Assignment 2

Instructions: Make an R Notebook and in it answer the questions below. When you are done, hand in on Quercus the *output* from Previewing (or Knitting) your Notebook. Do *not* hand in the Notebook itself. You want to show that you can (i) write code that will answer the questions, (ii) run that code and get some sensible output, (iii) write some words that show you know what is going on and that reflect your conclusions about the data. Your goal is to convince the grader that you *understand* what you are doing: not only doing the right thing, but making it clear that you know *why* it's the right thing.

Do *not* expect to get help on this assignment. The purpose of the assignments is for you to see how much *you* have understood. You will find that you also learn something from grappling with the assignments. The time to get help is after you watch the lectures and work through the problems from PASIAS, via tutorial and the discussion board, that is *before* you start work on the assignment. The only reasons to contact the instructor while working on an assignment are to report (i) something missing like a data file that cannot possibly be read, (ii) something *beyond your control* that makes it impossible to finish the assignment in time after you have started it.

You have 4 hours to complete this assignment after you start it.

1. The data set at http://ritsokiguess.site/STAC32/cholest.csv contains cholesterol measurements for heart attack patients (at several different times) as well as for a group of control patients. We will focus on the control patients in this question.

   (a) Read in and display (some of) the data.

Solution: This is (as you might guess) a `.csv`, so:

```
my_url <- "http://ritsokiguess.site/STAC32/cholest.csv"
cholest <- read_csv(my_url)
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   `2-Day` = col_double(),
##   `4-Day` = col_double(),
##   `14-Day` = col_double(),
##   control = col_double()
## )
```

```
cholest
```

```
## # A tibble: 30 x 4
##    `2-Day` `4-Day` `14-Day` control
##      <dbl>   <dbl>    <dbl>   <dbl>
##  1     270     218      156     196
##  2     236     234       NA     232
##  3     210     214      242     200
##  4     142     116       NA     242
##  5     280     200       NA     206
##  6     272     276      256     178
##  7     160     146      142     184
##  8     220     182      216     198
##  9     226     238      248     160
## 10     242     288       NA     182
## # ... with 20 more rows
```

Note for yourself that there are 30 observations (and some missing ones), and a column called `control` that is the one we'll be working with.

Extra: the 2-day, 4-day and 14-day columns have the funny "backticks" around their names, because a column name cannot contain a `-` or start with a number. This is not a problem here, since we won't be using those columns, but if we wanted to, this would not work:

```
cholest %>% summarize(xbar = mean(2-Day))
```

```
## Error: Problem with `summarise()` input `xbar`.
## x object 'Day' not found
## i Input `xbar` is `mean(2 - Day)`.
```

because it is looking for a column called `Day`, which doesn't exist. The meaning of `2-Day` is "take the column called `Day` and subtract it from 2". To make this work, we have to supply the backticks ourselves:

```
cholest %>% summarize(xbar = mean(`2-Day`, na.rm = TRUE))
```

```
## # A tibble: 1 x 1
##    xbar
##   <dbl>
## 1  254.
```

This column also has missing values (at the bottom), so here I've asked to remove the missing values[1] before working out the mean. Otherwise the mean is, unhelpfully, missing as well.

You might imagine that dealing with column names like this would get annoying. There is a package called `janitor` that has a function called `clean_names` to save you the trouble. Install it first, then load it:

```
library(janitor)
```

and then pipe your dataframe into `clean_names` and see what happens:

```
cholest %>% clean_names() -> cholest1
cholest1
```

```
## # A tibble: 30 x 4
##    x2_day x4_day x14_day control
##     <dbl>  <dbl>   <dbl>   <dbl>
##  1    270    218     156     196
##  2    236    234      NA     232
##  3    210    214     242     200
##  4    142    116      NA     242
##  5    280    200      NA     206
##  6    272    276     256     178
##  7    160    146     142     184
##  8    220    182     216     198
##  9    226    238     248     160
## 10    242    288      NA     182
## # ... with 20 more rows
```

These are all legit column names; the `-` has been replaced by an underscore, and each of the first three column names has gained an `x` on the front so that it no longer starts with a number. This then works:

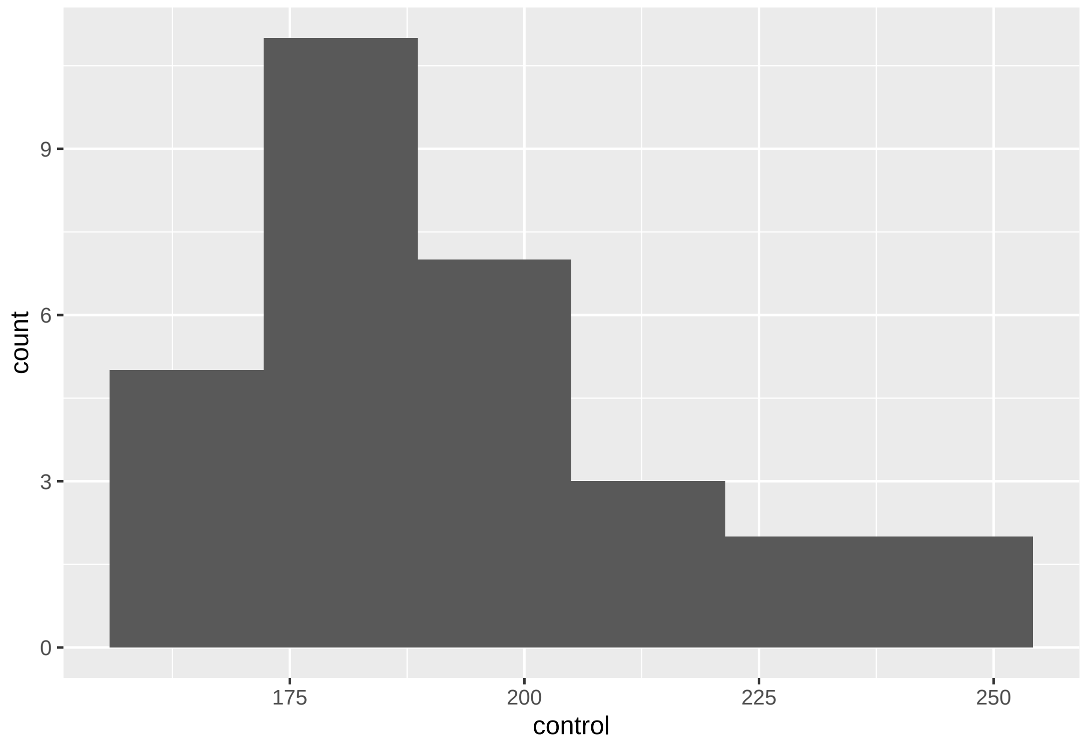
```
cholest1 %>% summarize(xbar = mean(x2_day, na.rm = TRUE))

## # A tibble: 1 x 1
##    xbar
##   <dbl>
## 1  254.
```

(b) Make a suitable plot of the cholesterol levels of the control patients, and comment briefly on the shape of the distribution.

Solution: There is one quantitative variable, so a histogram, as ever:

```
ggplot(cholest, aes(x=control)) + geom_histogram(bins=6)
```



Pick a number of bins that shows the shape reasonably well. Too many or too few won't. (Sturges' rule says 6, since there are 30 observations and $2^5 = 32$.) Seven bins also works, but by the time you get to 8 bins or more, you are starting to lose a clear picture of the shape. Four bins is, likewise, about as low as you can go before getting too crude a picture.

Choosing one of these numbers of bins will make it clear that the distribution is somewhat skewed to the right.

(c) It is recommended that people in good health, such as the Control patients here, keep their cholesterol level below 200. Is there evidence that the mean cholesterol level of the population of people of which the Control patients are a sample is less than 200? Show that you understand the process, and state your conclusion in the context of the data.

Solution: The word "evidence" means to do a hypothesis test and get a P-value. Choose an α first, such as 0.05.

Testing a mean implies a one-sample *t*-test. We are trying to prove that the mean is less than 200, so that's our alternative: $H_a : \mu < 200$, and therefore the null is that the mean is equal to 200: $H_0 : \mu = 200$. (You might think it makes more logical sense to have $H_0 : \mu \geq 200$, which is also fine. As long as the null hypothesis has an equals in it in a logical place, you are good.)

```
with(cholest, t.test(control, mu=200, alternative = "less"))
```

```
##
##  One Sample t-test
##
## data:  control
## t = -1.6866, df = 29, p-value = 0.05121
## alternative hypothesis: true mean is less than 200
## 95 percent confidence interval:
##      -Inf 200.0512
## sample estimates:
## mean of x
##  193.1333
```

This is also good:

```
t.test(cholest$control, mu=200, alternative = "less")
```

```
##
##  One Sample t-test
##
## data:  cholest$control
## t = -1.6866, df = 29, p-value = 0.05121
## alternative hypothesis: true mean is less than 200
## 95 percent confidence interval:
##      -Inf 200.0512
## sample estimates:
## mean of x
##  193.1333
```

I like the first version better because a lot of what we do later involves giving a data frame, and then working with things in that data frame. This is more like that.

This test is *one*-sided because we are looking for evidence of *less*; if the mean is actually *more* than 200, we don't care about that. For a one-sided test, R requires you to say which side you are testing.

The P-value is not (quite) less than 0.05, so we cannot quite reject the null. Therefore, there is no evidence that the mean cholesterol level (of the people of which the control group are a sample) is less than 200. Or, this mean is not significantly less than 200. Or, we conclude that this mean is equal to 200. Or, we conclude that this mean could be 200. Any of those.

If you chose a different α, draw the right conclusion for the α you chose. For example, with $\alpha = 0.10$, we *do* have evidence that the mean is less than 200. Being consistent is more important than getting the same answer as me.

Writing out all the steps correctly shows that you understand the process. Anything less doesn't.

(d) What values could the population mean cholesterol level take? You might need to get some more output to determine this.

Solution:

This is *not* quoting the sample mean, giving that as your answer, and then stopping. The sample mean should, we hope, be somewhere the population mean, but it is almost certainly not the same as the population mean, because there is variability due to random sampling. (This is perhaps the most important thing in all of Statistics: recognizing that variability exists and dealing with it.)

With that in mind, the question means to get a range of values that the population mean could be: that is to say, a confidence interval. The one that came out of the previous output is one-sided, to go with the one-sided test, but confidence intervals for us are two-sided, so we have to run the test again, but two-sided, to get it. To do that, take out the "alternative", thus (you can also take out the null mean, since a confidence interval has no null hypothesis):

```r
with(cholest, t.test(control))
```

```
##
##  One Sample t-test
##
## data:  control
## t = 47.436, df = 29, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  184.8064 201.4603
## sample estimates:
## mean of x
##  193.1333
```

With 95% confidence, the population mean cholesterol level is between 184.8 and 201.5.

You need to state the interval, and you also need to round off the decimal places to something sensible. This is because in your statistical life, you are providing results to someone else *in a manner that they can read and understand.* They do not have time to go searching in some output, or to fish through some excessive number of decimal places. If that's what you give them, they will ask you to rewrite your report, wasting everybody's time when you could have done it right the first time.

How many decimal places is a good number? Look back at your data. In this case, the cholesterol values are whole numbers (zero decimal places). A confidence interval is talking about a mean. In this case, we have a sample size of 30, which is between 10 and 100, so we can justify one extra decimal place beyond the data, here one decimal altogether, or two *at the absolute outside*. (Two is more justifiable if the sample size is bigger than 100.) See, for example, this, in particular the piece at the bottom.

(e) Explain briefly why you would be reasonably happy to trust the t procedures in this question. (There are two points you need to make.)

Solution: The first thing is to look back at the graph you made earlier. This was skewed to the right ("moderately" or "somewhat" or however you described it). This would seem to say that the t procedures were not very trustworthy, since the population distribution doesn't look very normal in shape.

However, the second thing is to look at the sample size. We have the central limit theorem, which says (for us) that the larger the sample is, the less the normality matters, when it comes to estimating the mean. Here, the sample size is 30, which, for the central limit theorem, is large enough to overcome moderate non-normality in the data.

My take, which I was trying to guide you towards, is that our non-normality was not too bad, and so our sample size is large enough to trust the t procedures we used.

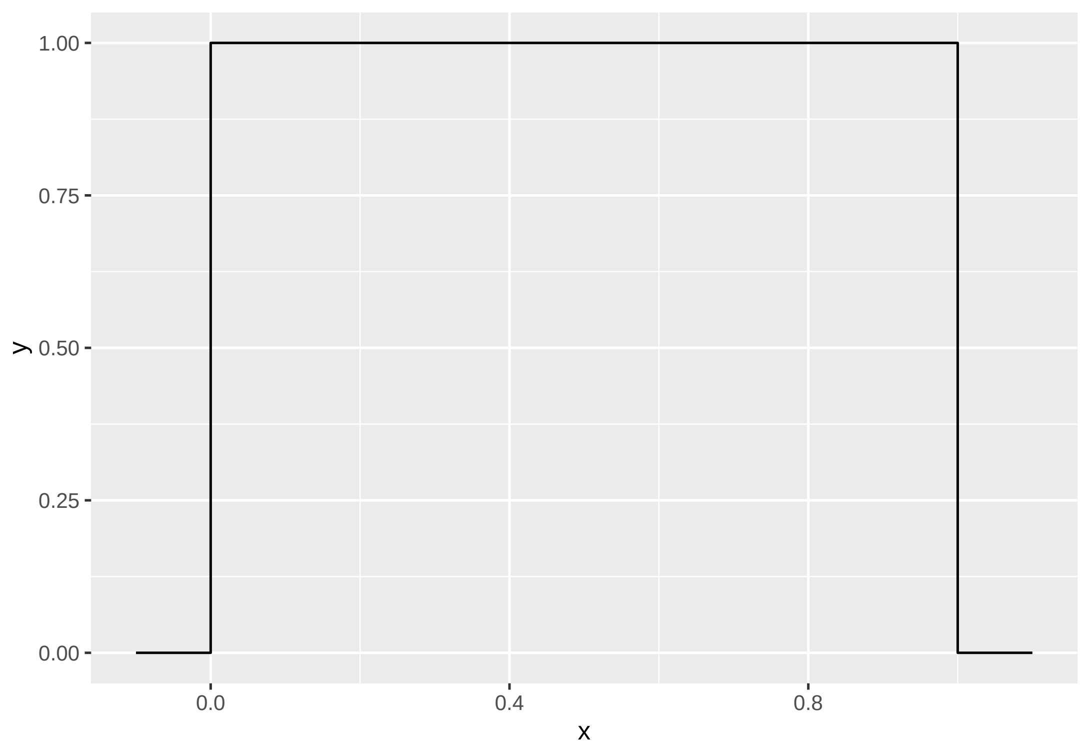
Extra 1: **There is nothing magical about a sample size of 30.** What matters is the tradeoff between sample size and the extent of the non-normality. If your data is less normal, you need a larger sample size to overcome it. Even a sample size of 500 might not be enough if your distribution is very skewed, or if you have extreme outliers.

The place $n = 30$ comes from is back from the days when we only ever used printed tables. In most textbooks, if you printed the t-table on one page in a decent-sized font, you'd get to about 29 df before running out of space. Then they would say "∞ df" and put the normal-distribution z numbers in. If the df you needed was bigger than what you had in the table, you used this last line: that is, you called the sample "large". Try it in your stats textbooks: I bet the df go up to 30, then you get a few more, then the z numbers.

Extra 2: By now you are probably thinking that this is very subjective, and so it is. What actually matters is the shape of the thing called the *sampling distribution of the sample mean*. That is to say, what kind of sample means you might get in repeated samples from your population. The problem is that you don't know what the population looks like.[2] But we can fake it up, in a couple of ways: (a) we can play what-if and pretend we know what the population looks like (to get some understanding for "populations like that"), or (b) we can use a technique called the "bootstrap" that will tell us what kind of sample means we might get from the population that *our* sample came from (this seems like magic and, indeed, is).

The moral of the story is that the central limit theorem is more powerful than you think.

To illustrate my (a), let's pretend the population looks like this, with a flat top:



Only values between 0 and 1 are possible, and each of those is equally likely. Not very normal in shape. So let's take some random samples of size *three*, not in any sense a large sample, from this population, and see what kind of sample means we get. This technique is called *simulation*: rather than working out the answer by math, we're letting the computer approximate the answer for us. Here's one simulated sample:

```
u <- runif(3)
u
```

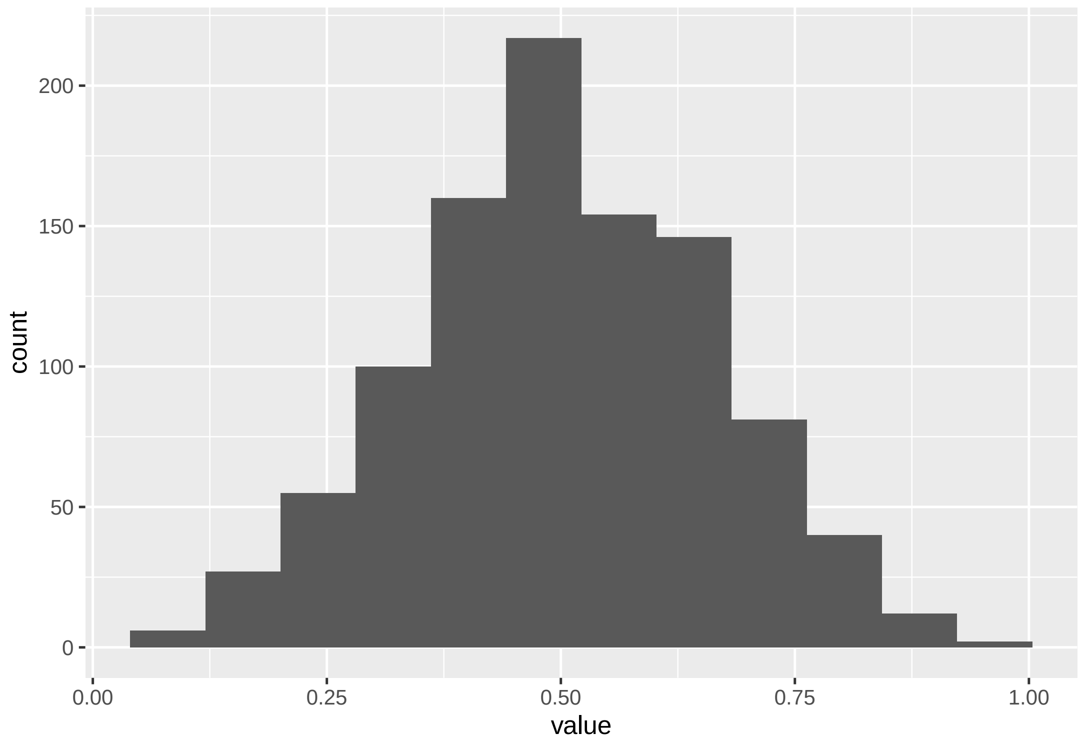
```
## [1] 0.9475841 0.1245953 0.2277288
```

```
mean(u)
```

```
## [1] 0.4333027
```

and here's the same thing 1000 times, including a histogram of the sample means:

```
rerun(1000, runif(3)) %>%
    map_dbl(~mean(.)) %>%
    enframe() %>%
    ggplot(aes(x=value)) + geom_histogram(bins=12)
```



This is our computer-generated assessment of what the sampling distribution of the sample mean looks like. Isn't this looking like a normal distribution?

Let's take a moment to realize what this is saying. If the population looks like the flat-topped uniform distribution, the central limit theorem kicks in for a sample of size *three*, and thus if your population looks like this, t procedures will be perfectly good for $n = 3$ or bigger, *even though the population isn't normal.*

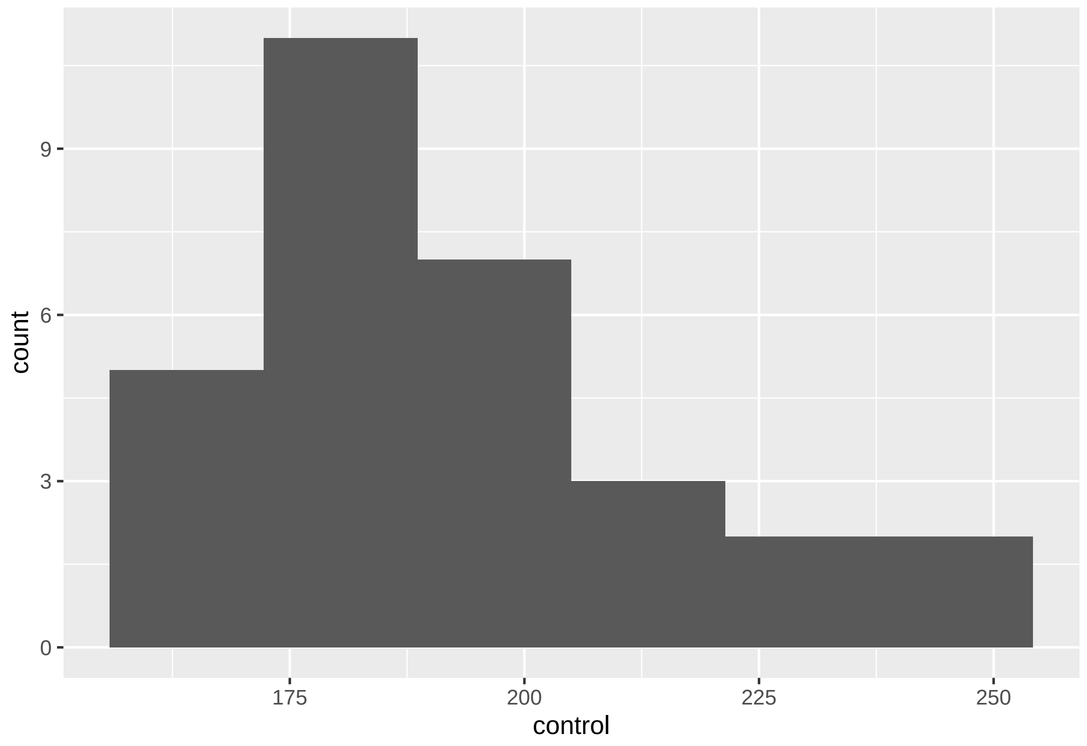
Thus, when you're thinking about whether to use a t-test or something else (that we'll learn about later), the distribution shape matters, *but so does the sample size.*

I should say a little about my code. I'm not expecting you to figure out details now (we see the ideas properly in simulating power of tests), but in words, one line at a time:

- generate 1000 ("many") samples each of 3 observations from a uniform distribution
- for each sample, work out the mean of it
- turn those sample means into a data frame with a column called `value`
- make a histogram of those.

Now, the central limit theorem doesn't always work as nicely as this, but maybe a sample size of 30 is large enough to overcome the skewness that we had:

```
ggplot(cholest, aes(x=control)) + geom_histogram(bins=6)
```



That brings us to my (b) above.

The sample that we had is in some sense an "estimate of the population". To think about the sampling distribution of the sample mean, we need more estimates of the population. How might we get those? The curious answer is to *sample from the sample*. This is the idea behind the *bootstrap*. (This is what Lecture 3c is about.) The name comes from the expression "pulling yourself up by your own bootstraps", meaning "to begin an enterprise or recover from a setback without any outside help" (from here), something that should be difficult or impossible. How is it possible to understand a sampling distribution with only one sample?

We have to be a bit careful. Taking a sample from the sample would give us the original sample back. So, instead, we sample *with replacement*, so that each bootstrap sample is different:

```
sort(cholest$control)
```

```
##  [1] 160 162 164 166 170 176 178 178 182 182 182 182 182 184 186 188 196 198 198
## [20] 198 200 200 204 206 212 218 230 232 238 242
```

```
sort(sample(cholest$control, replace=TRUE))
```

```
##  [1] 164 166 166 166 166 176 178 178 182 182 182 182 182 188 198 198 198 200 200
## [20] 200 200 204 206 206 218 218 230 232 232 242
```

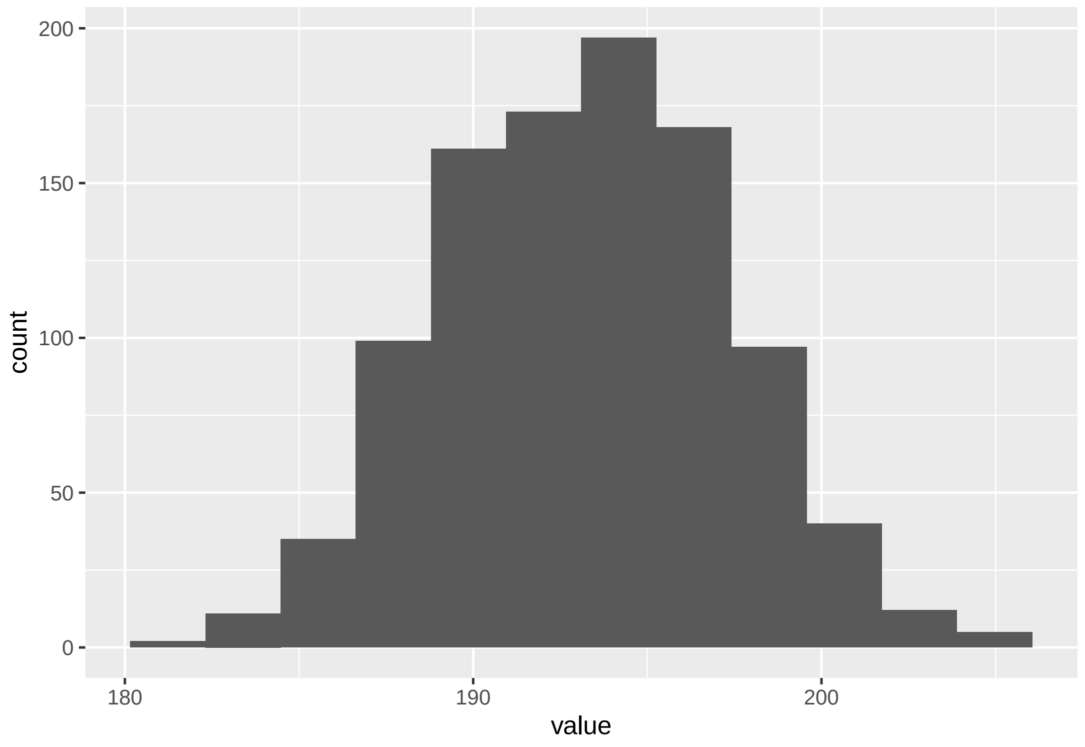
A bootstrap sample contains repeats of the original data values, and misses some of the others. Here, the original data had values 160 and 162 that are missing in the bootstrap sample; the original data had one value 166, but the bootstrap sample has *four*! I sorted the data and the bootstrap sample to make this clearer; you will not need to sort. This is a perfectly good bootstrap sample:

```
sample(cholest$control, replace = TRUE)
```

```
##  [1] 242 232 198 160 242 182 182 182 198 162 212 198 242 204 242 242 170 198 182
## [20] 206 232 170 218 188 166 178 164 160 218 196
```

So now we know what to do: take lots of bootstrap samples, work out the mean of each, plot the means, and see how normal it looks. The only new idea here is the sampling with replacement:

```
rerun(1000, sample(cholest$control, 30, replace = TRUE)) %>%
  map_dbl(~mean(.)) %>%
  enframe() %>%
  ggplot(aes(x=value)) + geom_histogram(bins=12)
```



That looks pretty normal, not obviously skewed, and so the t procedures we used will be reliable enough.

2. Two groups of students (in a class at a American university) were asked what they thought the population of Canada was. (The correct answer at the time was just over 30 million.) Some of the students, before having to answer this, were told that the population of the United States was about 270 million. The other students in the class were told that the population of Australia was about 18 million. The data are in http://ritsokiguess.site/STAC32/anchoring.csv. The first column contains the country whose population the student was told, and the second contains the student's guess at the population of Canada.

   You might wonder how being told the population of an unrelated country would have any impact on a student's guess at the population of Canada. Psychology says it does: it's called the *anchoring effect*, and the idea is that the number mentioned first acts as an "anchor": a person's guess will be closer to the anchor than it would have been otherwise. In this case, that would mean that the guesses for the students given the US as an anchor will be higher than for the students given Australia as an anchor.

We are interested in seeing whether there is evidence for that here.

(a) Read in and display (some of) the data.

Solution:

I made it as easy as I could:

```
my_url <- "http://ritsokiguess.site/STAC32/anchoring.csv"
canada <- read_csv(my_url)
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   anchor = col_character(),
##   estimate = col_double()
## )
```

```
canada
```

```
## # A tibble: 21 x 2
##    anchor estimate
##    <chr>     <dbl>
##  1 US         20
##  2 US         90
##  3 US          1.5
##  4 US        100
##  5 US        132
##  6 US        150
##  7 US        130
##  8 US         40
##  9 US        200
## 10 US         20
## # ... with 11 more rows
```

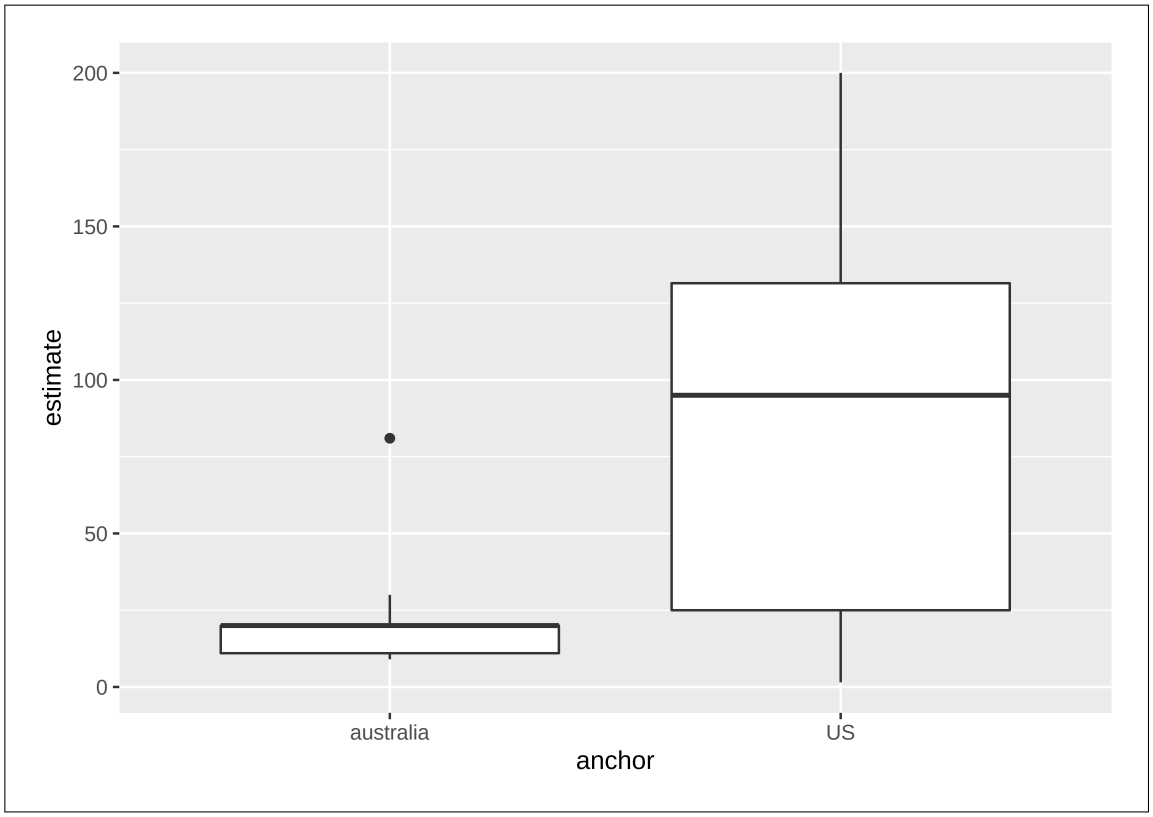
You might need to scroll down to see that both "anchor" countries are indeed represented.

(b) Draw a suitable graph of these data.

Solution:

One categorical variable and one quantitative one, so a boxplot:

```
ggplot(canada, aes(x = anchor, y = estimate)) + geom_boxplot()
```



(c) Explain briefly why a Welch t-test would be better than a pooled t-test in this case.

Solution:

The decision between these two tests lies in whether you think the two groups have equal spread (variance, strictly). Here, the spread for the US group is much larger than for the Australia group, even taking into account the big outlier in the latter group. Since the spreads are different, we should do a Welch t-test rather than a pooled one.

Make sure you answer the question I asked, not the one you think I should have asked.

There is a separate question about whether the groups are close enough to normal, but I wasn't asking about that here. I was asking: *given* that we have decided to do some kind of t-test, why is the Welch one better than the pooled one? I am not asking whether we should be doing any kind of t-test at all; if I had, you could *then* reasonably talk about the outlier in the Australia group, and other possible skewness in its distribution, but that's not what I asked about.

(d) Run a suitable Welch t-test and display the output.

Solution:

The word "suitable" is a hint that you may have to think a bit about how you run the test. If the anchoring effect is real, the mean of the guesses for the students told the population of the US will be higher on average than for those told the population of Australia, so we want a one-sided alternative. Australia is before the US alphabetically, so the alternative has to be `less`:

```r
t.test(estimate~anchor, data = canada, alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  estimate by anchor
## t = -3.0261, df = 10.558, p-value = 0.006019
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##       -Inf -26.63839
## sample estimates:
## mean in group australia        mean in group US
##                22.45455                88.35000
```

Note that the Welch test is the default, so you don't have to do anything special to get it. Your output will tell you that a Welch test is what you have. It's if you want a *pooled* test that you have to ask for it specifically (with `var.equal = TRUE`).

If you get a P-value close to 1, this is often an indication that you have the alternative the wrong way around.

(e) What do you conclude from your test, in the context of the data?

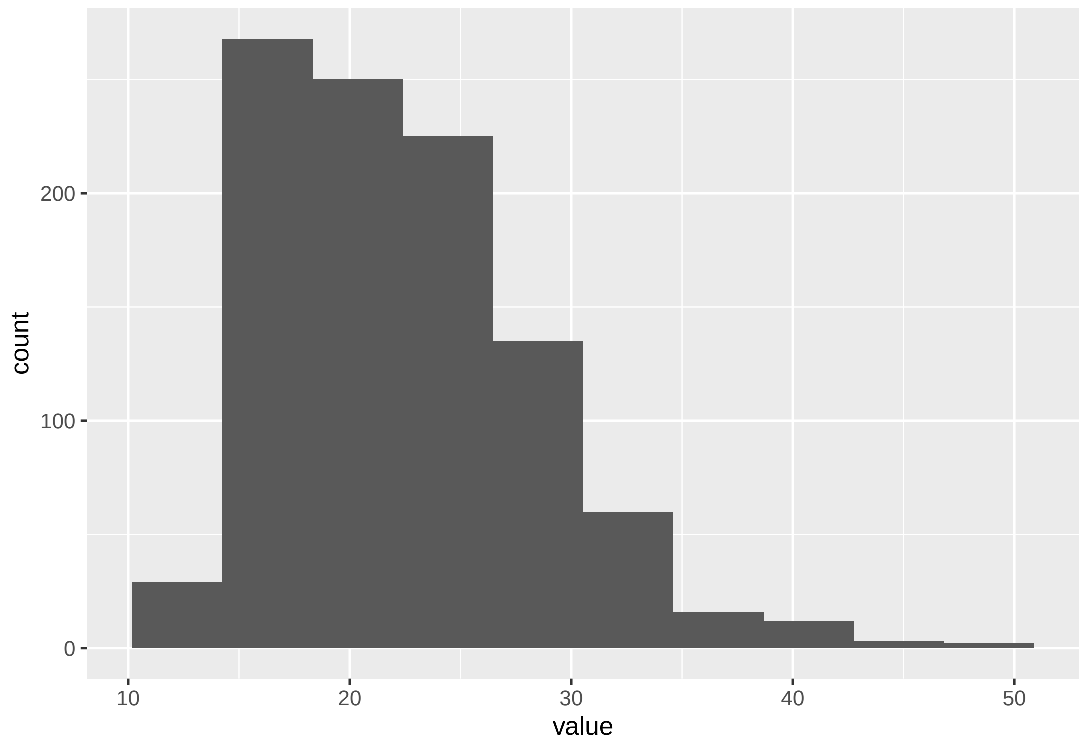
Solution:

The P-value is definitely less than 0.05, so we reject the null hypothesis (which says that the mean guess is the same regardless of the anchor the student was given). So we have evidence that the mean guess is higher for the students who were given the US population first.

Extra 1: this is perhaps the place to think about what effect that outlier in the `australia` group might have had. Since it is a high outlier, its effect will be to make the the `australia` mean higher than it would have been otherwise, and therefore to make the two group means closer together. Despite this, the difference still came out strongly significant, so that we can be *even more sure than the P-value says* that there is a real difference between the means of estimates of the population of Canada. (To say it differently, if the outlier had not been there, the difference in means would have been even bigger and thus even more significant.)

Extra 2: if you are still worried about doing a two-sample *t*-test here, you might consider looking at the bootstrapped sampling distribution of the sample mean of the `australia` group:

```r
canada %>% filter(anchor == "australia") -> oz
rerun(1000, sample(oz$estimate, replace = TRUE)) %>%
  map_dbl(~mean(.)) %>%
  enframe() %>%
  ggplot(aes(x = value)) + geom_histogram(bins=10)
```



This is indeed skewed to the right (though, with 11 observations, not nearly so non-normal as the original data), and so the P-value we got from the *t*-test may not be reliable. But, as discussed in Extra 1, the "correct" P-value is, if anything, *even smaller* than the one we got, and so the conclusion we drew earlier (that there is a significant anchoring effect) is not going to change.

Extra 3: looking even further ahead, there is a test that definitely *does* apply here, called Mood's Median Test. You won't have installed the package yet, so this won't work for you just yet (read ahead if you want to learn more), but here's how it goes:

```
library(smmr)
median_test(canada, estimate, anchor)
```

```
## $table
##             above
## group       above below
##   australia     2     5
##   US            7     1
##
## $test
##        what      value
## 1 statistic 5.40178571
## 2        df 1.00000000
## 3   P-value 0.02011616
```

This does (as it is written) a two-sided test, because it can also be used for comparing more than two groups. Since we want a one-sided test here, you can (i) check that we are on the correct side (we are)[3] (ii) halve the P-value to get 0.010.

This is a P-value you can trust. It is not smaller than the *t*-test one, perhaps because this test is less powerful than the *t*-test in most cases.[4]

Notes

1. In R, missing values are labelled NA, and “rm” is Unix/C shorthand for “remove”.

2. If you did, all your problems would be over.

3. The test works by comparing the data values in each group to the overall median. The students who were given Australia as an anchor mostly guessed below the overall median, and the students given the US as an anchor mostly guessed above.

4. It uses the data less efficiently than the *t*-test; it just counts the number of values above and below the overall median in each group, rather than using the actual numbers to compute means.