Inference for two independent means

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Introduction

If we have a categorical variable with two categories and a numerical variable, we can think of the the categorical variable as explanatory and the numerical variable as response. The idea is that the two categories sort your numerical data into two groups which can be compared. Assuming the two groups are independent of each other, we can use them as samples of two larger populations. This leads to inference to decide if the difference between the two groups is statistically significant and then estimate the difference between the two populations represented. The relevant hypothesis test is called a two-sample t-test (or Welch's t-test, to be specific).

Instructions

Presumably, you have already created a new project and downloaded this file into it. Please knit the document and work back and forth between this R Markdown file and the PDF output as you work through this module.

When you are finished with the assignment, knit to PDF one last time, proofread the PDF file **carefully**, export the PDF file to your computer, and then submit your assignment.

Sometimes you will be asked to add your own R code. That will appear in this document as a code chunk with a request for you to add your own code, like so:

```
## Add code here to [do some task]...
```

Be sure to remove the line `## Add code here to [do some task]...` when you have added your own code.

Sometimes you will be asked to type up your thoughts. That will appear in the document as follows:

Please write up your answer here.

Again, please be sure to remove the line "Please write up your answer here" when you have written up your answer. In these areas of the assignment, please use contextually meaningful full sentences/paragraphs (unless otherwise indicated) and proper spelling, grammar, punctuation, etc. This is not R code, but rather a free response section where you talk about your analysis and conclusions. If you need to use some R code as well, you can use inline R code inside the block between `\begin{answer}` and `\end{answer}`, or if you need an R code chunk, please go outside the `answer` block and start a new code chunk.

Load Packages

We load the standard `mosaic` package as well as the `MASS` for the `cabbages` data. The `broom` package gives us tidy output.

```
library(MASS)
library(broom)
library(mosaic)
```

We set the seed to make our simulations reproducible.

```
set.seed(1729)
```

Research question

We have data on two cultivars of cabbage called "c39" and "c52". Is there a difference in weight of the cabbage heads between these two varieties?

Every day I'm shuffling

Whenever there are two groups, the obvious null hypothesis is that there is no difference between them.

Consider the cultivar types c39 and c52. If there were truly no difference in weight between these cultivars, then it shouldn't matter if we know the cultivar or not. It becomes irrelevant under the assumption of the null.

We can simulate this assumption by shuffling the names of the cultivars. More concretely, we can randomly assign cultivar labels to each head of cabbage and then calculate the average weight in each cultivar groups. Since the cultivar labels are random, there's no reason to expect a difference between the two average weights other than random fluctuations due to sampling variability.

The actual mean weights of the c39 and c52 cultivars can be found using the `mean` command and the tilde notation. The following command should be read aloud as "calculate the mean head weight *by* cultivar type," or "*grouped by* cultivar type."

```
mean(HeadWt ~ Cult, data = cabbages)
```

```
##      c39      c52
## 2.906667 2.280000
```

The difference between the means is calculated with the `diffmean` command. We'll store this result as `obs_diff` for "observed difference".

```
obs_diff <- diffmean(HeadWt ~ Cult, data = cabbages)
obs_diff
```

```
##   diffmean
## -0.6266667
```

(Note that the order of subtraction here is c52 minus c39.)

This is the list of cultivars in the actual data:

```
cabbages$Cult
```

```
##  [1] c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39
## [18] c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c39 c52 c52 c52 c52
## [35] c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52 c52
## [52] c52 c52 c52 c52 c52 c52 c52 c52 c52
## Levels: c39 c52
```

This is what happens when we `shuffle` them.

```
shuffle(cabbages$Cult)
```

```
##  [1] c52 c39 c52 c39 c52 c39 c39 c39 c52 c52 c39 c39 c39 c52 c39 c52 c52
## [18] c52 c52 c52 c52 c39 c39 c52 c39 c39 c52 c39 c52 c39 c39 c52 c52 c52
## [35] c39 c39 c52 c39 c52 c52 c52 c52 c39 c39 c39 c52 c52 c52 c39 c52 c39
## [52] c39 c52 c39 c39 c52 c39 c52 c39 c39
## Levels: c39 c52
```

Now we can calculate the group means and their difference for shuffled data. Let's do it few times.

```
diffmean(HeadWt ~ shuffle(Cult), data = cabbages)
```

```
##   diffmean
## 0.07333333
```

```
diffmean(HeadWt ~ shuffle(Cult), data = cabbages)
```

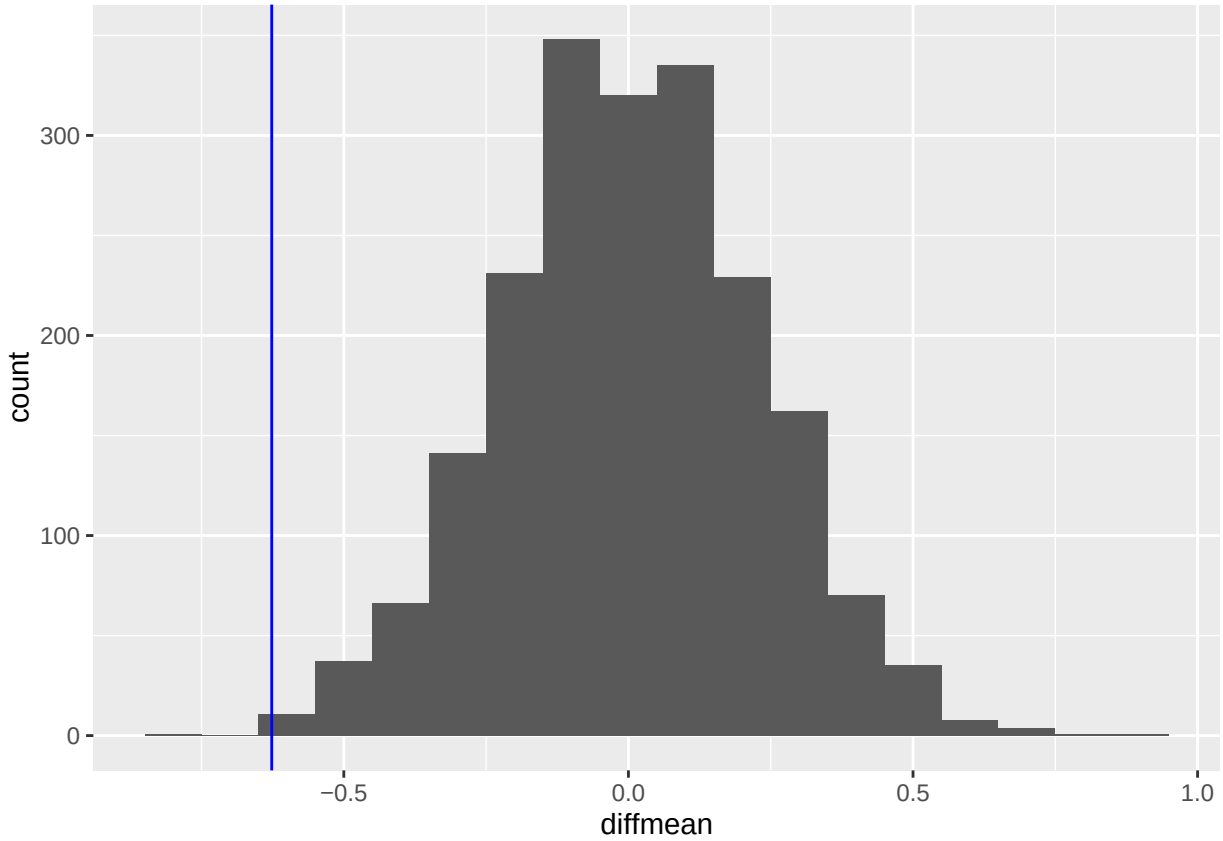
```
##   diffmean
## -0.1866667
```

```
diffmean(HeadWt ~ shuffle(Cult), data = cabbages)
```

```
##   diffmean
## 0.08666667
```

We use the `do` command to do this a bunch of times and graph the results along with our observed difference.

```
sims <- do(2000) * diffmean(HeadWt ~ shuffle(Cult), data = cabbages)
ggplot(sims, aes(x = diffmean)) +
    geom_histogram(binwidth = 0.1) +
    geom_vline(xintercept = obs_diff, color = "blue")
```



No surprise that this histogram looks nearly normal, centered at zero. Our observed difference is quite far out into the tail of this simulated sampling distribution, so it appears that our actual data would be unlikely due to pure chance alone if the null hypothesis were true.

We can even find a P-value by calculating how many of our sampled values are as extreme or more extreme than the observed data difference. The command below accomplishes this by calculating the percentage of samples in the left tail and then multiplying by 2 to make it a two-sided test. (It's two-sided because we didn't have any preconceptions about which cultivar would be heavier.)

```
2 * prop(sims$diffmean <= obs_diff)
```

```
##  TRUE
## 0.003
```

Indeed, this is a small P-value.

The sampling distribution model

In the previous section, we simulated the sampling distribution under the assumption of a null hypothesis of no difference between the groups. It certainly looked like a normal model, but which normal model? The center is obviously zero, but what about the standard deviation?

Let's assume that both groups come from populations that are normally distributed with normal models $N(\mu_1, \sigma_1)$ and $N(\mu_2, \sigma_2)$. If we take samples of size n_1 from group 1 and n_2 from group 2, some fancy math shows that the distribution of the differences between sample means is

$$N\left(\mu_1 - \mu_2, \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}\right).$$

Under the assumption of the null, the difference of the means is zero ($\mu_1 - \mu_2 = 0$). Unfortunately, though, we make no assumption on the standard deviations.

If we were testing two proportions with categorical data, we could pool our data. If the groups are truly equal, then they share the same proportion, so we can use a pooled proportion to estimate it. With numerical data, we can calculate a pooled mean, but that doesn't help with the unknown standard deviations. Nothing in the null hypothesis suggests that the standard deviations of the two groups should be the same.[1]

It should be clear that the only solution is to substitute the sample standard deviations s_1 and s_2 for the population standard deviations σ_1 and σ_2. However, s_1 and s_2 are not perfect estimates of σ_1 and σ_2; they are subject to sampling variability too. This extra variability means that a normal model is no longer appropriate as the sampling distribution model.

In the one-sample case, a Student t model with $df = n - 1$ was the right choice. In the two-sample case, we don't know the right answer. Yes, you read that correctly. Statisticians have not found a formula for the correct sampling distribution. It is a famous unsolved problem, called the Behrens-Fisher problem.

Several researchers have proposed solutions that are "close" though. One compelling one is called "Welch's t-test". Welch showed that even though it's not quite right, a Student t model is very close as long as you pick the degrees of freedom carefully. Unfortunately, the way to compute the right degrees of freedom is crazy complicated. Fortunately, R is good at crazy complicated computations. The `t.test` command uses the Welch's t-test by default when there are two groups.

Let's go through the full rubric using the cabbage example.

Exploratory data analysis

Use data documentaton (help files, code books, Google, etc.), the str command, and other summary functions to understand the data.

[Type `library(MASS)` then `?cabbages` to read the help file.]

```
str(cabbages)
```

```
## 'data.frame':    60 obs. of  4 variables:
##  $ Cult  : Factor w/ 2 levels "c39","c52": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Date  : Factor w/ 3 levels "d16","d20","d21": 1 1 1 1 1 1 1 1 1 1 ...
##  $ HeadWt: num  2.5 2.2 3.1 4.3 2.5 4.3 3.8 4.3 1.7 3.1 ...
##  $ VitC  : int  51 55 45 42 53 50 50 52 56 49 ...
```

Prepare the data for analysis.

The cultivar variable `Cult` is already a factor variable, as it should be.

[1] In the extremely rare situation in which one can assume equal standard deviations in the two groups, then there is a way to run a pooled t test. But this "extra" assumption of equal standard deviations is typically questionable, and it's impossible to check anyway.

Make tables or plots to explore the data visually.

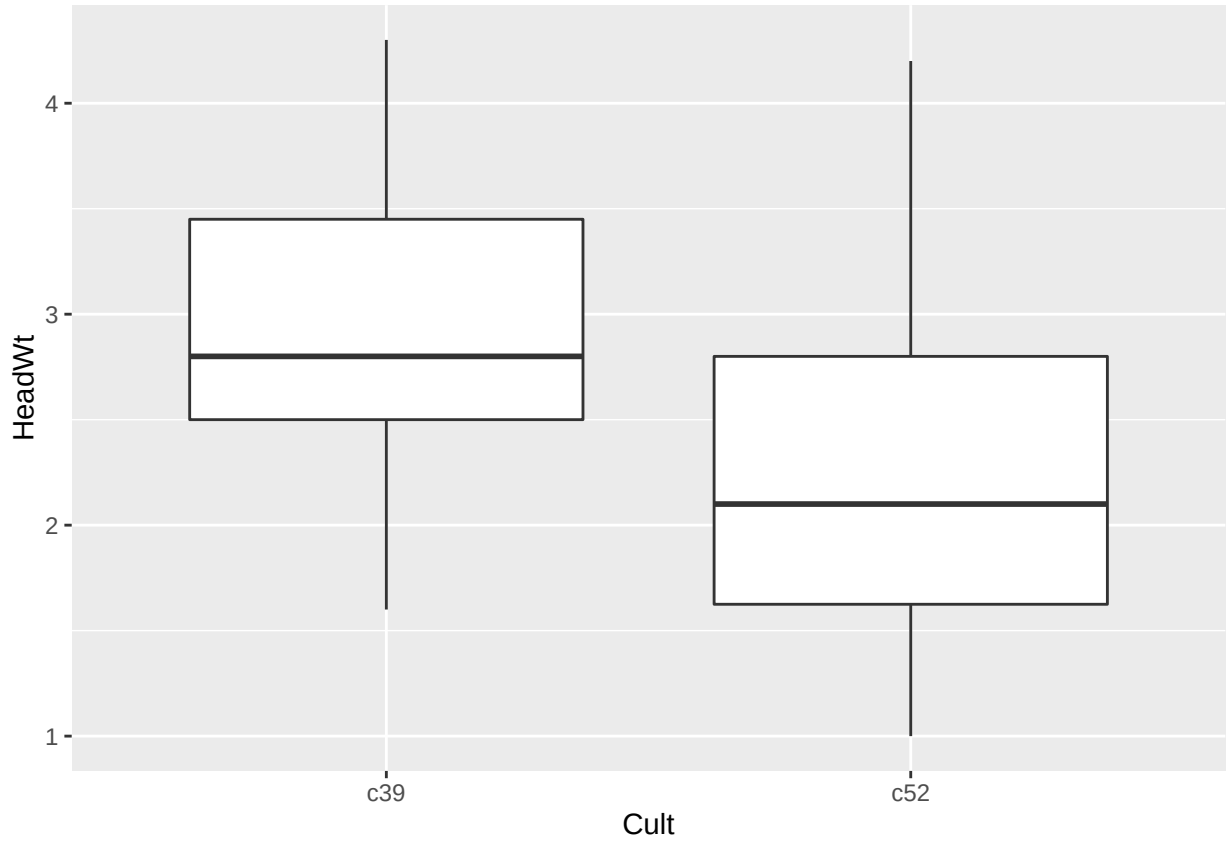
How many cabbages of each cultivar type do we have?

```
table(cabbages$Cult)
```

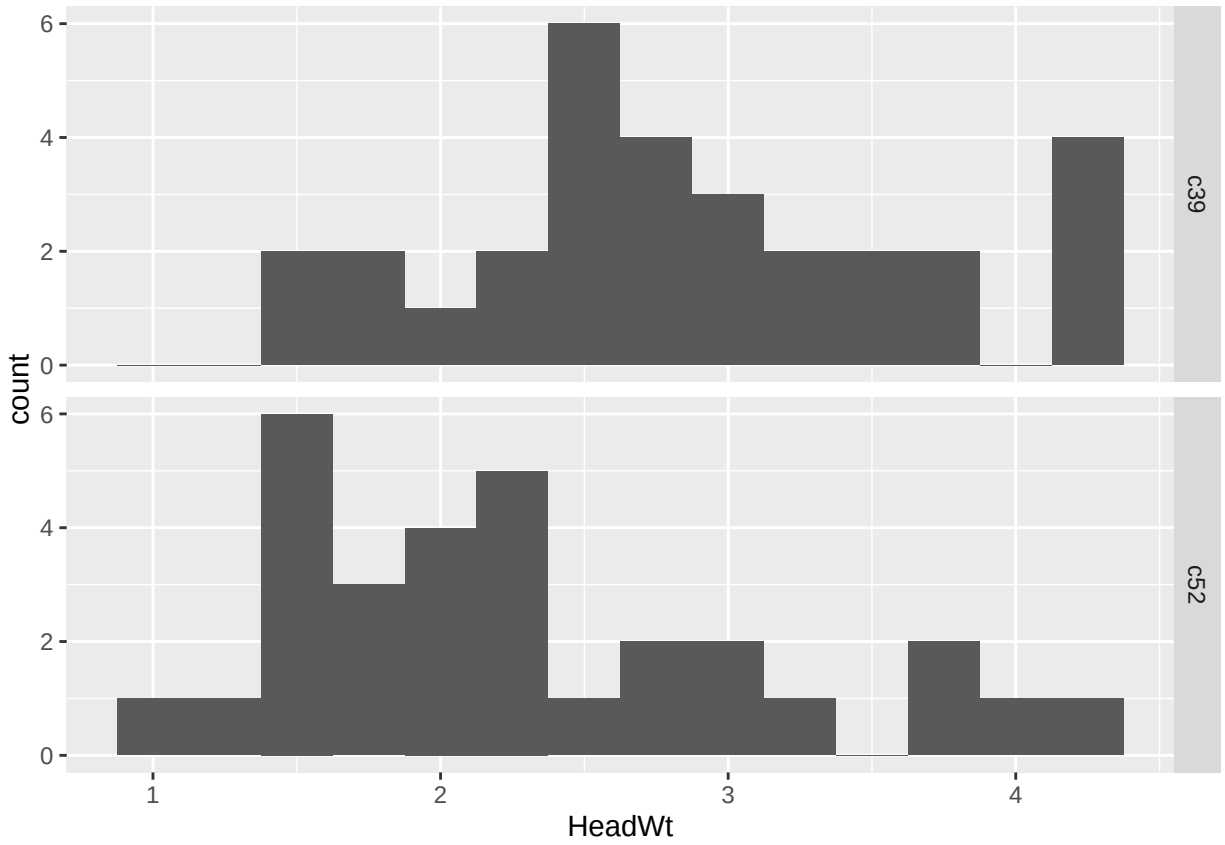
```
##
## c39 c52
##  30  30
```

With a categorical explanatory variable and a numerical response variable, there are two useful plots: a side-by-side boxplot and a stacked histogram.

```
ggplot(cabbages, aes(x = Cult, y = HeadWt)) +
    geom_boxplot()
```

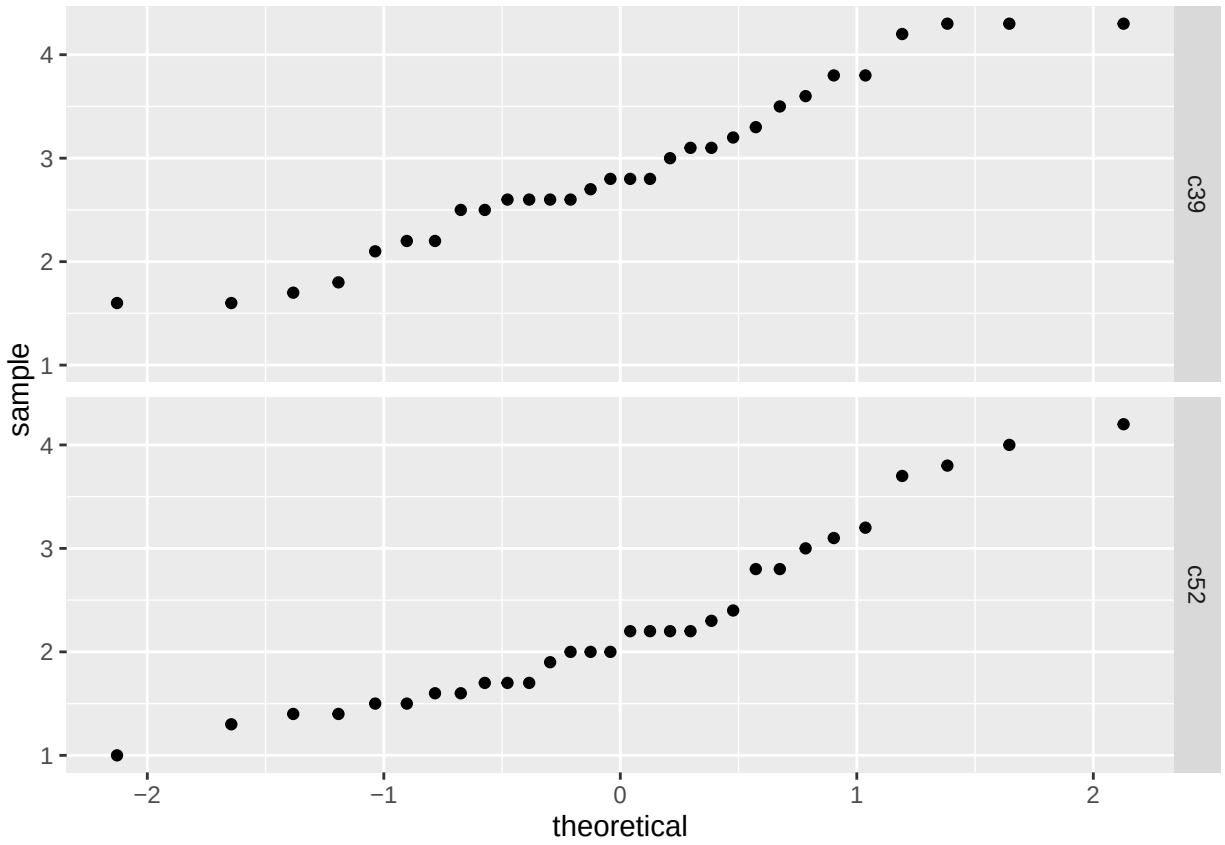



```
ggplot(cabbages, aes(x = HeadWt)) +
    geom_histogram(binwidth = 0.25) +
    facet_grid(Cult ~ .)
```



The individual group histograms looks reasonably normal, although it's a bit hard to tell with a sample size of 30 in each group. Here are the QQ plots to give us another way to ascertain normality of the data.

```
ggplot(cabbages, aes(sample = HeadWt)) +
    geom_qq() +
    facet_grid(Cult ~ .)
```



Commentary: The boxplots and histograms show why statistical inference is so important. It's clear that there is some difference between the two groups, but it's not obvious if that difference will turn out to be statistically significant. There appears to be a lot of variability in both groups, and both groups have a fair number of lighter and heavier cabbage heads.

Hypotheses

Identify the sample (or samples) and a reasonable population (or populations) of interest.

The samples consist of 30 cabbages from the c39 group and 30 cabbages from the c52 group. The populations are all cabbages of variety c39 and all cabbages of variety c52.

Express the null and alternative hypotheses as contextually meaningful full sentences.

H_0: There is no difference in the head weight of c39 cabbages and c52 cabbages.

H_A: There is a difference in the head weight of c39 cabbages and c52 cabbages.

Express the null and alternative hypotheses in symbols.

$H_0 : \mu_{c39} - \mu_{c52} = 0$

$H_A : \mu_{c39} - \mu_{c52} \neq 0$

Commentary: Pay close attention to the order of subtraction. It's easiest to make your hypotheses match the order of the `t.test` command we use later in the rubric. **It is the oppposite of the `diffmean` command!** How do we know? Let's run the `t.test` command a little early and look at the output.

```
cabbage_test <- tidy(t.test(HeadWt ~ Cult, data = cabbages))
cabbage_test
```

```
##    estimate estimate1 estimate2 statistic     p.value parameter  conf.low
## 1 0.6266667  2.906667      2.28  2.920875 0.004971691  57.77675 0.1971677
##   conf.high                  method alternative
## 1  1.056166 Welch Two Sample t-test   two.sided
```

The `estimate` is positive, obtained by subtracting `estimate1` minus `estimate2`. Looking back to the mean of both groups that we calculated with the `mean` command, we can see that `estimate1` corresponds to the c39 group and `estimate2` corresponds to the c52 group.

Model

Identify the sampling distribution model.

We use a t model. Since we ran the `t.test` command already, we can see the degrees of freedom:

```
cabbage_test$parameter
```

```
## [1] 57.77675
```

Commentary: For Welch's t test, the degrees of freedom won't usually be a whole number. Be sure you understand that the formula is no longer $df = n - 1$. That doesn't even make any sense as there isn't a single n in a *two*-sample test.

Check the relevant conditions to ensure that model assumptions are met.

- Random
  - We have no information at all about these cabbages. We hope that the 30 we have of each kind are representative of all cabbages from the two cultivars.
- 10%
  - 30 is less than 10% of all c39 cabbages and 30 is less than 10% of all c52 cabbages.
- Nearly normal
  - We have to check this for both groups. Since the sample sizes are 30 in each group, though, we meet the condition automatically.

Mechanics

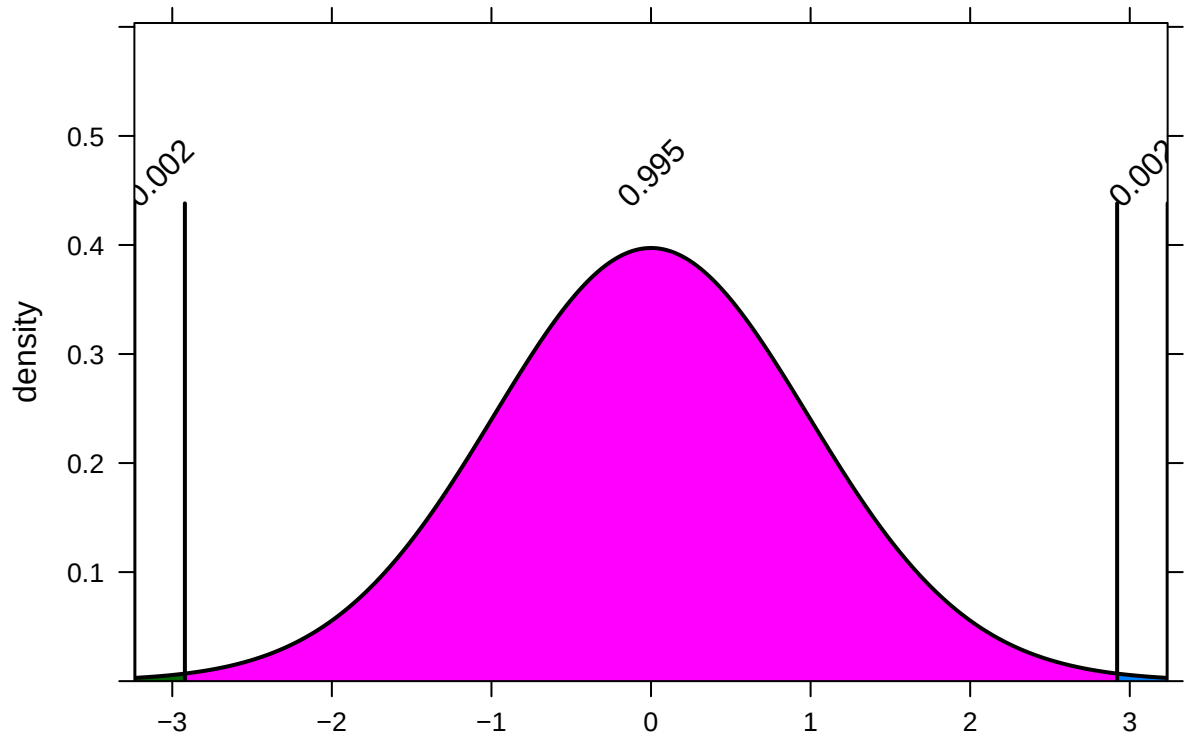
Compute the test statistic.

```
t <- cabbage_test$statistic
t
```

```
## [1] 2.920875
```

Plot the null distribution.

```
pdist("t", df = cabbage_test$parameter, q = c(-t, t))
```




```
## [1] 0.002485846 0.997514154
```

Calculate the P-value.

```
cabbage_test$p.value
```

```
## [1] 0.004971691
```

Conclusion

State the statistical conclusion.

We reject the null hypothesis.

State (but do not overstate) a contextually meaningful conclusion.

We have sufficient evidence that there is a difference in the head weight of c39 cabbages and c52 cabbages.

Identify the possibility of either a Type I or Type II error and state what making such an error means in the context of the hypotheses.

If we've made a Type I error, then that means that there might be no difference in the head weight of c39 cabbages and c52 cabbages, but we got some unusual samples that showed a difference.

Confidence interval

Conditions

There are no additional conditions to check.

Calculation

```
cabbage_test$conf.low
```

```
## [1] 0.1971677
```

```
cabbage_test$conf.high
```

```
## [1] 1.056166
```

Conclusion

We are 95% confident that the true difference in mean head weight between c52 and c39 cabbages is captured in the interval (0.1971677 kg, 1.0561656 kg). We obtained this by subtracting c39 minus c52.

Your turn

Continue to use the `cabbage` data set. This time, explore the ascorbic acid (vitamin C) content of each of the two cultivars.