Bootstrap for sampling distribution of sample mean

Assessing assumptions

- Our t-tests assume normality of variable being tested
- but, Central Limit Theorem says that normality matters less if sample is "large"
- in practice "approximate normality" is enough, but how do we assess whether what we have is normal enough?
- so far, use histogram/boxplot and make a call, allowing for sample size.

What actually has to be normal

- is: **sampling distribution of sample mean**
- the distribution of sample mean over *all possible samples*
- but we only have *one* sample!
- Idea: assume our sample is representative of the population, and draw samples from our sample (!), with replacement.
- This gives an idea of what different samples from the population might look like.
- Called *bootstrap*, after expression “to pull yourself up by your own bootstraps”.

Packages

```
library(tidyverse)
```

Blue Jays attendances

```
jays$attendance
```

```
 [1] 48414 17264 15086 14433 21397 34743 44794 14184 15606
[10] 18581 19217 21519 21312 30430 42917 42419 29306 15062
[19] 16402 19014 21195 33086 37929 15168 17276
```

- A bootstrap sample:

```
s <- sample(jays$attendance, replace = TRUE)
s
```

```
 [1] 21195 34743 21312 44794 16402 19014 34743 21195 17264
[10] 18581 19014 19217 34743 19217 14433 15062 16402 15062
[19] 34743 15062 15086 15168 15086 48414 30430
```

Sorting

- It is easier to see what is happening if we sort both the actual attendances and the bootstrap sample:

```
sort(jays$attendance)
```

```
 [1] 14184 14433 15062 15086 15168 15606 16402 17264 17276
[10] 18581 19014 19217 21195 21312 21397 21519 29306 30430
[19] 33086 34743 37929 42419 42917 44794 48414
```

```
sort(s)
```

```
 [1] 14433 15062 15062 15062 15086 15086 15168 16402 16402
[10] 17264 18581 19014 19014 19217 19217 21195 21195 21312
[19] 30430 34743 34743 34743 34743 44794 48414
```

Getting mean of bootstrap sample

- A bootstrap sample is same size as original, but contains repeated values (eg. 15062) and missing ones (42917).
- We need the mean of our bootstrap sample:

```
mean(s)
```

```
[1] 23055.28
```

- This is a little different from the mean of our actual sample:

```
mean(jays$attendance)
```

```
[1] 25070.16
```

- Want a sense of how the sample mean might vary, if we were able to take repeated samples from our population.
- Idea: take lots of *bootstrap* samples, and see how *their* sample means vary.

Setting up bootstrap sampling

- Begin by setting up a dataframe that contains a row for each bootstrap sample. I usually call this column `sim`. Do just 4 to get the idea:

```
tibble(sim = 1:4)
```

```
# A tibble: 4 x 1
    sim
  <int>
1     1
2     2
3     3
4     4
```

Drawing the bootstrap samples

- Then set up to work one row at a time, and draw a bootstrap sample of the attendances in each row:

```
tibble(sim = 1:4) %>%
  rowwise() %>%
  mutate(sample = list(sample(jays$attendance,
                              replace = TRUE)))
```

```
# A tibble: 4 x 2
# Rowwise:
    sim sample
  <int> <list>
1     1 <dbl [25]>
2     2 <dbl [25]>
3     3 <dbl [25]>
4     4 <dbl [25]>
```

- Each row of our dataframe contains *all* of a bootstrap sample of 25

Sample means

- Find the mean of each sample:

```
tibble(sim = 1:4) %>%
  rowwise() %>%
  mutate(sample = list(sample(jays$attendance,
                              replace = TRUE))) %>%
  mutate(my_mean = mean(sample))
```

```
# A tibble: 4 x 3
# Rowwise:
    sim sample     my_mean
  <int> <list>       <dbl>
1     1 <dbl [25]>  28472.
2     2 <dbl [25]>  28648.
3     3 <dbl [25]>  23329.
4     4 <dbl [25]>  24808.
```

- These are (four simulated values of) the bootstrapped sampling

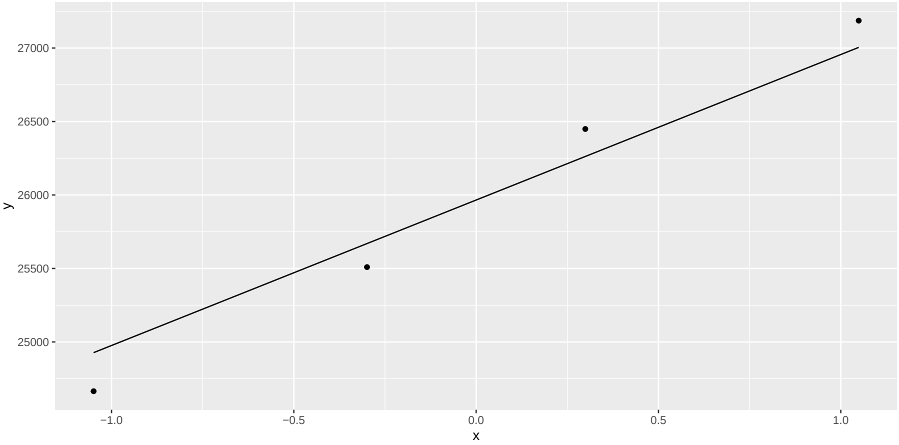
Make a normal quantile plot of them

- rather pointless here, but to get the idea:

```
tibble(sim = 1:4) %>%
  rowwise() %>%
  mutate(sample = list(sample(jays$attendance, replace = TRUE)
  mutate(my_mean = mean(sample)) %>%
  ggplot(aes(sample = my_mean)) +
    stat_qq() + stat_qq_line() -> g
```

The (pointless) plot

```
g
```



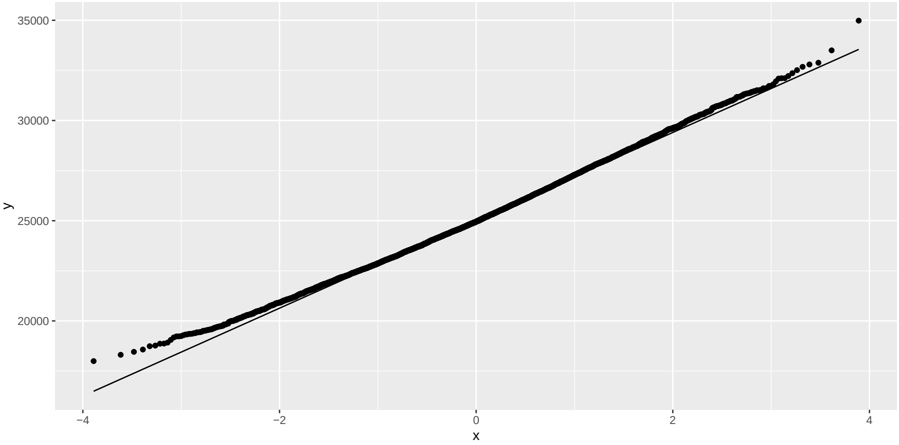
Now do again with a decent number of bootstrap samples

- say 10000, to get a good look at the tails:

```
tibble(sim = 1:10000) %>%
  rowwise() %>%
  mutate(sample = list(sample(jays$attendance,
                              replace = TRUE))) %>%
  mutate(my_mean = mean(sample)) %>%
  ggplot(aes(sample = my_mean)) +
    stat_qq() + stat_qq_line() -> g
```

The (better) plot

```
g
```



Comments

- This is very close to normal (only very slightly right-skewed)
- The bootstrap says that the sampling distribution of the sample mean is close to normal, even though the distribution of the data is not
- A sample size of 25 is big enough to overcome the skewness that we saw
- This is the Central Limit Theorem in practice
- It is surprisingly powerful.
- Thus, the t-test is actually perfectly good here.

Comments on the code 1/2

- You might have been wondering about this:

```
tibble(sim = 1:4) %>%
  rowwise() %>%
  mutate(sample = list(sample(jays$attendance,
                               replace = TRUE)))
```

```
# A tibble: 4 x 2
# Rowwise:
    sim sample
  <int> <list>
1     1 <dbl [25]>
2     2 <dbl [25]>
3     3 <dbl [25]>
4     4 <dbl [25]>
```

Comments on the code 2/2

- how did we squeeze all 25 sample values into one cell?
  - sample is a so-called "list-column" that can contain anything.
- why did we have to put `list()` around the `sample()`?
  - because `sample` produces a collection of numbers, not just a single one
  - the `list()` signals this: "make a list-column of samples".

Two samples

- Assumption: *both* samples are from a normal distribution.
- In this case, each sample should be "normal enough" given its sample size, since Central Limit Theorem will help.
- Use bootstrap on each group independently, as above.

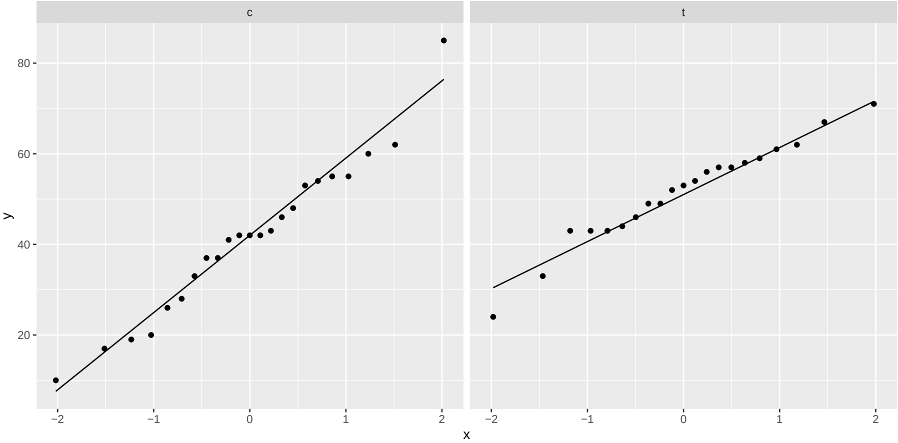
Kids learning to read

```
# A tibble: 44 x 2
   group score
   <chr> <dbl>
 1 t        24
 2 t        61
 3 t        59
 4 t        46
 5 t        43
 6 t        44
 7 t        52
 8 t        43
 9 t        58
10 t        67
# i 34 more rows
```

```
ggplot(kids, aes(x=group, y=score)) + geom_boxplot()
```

or, a normal quantile plot

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



Getting just the control group

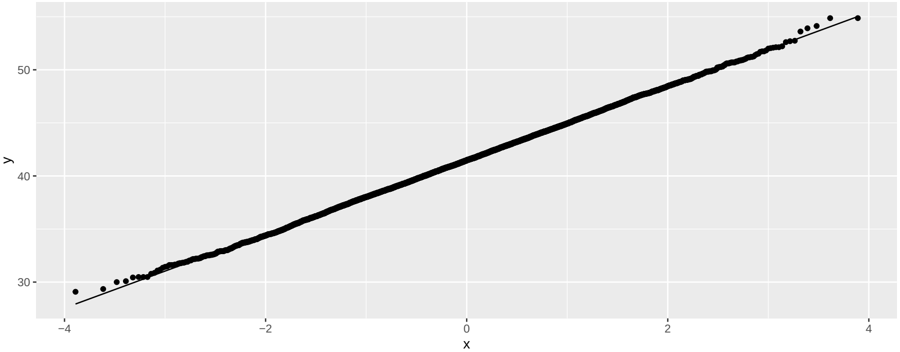
- Use `filter` to select rows where something is true:

```
kids %>% filter(group == "c") -> controls
controls
```

```
# A tibble: 23 x 2
   group score
   <chr> <dbl>
 1 c        42
 2 c        33
 3 c        46
 4 c        37
 5 c        43
 6 c        41
 7 c        10
 8 c        42
 9 c        55
10 c        19
# i 13 more rows
```

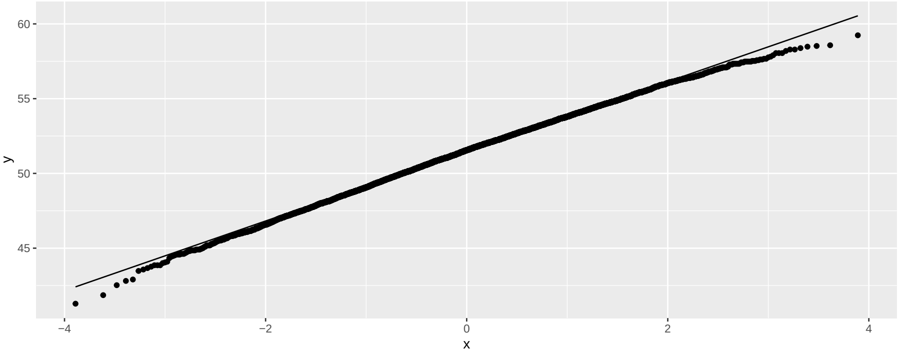
Bootstrap these

```
tibble(sim = 1:10000) %>%
  rowwise() %>%
  mutate(sample = list(sample(controls$score, replace = TRUE))
  mutate(my_mean = mean(sample)) %>%
  ggplot(aes(sample = my_mean)) + stat_qq() + stat_qq_line()
```



… and the treatment group:

```
kids %>% filter(group == "t") -> treats
tibble(sim = 1:10000) %>%
  rowwise() %>%
  mutate(sample = list(sample(treats$score, replace = TRUE)))
  mutate(my_mean = mean(sample)) %>%
  ggplot(aes(sample = my_mean)) + stat_qq() + stat_qq_line()
```



Comments

- sampling distributions of sample means both look pretty normal, though treatment group is a tiny bit left-skewed
- as we thought, no problems with our two-sample t at all.