

## The bootstrap revisited

## Packages for this section

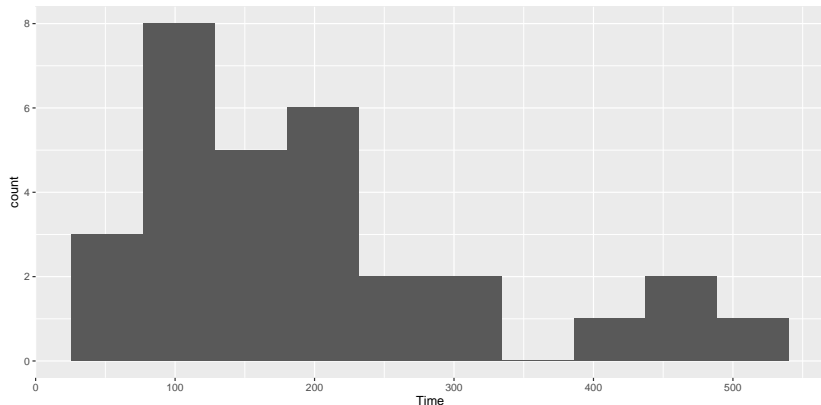
```
library(tidyverse)  
library(bootstrap)
```

Source: Hesterberg et al

# Is my sampling distribution normal enough?

- Recall IRS data (used as a motivation for the sign test) :

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



- $t$  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] 201.2
```

- ▶ 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
```

```
# Rowwise:
```

```
      sim boot_sample  
  <int> <list>  
1      1 1 <dbl [30]>  
2      2 2 <dbl [30]>  
3      3 3 <dbl [30]>  
4      4 4 <dbl [30]>  
5      5 5 <dbl [30]>  
6      6 6 <dbl [30]>  
7      7 7 <dbl [30]>  
8      8 8 <dbl [30]>  
9      9 9 <dbl [30]>  
10     10 10 <dbl [30]>  
# i 990 more rows
```



## 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

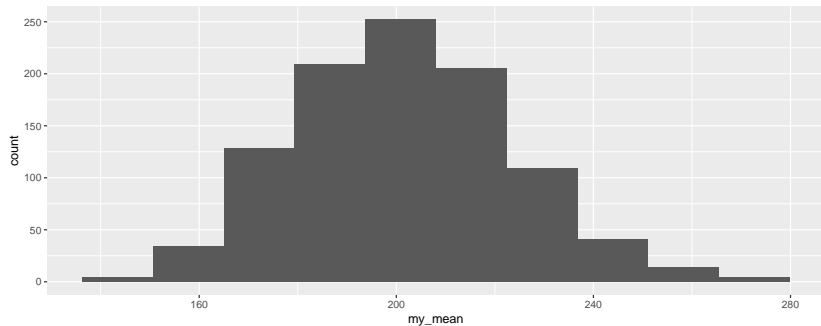
# Rowwise:

	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.

# i 990 more rows

# Sampling distribution of sample mean

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

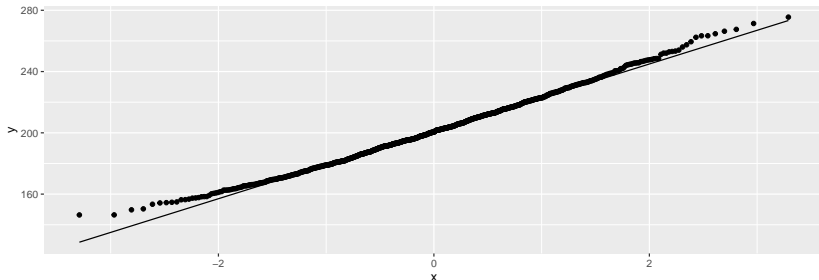


► Is that a slightly long right tail?

# 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

```
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

```
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

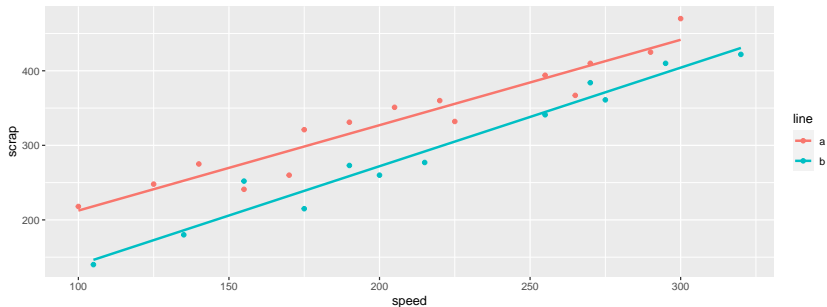
Recall the soap data:

```
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     1    218   100 a
2     2     2    248   125 a
3     3     3    360   220 a
4     4     4    351   205 a
5     5     5    470   300 a
6     6     6    394   255 a
7     7     7    332   225 a
8     8     8    321   175 a
9     9     9    410   270 a
10    10    10    260   170 a
```

# Scatterplot

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



## 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     24   252   155 b
2     22   260   200 b
3     16   140   105 b
4     25  422   320 b
5     16   140   105 b
6     19  341   255 b
7     19  341   255 b
8     19  341   255 b
9     17  277   215 b
10    16   140   105 b
11    20   215   175 b
12    18  384   270 b
```

## Bootstrapping a correlation 2/2

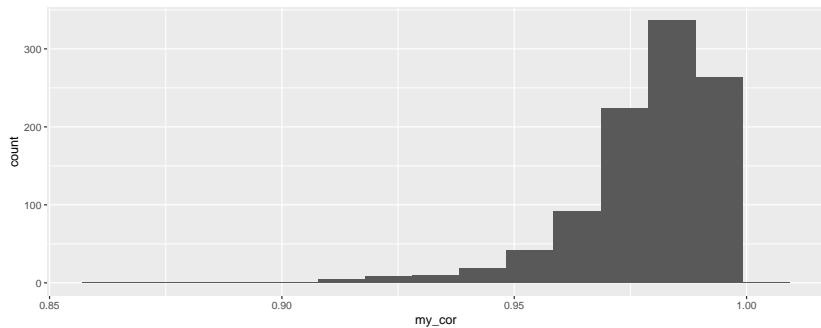
1000 times:

```
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%
0.9415748	0.9962462

- ▶ 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 0.9947799
```

## Comparing the results

```
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 0.942 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()
```

