Comparing two groups

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Recall any hypothesis testing follows boradly-speaking these steps:

1. Choose a significance level (alpha)
2. Formulate a null hypothesis, H0
3. Formulate an alternative hypothesis, H1
4. Gather data, calculate a test statistic, e.g. T or F
5. Determine the probability (p-value) of obtaining T or F “or a more extreme value” under H0
6. If p <= alpha, reject H0

And the basic process is:

- Set up a hypothesis, and assume that it is true.
- Gather data from some real-world experiment that is relevant to the hypothesis.
- Make a determination about the hypothesis, based on the idea of “how likely is our data given the hypothesis?”

Let’s go through an example.

First let’s load the R libraries.

```
library(tidyverse)
```

We have some data from @Johnson2008 called `F1_data.txt`.

```
f1 <- read_csv('data/F1_data.txt')
```

Let’s have a look at the data.

```
head(f1)
```

```
## # A tibble: 6 x 4
##   female  male vowel language
##    <dbl> <dbl> <chr> <chr>
## 1    391   339 i     W.Apache
## 2    561   512 e     W.Apache
## 3    826   670 a     W.Apache
## 4    453   427 o     W.Apache
## 5    358   291 i     CA English
## 6    454   406 e     CA English
```

And the structure `str()` of the data?

```
str(f1)
```

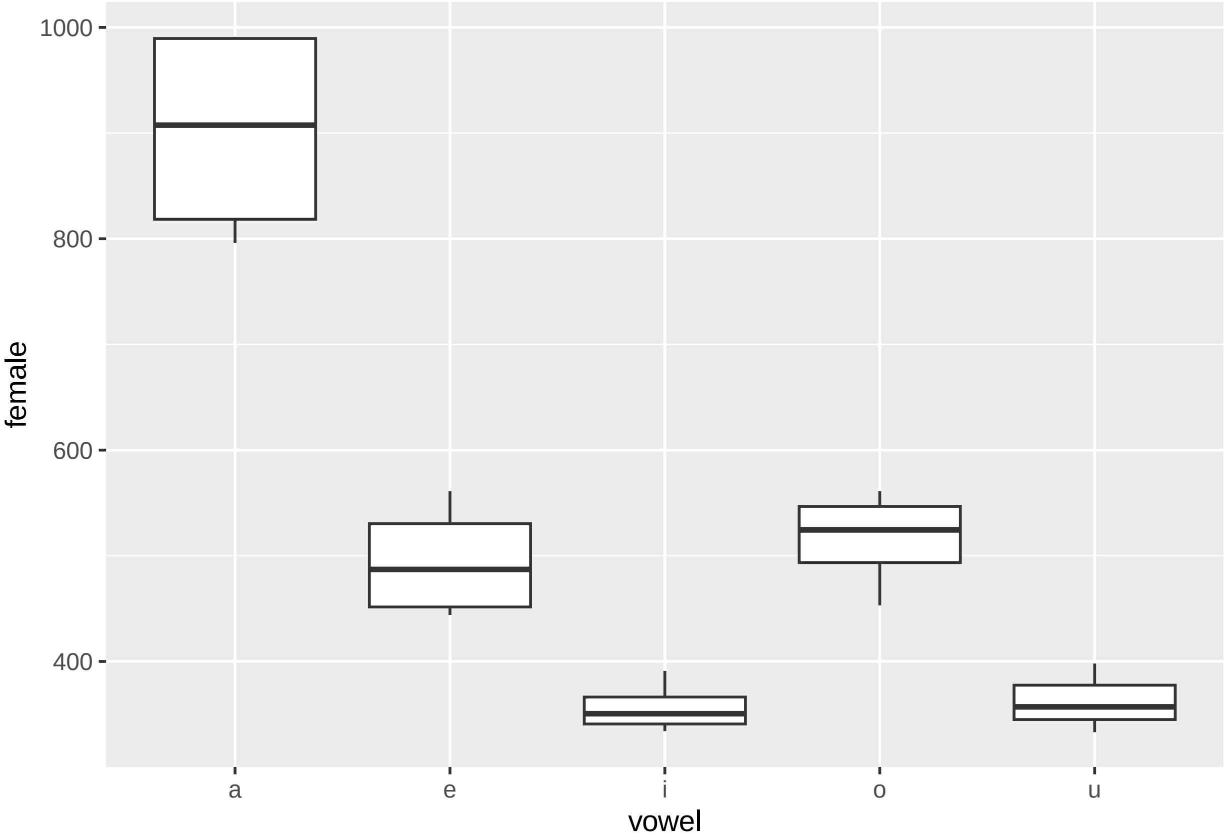
```
## spc_tbl_ [19 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ female  : num [1:19] 391 561 826 453 358 454 991 561 398 334 ...
##  $ male    : num [1:19] 339 512 670 427 291 406 706 439 324 307 ...
##  $ vowel   : chr [1:19] "i" "e" "a" "o" ...
##  $ language: chr [1:19] "W.Apache" "W.Apache" "W.Apache" "W.Apache" ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   female = col_double(),
##   ..   male = col_double(),
##   ..   vowel = col_character(),
##   ..   language = col_character()
##   .. )
##  - attr(*, "problems")=<externalptr>
```

For each observation (row) the variables for the columns (male and female) record the F1 formant measures values in frequency in Hz. Formants are the distinctive properties of vowels in the acoustic signal in speech. Formants F1-F3 allow us to identify different vowels.

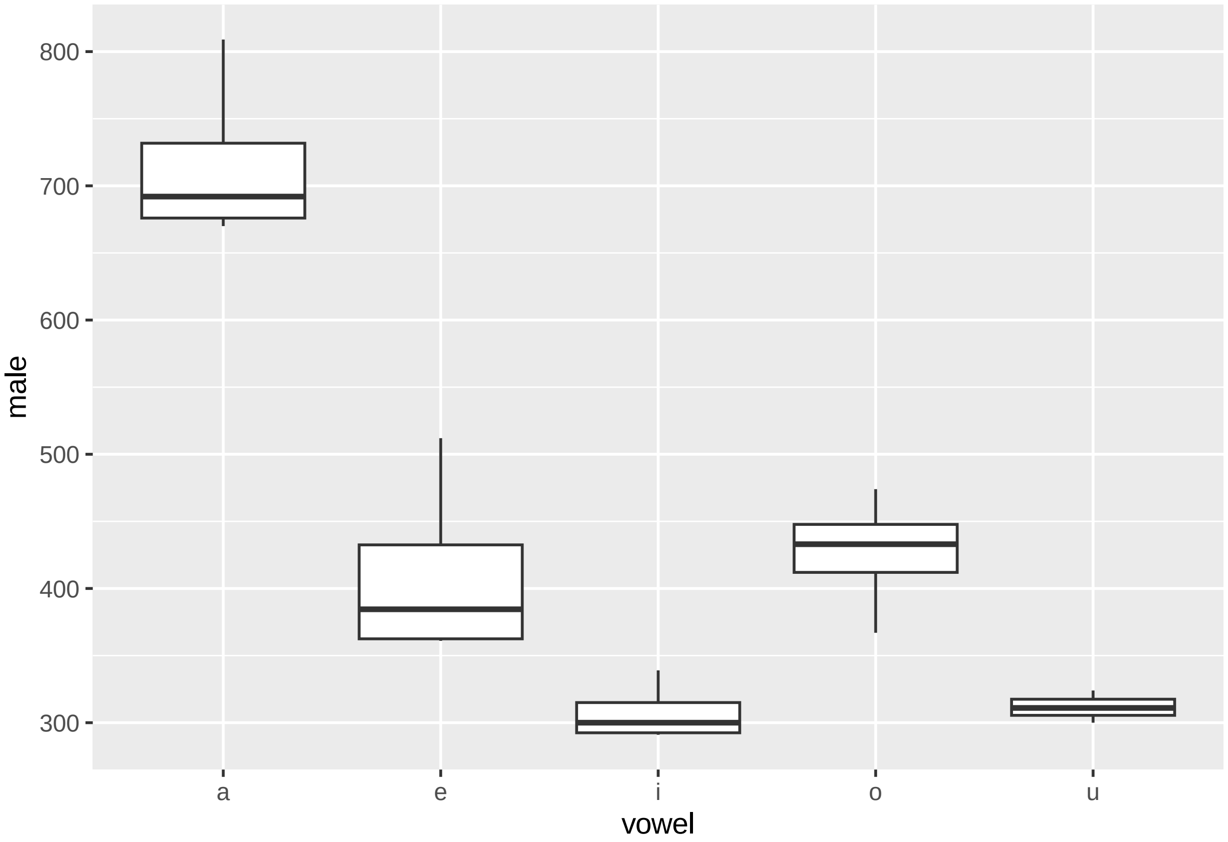
The data include 19 observations from male and female speakers from four different languages producing different cardinal vowels. We can do some visual explorations of the data.

A quick way to look at the data.

```
ggplot(data = f1, aes(x = vowel, y = female)) +
  geom_boxplot()
```



```
ggplot(data = f1, aes(x = vowel, y = male)) +
  geom_boxplot()
```



The problem is the input data is not in a format that is particularly easy to plot as a box plot. So, what do we do? Transform it into a format that is easy to plot. (Remember, something like 80% of your time is getting the data in formats that are useful for particular purposes.)

There are many ways to transform the data. Often it helps to first think about what format you need to get to – I often do this on scrap paper and then think about the code needed. (Remember with code there's going to typically myriad ways of doing the same thing.)

What do we want? We want to be able to group on the male and female variable – but right now they are in columns.

Here's a not particularly elegant, but arguably readable way, to transform the data.

```
men <- f1 %>% select(male, vowel, language)
women <- f1 %>% select(female, vowel, language)

men <- men %>% rename(F1 = male)
men$sex <- 'male'
men
```

```
## # A tibble: 19 x 4
##       F1 vowel language   sex
##    <dbl> <chr> <chr>      <chr>
##  1   339 i     W.Apache   male
##  2   512 e     W.Apache   male
##  3   670 a     W.Apache   male
##  4   427 o     W.Apache   male
##  5   291 i     CA English male
##  6   406 e     CA English male
##  7   706 a     CA English male
## 8    439 o     CA English male
## 9    324 u     CA English male
## 10   307 i     Ndumbea    male
## 11   361 e     Ndumbea    male
## 12   678 a     Ndumbea    male
## 13   474 o     Ndumbea    male
## 14   311 u     Ndumbea    male
## 15   293 i     Sele       male
## 16   363 e     Sele       male
## 17   809 a     Sele       male
## 18   367 o     Sele       male
## 19   300 u     Sele       male
```

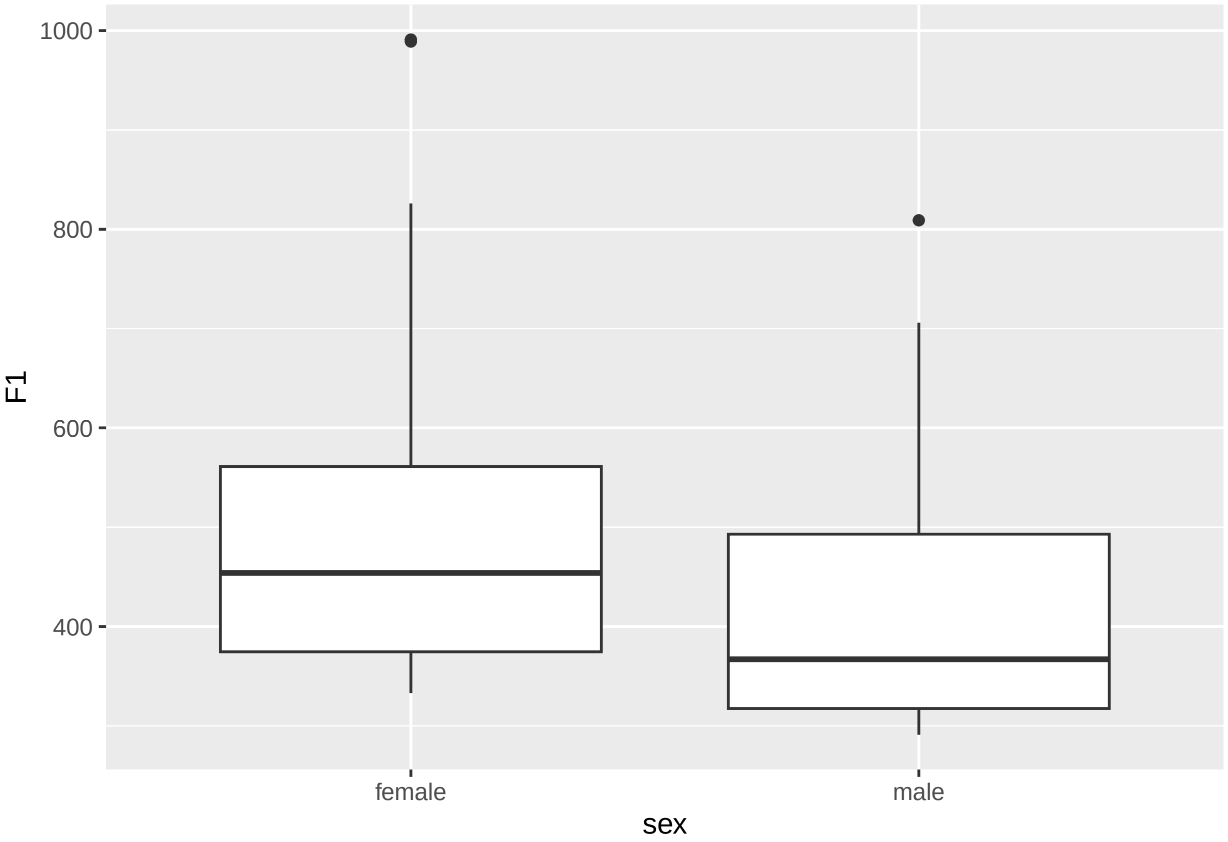
```
women <- women %>% rename(F1 = female)
women$sex <- 'female'
women
```

```
## # A tibble: 19 x 4
##        F1 vowel language   sex
##     <dbl> <chr> <chr>      <chr>
##  1   391 i     W.Apache   female
##  2   561 e     W.Apache   female
##  3   826 a     W.Apache   female
##  4   453 o     W.Apache   female
##  5   358 i     CA English female
##  6   454 e     CA English female
##  7   991 a     CA English female
##  8   561 o     CA English female
##  9   398 u     CA English female
## 10   334 i     Ndumbea    female
## 11   444 e     Ndumbea    female
## 12   796 a     Ndumbea    female
## 13   542 o     Ndumbea    female
## 14   333 u     Ndumbea    female
## 15   343 i     Sele       female
## 16   520 e     Sele       female
## 17   989 a     Sele       female
## 18   507 o     Sele       female
## 19   357 u     Sele       female
```

```
df <- rbind(women, men)
```

Now we have something a bit easier to work with.

```
ggplot(data = df, aes(sex, F1)) +
  geom_boxplot()
```



Now we want to ask if there is a statistically significant difference between the F1 values of women and men in the sample. One way we can do this is by comparing the mean of the two groups.

First we state our hypothesis:

- H0 (null hypothesis): there is **no difference** between the mean value of F1 for women and men
- H1 (alternative hypothesis): there is a difference

Next we identify which statistical test we can use.

T-tests are for comparing the means of two groups (e.g., the average heights of men and women). It is a parametric test based on the Student's T distribution. Essentially, you test the significance of the difference of the mean values when the sample size is small (i.e, less than 30) and when the population standard deviation is not available.

Assumptions of this test:

- Population distribution is normal
- Samples are random and independent
- The sample size is small
- Population standard deviation is not known

In this case of our data, we have paired data, i.e., each row has an associated group (woman and man), in which the speakers produced the same vowel. The paired t-test allows us to test for significance between two paired groups.

How do we know our data is paired?

Now we search for examples of how we can do a paired t-test in R and figure out what the function is called and which parameters it needs.

```
t.test(f1$female, f1$male, paired=T, alternative="greater")
```

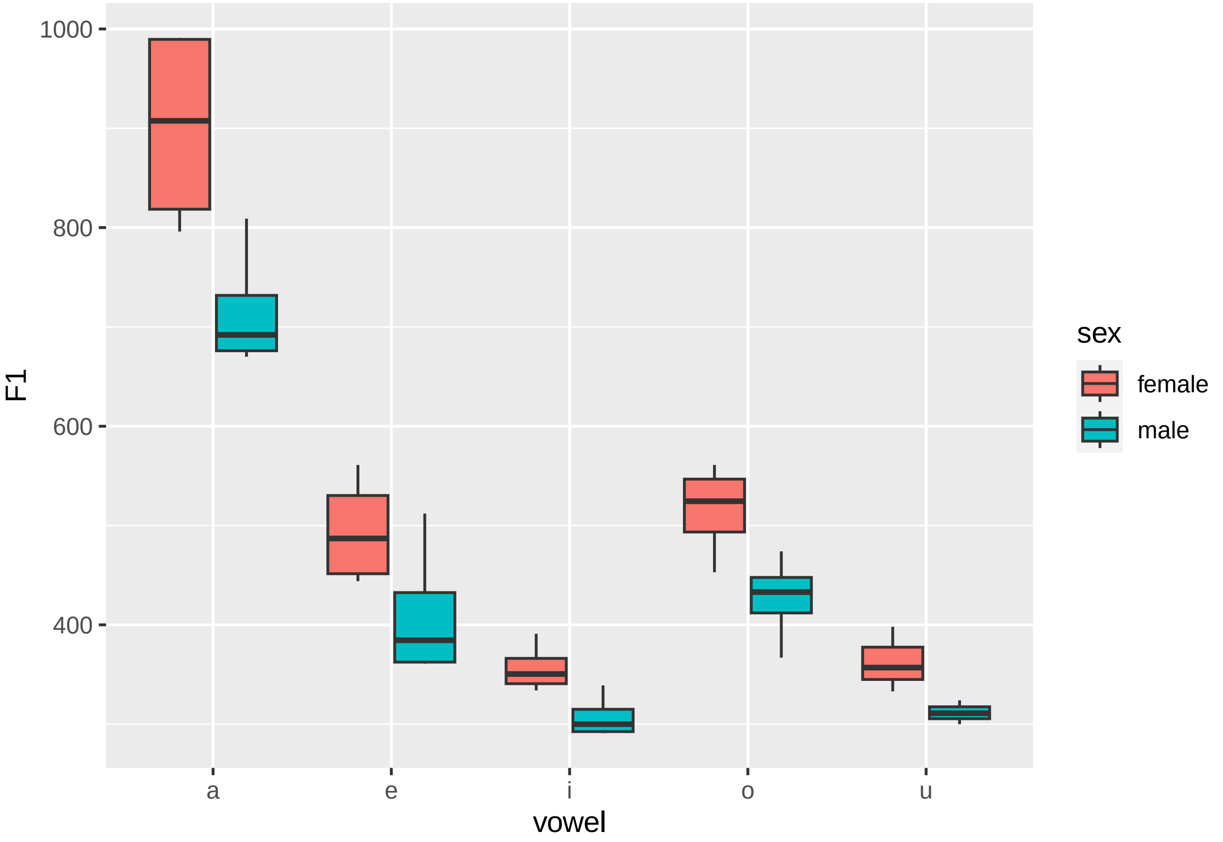
```
##
##  Paired t-test
##
## data:  f1$female and f1$male
## t = 6.1061, df = 18, p-value = 4.538e-06
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  67.11652      Inf
## sample estimates:
## mean of the differences
##                93.73684
```

And now we interpret the results and either accept or reject the null hypothesis.

Is there a statistically significant difference between the means?

What could we do from here? One idea would be to dig deeper into the data. For example, do we see differences within **each** vowel?

```
ggplot(data = df, aes(vowel, F1, fill=sex)) +
  geom_boxplot()
```


F1
a
e
i
o
u
vowel
sex
female
male