The Bootstrap

Packages for this section

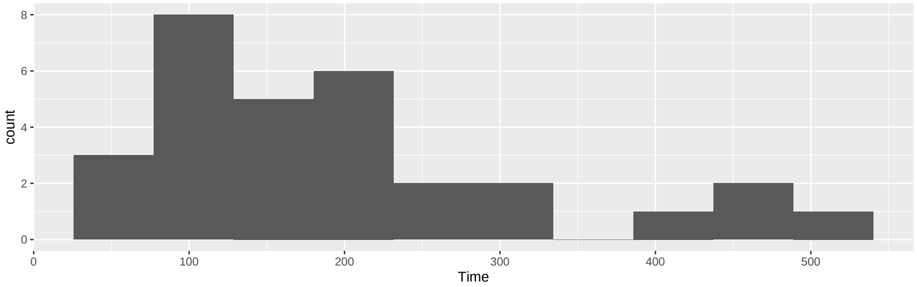
```r
library(tidyverse)
library(bootstrap)
```

My source for this

Is my sampling distribution normal enough?

- Recall the IRS data that we used as a motivation for the sign test:

```
ggplot(irs, aes(x=Time))+geom_histogram(bins=10)
```



- We said that a t procedure for the mean would not be a good idea because the distribution is skewed.

What *actually* matters

- It's not the distribution of the *data* that has to be approx normal (for a t procedure).
- What matters is the *sampling distribution of the sample mean*.
- If the sample size is large enough, the sampling distribution will be normal enough even if the data distribution is not.
  - This is why we had to consider the sample size as well as the shape.
- But how do we know whether this is the case or not? We only have *one* sample.

The (nonparametric) bootstrap

- Typically, our sample will be reasonably representative of the population.
- Idea: pretend the sample *is* the population, and sample from it *with replacement*.
- Calculate test statistic, and repeat many times.
- This gives an idea of how our statistic might vary in repeated samples: that is, its sampling distribution.
- Called the **bootstrap distribution** of the test statistic.
- If the bootstrap distribution is approx normal, infer that the true sampling distribution also approx normal, therefore inference about the mean such as t is good enough.
- If not, we should be more careful.

Why it works

- We typically estimate population parameters by using the corresponding sample thing: eg. estimate population mean using sample mean.
- This called **plug-in principle**.
- The fraction of sample values less than a value x called the **empirical distribution function** (as a function of x).
- By plug-in principle, the empirical distribution function is an estimate of the population CDF.
- In this sense, the sample *is* an estimate of the population, and so sampling from it is an estimate of sampling from the population.

Bootstrapping the IRS data

- Sampling with replacement is done like this (the default sample size is as long as the original data):

```
boot <- sample(irs$Time, replace=T)
mean(boot)
```

```
## [1] 216.9333
```

- That's one bootstrapped mean. We need a whole bunch.

A whole bunch

- Use the same idea as for simulating power:

```
tibble(sim = 1:1000) %>%
  rowwise() %>%
  mutate(boot_sample = list(sample(irs$Time, replace = TRUE)))
```

```
## # A tibble: 1,000 x 2
##       sim boot_sample
##     <int> <list>
##  1      1 <dbl [30]>
##  2      2 <dbl [30]>
##  3      3 <dbl [30]>
##  4      4 <dbl [30]>
##  5      5 <dbl [30]>
##  6      6 <dbl [30]>
##  7      7 <dbl [30]>
##  8      8 <dbl [30]>
##  9      9 <dbl [30]>
## 10     10 <dbl [30]>
```

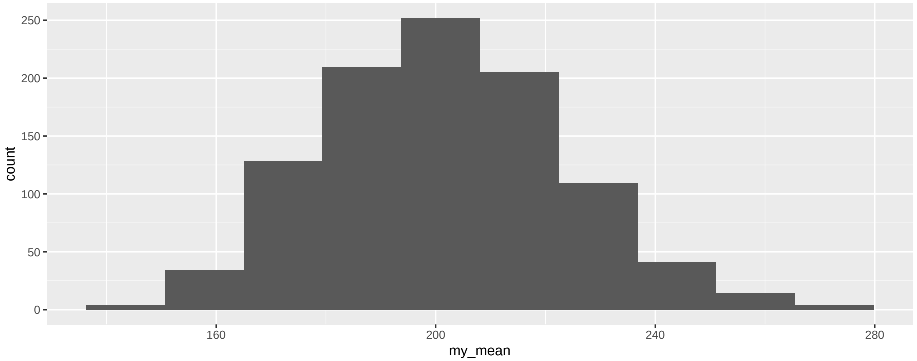
Get the mean of each of those

```
tibble(sim = 1:1000) %>%
  rowwise() %>%
  mutate(boot_sample = list(sample(irs$Time, replace = TRUE))) %>%
  mutate(my_mean = mean(boot_sample)) -> samples
samples
```

```
## # A tibble: 1,000 x 3
##       sim boot_sample my_mean
##     <int> <list>        <dbl>
##  1      1 <dbl [30]>     196
##  2      2 <dbl [30]>     202.
##  3      3 <dbl [30]>     263.
##  4      4 <dbl [30]>     173.
##  5      5 <dbl [30]>     204.
##  6      6 <dbl [30]>     197.
##  7      7 <dbl [30]>     210.
##  8      8 <dbl [30]>     160.
##  9      9 <dbl [30]>     198.
## 10     10 <dbl [30]>     178.
```

Sampling distribution of sample mean

```
ggplot(samples, aes(x=my_mean)) + geom_histogram(bins=10)
```

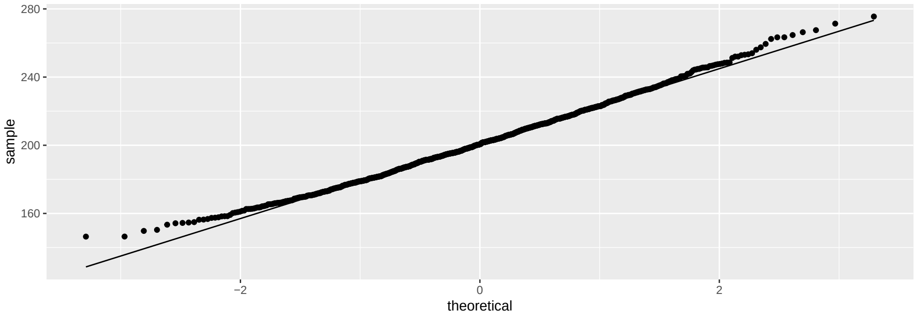


- Is that a slightly long right tail?

Normal quantile plot

might be better than a histogram:

```
ggplot(samples, aes(sample = my_mean)) +
  stat_qq()+stat_qq_line()
```



- a very very slight right-skewness, but very close to normal.

Confidence interval from the bootstrap distribution

There are two ways (at least):

- percentile bootstrap interval: take the 2.5 and 97.5 percentiles (to get the middle 95%). This is easy, but not always the best:

```
(b_p=quantile(samples$my_mean, c(0.025, 0.975)))
```

```
##      2.5%     97.5%
## 162.5775 246.9092
```

- bootstrap t: use the SD of the bootstrapped sampling distribution as the SE of the estimator of the mean and make a t interval:

```
n <- length(irs$Time)
t_star <- qt(0.975, n-1)
b_t <- with(samples, mean(my_mean)+c(-1, 1)*t_star*sd(my_mean))
b_t
```

```
## [1] 156.5070 246.4032
```

Comparing

- get ordinary t interval:

```
my_names=c("LCL", "UCL")
o_t <- t.test(irs$Time)$conf.int
```

- Compare the 2 bootstrap intervals with the ordinary t-interval:

```
tibble(limit=my_names, o_t, b_t, b_p)
```

```
## # A tibble: 2 x 4
##   limit   o_t   b_t   b_p
##   <chr> <dbl> <dbl> <dbl>
## 1 LCL    155.  157.  163.
## 2 UCL    247.  246.  247.
```

- The bootstrap t and the ordinary t are very close
- The percentile bootstrap interval is noticeably shorter (common) and higher (skewness).

Which to prefer?

- If the intervals agree, then they are all good.
- If they disagree, they are all bad!
- In that case, use BCA interval (over).

Bias correction and acceleration

- this from “An introduction to the bootstrap”, by Brad Efron and Robert J. Tibshirani.
- there is way of correcting the CI for skewness in the bootstrap distribution, called the BCa method
- complicated (see the Efron and Tibshirani book), but implemented in `bootstrap` package.

Run this on the IRS data:

```
bca=bcanon(irs$Time, 1000, mean)
bca$confpoints
```

```
##      alpha bca point
## [1,] 0.025  161.8333
## [2,] 0.050  168.0667
## [3,] 0.100  174.8333
## [4,] 0.160  180.7667
## [5,] 0.840  224.1333
## [6,] 0.900  232.3000
## [7,] 0.950  241.9333
## [8,] 0.975  253.7333
```

use 2.5% and 97.5% points for CI

```r
bca$confpoints %>% as_tibble() %>%
  filter(alpha %in% c(0.025, 0.975)) %>%
  pull(`bca point`) -> b_bca
b_bca
```

```
## [1] 161.8333 253.7333
```

Comparing

```r
tibble(limit=my_names, o_t, b_t, b_p, b_bca)
```

```
## # A tibble: 2 x 5
##   limit   o_t   b_t   b_p b_bca
##   <chr> <dbl> <dbl> <dbl> <dbl>
## 1 LCL    155.  157.  163.  162.
## 2 UCL    247.  246.  247.  254.
```

- The BCA interval says that the mean should be estimated even higher than the bootstrap percentile interval does.
- The BCA interval is the one to trust.

Bootstrapping the correlation

Recall the soap data:

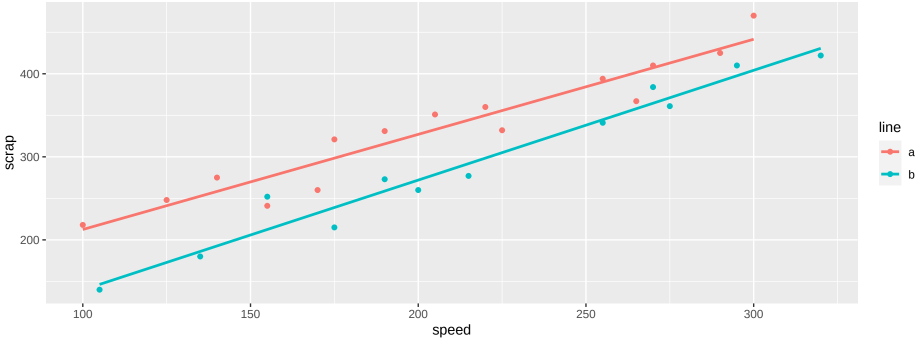
```
url <- "http://ritsokiguess.site/datafiles/soap.txt"
soap <- read_delim(url," ")
soap
```

```
## # A tibble: 27 x 4
##      case scrap speed line
##     <dbl> <dbl> <dbl> <chr>
##  1      1   218   100 a
##  2      2   248   125 a
##  3      3   360   220 a
##  4      4   351   205 a
##  5      5   470   300 a
##  6      6   394   255 a
##  7      7   332   225 a
##  8      8   321   175 a
```

Scatterplot

```r
ggplot(soap, aes(x=speed, y=scrap, colour=line))+
  geom_point()+geom_smooth(method="lm", se=F)
```

```
## `geom_smooth()` using formula 'y ~ x'
```



Comments

- Line B produces less scrap for any given speed.
- For line B, estimate the correlation between speed and scrap (with a confidence interval.)

Extract the line B data; standard correlation test

```
soap %>% filter(line=="b") -> line_b
with(line_b, cor.test(speed, scrap))
```

```
##
##  Pearson's product-moment correlation
##
## data:  speed and scrap
## t = 15.829, df = 10, p-value = 2.083e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9302445 0.9947166
## sample estimates:
##       cor
## 0.9806224
```

Bootstrapping a correlation 1/2

- This illustrates a different technique: we need to keep the x and y values *together*.
- Sample *rows* of the data frame rather than individual values of `speed` and `scrap`:

```
line_b %>% sample_frac(replace=T)
```

```
## # A tibble: 12 x 4
##     case scrap speed line
##    <dbl> <dbl> <dbl> <chr>
##  1    19   341   255 b
##  2    19   341   255 b
##  3    19   341   255 b
##  4    17   277   215 b
##  5    16   140   105 b
##  6    20   215   175 b
##  7    18   384   270 b
##  8    19   341   255 b
##  9    21   180   135 b
## 10    26   273   190 b
## 11    17   277   215 b
## 12    27   410   295 b
```

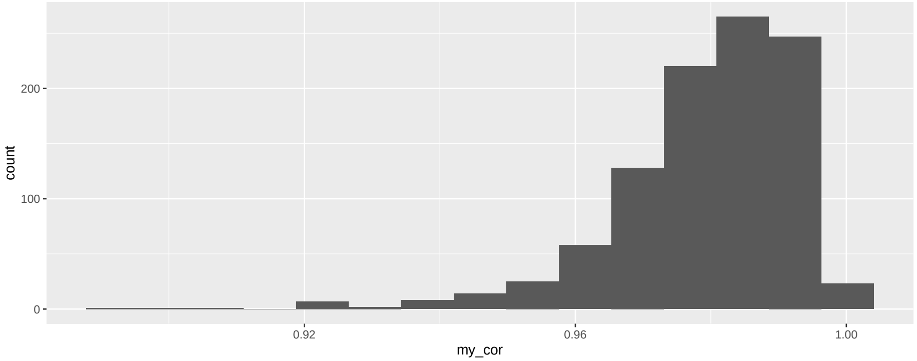
Bootstrapping a correlation 2/2

1000 times:

```
tibble(sim = 1:1000) %>%
  rowwise() %>%
  mutate(boot_df = list(sample_frac(line_b, replace = TRUE)))
  mutate(my_cor = with(boot_df, cor(speed, scrap))) -> cors
```

A picture of this

```
ggplot(cors, aes(x=my_cor))+geom_histogram(bins=15)
```



Comments and next steps

- This is very left-skewed.
- Bootstrap percentile interval is:

```
(b_p=quantile(cors$my_cor, c(0.025, 0.975)))
```

```
##      2.5%     97.5% 
## 0.9450798 0.9962227
```

- We probably need the BCA interval instead.

Getting the BCA interval 1/2

- To use bcanon, write a function that takes a vector of row numbers and returns the correlation between speed and scrap for those rows:

```
theta=function(rows, d) {
  d %>% slice(rows) %>% with(., cor(speed, scrap))
}
theta(1:3, line_b)
```

```
## [1] 0.9928971
```

```
line_b %>% slice(1:3)
```

```
## # A tibble: 3 x 4
##    case scrap speed line
##   <dbl> <dbl> <dbl> <chr>
## 1    16   140   105 b
## 2    17   277   215 b
## 3    18   384   270 b
```

- That looks about right.

Getting the BCA interval 2/2

- Inputs to `bcanon` are now:
  - row numbers (1 through 12 in our case: 12 rows in `line_b`)
  - number of bootstrap samples
  - the function we just wrote
  - the data frame:

```
points=bcanon(1:12, 1000, theta, line_b)$confpoints
points %>% as_tibble() %>%
  filter(alpha %in% c(0.025, 0.975)) %>%
  pull(`bca point`) -> b_bca
b_bca
```

```
## [1] 0.9314334 0.9947634
```

Comparing the results

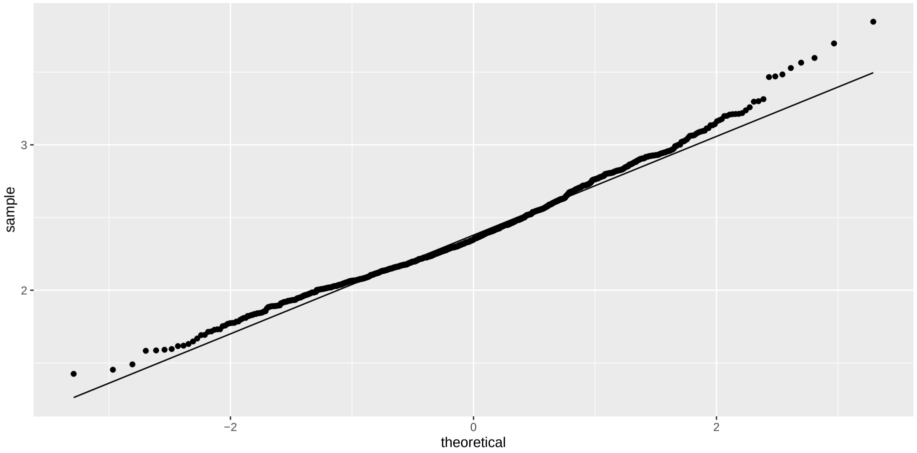
```r
tibble(limit=my_names, o_c, b_p, b_bca)
```

```
## # A tibble: 2 x 4
##   limit   o_c   b_p b_bca
##   <chr> <dbl> <dbl> <dbl>
## 1 LCL   0.930 0.945 0.931
## 2 UCL   0.995 0.996 0.995
```

- The bootstrap percentile interval doesn't go down far enough.
- The BCA interval seems to do a better job in capturing the skewness of the distribution.
- The ordinary confidence interval for the correlation is very similar to the BCA one, and thus seems to be trustworthy here even though the correlation has a very skewed distribution. (`cor.test` uses the Fisher z transformation which "spreads out" correlations close to 1).

The z-transformed bootstrapped correlations

```
cors %>%
  mutate(z = 0.5 * log((1+my_cor)/(1-my_cor))) %>%
  ggplot(aes(sample=z)) + stat_qq() + stat_qq_line()
```


sample
theoretical