Simulation and the bootstrap

packages

library(tidyverse)

Simulation

- Sometimes you know the exact mathematical answer to a problem, eg:
 - $\blacktriangleright X_1, \dots X_n \sim N(\mu, \sigma^2)$, what is distribution of \bar{X} ? (Ans: $N(\mu, \sigma^2/n)$.)
- More often, though, you don't:
 - if $X \sim Bin(2,0.5), Y \sim Bin(3,0.2)$, what is dist of Z = X + Y?
- Simulation: generate random X and Y, calculate sum, repeat many times. Gives you (approx) dist of X + Y without any mathematics!

Random numbers in R

- R knows about a lot of distributions, eg: norm binom pois exp gamma t chisq (type ?distributions in Console to see more)
- ▶ to generate random numbers from a distribution, put r on front of these; inputs are number of random values to generate, and parameters of distribution to simulate from.
- **E**xamples:

rpois(10, 3.5)

```
rnorm(5, 100, 15)
[1] 111.96072 89.80331 113.74231 90.74167 89.86461
and
```

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

Our problem: simulating once

if $X \sim Bin(2,0.5), Y \sim Bin(3,0.2)$, what is dist of Z = X + Y?

[1] 1

У

[1] 1

x + y

[1] 2

To simulate many times: - set up dataframe with space for each simulated value - work rowwise - do one simulation per row

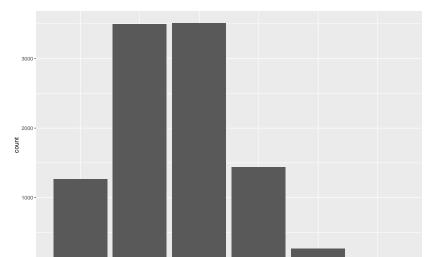
Simulating many times

```
tibble(sim = 1:10000) %>%
 rowwise() %>%
 mutate(x = rbinom(1, 2, 0.5),
        y = rbinom(1, 3, 0.2),
        z = x + y) \rightarrow d
d
# A tibble: 10,000 x 4
# Rowwise:
    sim x y
  <int> <int> <int> <int>
   5 1
      6 2
```

Distribution of sum

Make a bar chart rather than a histogram because distribution of ${\cal Z}$ is discrete:

$$ggplot(d, aes(x = z)) + geom_bar()$$



(Simulated) probability that the sum is at least 4:

Only this much:

```
285/10000
```

[1] 0.0285

A sum of 5 is possible though very unlikely.

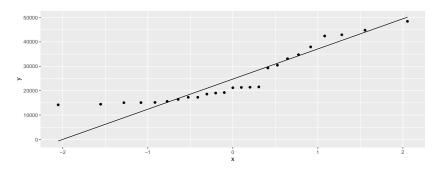
The bootstrap

Source: Hesterberg et al

- Sampling distribution of a statistic is distribution of that statistic over "all possible samples" from population of interest.
- "Plug-in principle": sample mean estimates population mean, sample variance estimates population variance, etc.
- Also, sample is estimate of population (precisely, proportion of sample values $\leq x$ estimates probability of drawing value $\leq x$ from population, for any x).
- As long as your sample is representative, sampling from the sample (!) is an estimate of sampling from the population. Called a bootstrap sample.
- Sample from sample *with* replacement, or else you get original sample back.

Blue Jays attendances:

```
ggplot(jays, aes(sample = attendance)) +
stat_qq() + stat_qq_line()
```



- t procedure for the mean may not be a good idea because the distribution is skewed.
- Previously: hand-waving with sample size.

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.
- Use the bootstrap to simulate sampling distribution.

Simulating the sampling distribution of sample statistic

- Sample from our sample with replacement.
- Calculate statistic
- Repeat many times (simulation).
- This gives an idea of how our statistic might vary in repeated samples: that is, its sampling distribution.
- Called the bootstrap distribution of the 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.

Bootstrapping the Blue Jays attendances

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

```
boot <- sample(jays$attendance, replace=TRUE)
sort(jays$attendance)</pre>
```

```
[1] 14184 14433 15062 15086 15168 15606 16402 17264 17276 [13] 21195 21312 21397 21519 29306 30430 33086 34743 37929 [25] 48414
```

```
sort(boot)
```

```
[1] 14184 14433 14433 15086 15086 15168 15168 16402 17264 [13] 17276 17276 18581 19014 21312 21519 33086 37929 42419 [25] 48414
```

```
mean(boot)
```

[1] 23764.76

A whole bunch

4 5

▶ We are now doing a simulation. I like 10,000 samples when testing for normality:

```
tibble(sim = 1:10000) %>%
  rowwise() %>%
  mutate(boot_sample = list(sample(jays$attendance, replace
  mutate(my_mean = mean(boot_sample)) -> samples
samples
```

```
# Rowwise:
sim boot_sample my_mean
<int> <1 1 <dbl [25]> 23055.
```

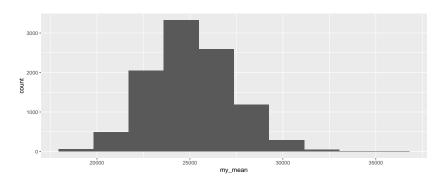
2 <dbl [25]> 25513. 3 <dbl [25]> 25563. 4 <dbl [25]> 29198.

5 <dbl [25]> 23615.

A tibble: 10,000 x 3

Sampling distribution of sample mean

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

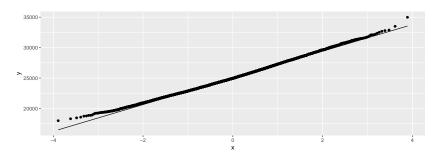


Is that a slightly long right tail?

Normal quantile plot

might be better than a histogram:

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

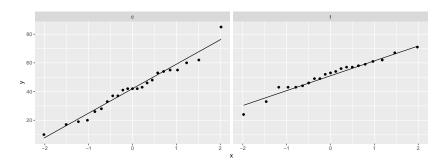


- a very very slight right-skewness, but very close to normal.
- \blacktriangleright hence the t-test is fine for the Blue Jays attendances.

Kids learning to read

Normal quantile plots, one for each sample:

```
ggplot(kids, aes(sample = score)) +
  stat_qq() + stat_qq_line() +
  facet_wrap(~ group)
```



These both look close to normal.

Control group

- ► Pull out control group children
- ▶ Obtain bootstrap sampling distribution of scores

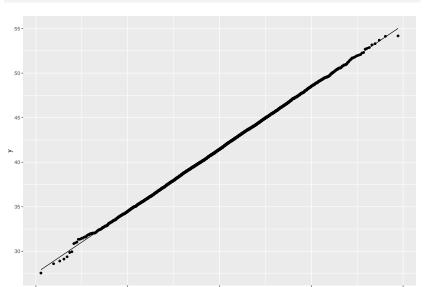
```
kids %>% filter(group == "c") -> controls
tibble(sim = 1:10000) %>%
   rowwise() %>%
   mutate(my_sample = list(sample(controls$score, replace =
   mutate(my_mean = mean(my_sample)) -> samples1
samples1
```

```
# A tibble: 10,000 x 3
# Rowwise:
    sim my sample my_mean
```

- 3 3 <dbl [23]> 44.3 4 4 <dbl [23]> 40.8

The bootstrap sampling distribution

```
ggplot(samples1, aes(sample = my_mean)) +
  stat_qq() + stat_qq_line()
```

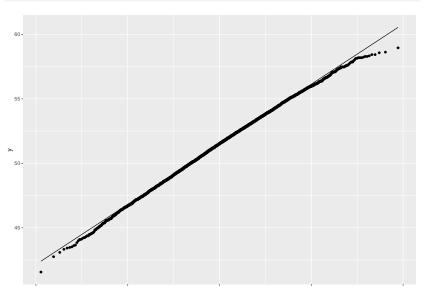


Same, for treatment group

```
kids %>% filter(group == "t") -> treated
tibble(sim = 1:10000) %>%
   rowwise() %>%
   mutate(my_sample = list(sample(treated$score, replace = "mutate(my_mean = mean(my_sample)) -> samples2
```

The bootstrap sampling distribution

```
ggplot(samples2, aes(sample = my_mean)) +
  stat_qq() + stat_qq_line()
```



Pain relief

▶ With matched pairs, assumption is of normality of differences:

```
pain %>% mutate(diff = druga - drugb) -> pain
pain
```

```
A tibble: 12 x 4
  subject druga drugb diff
    <dbl> <dbl> <dbl> <dbl>
1
           2
                 3.5 - 1.5
2
        2 \quad 3.6 \quad 5.7 \quad -2.1
3
        3 2.6 2.9 -0.300
4
        4 2.6 2.4 0.200
5
        5 7.3 9.9 -2.6
6
        6 3.4 3.3 0.100
        7
           14.9 16.7 -1.80
8
        8
           6.6 6 0.600
9
        9 2.3 3.8 -1.5
10
       10
                 4
           2
                      -2
```

Bootstrap sampling distribution of differences

3 <dbl [12]> -2.66

5 <dbl [12]> -0.975

6 <dbl [12]> -2.25

7 <dbl [12]> -2.32

8 <dbl [12]> -1.84

4 <dbl [12]> -2.9

3

4

5

6

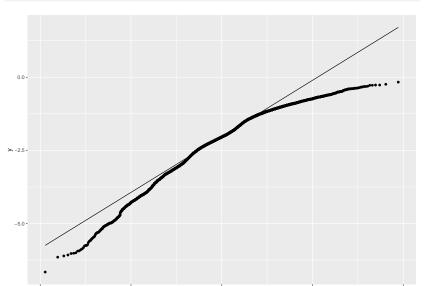
7

8

```
tibble(sim = 1:10000) %>%
 rowwise() %>%
 mutate(my_sample = list(sample(pain$diff, replace = TRUE)
 mutate(my_mean = mean(my_sample)) -> samples
samples
# A tibble: 10,000 x 3
# Rowwise:
     sim my sample my mean
   <int> <list> <dbl>
 1
      1 <dbl [12]> -1.82
      2 <dbl [12]> -3.58
```

Assess it for normality

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



Histogram with many bins

 $ggplot(samples, aes(x = my_mean)) + geom_histogram(bins = 0)$

