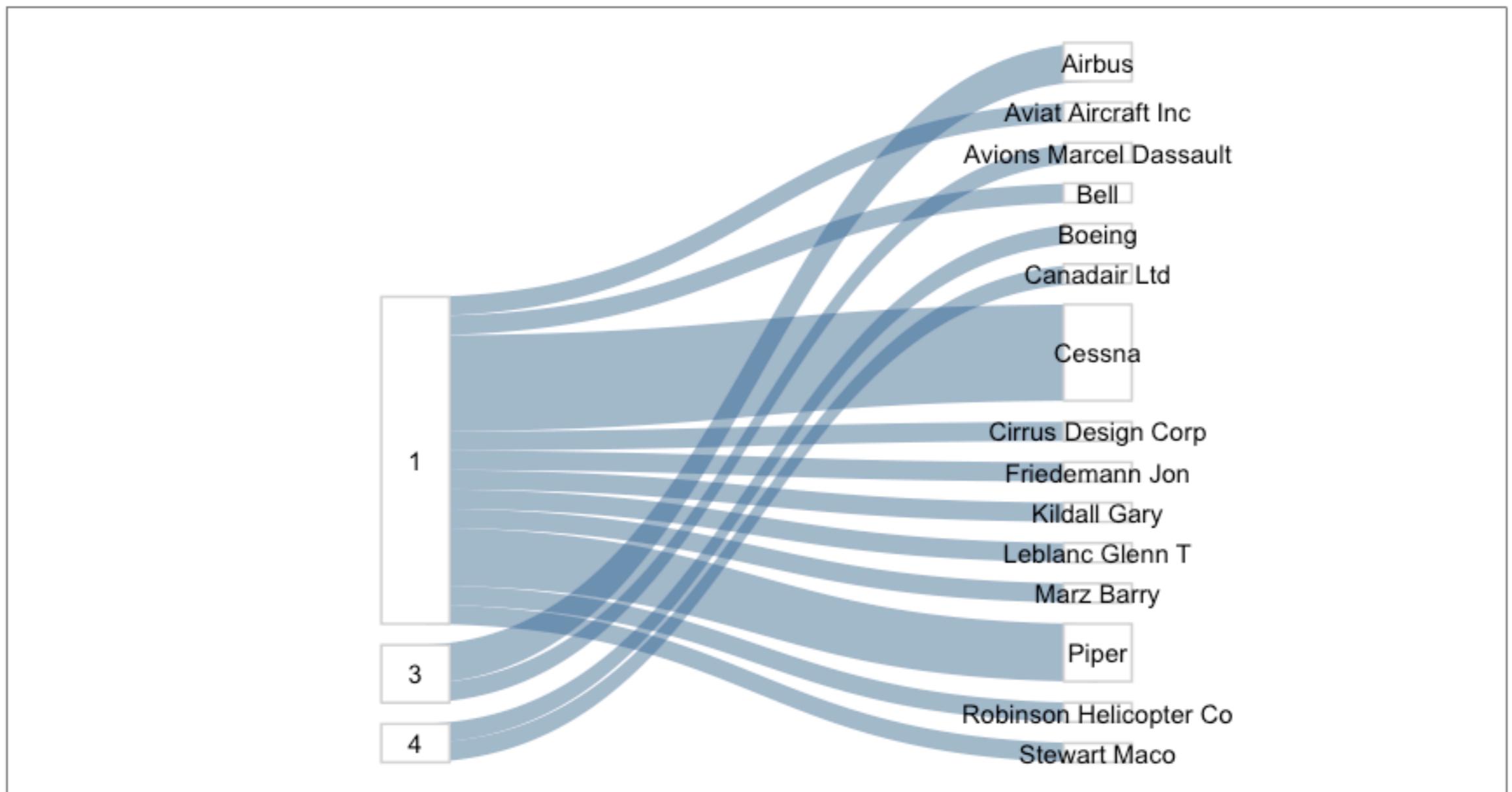


Grouping by Manufacturer and Number of Engines - Planes made after 1960 and excluding 2-engine aircraft

```
prep_planes <- planes %>%
  filter(year > 1960) %>%
  filter(engines != 2) %>%
  select(manufacturer, engines) %>%
  mutate(manufacturer = str_to_title(manufacturer))

> prep_planes %>%
+   group_by(manufacturer, engines) %>%
+   summarise(n())
# A tibble: 15 x 3
# Groups:   manufacturer [15]
  manufacturer       engines `n()`
  <chr>                <int> <int>
1 Airbus                  3      2
2 Aviat Aircraft Inc     1      1
3 Avions Marcel Dassault 3      1
4 Bell                     1      1
5 Boeing                   4      1
6 Canadair Ltd            4      1
7 Cessna                   1      5
8 Cirrus Design Corp      1      1
9 Friedemann Jon          1      1
10 Kildall Gary           1      1
11 Leblanc Glenn T        1      1
12 Marz Barry              1      1
13 Piper                    1      3
14 Robinson Helicopter Co 1      1
15 Stewart Maco            1      1
```

```
prep_planes %>%
  gather_set_data(1:2) %>%
  ggplot(aes(x = x, id = id, split = y, value = 1)) +
  geom_parallel_sets(aes(fill = engines), show.legend = FALSE, alpha = 0.5) +
  geom_parallel_sets_axes(axis.width = 0.1, color = "lightgrey", fill =
"white") +
  geom_parallel_sets_labels(angle = 0) +
  theme_no_axes()
```



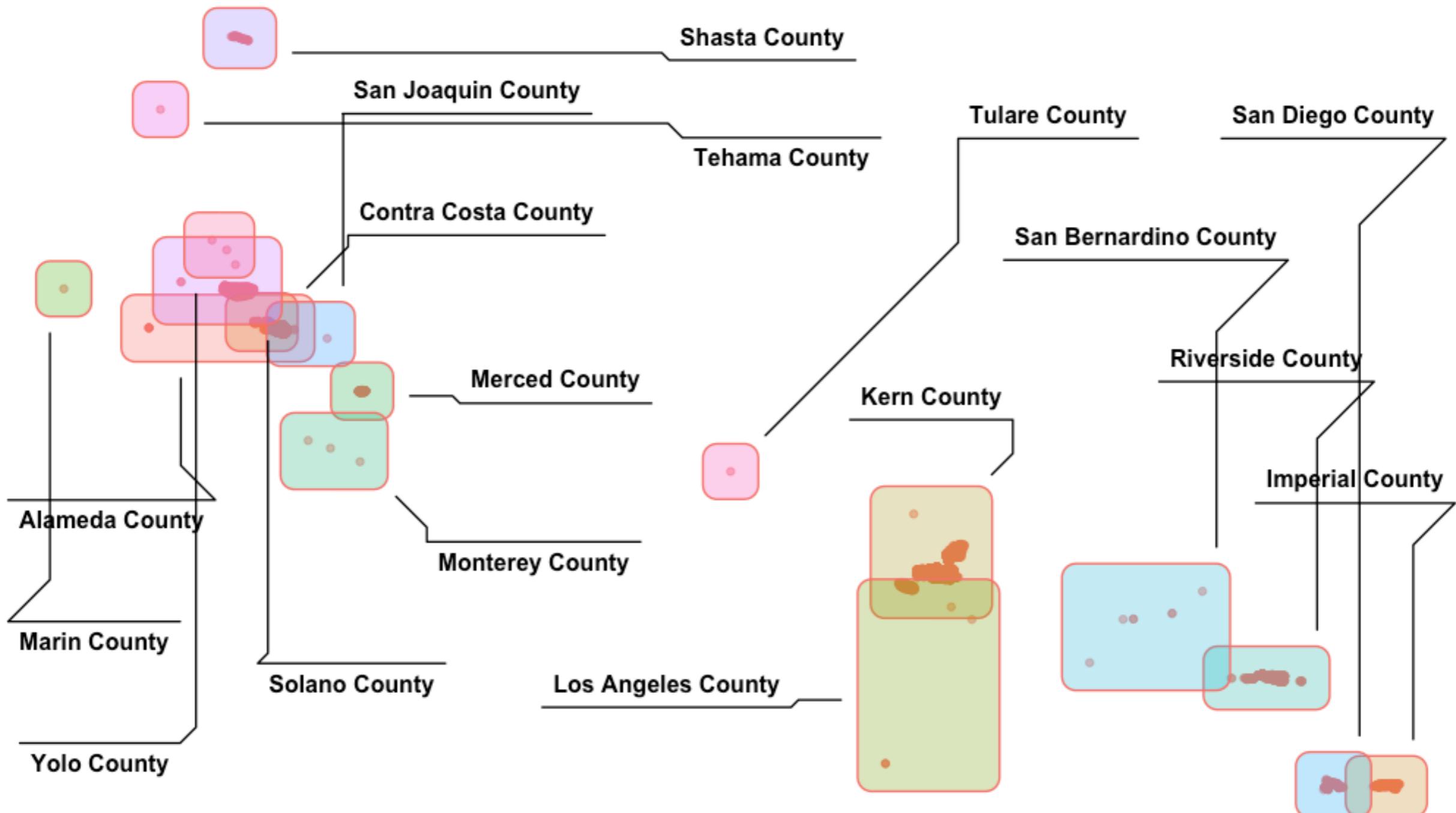
Another dataset

Plot of Windfarms in Continental US

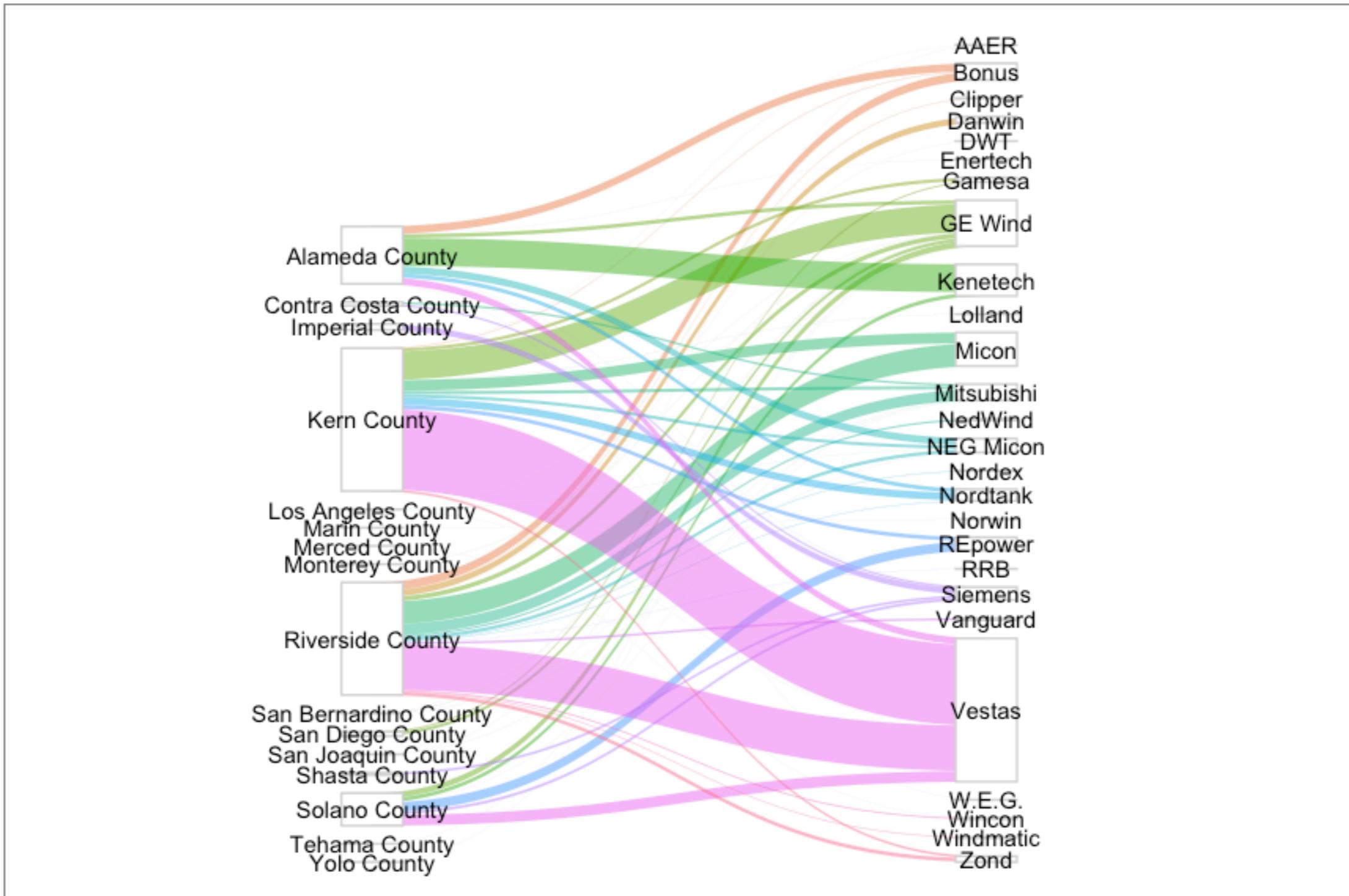


Focusing on California and Group by County

Plot of Windfarms in California Grouped by County

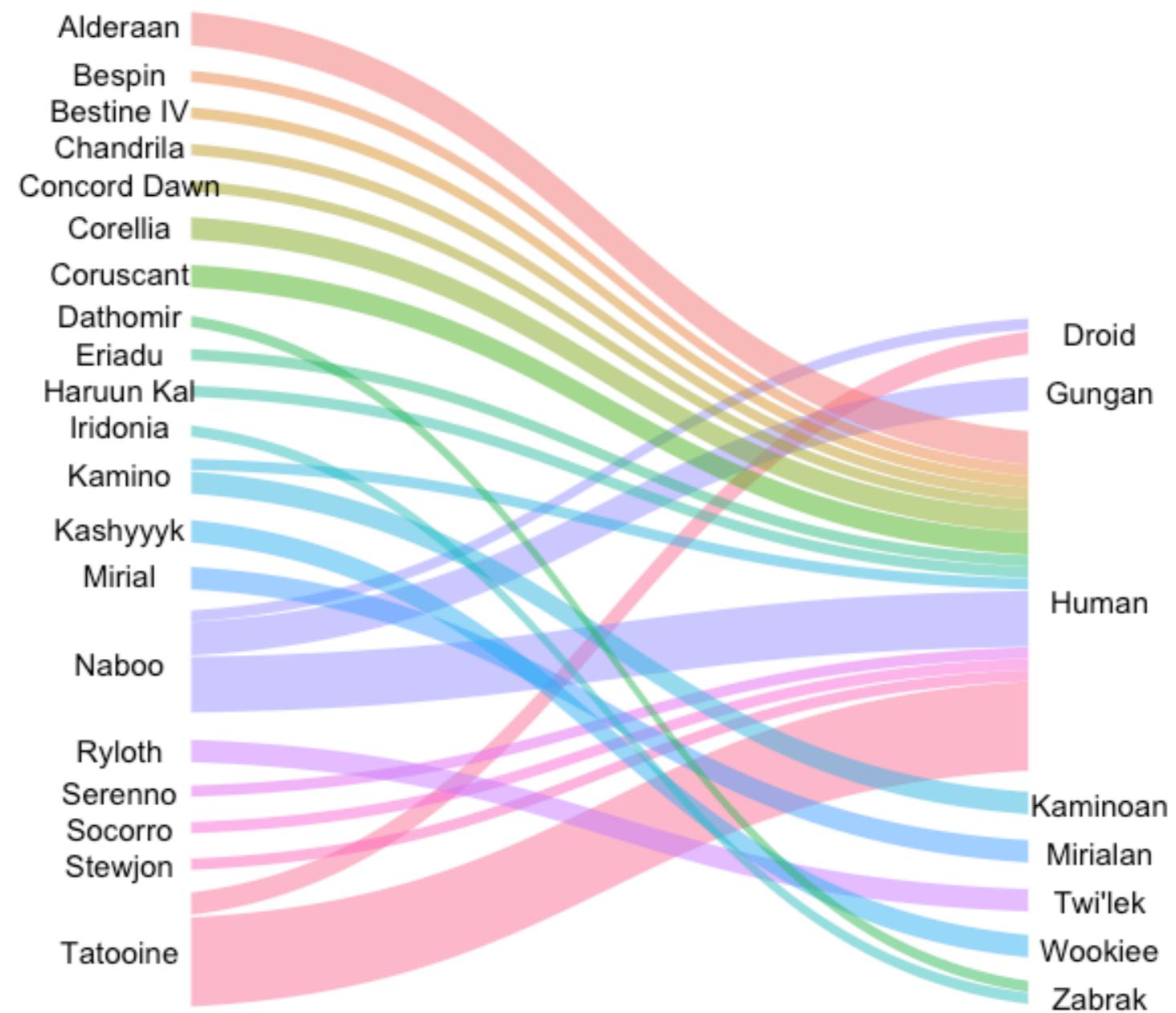


California - Mapping of Wind Turbine Manufacturer to County



The Star Wars dataset - with some minor aesthetics tweaks

Mapping of Homeworlds to Species in the Star Wars Universe



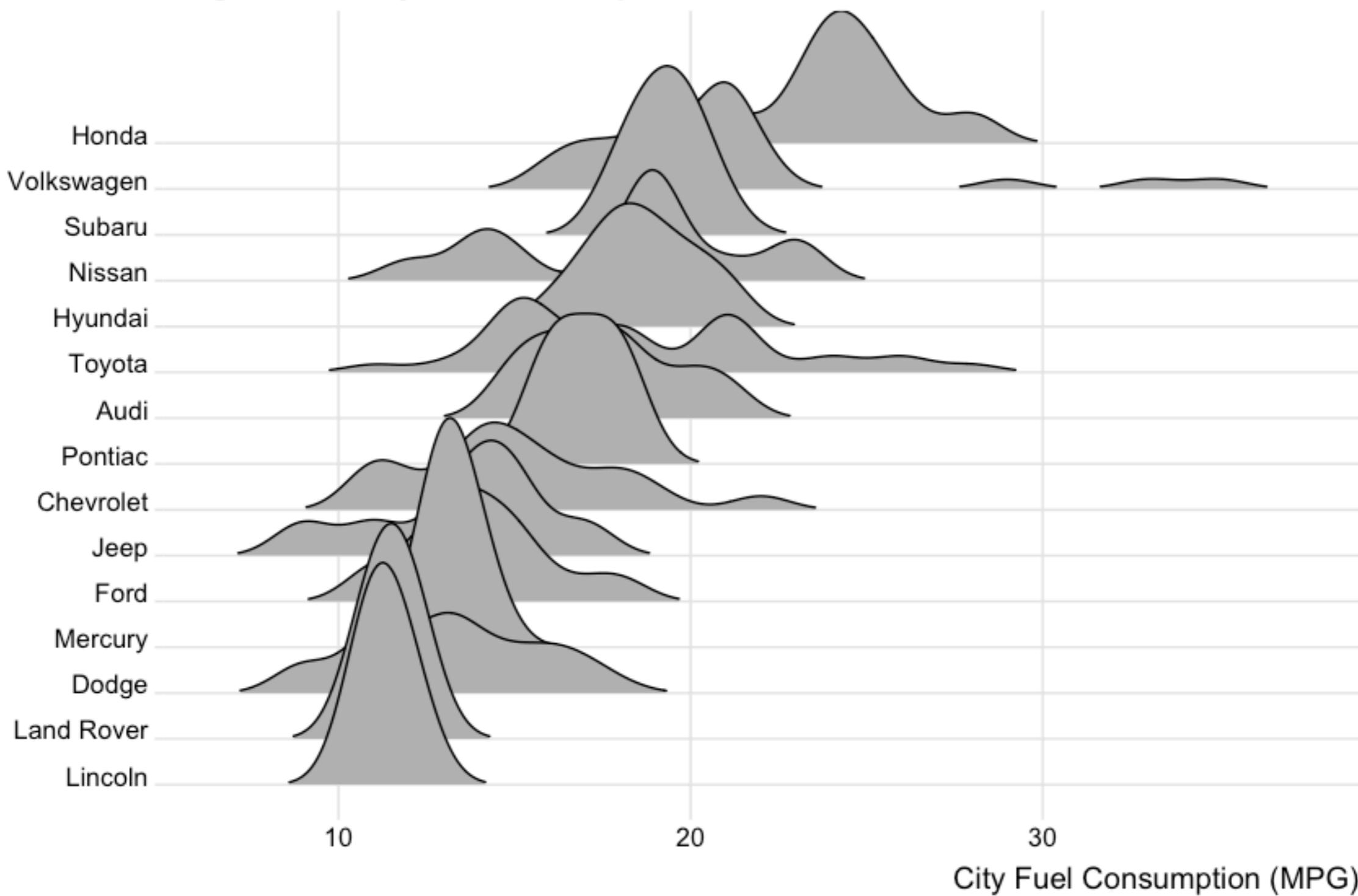
Ridge Plots with ggridges

Ridge Plots allow you to plot multiple histograms on the same group - good for quickly comparing different samples from a population (for example).

```
library(tidyverse)
library(ggridges)

mpg %>%
  mutate(manufacturer = str_to_title(manufacturer)) %>%
  ggplot(aes(x = cty, y = fct_reorder(manufacturer, cty), group = manufacturer)) +
  geom_density_ridges(scale = 5, size = 0.5, rel_min_height = 0.01) +
  labs(title = "Ridge Plot of City Fuel Consumption for Different Car
Manufacturers",
       x = "City fuel consumption (mpg)",
       y = NULL) +
  theme_ridges()
```

Ridge Plot of City Fuel Consumption for Different Car Manufacturers



Get ready to code...

Have a go at visualising a new dataset using one or more of these techniques - choose one from TidyTuesday:

<https://github.com/rfordatascience/tidytuesday>

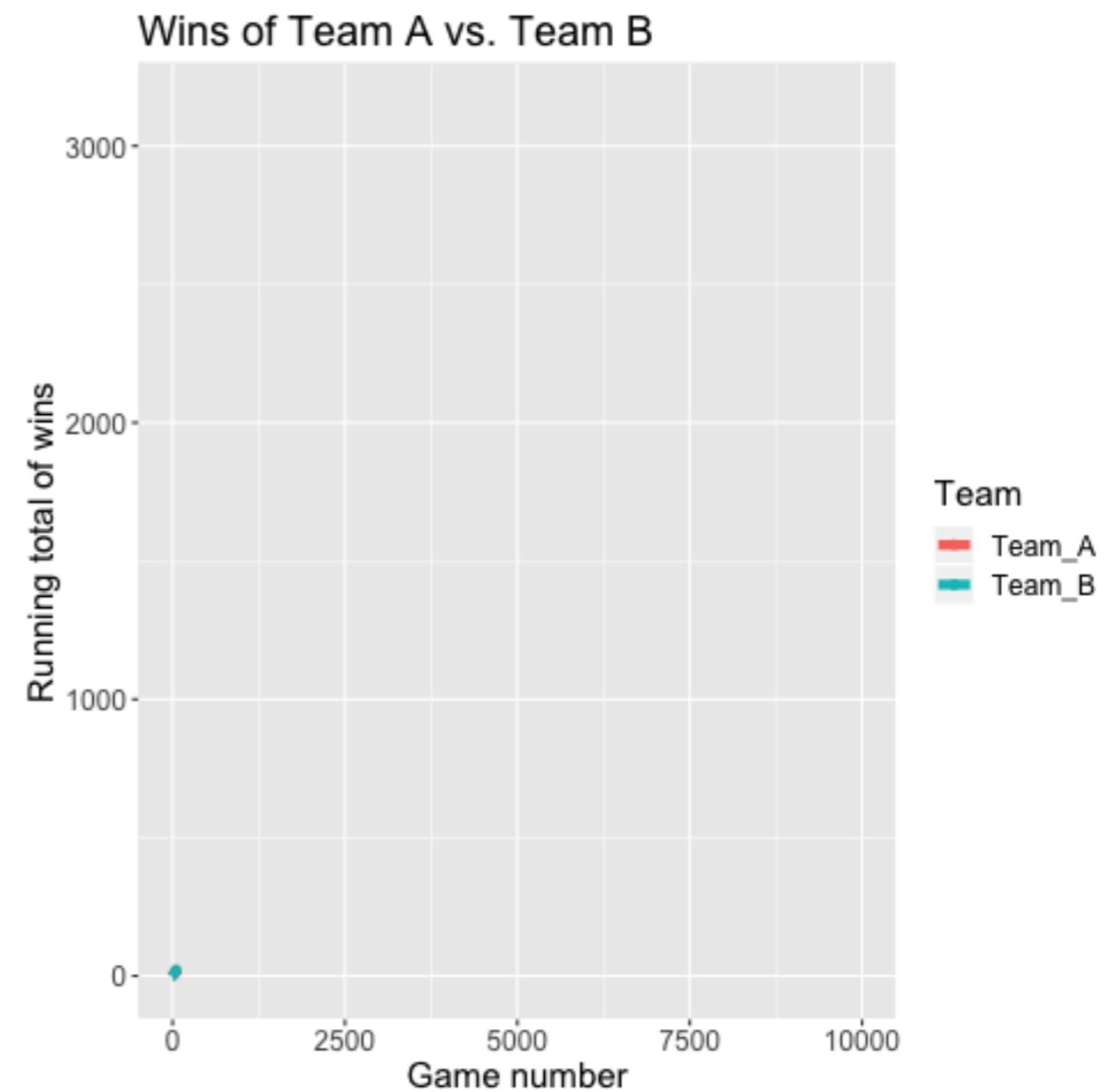
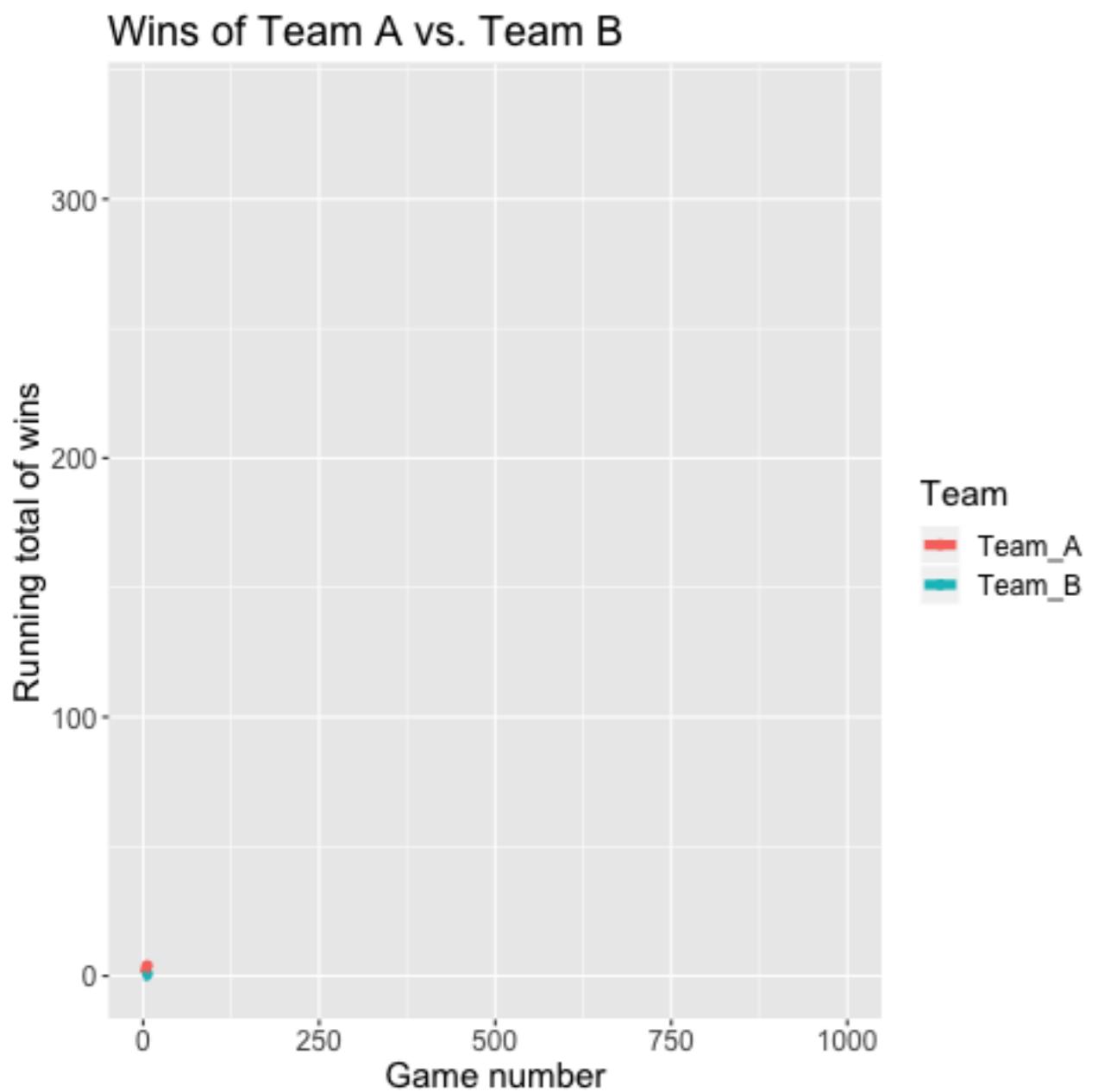
Animations - Hockey game simulation

Imagine a hockey game where we know that Team A scores exactly 1 goal for sure and Team B takes 20 shots, each with a 5.5% chance of going in.

Which team would you rather be?

(nothing additional happens if you tie.)

Animation of the first 1,000 games on the left and 10,000 on the right.



We can code it to simulate the outcomes of 100,000 such games...

```
set.seed(1234)

team_b_goals <- NULL

for(i in 1:100000) {
  score <- sum(sample(c(1, 0), size = 20, replace = TRUE, prob = c(0.055, 1-.055)))
  team_b_goals <- c(team_b_goals, score)}

team_a_goals <- rep(1, 100000)

all_games <- as.tibble(cbind(team_a_goals, team_b_goals))
```

```
> nrow(filter(all_games, team_a_goals > team_b_goals))
[1] 32022
> nrow(filter(all_games, team_a_goals < team_b_goals))
[1] 30337
> nrow(filter(all_games, team_a_goals == team_b_goals))
[1] 37641
```

We see that out of 100,000 simulations, Team A wins on 32,022 occasions. Team B wins on 30,337 occasions and there are 37,641 ties.

The gganimate package

- The `gganimate` package needs to be installed separately from the core `tidyverse` packages.
- It follows the Tidyverse philosophy and extends the capabilities of the `ggplot()` function - in many ways it's like adding an extra layer to your plots in the same way you might use `facet_wrap()` but specifying parameters related to your animation frames (and how to transition between those frames).
- Let's look at some examples...

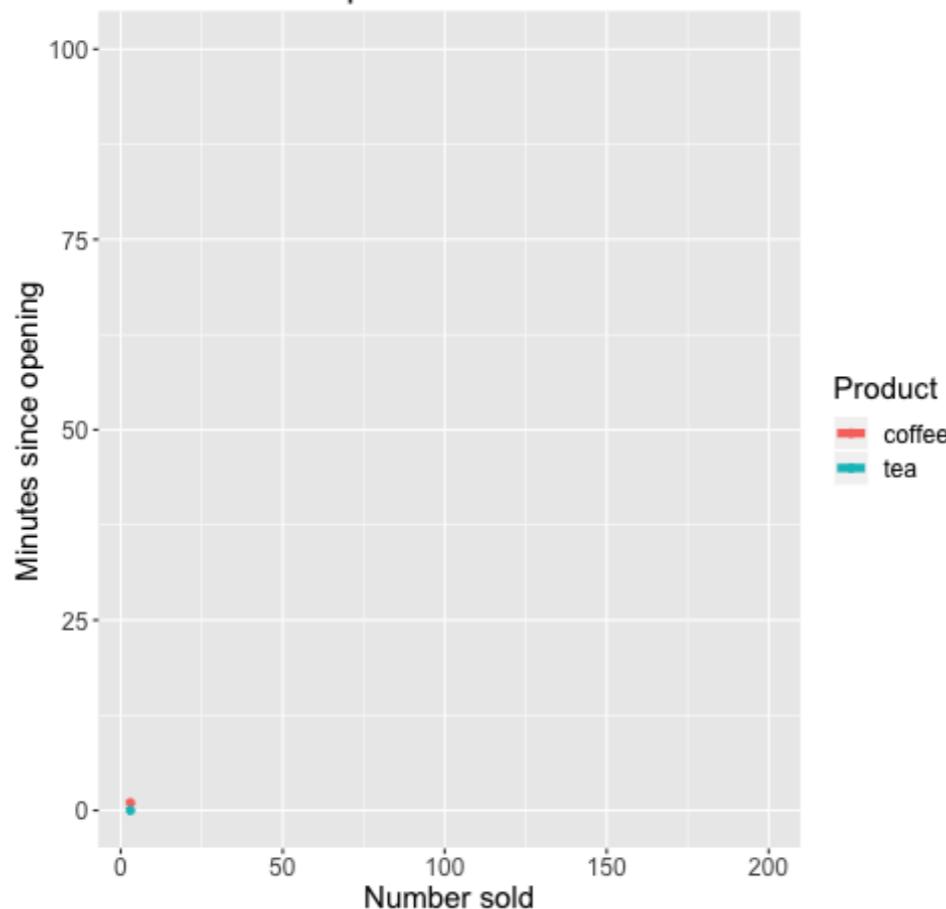
The data

- Our data set contains information from a cafe about the number of teas and coffees (Product) sold (n_sold) from minutes since opening (Time).

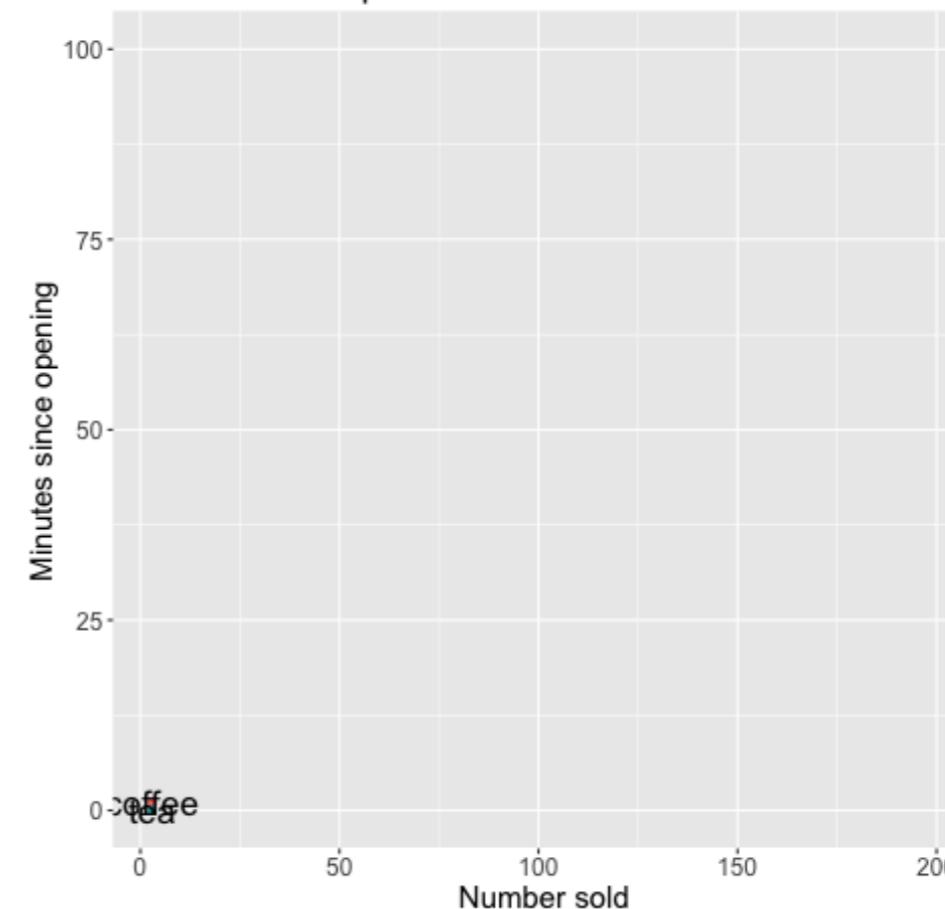
```
> str(data)
Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
$ Product: Factor w/ 2 levels "coffee","tea": 1 1 1 1 1 1 1 1 1 1 ...
$ Time    : int 3 8 9 10 12 13 14 15 20 22 ...
$ n_sold  : int 1 2 3 4 5 6 7 8 9 10 ...

> head(data)
# A tibble: 6 x 3
  Product  Time n_sold
  <fct>    <int>  <int>
1 coffee      3      1
2 coffee      8      2
3 coffee      9      3
4 coffee     10      4
5 coffee     12      5
6 coffee     13      6
```

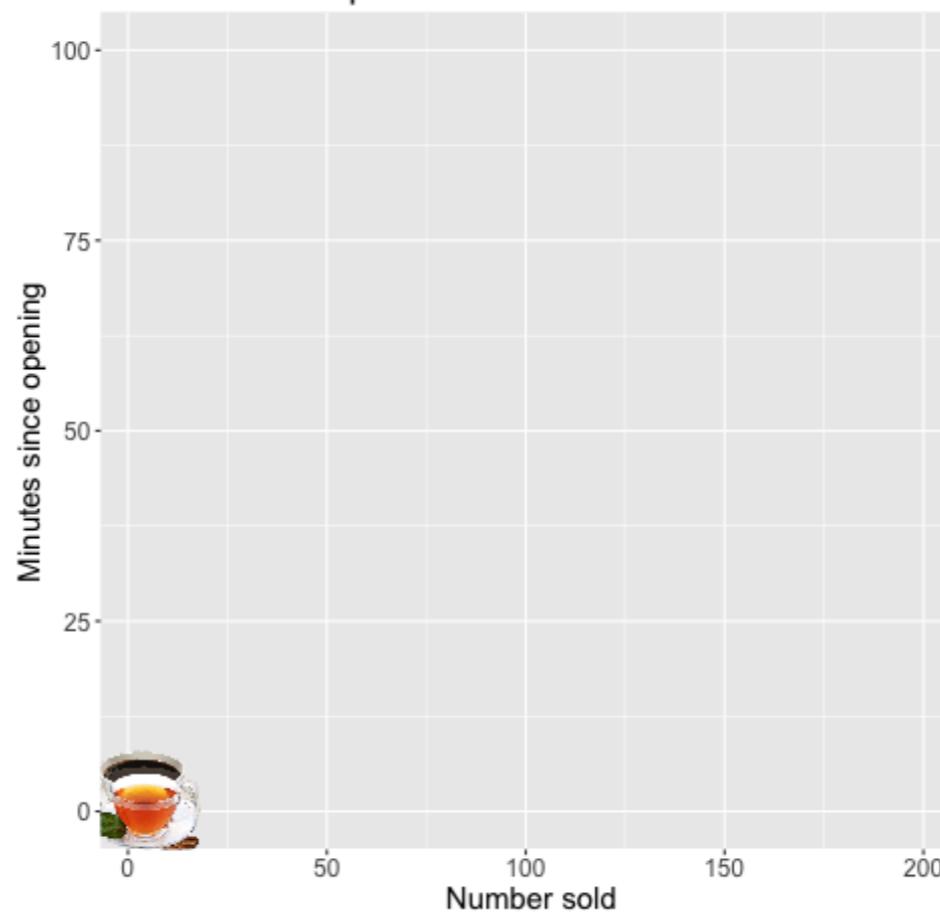
Coffee and tea purchases in a fictitious cafe



Coffee and tea purchases in a fictitious cafe



Coffee and tea purchases in a fictitious cafe



```

library(gganimate)

# Just animated lines
data %>%
  ggplot(aes(x = n_sold, y = Time, group = Product, colour = Product)) +
  geom_point() +
  geom_line(size = 2) +
  coord_flip() +
  transition_reveal(Time) +
  labs(title = "Coffee and tea purchases in a fictitious cafe",
       x = "Minutes since opening",
       y = "Number sold") +
  theme(text = element_text(size = 15))

# With text labels
data %>%
  ggplot(aes(x = n_sold, y = Time, group = Product, colour = Product)) +
  geom_point() +
  geom_line(size = 2) +
  coord_flip() +
  geom_text(aes(label = Product), size = 6, colour = "black") +
  transition_reveal(Time) +
  guides(colour = FALSE) +
  labs(title = "Coffee and tea purchases in a fictitious cafe",
       x = "Minutes since opening",
       y = "Number sold") +
  theme(text = element_text(size = 15))

```

- The `transition_reveal()` function allows you to reveal the data gradually by whatever labelled parameter you specify.

```
library(ggimage)

# Add .png images to animation
data_recoded <- mutate(data, image = recode(Product,
                                              "coffee" = "coffee.png",
                                              "tea" = "tea.png"))

data_recoded %>%
  ggplot(aes(x = n_sold, y = Time, group = image)) +
  coord_flip() +
  geom_line(size = 2, aes(colour = image)) +
  geom_image(aes(image = image), size = .15) +
  transition_reveal(Time) +
  guides(colour = FALSE) +
  labs(title = "Coffee and tea purchases in a fictitious cafe",
       x = "Minutes since opening",
       y = "Number sold") +
  theme(text = element_text(size = 15))
```

Animating aspects of the NHANES dataset:

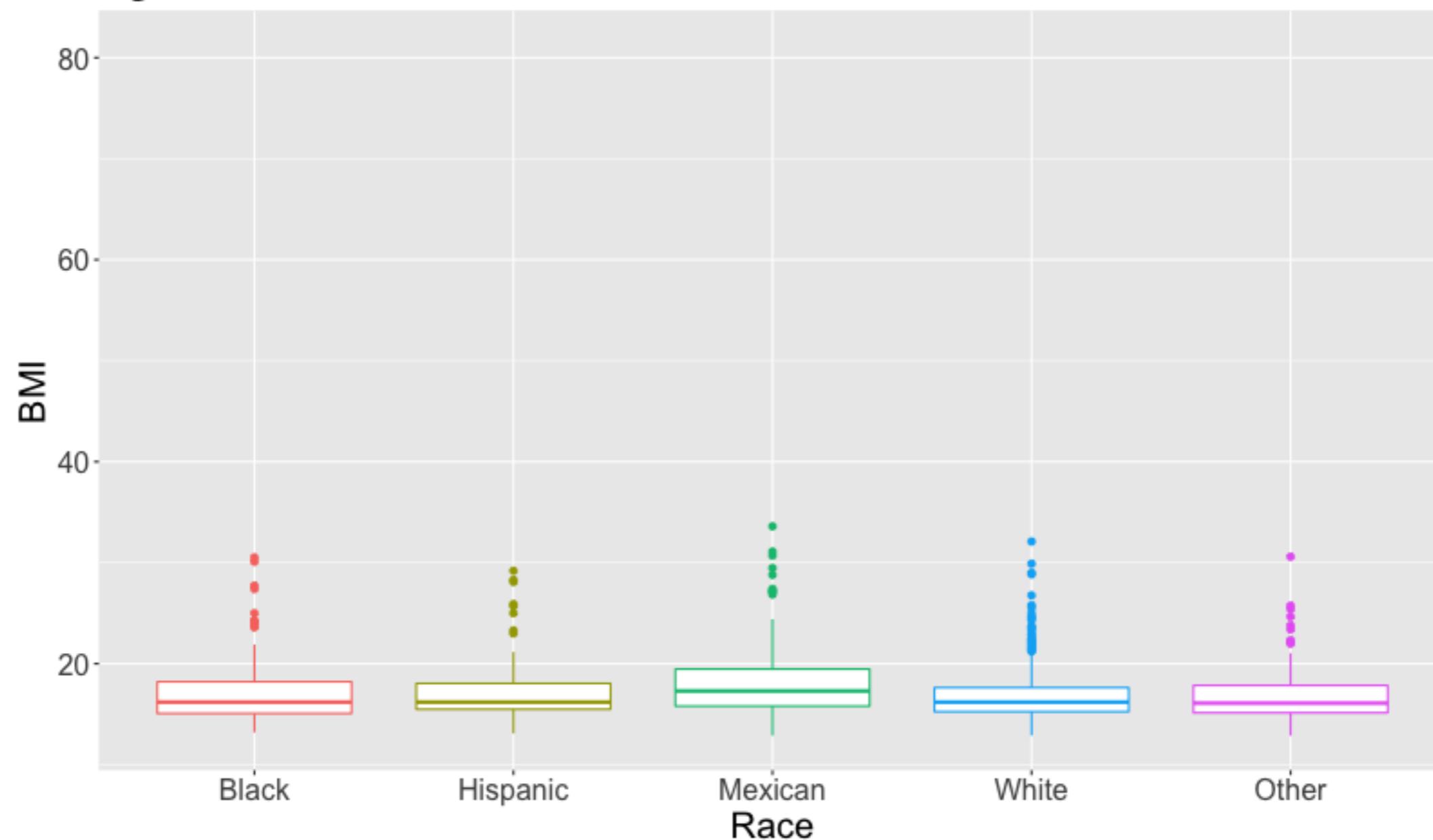
This is survey data collected by the US National Center for Health Statistics (NCHS) which has conducted a series of health and nutrition surveys since the early 1960's. Since 1999 approximately 5,000 individuals of all ages are interviewed in their homes every year and complete the health examination component of the survey. The health examination is conducted in a mobile examination centre (MEC).

```
library(NHANES)

# Boxplot of BMI by Race and AgeDecade
NHANES %>%
  distinct(ID, .keep_all = TRUE) %>%
  ggplot(aes(x = Race1, y = BMI, colour = Race1)) +
  geom_boxplot() +
  guides(colour = FALSE) +
  labs(x = "Race", title = "Age = {closest_state}") +
  transition_states(AgeDecade)
```

- Think of `transition_states()` like `facet_wrap()` with the transition between each panel animated. The variable `{closest_state}` is available from the `transition_states()` function and can be used outside the function (like I am in the title here).

Age = 0-9



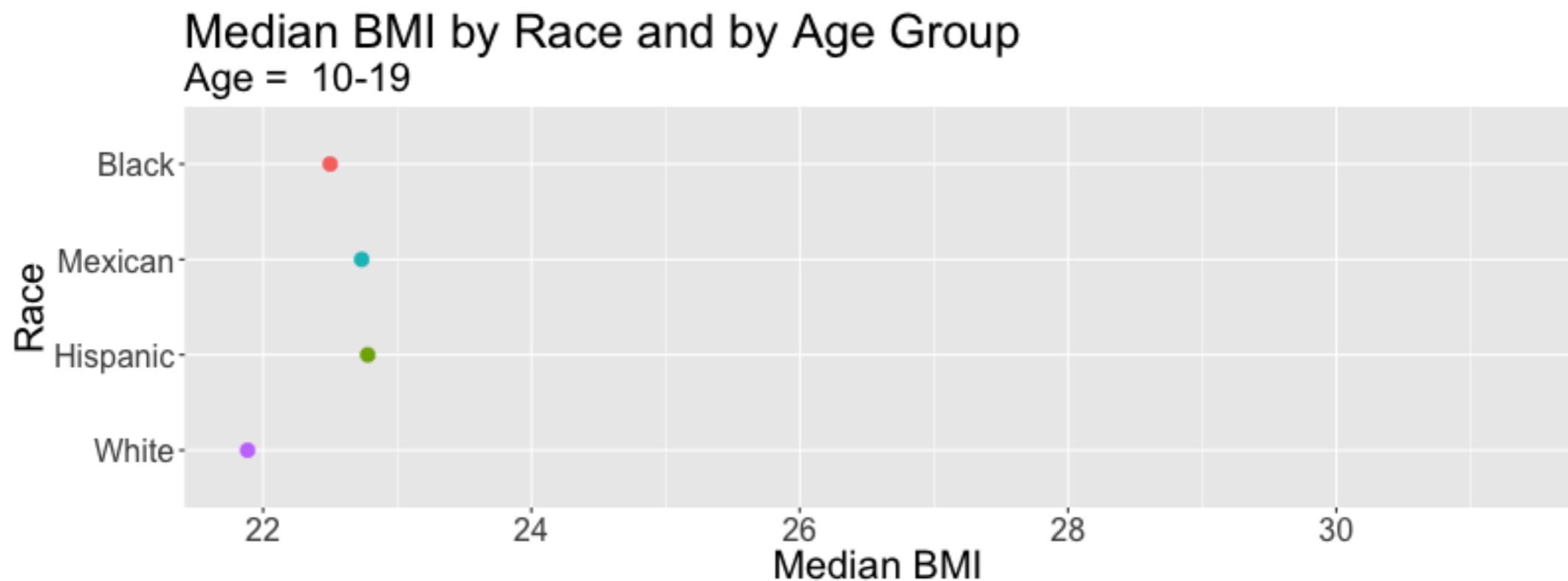
```

NHANES_tidy <- NHANES %>%
  filter(Race1 != "Other") %>%
  filter(as.character(AgeDecade) != " 0-9")

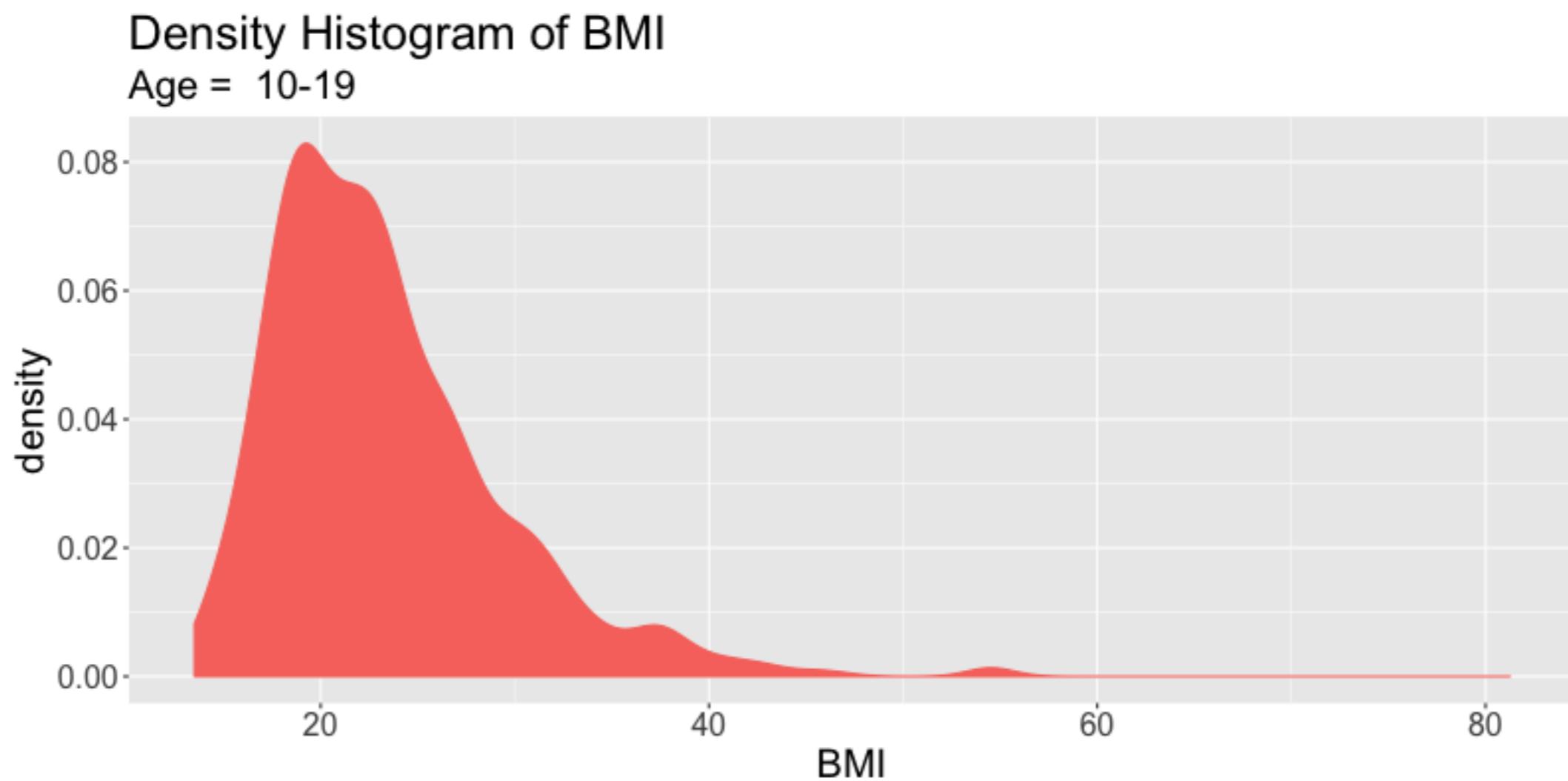
my_plot <- NHANES_tidy %>%
  mutate(AgeDecade = fct_drop(AgeDecade, " 0-9")) %>%
  group_by(AgeDecade, Race1) %>%
  summarise(median_BMI = median(BMI, na.rm = TRUE)) %>%
  ggplot(aes(x = median_BMI, y = reorder(Race1, median_BMI), colour = Race1)) +
  geom_point(size = 3) +
  labs(x = "Median BMI", y = "Race", title = "Median BMI by Race and by Age Group",
       subtitle = "Age = {closest_state}") +
  transition_states(AgeDecade) +
  theme(text = element_text(size = 20)) +
  guides(colour = FALSE)

animate(my_plot, height = 300, width = 800)
anim_save("example_plot.gif")

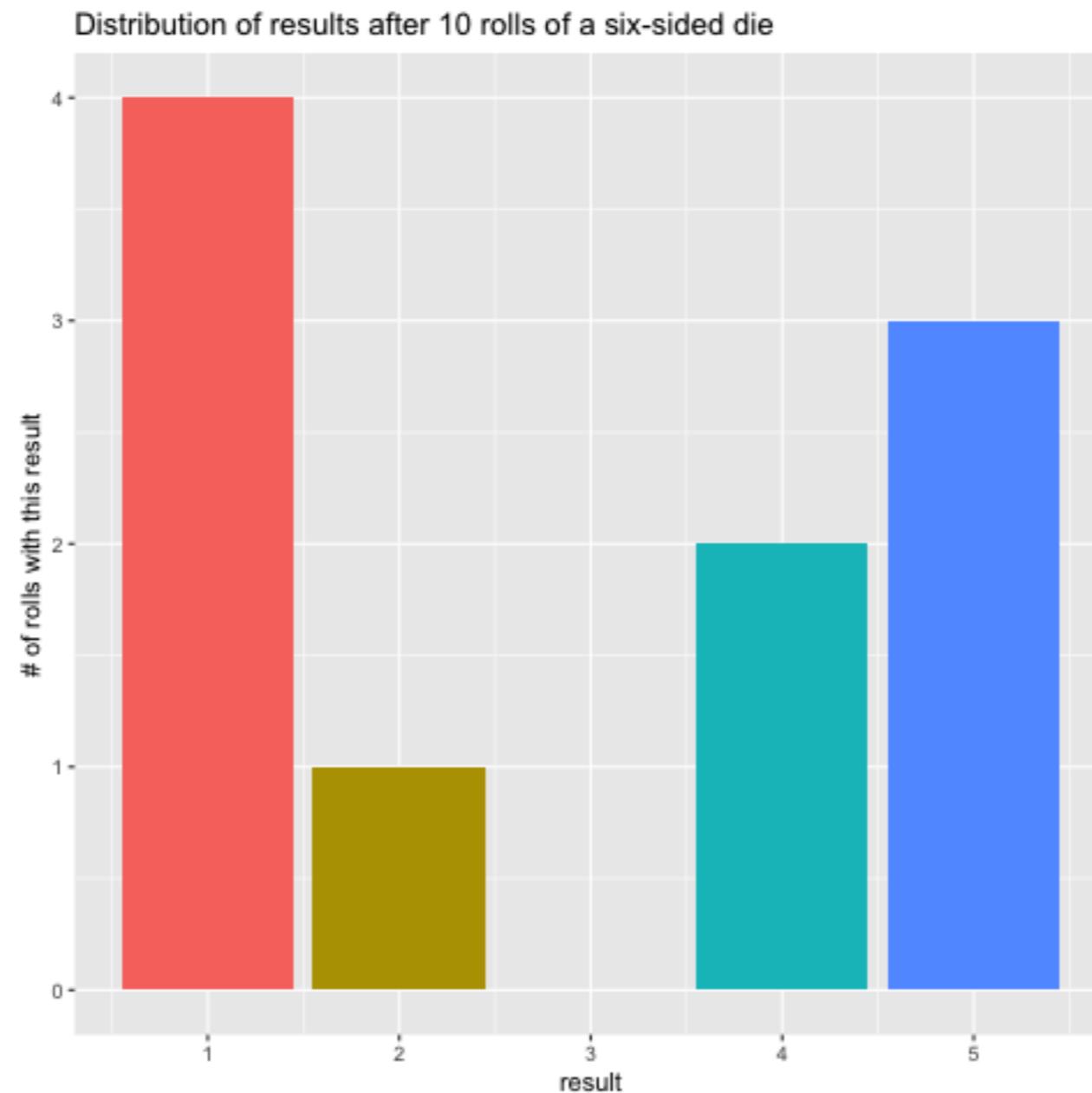
```



Animated density histogram of BMI



Simulation of 10,000 dice rolls by @drob



<https://twitter.com/drob/status/1100182329350336513>

- You can see some really nice slides of examples by the author of the package (Thomas Lin Pedersen, Twitter @thomasp85) from the 2019 RStudio Conference at the following:

<https://www.data-imaginist.com/slides/rstudioconf2019/assets/player/keynotedhtmlplayer#11>

Visualising Likert Scale Data

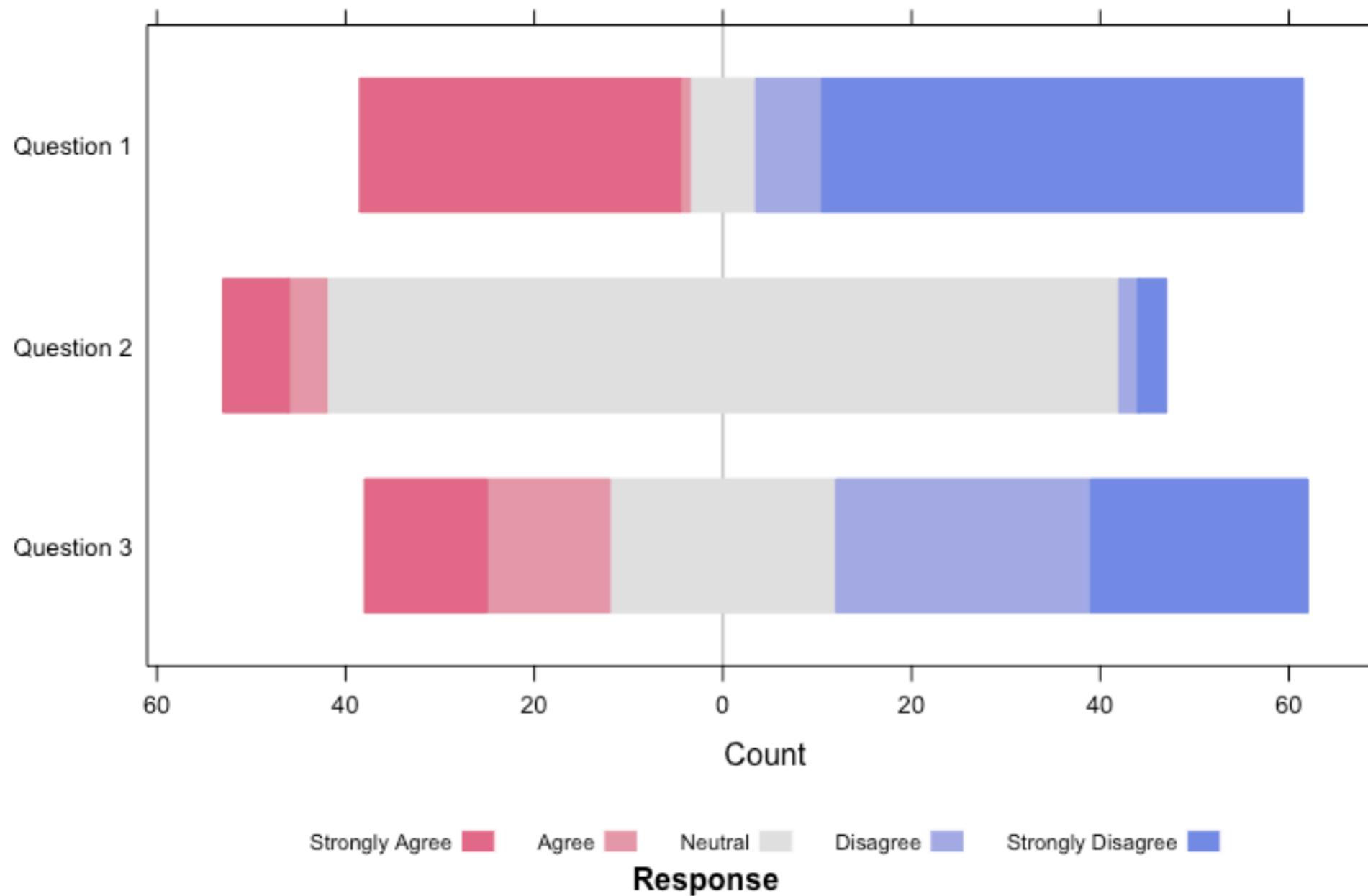
Imagine you asked 100 people to respond to three questions using a 5-point Likert scale - their data might look like this:

	Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
Question 1	34	1	7	7	51
Question 2	7	4	84	2	3
Question 3	13	13	24	27	23

How might you best communicate the data? It might be misleading to report a measure of central tendency as the mean, median, and mode for Question 2 will all suggest people were Neutral (and ignore those in the tails).

One option is via a diverging stacked bar chart using the `likert()` function in the package `HH...`

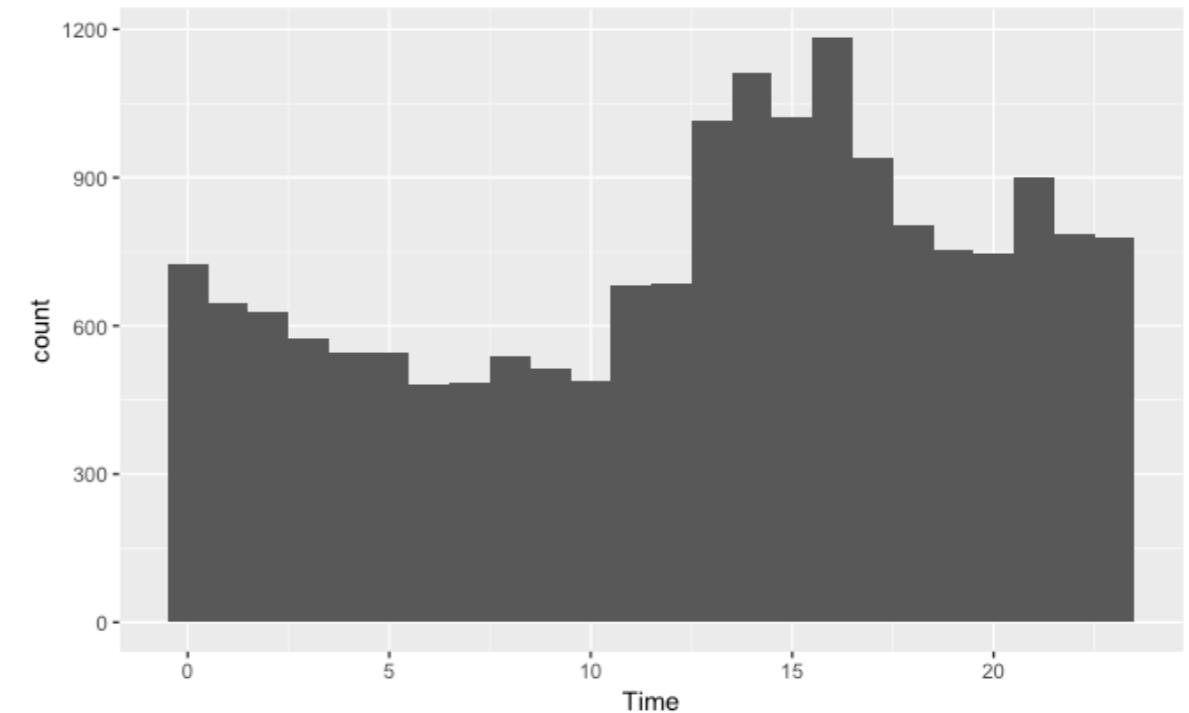
Diverging Stacked Bar Chart for Likert Scale Data



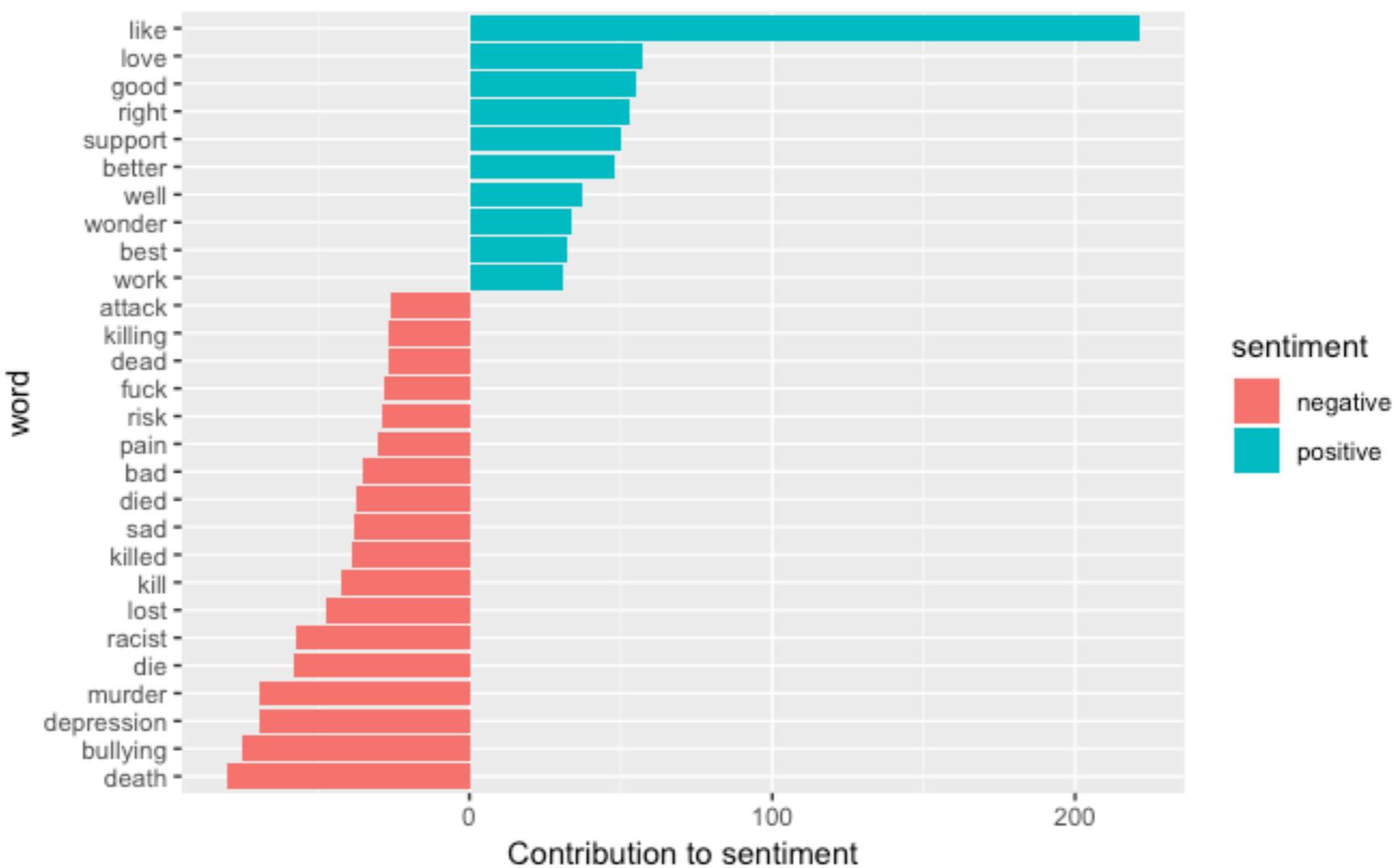
Visualising Text Data

- We can use the `rtweet` package by Mike Kearney to scrape data from Twitter using the `search_tweets()` function. In this case I'm scraping Twitter for mentions of the word 'suicide' in Tweets, extracting the time the Tweet was created and then plotting on a histogram.

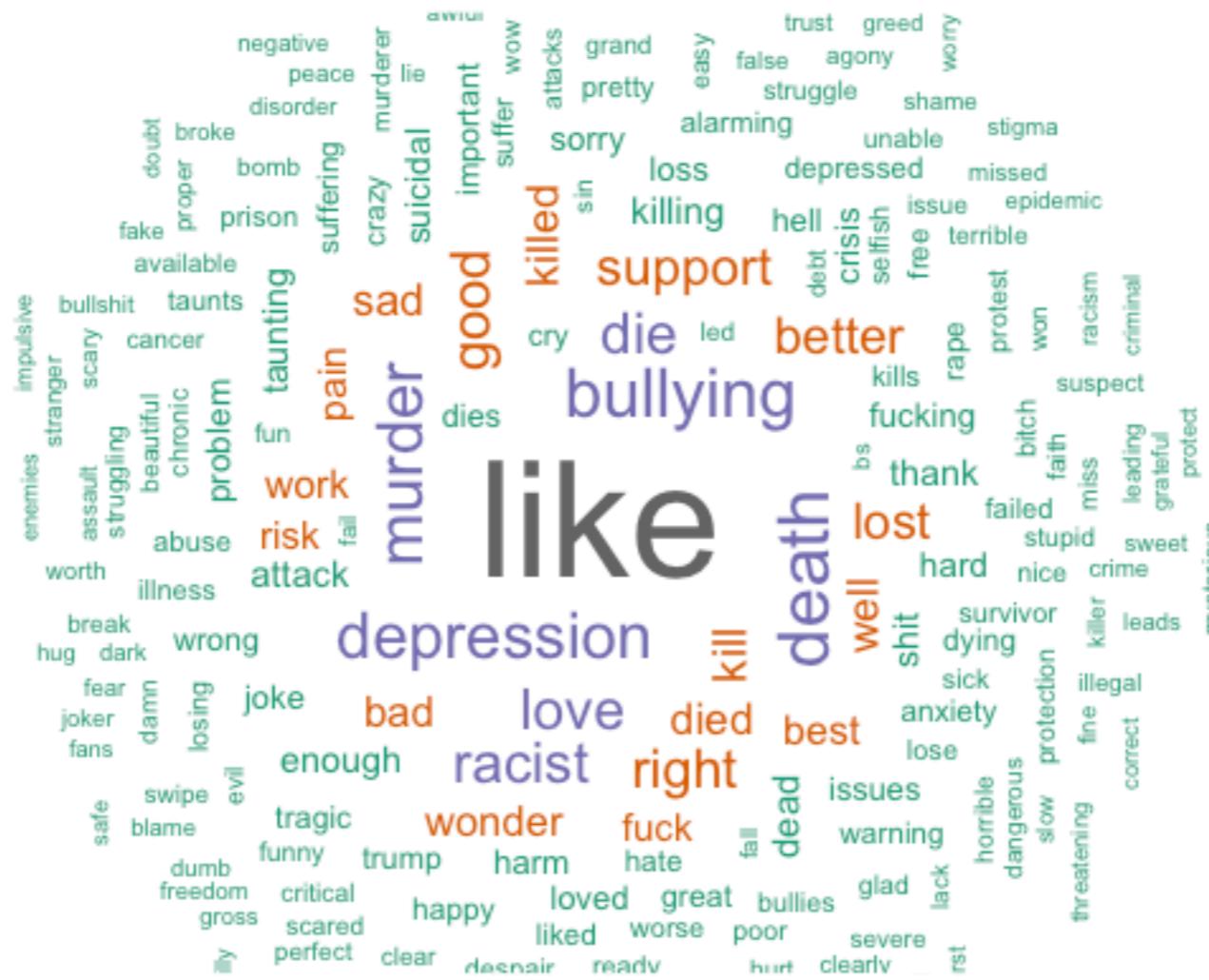
```
tweets <- search_tweets(q = "suicide", n =  
1000, include_rts = FALSE, retryonratelimit =  
TRUE)  
  
time <- tibble(Time = hour(tweets$created_at))  
  
time %>%  
  filter(!is.na(Time)) %>%  
  ggplot(aes(x = Time)) +  
  geom_histogram()
```



- Now I'm using the tidytext package to do a sentiment analysis associated with the words in Tweets mentioning 'suicide' created between midnight and 6AM.



- And visualising the content of the Tweets as a Wordcloud using the `wordcloud` package.



Searching for mentions of “Opeth”

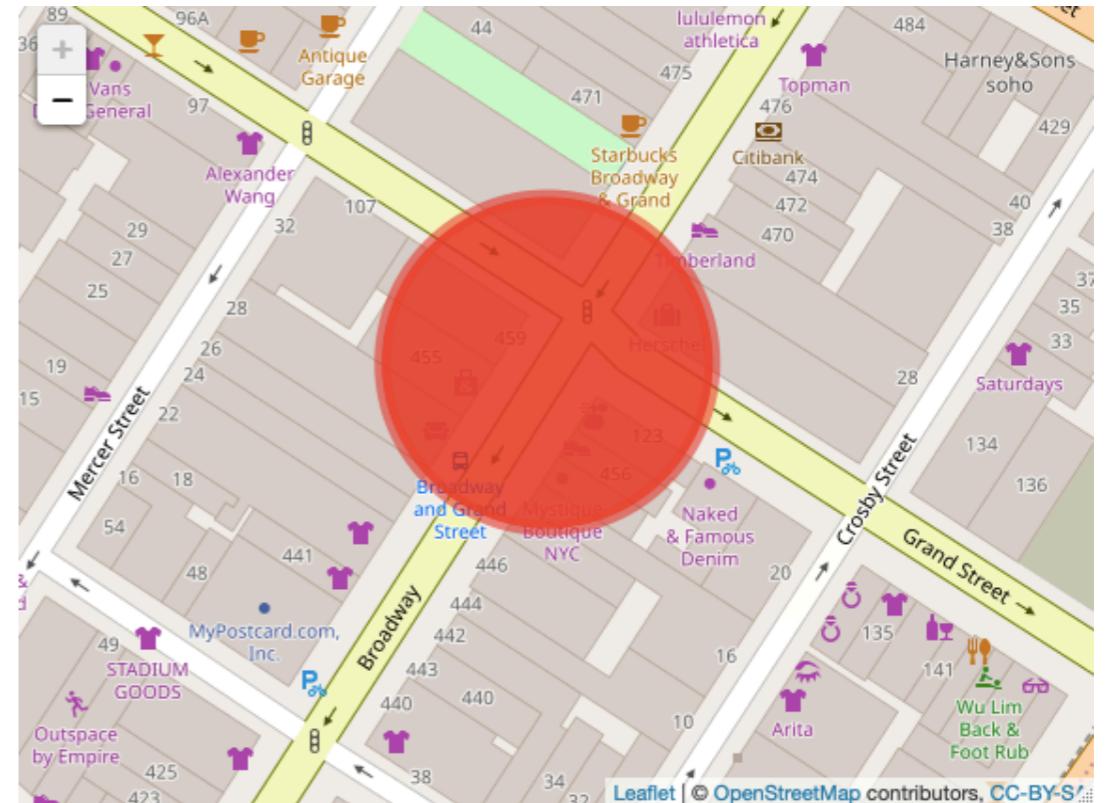
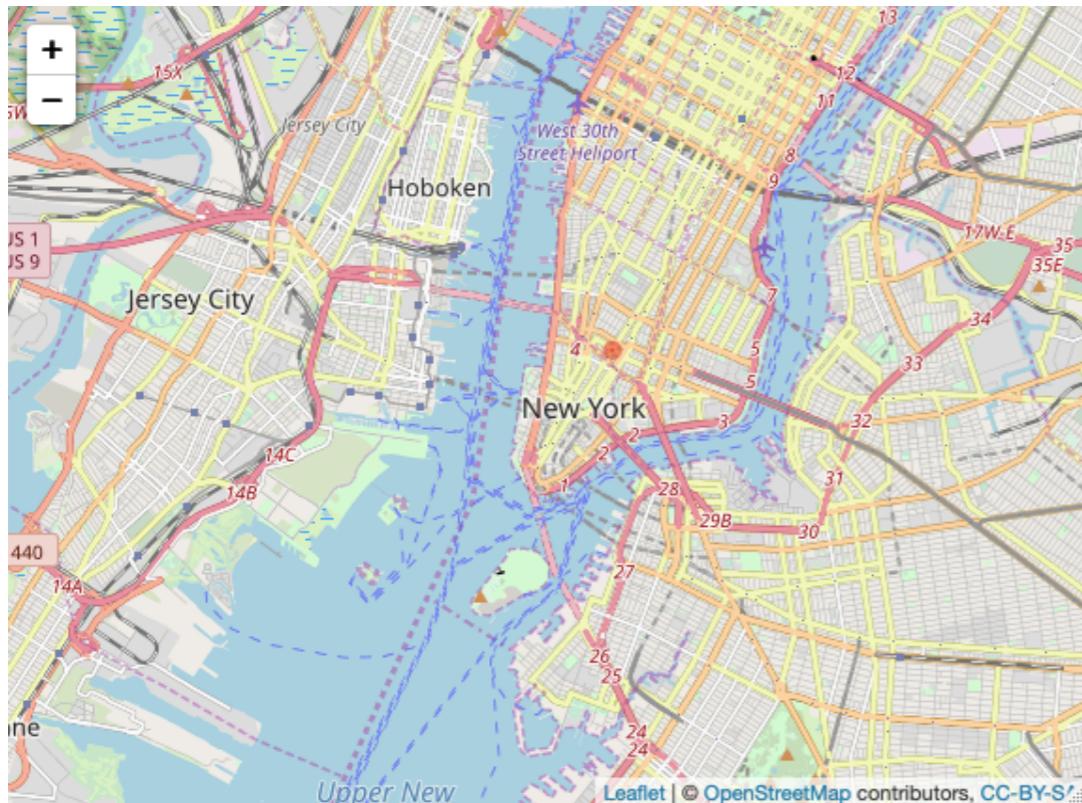
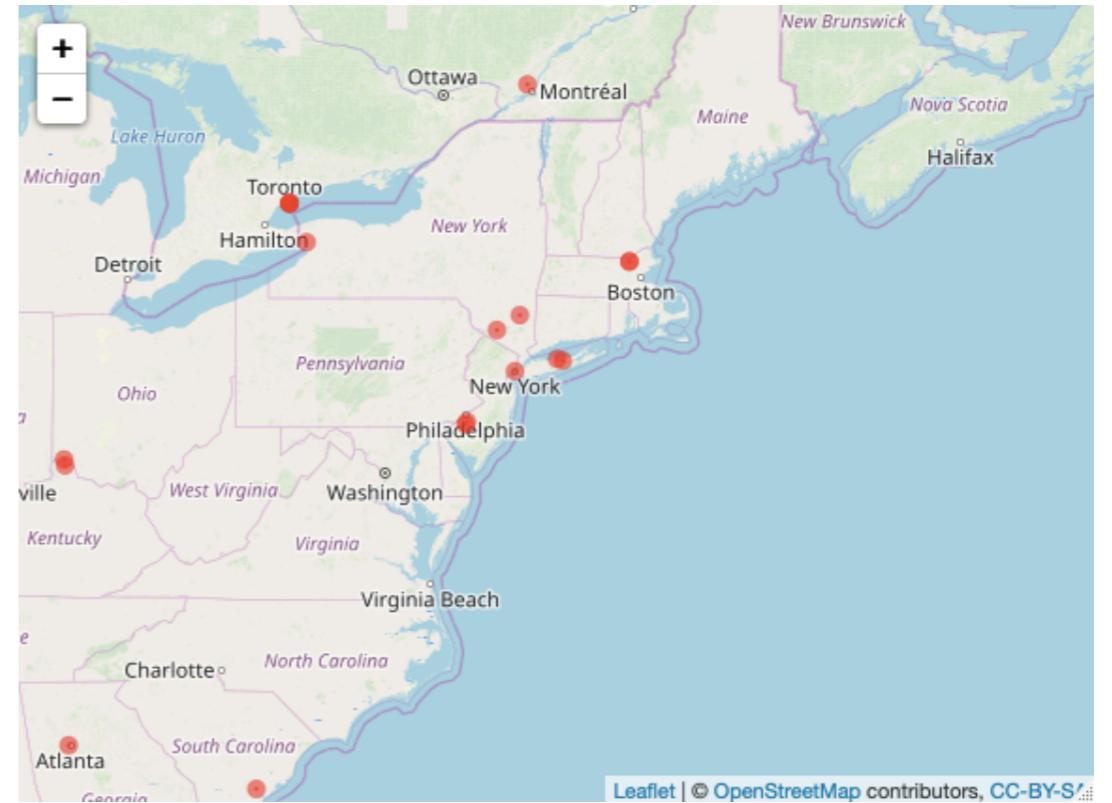
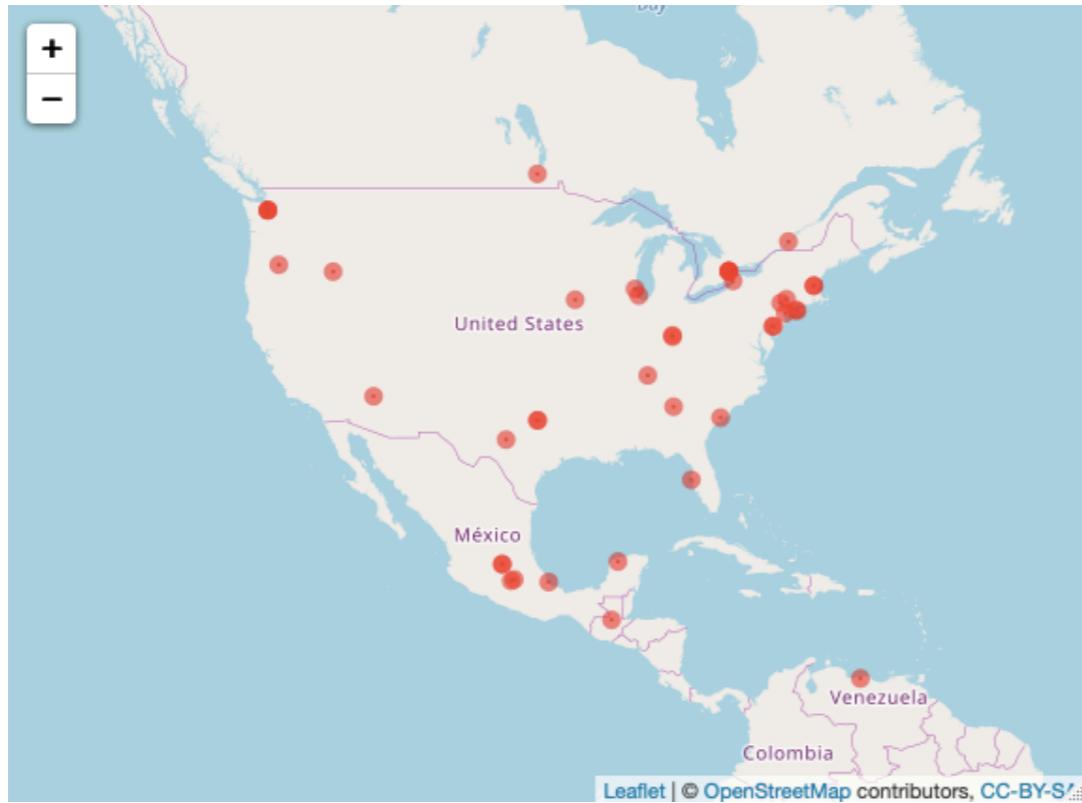


Geospatial plotting

- Some Tweets have associated with them the latitude and longitude of where they were tweeted from - we can use the leaflet package to extract these coordinates and plot the location of tweets with geospatial tagging on a map...



...and the map is zoomable

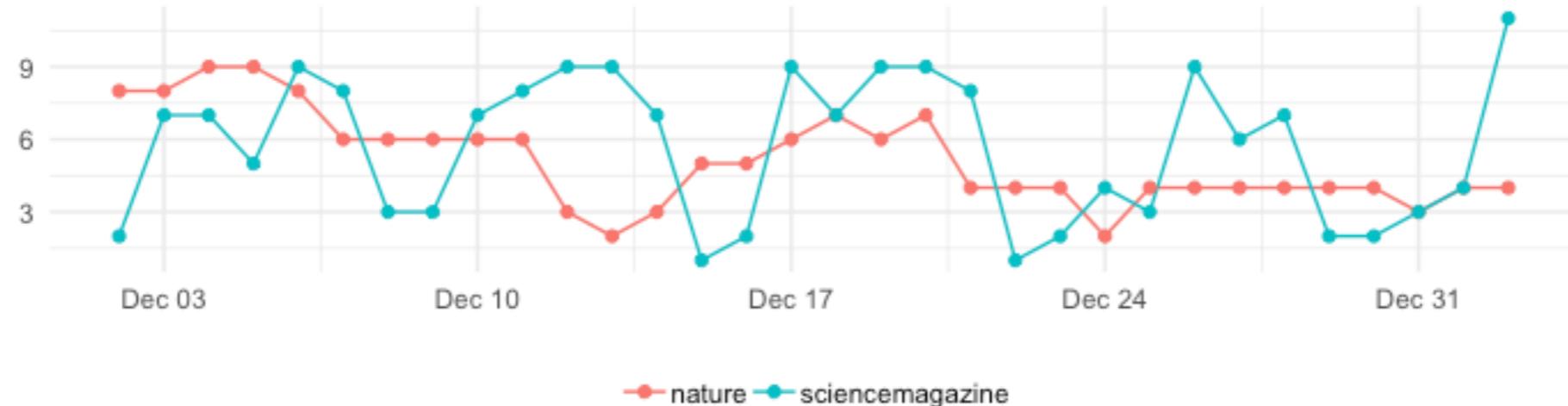


Collecting the number of Tweets from two timelines

```
tmbs <- get_timelines(c("Nature", "sciencemagazine"), n = 1000)
tmbs %>%
  filter(created_at > "2018-12-1") %>%
  group_by(screen_name) %>%
  ts_plot("days", trim = 1L) +
  geom_point() +
  theme_minimal() +
  theme(
    legend.title = ggplot2::element_blank(),
    legend.position = "bottom",
    plot.title = ggplot2::element_text(face = "bold")) +
  labs(
    x = NULL, y = NULL,
    title = "Frequency of Twitter statuses posted by the journals Nature and Science",
    subtitle = "Twitter status (tweet) counts aggregated by day",
    caption = "\nSource: Data collected from Twitter's REST API via rtweet"
)
```

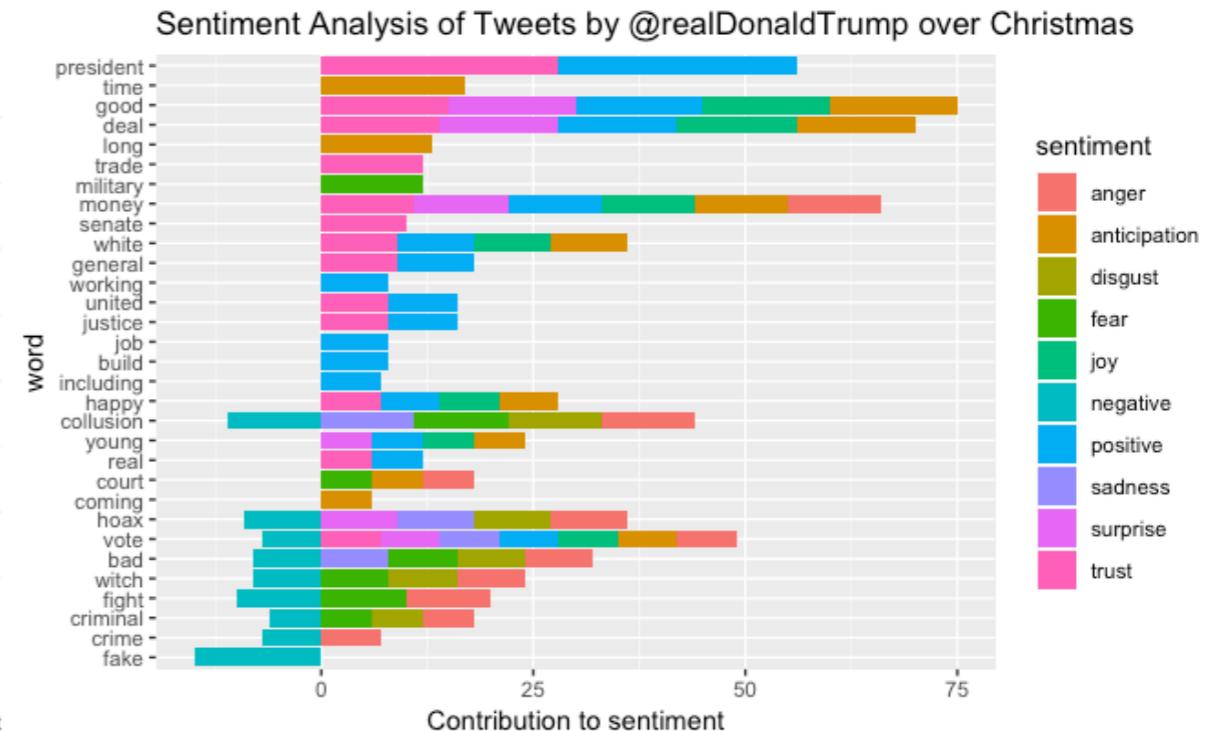
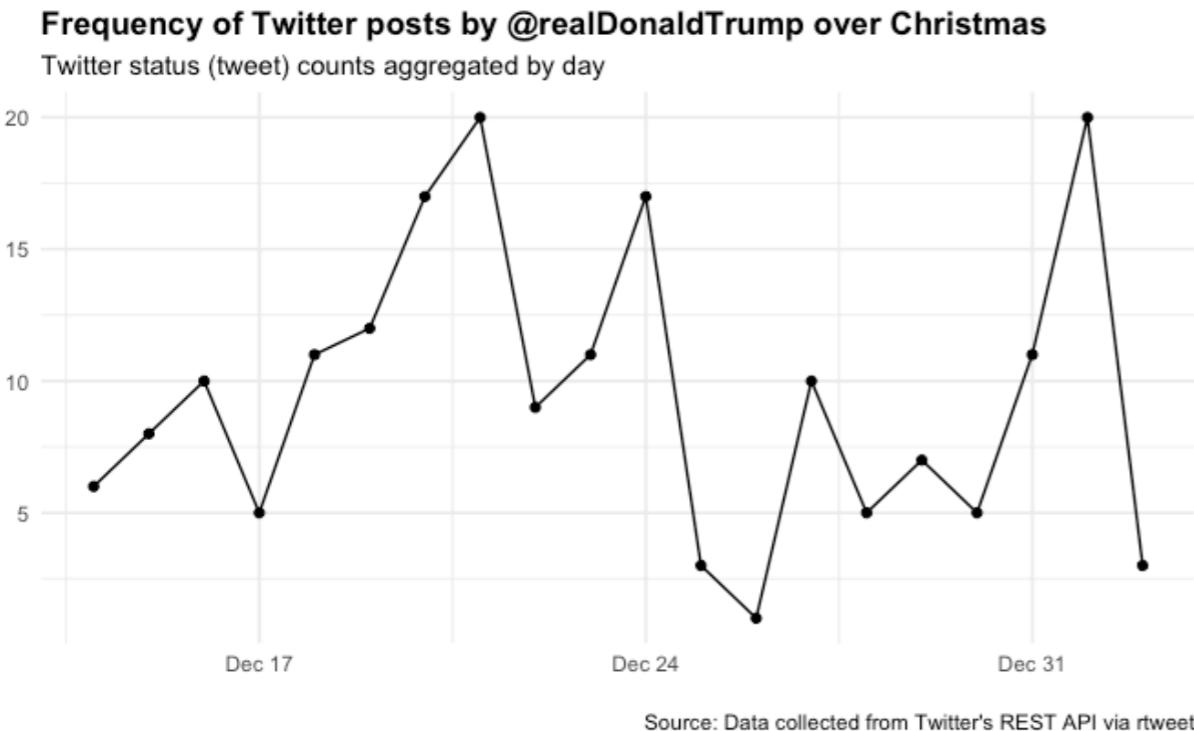
Frequency of Twitter statuses posted by the journals Nature and Science

Twitter status (tweet) counts aggregated by day

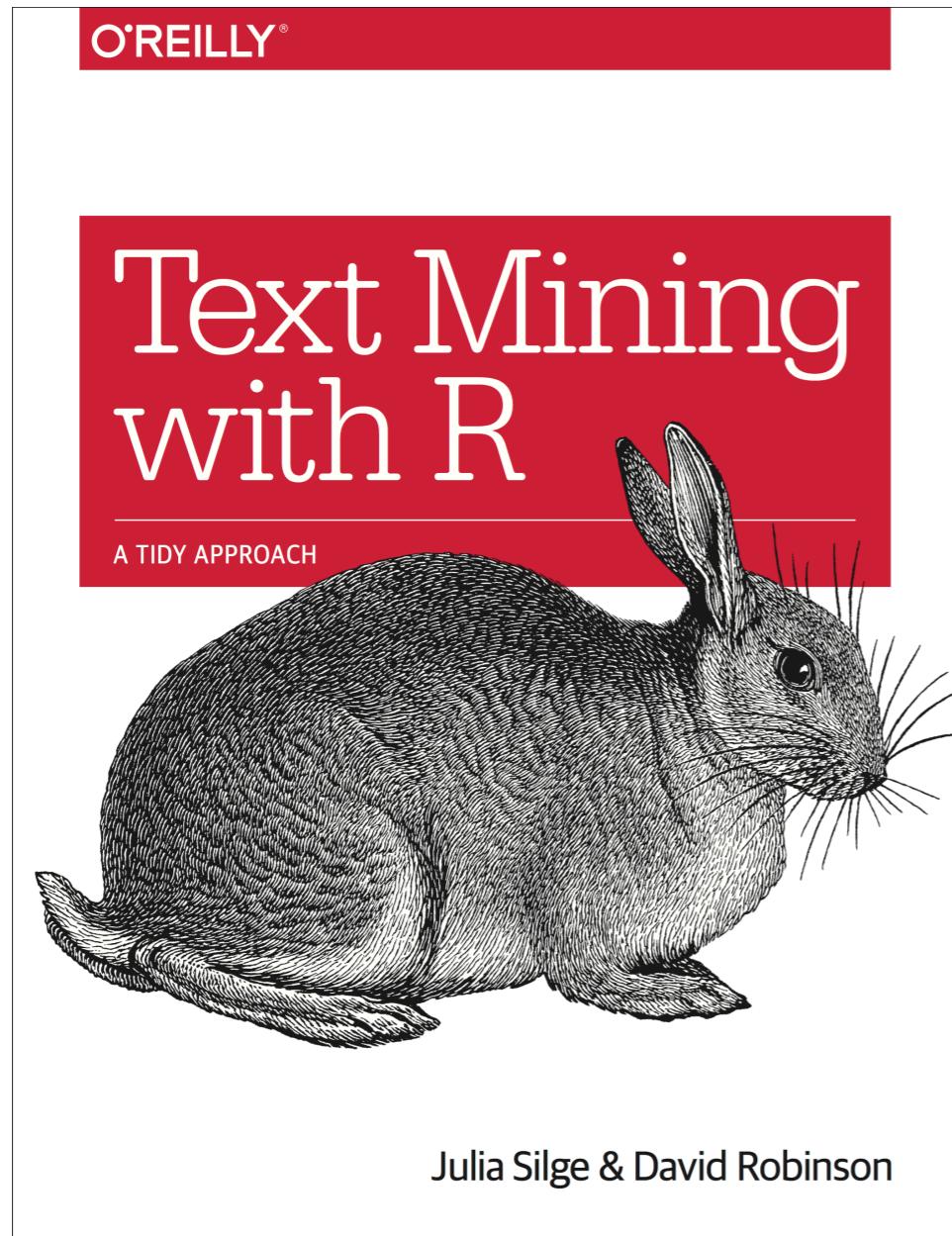


Source: Data collected from Twitter's REST API via rtweet

Collecting Tweets from one timeline



A good, detailed text mining book for those working on qualitative projects...



<https://www.tidytextmining.com>

Reading in texts using the `gutenbergr` package

```
titles <- c("Twenty Thousand Leagues under the Sea", "The War of the Worlds")
books <- gutenberg_works(title %in% titles) %>%
  gutenberg_download(meta_fields = "title")

> books
# A tibble: 18,609 x 3
  gutenberg_id text
  <int> <chr>
1          36 The War of the Worlds
2          36 ""
3          36 by H. G. Wells [1898]
4          36 ""
5          36 ""
6          36 "    But who shall dwell in these worlds if they be"
7          36 "    inhabited? . . . Are we or they Lords of the"
8          36 "    World? . . . And how are all things made for man?--"
9          36 "        KEPLER (quoted in The Anatomy of Melancholy)"
10         36 ""
# ... with 18,599 more rows
```

	text	title
1	The War of the Worlds	The War of the Worlds
2	"	The War of the Worlds
3	by H. G. Wells [1898]	The War of the Worlds
4	"	The War of the Worlds
5	"	The War of the Worlds
6	" But who shall dwell in these worlds if they be"	The War of the Worlds
7	" inhabited? . . . Are we or they Lords of the"	The War of the Worlds
8	" World? . . . And how are all things made for man?--"	The War of the Worlds
9	" KEPLER (quoted in The Anatomy of Melancholy)"	The War of the Worlds
10	"	The War of the Worlds

- In the above code I read in two books using the `gutenbergr` package which reads them from the Project Gutenberg library (containing over 58,000 free books). The object `books` contains the text of both books contained in the “text” column

```
text_waroftheworlds <- books %>%
  filter(title == "The War of the Worlds") %>%
  unnest_tokens(word, text) %>%
  anti_join(stop_words)

text_underthesea <- books %>%
  filter(title == "Twenty Thousand Leagues under the Sea") %>%
  unnest_tokens(word, text) %>%
  anti_join(stop_words)
```

- I then filter by book title and ‘unnest’ the text of each book so that we have one column in each of two dataframes corresponding to the words in each book...

```
> text_waroftheworlds
# A tibble: 60,513 x 3
  gutenberg_id title          word
  <int> <chr>        <chr>
1           36 The War of the Worlds the
2           36 The War of the Worlds war
3           36 The War of the Worlds of
4           36 The War of the Worlds the
5           36 The War of the Worlds worlds
6           36 The War of the Worlds by
7           36 The War of the Worlds h
8           36 The War of the Worlds g
9           36 The War of the Worlds wells
10          36 The War of the Worlds 1898
# ... with 60,503 more rows
```

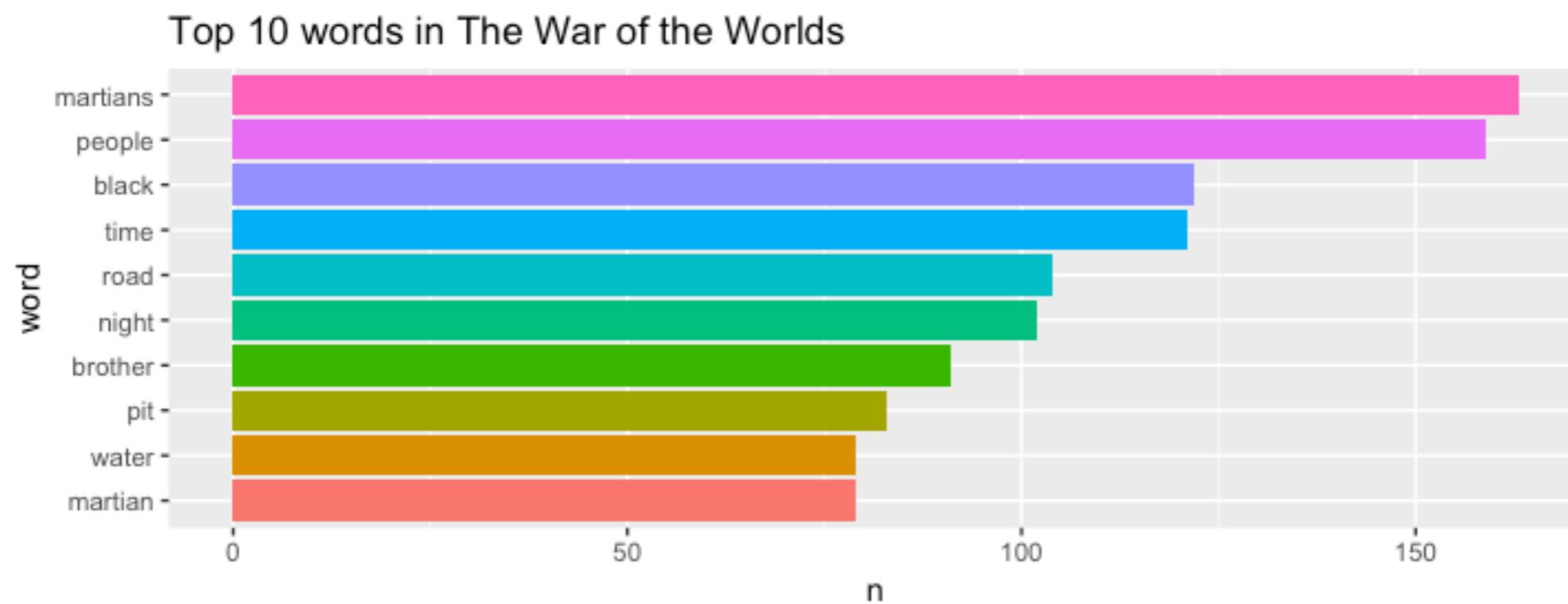
- If I hadn't use the `anti_join(stopwords)` call I would end up with a data frame like the above containing lots of common function words.

- But by adding the `anti_join(stopwords)` line to my code I exclude all stop words (the common function words) and end up with:

```
> text_waroftheworlds
# A tibble: 22,583 x 3
  gutenberg_id title          word
        <int> <chr>        <chr>
1            36 The War of the Worlds war
2            36 The War of the Worlds worlds
3            36 The War of the Worlds 1898
4            36 The War of the Worlds dwell
5            36 The War of the Worlds worlds
6            36 The War of the Worlds inhabited
7            36 The War of the Worlds lords
8            36 The War of the Worlds world
9            36 The War of the Worlds kepler
10           36 The War of the Worlds quoted
# ... with 22,573 more rows
```

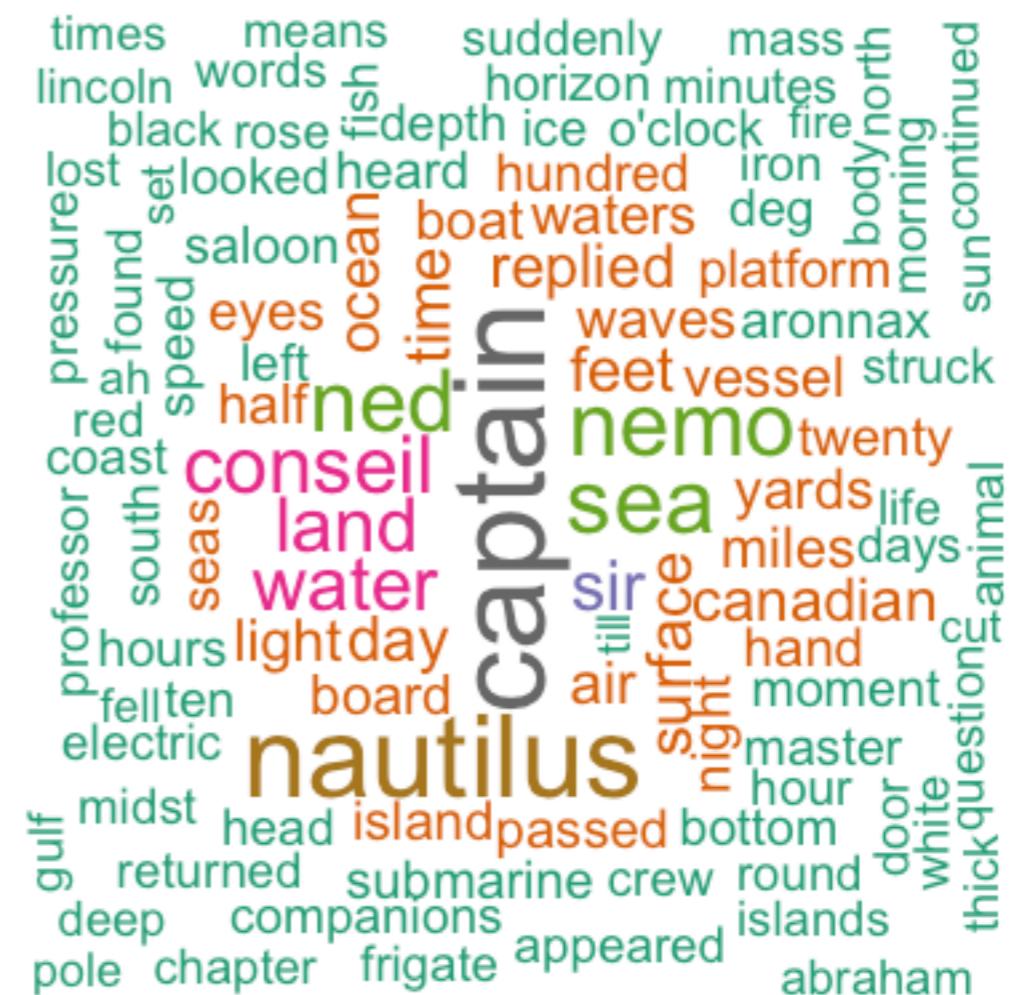
- I can plot the top 10 most common words in The War of the Worlds with this code:

```
text_waroftheworlds %>%
  count(word) %>%
  top_n(10) %>%
  mutate(word = reorder(word, n)) %>%
  ggplot(aes(x = word, y = n, fill = word)) +
  geom_col() +
  coord_flip() +
  guides(fill = FALSE) +
  labs(title = "Top 10 word in The War of the Worlds")
```



- Plotting a wordcloud based on the words in 20,000 Leagues Under the Sea.

```
text_underthesea_count <- text_underthesea %>%  
  count(word) %>%  
  top_n(200)  
  
wordcloud(words = text_underthesea_count$word,  
          freq = text_underthesea_count$n,  
          min.freq = 1,  
          scale = c(3, 1),  
          max.words = 200,  
          random.order = FALSE,  
          rot.per = 0.35,  
          colors = brewer.pal(8, "Dark2"))
```



BBC-style Visualisations

- The BBC have published their R graphics cookbook for generating data visualisations following the BBC style guide.

- The cookbook can be found here:

<https://bbc.github.io/rcookbook/#how does the bbplot package work>

- With the `bbplot` package containing the functions used to generate BBC-style visualisations available on GitHub:

<https://github.com/bbc/bbplot>

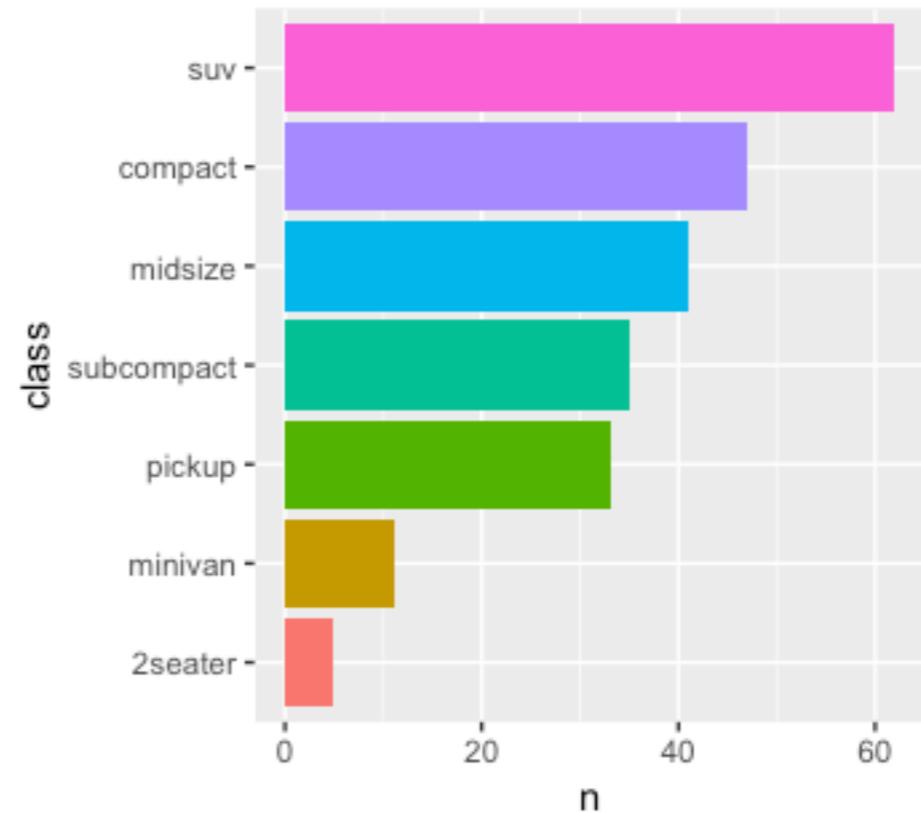
- Let's start with a basic plot - we're going to use the built-in mpg dataset.

```
devtools::install_github('bbc/bbplot')

library(tidyverse)
library(bbplot)

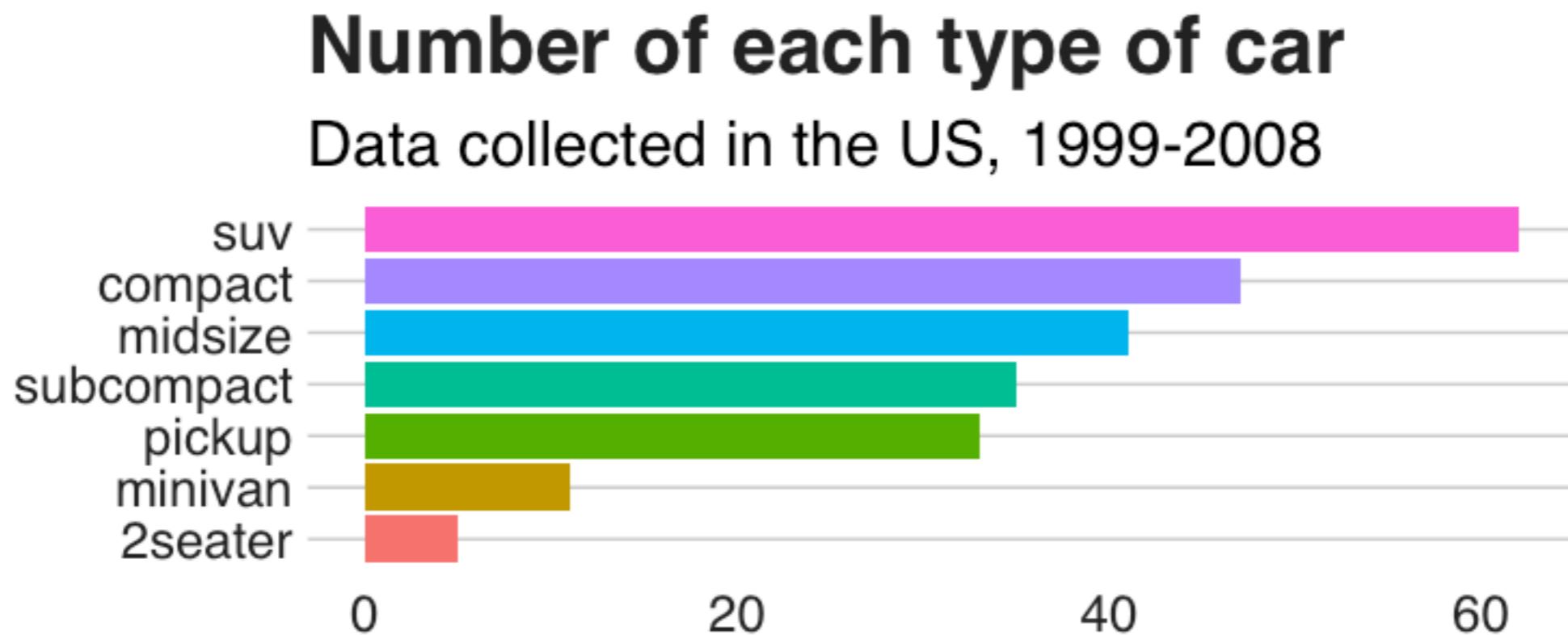
my_plot <- mpg %>%
  count(class) %>%
  mutate(class = fct_reorder(class, n)) %>%
  ggplot(aes(x = class, y = n, fill = class)) +
  geom_col() +
  coord_flip() +
  guides(fill = FALSE)

my_plot
```



- We can add an extra parameter to our ggplot code to set the BBC theme using `bbc_style()`:

```
my_plot <- mpg %>%
  count(class) %>%
  mutate(class = fct_reorder(class, n)) %>%
  ggplot(aes(x = class, y = n, fill = class)) +
  geom_col() +
  coord_flip() +
  guides(fill = FALSE) +
  bbc_style() +
  labs(title = "Number of each type of car",
       subtitle = "Data collected in the US, 1999-2008")
```



Get ready to code...

- The worksheet contains a number of possible exercises to work on - you probably won't have time to do them all so start with the one you think will be more interesting/useful to you!