Comparing Groups and Hypothesis Testing

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Contents

We've mainly reviewed about informally comparing the distribution of data in different groups. Now we want to explore tools about how to use statistics to make this more formal – specifically to quantify whether the differences we see are due to natural variability or something deeper.

We will first consider the setting of comparing two groups. Depending on whether you took STAT 20 or Data 8, you may be more familiar with one set of tools than the other.

In addition to the specific hypothesis tests we will discuss (review), we have the following goals:

- abstract the ideas of hypothesis testing, in particular what it means to be "valid", what makes a good procedure
- dig a little deeper as to what assumptions we are making in using a particular test
- Two paradigms of hypothesis testing:
  - parametric ideas of hypothesis testing
  - resampling methods for hypothesis testing

The Question Recall the airline data, with different airline carriers. We could ask the question about whether the distribution of flight delays is different between carriers. If we wanted to ask whether United was more likely to have delayed flights than American Airlines, how might we quantify this?

What happens here when I take the mean of all our observations?

```
flightSubset <- flightSFOSRS[flightSFOSRS$Carrier %in%
    c("UA", "AA"), ]
mean(flightSubset$DepDelay)
```

```
## [1] NA
```

We can use a useful function 'tapply' that will do calculations by group.

```
tapply(X = flightSubset$DepDelay, flightSubset$Carrier,
    mean)
```

```
## AA UA
## NA NA
```

```
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    mean, na.rm = TRUE)
```

```
##        AA        UA
##  7.728294 12.255649
```

```
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    function(x) {
        mean(x, na.rm = TRUE)
    })
```

```
##        AA        UA
##  7.728294 12.255649
```

```
f <- function(x) {
    mean(x, na.rm = TRUE)
}
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    FUN = f)
```

```
##        AA        UA
##  7.728294 12.255649
```

```
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    function(x) {
        median(x, na.rm = TRUE)
    })
```

```
## AA UA
## -2 -1
```

```
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    function(x) {
        sum(x > 0 | is.na(x))/length(x)
    })
```

```
##        AA        UA
## 0.3201220 0.4383791
```

```
tapply(flightSubset$DepDelay, flightSubset$Carrier,
    function(x) {
        sum(x > 15 | is.na(x))/length(x)
    })
```

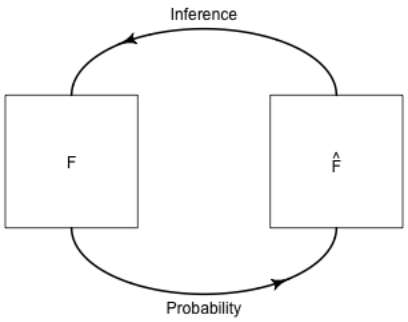
```
##        AA        UA
## 0.1554878 0.2046216
```

```
tapply(flightSubset$Cancelled, flightSubset$Carrier,
    mean)
```

```
##          AA          UA
## 0.005081301 0.007032820
```

These are **statistics** that we can calculate from the data. A statistic is *any* function of the input data sample.

Once we've decided on a statistic, we want to ask whether this is a meaningful difference between our groups. Specifically, with different data samples, the statistic would change. **Inference** is the process of using statistical tools to evaluate whether the statistic observed indicates some kind of actual difference, or whether we could see such a value due to random chance even if there was no difference.



Therefore, to use the tools of statistics – to say something about the generating process – we must have be able to define a random process that we posit created the data.

1 Hypothesis Testing

Recall the components of **hypothesis testing**.

- Hypothesis testing sets up a **null hypothesis** which describes a feature of the population data that we want to test – for example, are the medians of the two populations the same?
- In order to assess this question, we need to know what would be the distribution of our sample statistic if that null hypothesis is true. To do that, we have to go further than our null hypothesis and further describe the random process that could have created our data if the null hypothesis is true. If we know this process, it will define the specific probability distribution of our statistic if the null hypothesis was true. This is called the **null distribution**.

  The null distribution makes specific the qualitative question "this difference might be just due to chance", since there are a lot of ways "chance" could have created non-meaninful differences between our populations.
- How do we determine whether the null hypothesis is a plausible explanation for the data? We take the value of the statistic we actually observed in our data, and we determine whether this observed value is too unlikely under the null distribution to be plausible.

Specifically, we calculate the probability (under the null distribution) of randomly getting a statistic X under the null hypothesis *as extreme as or more extreme* than the statistic we observed in our data (x_{obs}). This probability is called a **p-value**.

"Extreme" means values of the test-statistic that are unlikely under the null hypothesis we are testing. In almost all tests it means large numeric values of the test-statistic, but whether we mean large positive values, large negative values, or both depends on how we define the test-statistic and which values constitute divergence from the null hypothesis. For example, if our test statistic is the *absolute* difference in the medians of two groups, then large positive values are stronger evidence of not following the null distribution:

$$\text{p-value}(x_{obs}) = P_{H_0}(X \geq x_{obs})$$

If we were looking at just the difference, large positive *or* negative values are evidence against the null that they are the same,

$$\text{p-value}(x_{obs}) = P_{H_0}(X \leq -x_{obs}, X \geq x_{obs}) = 1 - P_{H_0}(-x_{obs} \leq X \leq x_{obs}).^1$$

- If the observed statistic is too unlikely under the null hypothesis we can say we **reject the null hypothesis** or that we have a **statistically significant** difference.

  How unlikely is *too* unlikely? Often a proscribed cutoff value of 0.05 is used so that p-values *less* than that amount are considered too extreme. But there is nothing magical about 0.05, it's just a common standard if you have to make a "Reject"/"Don't reject" decision. Such a standard cutoff value for a decision is called a **level**. Even if you need to make a Yes/No type of decision, you should report the p-value as well because it gives information about *how* discordant with the null hypothesis the data is.

1.1 Where did the data come from? Valid tests & Assumptions

Just because a p-value is reported, doesn't mean that it is correct. You must have a **valid** test. A valid test simply means that the p-value (or level) that you report is accurate. This is only true if the null distribution of the test statistic is correctly identified. To use the tools of statistics, we must assume some kind of random process created the data. When your data violates the assumptions of the data generating process, your p-value can be quite wrong.

[1] In fact the distribution of X and $|X|$ are related, and thus we can simplify our life by considering just $|X|$.

What does this mean? After all, the whole point is that we're trying to detect when the statistic doesn't follow the null hypothesis distribution. So we know it may not be true!

Usually, we are asking about one specific feature of the random process – that is our actual null hypothesis we want to test. The random process that we further assume in order to get a precise null statistic, however, will have further assumptions. Sometimes we can know these assumptions are true, but often not; knowing where your data came from and how it is collected is critical for assessing these questions. So we need to always think deeply about where the data come from, how they were collected, etc.

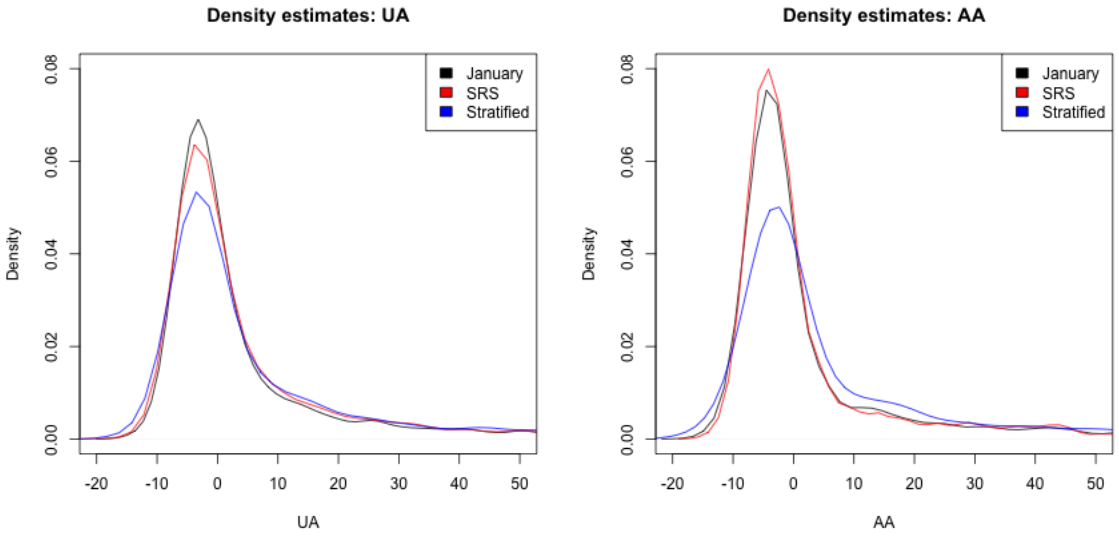
Complete Census For example, for the airline data, we have one dataset that gives *complete* information about the month of January. We can ask questions about flights in January, and get the answer by calculating the relevant statistics. For example, if we want to know whether the average flight is more delayed on United than American, we calculate the means of both groups and simply compare them. End of story. We don't need the inference tools from above

Types of Samples For most of statistical applications, this is not the case. We have a *sample* of the entire population, and want to make statements about the entire population which we don't see. Notice that having a sample does not necessarily mean a random sample. For example, we have all of January which is a sample from the entire year, and there is no randomness involved in how we selected the data from the larger population. Some datasets might be a sample of the population with no easy way to describe the relationship between the sample and the population, for example data from volunteers or other *convenience samples* that pick the easiest to get data rather than randomly sampling from the population. Having convenience samples can make it quite fraught to try to make any conclusions about the population from the sample; generally we have to make assumptions about the data was collected, but because we did not control how the data is collected, we have no idea if the assumptions are true.

What problems do you have in trying to use the flight data on January to estimate something about the entire year?

What would be a better way to get flight data?

We discussed this issue for estimating histograms, where our histogram is a good estimate of the population when our data is a SRS, and otherwise may be quite off base. For example, here is the difference in our density estimates for three different kinds of sampling:



Recall there, that we said there we could find good estimates for other kind of random samples, though beyond the reach of this course. The key ingredient that is needed is to know the probability mechanism that drew the samples. This is the key difference between a random sample (of any kind) where we control the random process, and a sample of convenience – which may be random, but we don't know *how* the randomness was generated.

Assumptions versus reality A prominent statistician, George Box, gave the following famous quote,

All models are wrong but some are useful

All tests have assumptions, and most are often not met in practice. This is a continual problem in interpreting the results of statistical methods. Therefore there is a great deal of interest in understanding how badly the tests perform if the assumptions are violated; this is often called being **robust** to violations. We will try to emphasize both what the assumptions are, and how bad violations to the assumptions are.

For example, in practice, much of data that is available is not a carefully controlled random sample of the population, and therefore a sample of convenience in some sense (there's a reason we call them convenient!). Our goal is not to make say that analysis

of such data is impossible, but make clear about why this might make you want to be cautious about over-interpreting the results.

2 Permutation Tests

Suppose we want to compare the the proportion of flights with greater than 15 minutes delay time of United and American airlines. Then our test statistic will be the difference between that proportion

The permutation test is a very simple, straightforward mechanism for comparing two groups that makes very few assumptions about the distribution of the underlying data. The permutation test basicallly assumes that the data we saw we could have seen anyway even if we changed the group assignments (i.e. United or American). Therefore, any difference we might see between the groups is due to the luck of the assignment of those labels.

The null distribution for the test statistic (difference of the proportion) under the null hypothesis for a permutation tests is determined by making the following assumptions:

1. There is no difference between proportion of delays greater than 15 minutes between the two airlines,
$$H_0 : p_{UA} = p_{AA}$$
This is the main feature of the null distribution to be tested

2. The statistic observed is the result of randomly assigning the labels amongst the observed data.

   This is the additional assumption about the random process that allows for calculating a precise null distribution of the statistic. It basically expands our null hypothesis to say that the distribution of the data between the two groups is the same, and the labels are just random assignments to data that comes from the same distribution.

2.1 How do we implement it?

This is just words. We need to actually be able to compute probabilities under a specific distribution. In other words, if we were to have actually just randomly assigned labels to the data, we need to know what is the probablility we saw the median difference we actually saw?

How do you actually determine the null distribution for permutation tests?

The key assumption is that the data we measured (the flight delay) was fixed for each observation and completely independent from the airline the observation was assigned to. We imagine that the airline assignment was completely random and separate from the flight delays – a bunch of blank airplanes on the runway that we at the last minute assign to an airline, with crew and passengers (not realistic, but a thought experiment!)

If our data actually was from such a scenario, we could actually rerun the random assignment process. How? By randomly reassigning the labels. Since under the null we assume that the data we measured had nothing to do with those labels, we could have instead observed another assignment of those airline labels and seen the same data, just different labels on the planes. These are called **permutations** of the labels of the data.

We could enumerate all possible assignments of the observed delay data to airlines, and we would have the complete set potential flight delay datasets possible under the null hypothesis.

```
##   FlightDelay Observed Permutation1 Permutation2 Permutation3
## 1           5       UA           AA           UA           AA
## 2          -6       UA           UA           UA           UA
## 3         -10       AA           UA           UA           UA
## 4          -3       UA           UA           AA           UA
## 5          -3       UA           UA           AA           UA
## 6           0       UA           UA           UA           UA
```

For each of these permutations, I can calculate the median of those delays assigned to UA and those assigned to AA, and the difference between them

```
## Proportions per Carrier, each permutation:
##     Observed Permutation1 Permutation2 Permutation3
## AA 0.1554878    0.2063008    0.1951220    0.1910569
## UA 0.2046216    0.1878768    0.1915606    0.1929002

## Differences in Proportions per Carrier, each permutation:
##     Observed Permutation1 Permutation2 Permutation3
##  0.049133762 -0.018424055 -0.003561335  0.001843290
```

So in principle, it's straightforward – I just do this for every possible permutation, and get the difference of proportions. The result set of values gives the finite probability distribution

Too many! In practice: Random selection If we have, say, 14 observations with two groups of 7 each, how many permutations do we have?

So for even such a small dataset, we'd have to ennumerate almost 3500 permutations. In the airline data, we have 984, 2986 per airline. We can't even determine how many enumerations that is, much less actually enumerate them all.

Instead, we consider that there exists some such distribution and we are going to just estimate what it is. How? By creating a SRS from that distribution. Specifically, each possible permutation is an element of our sample space, and we need to randomly draw a permutation. We'll do this many times (i.e. many calls to the function `sample`), and this will create a SRS of permutations. Once we have a SRS of permutations, we can calculate the test statistic for each permutation, and get an estimate of the true null distribution. Unlike SRS of an actual population data, we can make the size of our SRS as large as our computer can handle to improve our estimate (though we don't in practice need it to be obscenely large)

Practically, this means we will repeating what we did above many times. The function `replicate` in R allows you to repeat something many times, so we will use this to repeat the sampling and the calculation of the difference in medians (in the accompanying R code, you will see that I wrote a little function to do this for any arbitrary statistic and I will use this function repeatedly in the lecture).

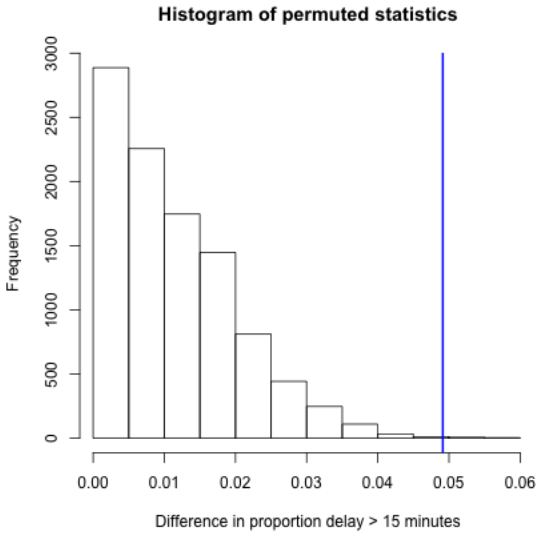
Proportion Later than 15 minutes Now we implement it on our the SRS version of our flight data for the difference in the propotions. Notice that I am going to make the statistic for which I compare the *absolute* difference between the proportion later than 15 minutes, so that large values are considered extreme.

Recall, our summary statistics

```
tapply(flightSFOSRS$DepDelay, flightSFOSRS$Carrier,
    propFun)[c("AA", "UA")]
```

```
##        AA        UA
## 0.1554878 0.2046216
```

Here is the histogram of what that gave me:



If my data came from the null, then this is the (estimate) of the actual distribution of what the test-statistic would be. How would I get a p-value from this? (what is the definition of a p-value once you know its distribution?)

```
## pvalue= 0.0011
```

So what conclusions would you draw from this permutation test?

What impact does it have? What conclusions would you be likely to make going forward?

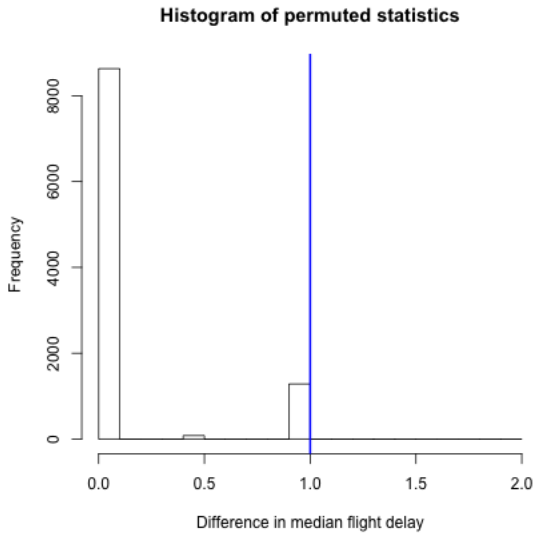
Why do I take the absolute difference? What difference does it make if you change the code to be only the difference?

Median difference What about if I look at the median flight delay? The first thing we might note is that there is a very small difference (1 minute). So even if we find something significant, who really cares? That is not going to change any opinions about which airline I fly. Statistical significance is not everything.

```
tapply(flightSFOSRS$DepDelay, flightSFOSRS$Carrier,
    function(x) {
        median(x, na.rm = TRUE)
    })[c("AA", "UA")]
```

```
## AA UA
## -2 -1
```

I can just quickly change the statistic I consider to be the absolute difference in the median instead of proportion late.




```
## pvalue= 0.1287
```

What is going on with our histogram?

What would have happened if we had defined our p-value as the probability of being *greater* rather than *greater than or equal to*? Where in the code was this done, and what happens if you change the code?

2.2 Assumptions: permutation tests

Let's discuss limitations of the permutation test.

Assumption of data generating process What assumption(s) are we making about the random process that generated this data in determining the null distribution? Does it make sense for our data?

Some datasets have this flavor. For example, if we wanted to decide which of two email solicitations for a political campaign are most likely to lead to someone to donate money, we could assign a sample of people on our mailing list to get one of the two. This would perfectly match the data generation assumed in the null hypothesis.

What if our assumption about random labels is wrong? Clearly random assignment of labels is not a good description for how any of the datasets regarding flight delay data were created. Does this mean the permutation test will be invalid? No, not necessarily. We just need that the null hypothesis have a random process that created the data that leads to a distribution of the permutation test that is equivalent to as if we randomly assigned labels.

Explicitly describing this assumption is beyond the level of this class[2], but an important example where they are valid is if each of your data observations can be considered a random, independent draw from the same distribution (assuming the null is true and the distributions are the same between groups). This is often abbreviated **i.i.d** (independent and identically distributed). This makes sense – the very act of permuting your data implies such an assumption about your data: that you have similar observations and the only thing different about them is which group they were assigned to.

Assuming your data is i.i.d is a common assumption that is thrown around, but is actually rather strong. For example, non-random samples do not have this property, because there is no randomness; convenience samples are unlikely to as well. However, permutation tests are a pretty good tool even in this setting, however, compared to the alternatives. Actual random assignments of the labels is the strongest such design of how to collect data.

[2]Namely, if the data can be assumed to be *exchangeable* under the null hypothesis, then the permutation test is also a valid test.

Inferring beyond the sample population Note that the randomness queried by our null hypothesis is all about the specific observations we have. Specifically the randomness is if we imagine that we assigned *these same people* different email solicitations – our null hypothesis asks what variation in our statistic would we expect? However, if we want to extend this to the general population, we have to make the assumption that these people's reaction are representative of the greater population.

For example, in our political email example we described above, if our sample of participants was only women, then the permutation test might have answered the question about any affect seend amongst these women was due to the chance assignment to these women. But that wouldn't answer our question very well about the general population of interest (that presumably includes men). Men might have very different reactions to the same email. Permutation tests do not get around the problem of a poor data sample. Random samples from the population are needed to be able to make the connection back to the general population.

So while permuting your data seems to intuitive and is often thought to make no assumptions, it does have assumptions about where your data are from. The assumptions for a permutation test are much less than some alternative tests (like the parametric tests we'll describe next), but it's useful to realize the limitations even for something as intuitive and as non-restrictive as permutation tests.

3 Parametric test: the T-test

In parametric testing, we assume the data comes from a specific family of distributions that share a functional form for their density, and define the features of interest for the null hypothesis based on this distribution.

Rather than resampling from the data, we will use the fact that we can analytically write down the density to determine the null distribution of the test statistic. For that reason, parametric tests tend to be limited to narrower class of statistics, since they have to be tractable for mathematical analysis.

3.1 Parameters

We have spoken about parameters in the context of parameters that define a family of distributions with the same mathematical form for the density. Much of the time the null hypothesis will be a direct hypotheses about the parameters that define our distribution. But the hypothesis could be something else about the distribution. For example, we could assume that the data comes from a normal distribution and our

null hypothesis could be about the .75 quantile of the distribution. So we can talk more generally about a parameter of any distribution as any numerical summary that we can get from a distribution. So the .75 quantile could be our parameter of interest. So just as a statistic is any function of our observed data, a **parameter** is a function of the true generating distribution F. We don't have to have assume that the data comes from any parametric distribution – every distribution has a .75 quantile. Parameters are often indicated with greek letters, like θ, α, β, σ.

If we assume our data is generated from one of a family of distributions defined by specific parameters (e.g. a normal distribution with unknown mean and variance) then those parameters completely define the distribution. Therefore any arbitrary parameter of the distribution can be written as a function of those parameters that define the distribution. So the 0.75 quantile of a normal distribution is a function of the mean μ and variance σ^2 of the normal distribution.

Statistics of our data sample are often chosen because they are estimates of our parameter. In that case they are often called the same greek letters as the parameter, only with a "hat" on top of them, e.g. $\hat{\theta}$, $\hat{\alpha}$, $\hat{\beta}$, $\hat{\sigma}$. Sometimes, however, a statistic will just be given a upper-case letter, like T or X, particularly when they are not estimating a parameter of the distribution.

3.2 More about the normal distribution and two group comparisons

Means and the normal distribution play a central role in many parametric tests, so lets review a few more facts.

Standardized Values If $X \sim N(\mu, \sigma^2)$, then

$$\frac{X - \mu}{\sigma} \sim N(0, 1)$$

This is called standardizing X.

Sums of normals If $X \sim N(\mu_1, \sigma_1^2)$ and $Y \sim N(\mu_2, \sigma_2^2)$ and X and Y are independent, then

$$X + Y \sim N(\mu_1 + \mu_2, \sigma_1^2 + \sigma_2^2)$$

CLT for differences of means We've reviewed that a sample mean of a SRS will have a sampling distribution that is roughly a normal distribution (the Central Limit

Theorem) – if we have a large enough sample size. Namely, that if $X_1, \ldots, X_n$ are a SRS from a distribution with mean μ and variance σ^2, then $\hat{\mu} = \bar{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$ will have a roughly normal distribution

$$N(\mu, \frac{\sigma^2}{n}).$$

If we have two groups,

- $X_1, \ldots, X_{n_1}$ a SRS from a distribution with mean μ_1 and variance σ_1^2, and
- $Y_1, \ldots, Y_{n_2}$ a SRS from a distribution with mean μ_2 and variance σ_2^2

Then if the X_i and Y_i are independent, then the central limit theorem applies and $\bar{X} - \bar{Y}$ will have a roughly normal distribution equal to

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

3.3 Testing of means

Let μ_{United}, and $\mu_{American}$ be the true means of the distribution of flight times of the two airlines in the population. We can write our null hypothesis as

$$H_0 : \mu_{AA} = \mu_{UA}$$

This could also be written as

$$H_0 : \mu_{AA} - \mu_{UA} = \delta = 0,$$

so we are testing whether a specific parameter $\delta = 0$.

Let's assume $X_1, \ldots, X_{n_1}$ is the data from United and $Y_1, \ldots, Y_{n_2}$ is the data from American. A natural sample statistic to estimate δ from our data would be

$$\hat{\delta} = \bar{X} - \bar{Y},$$

i.e. the difference in the means of the two groups.

Null distribution To do inference, we need to know the distribution of our statistic of interest. Our central limit theorem will tell us that under the null, for large sample sizes, the difference in means is distributed normally,

$$\bar{X} - \bar{Y} \sim N(0, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2})$$

We can thus use that distribution to determine whether the observed $\bar{X} - \bar{Y}$ is unexpected under the null (assuming we know σ_1 and σ_2!).

We can also equivalently standardize $\bar{X} - \bar{Y}$ and say,

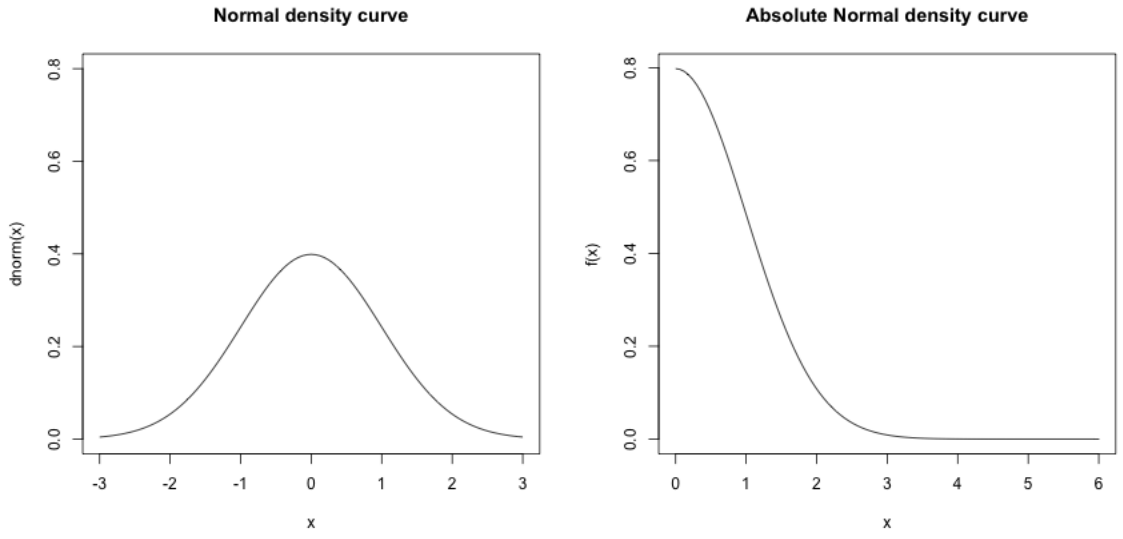
$$Z = \frac{\bar{X} - \bar{Y}}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} \sim N(0, 1)$$

Calculating a P-value Suppose that we observe a statistic $Z = 2$. To calculate the p-value we need to calculate the probability of getting a value as extreme as 2 or more under the null. What does extreme mean here? We need to consider what values of Z (or the difference in our means) would be considered evidence that the null hypothesis didn't explain the data. Going back to our example, $\bar{X} - \bar{Y}$ might correspond to $\bar{X}_{AA} - \bar{Y}_{UA}$, and clearly large positive values would be evidence that they were different. But large negative values also would be evidence that the means were different. Either is equally relevant as evidence that the null hypothesis doesn't explain the data.

So a reasonable definition of extreme is large values in either direction. This is more succinctly written as $|\bar{X} - \bar{Y}|$ being large.

So a better statistic is,

$$Z = \frac{|\bar{X} - \bar{Y}|}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$$



With this better Z statistic, what is the p-value if you observe $Z = 2$? How would

you calculate this using the standard normal density curve? With R?

This is often called a 'two-sided' t-statistic, and is the only one that we will consider.[3]

3.4 T-Test

The above test is actually just a thought experiment because Z is not in fact a statistic because we don't know σ_1 and σ_2. So we can't calculate Z from our data!

Instead you must estimate these unknown parameters with the **sample variance**

$$\hat{\sigma}_1^2 = \frac{1}{n-1}\sum(X_i - \bar{X})^2,$$

and the same for $\hat{\sigma}_2^2$. (Notice how we put a "hat" over a parameter to indicate that we've estimated it from the data.)

But once you must estimate the variance, you are adding additional variability to inference. Namely, before, assuming you knew the variances, you had

$$Z = \frac{|\bar{X} - \bar{Y}|}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}},$$

where only the numerator is random. Now we have

$$T = \frac{|\bar{X} - \bar{Y}|}{\sqrt{\frac{\hat{\sigma}_1^2}{n_1} + \frac{\hat{\sigma}_2^2}{n_2}}}.$$

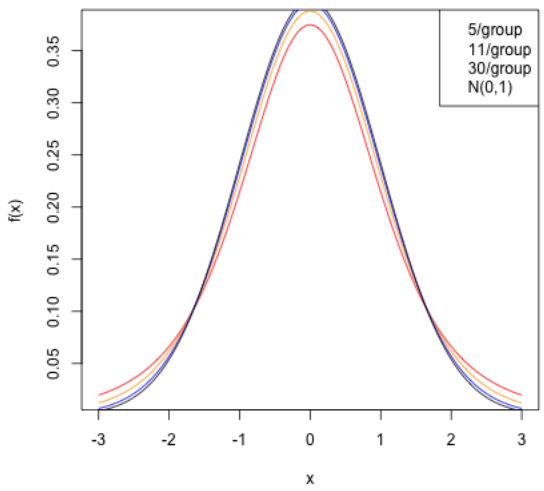
and the denominator is also random. T is called the **t-statistic**.

This additional uncertainty means seeing a large value of T is more likely than of Z. Therefore, T has a different distribution, and it's not $N(0,1)$.

Unlike the central limit theorem, that deals only with the distributions of means, when you add on estimating the variance terms determining even approximately what is the distribution of T is more complicated, and in fact depends on the distribution

[3]There are rare cases in comparing means where you might consider only evidence against the null that is positive (or negative). In this case you would then calculate the p-value correspondingly. These are called "one-sided" tests, for the same value of the observed statistic Z they give you smaller p-values, and they are usually only a good idea in very specific examples.

of the input data X_i and Y_i (unlike the central limit theorem). But if the distributions creating your data are reasonably close to normal distribution, then T follows what is called a t-distribution.



You can see that the t distribution is like the normal, only it has larger "tails" than the normal, meaning seeing large values is more likely than in a normal distribution.

What happens as you change the sample size?

Notice that if you have largish datasets (e.g. $> 30 - 50$ samples in *each* group) then you can see that the t-distribution is numerically almost equivalent to using the normal distribution, so that's why it's usually fine to just use the normal distribution to get p-values. Only in small samples sizes are there large differences.

Degrees of Freedom The t-distribution has one additional parameter called the **degrees of freedom**, often abreviated as *df*. This parameter has nothing to do with the mean or standard deviation of the data (since our t-statistic is already standardized), and depends totally on the sample size of our populations. The actual equation for the degrees of freedom is quite complicated:

$$df = \frac{\left(\frac{\hat{\sigma}_1^2}{n_1} + \frac{\hat{\sigma}_2^2}{n_2}\right)^2}{\frac{(\frac{\hat{\sigma}_1^2}{n_1})^2}{n_1 - 1} + \frac{(\frac{\hat{\sigma}_2^2}{n_2})^2}{n_2 - 1}}.$$

This is not an equation you need to learn or memorize, as it is implemented in R for you. A easy approximation for this formula is to use

$$df \approx min(n_1 - 1, n_2 - 1)$$

This approximation is mainly useful to try to understand how the degrees of freedom are changing with your sample size. Basically, the size of the smaller group is the important one. Having one huge group that you compare to a small group doesn't help much – you will do better to put your resources into increasing the size of the smaller group (in the actual formula it helps a little bit more, but the principle is the same).

3.5 Assumptions of the T-test

Parametric tests usually state their assumptions pretty clearly: they assume a parametric model generated the data in order to arrive at the mathematical description of the null distribution. For the t-test, we assume that the data $X_1, \ldots, X_{n_1}$ and $Y_1, \ldots, Y_{n_2}$ are normal to get the t-distribution.

What happens if this assumption is wrong? When will it still make sense to use the t-test?

If we didn't have to estimate the variance, the central limit theorem tells us the normality assumption will work for any distribution, *if* we have a large enough sample size.

What about the t-distribution? That's a little tricker. You still need a large sample size; you also need that the distribution of the X_i and the Y_i, while not required to be exactly normal, not be too far from normal. In particular, you want them to be symmetric (unlike our flight data).[4]

Generally, the t-statistic is reasonably robust to violations of these assumptions, particularly compared to other parametric tests, if your data is not too skewed and you have a largish sample size (e.g. 30 samples in a group is good). But the permutation test makes far fewer assumptions, and in particular is very robust to assumptions about the distribution of the data.

For small sample sizes (e.g. < 10 in each group), you certainly don't really have any good justification to use the t-distribution unless you have a reason to trust that the data is normally distributed (and with small sample sizes it is also very hard to justify this assumption by looking at the data).

[4]Indeed, the central limit theorem requires large data sizes, and how large a sample you need for the central limit theorem to give you a good approximation also depends on things about the distribution of the data, like how symmetric the distribution is.

3.6 Flight Data and Transformations

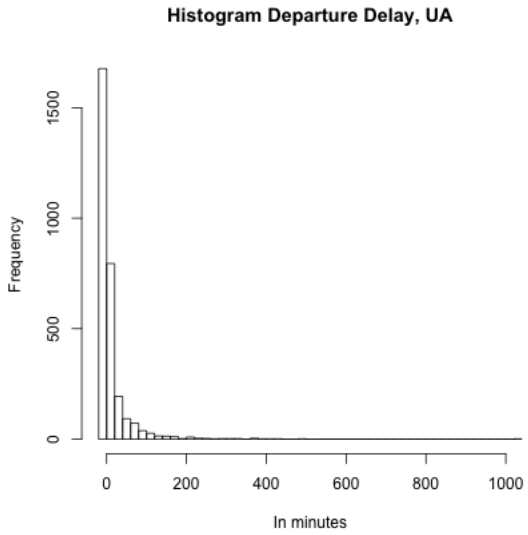
Let's consider the flight data. Recall, the t-statistic focuses on the difference in means. Why might this not be a compelling comparison?

```
tapply(flightSFOSRS$DepDelay, flightSFOSRS$Carrier,
    function(x) {
        mean(x, na.rm = TRUE)
    })[c("AA", "UA")]
```

```
##        AA        UA
##  7.728294 12.255649
```

Furthermore, you still – even with larger sample sizes – need to worry about the distribution of the data much more than with the permutation test. Very non-normal input data will not do well with the t-test, particularly if the data is **skewed**, meaning not symmetrically distributed around its mean.

Looking at the flight data, what would you conclude?



Note that nothing stops us from running the test, and it's a simple one-line code:

```
t.test(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "UA"], flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "AA"])
```

```
##
##  Welch Two Sample t-test
##
## data:  flightSFOSRS$DepDelay[flightSFOSRS$Carrier == "UA"] and flightSFOSRS$DepDel
## t = 2.8325, df = 1703.1, p-value = 0.004673
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.392379 7.662332
## sample estimates:
## mean of x mean of y
## 12.255649  7.728294
```

This is a common danger of parametric tests. They are implemented everywhere (there are on-line calculators that will compute this for you; excel will do this calculation), so people are drawn to doing this, while permutation tests are more difficult to find pre-packaged.

Direct comparison to the permutation test The permutation test can use any statistic we like, and the t-statistic is a perfectly reasonable way to compare two distributions. So we can compare the t-test to a permutation test of the mean *using the t-statistic*:

```
set.seed(489712)
tstatFun <- function(x1, x2) {
    abs(t.test(x1, x2)$statistic)
}
dataset <- flightSFOSRS
output <- permutation.test(group1 = dataset$DepDelay[dataset$Carrier ==
    "UA"], group2 = dataset$DepDelay[dataset$Carrier ==
    "AA"], FUN = tstatFun, n.repetitions = 10000)
cat("permutation pvalue=", output$p.value)
```

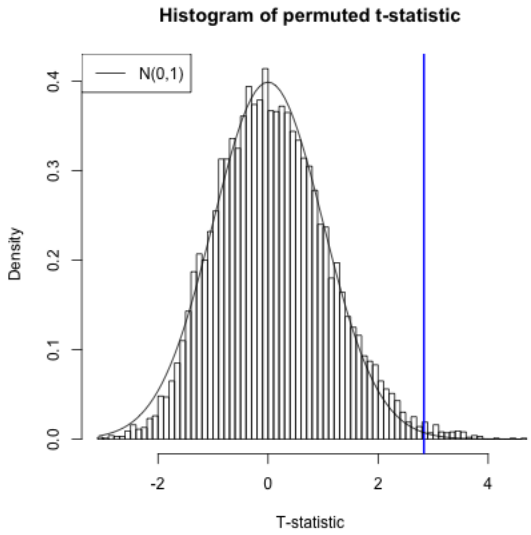
```
## permutation pvalue= 0.0076
```

```
tout <- t.test(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "UA"], flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
```

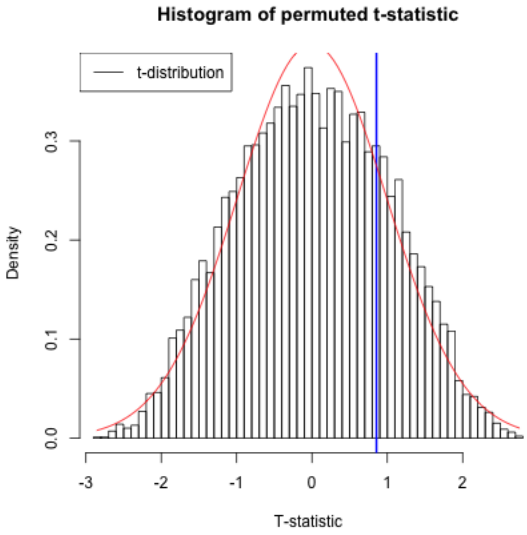
```
    "AA"])
cat("t-test pvalue=", tout$p.value)
```

```
## t-test pvalue= 0.004673176
```

We can compare the distribution of the permutation distribution of the t-statistic, and the density of the $N(0,1)$ that the parametric model assumes. We can see that they are quite close, even though our data is very skewed and clearly non-normal. Indeed for larger sample sizes, they will give similar results.



Smaller Sample Sizes If we had a smaller dataset we would not get such nice behavior. We can take a sample of our dataset to get a smaller sample of the data of size 20 and 30 in each group, and we can see that we do not get a permutation distribution that matches the (roughly) N(0,1) we use for the t-test.

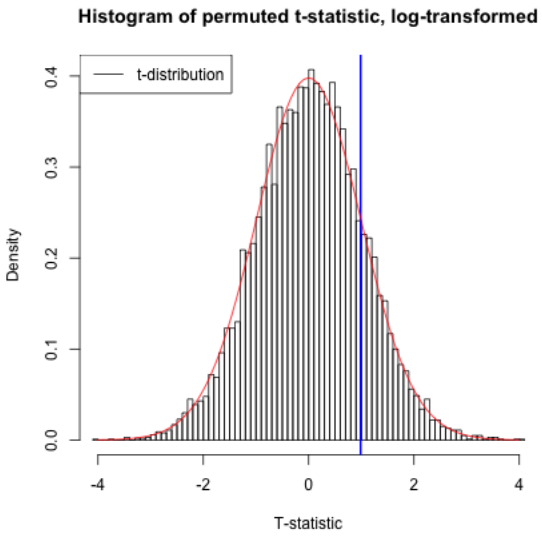



```
## pvalue permutation= 0.4446
## pvalue t.test= 0.394545
```

What different conclusions do you get from the two tests with these smaller data-sizes?

Transformations We saw that skewed data could be problematic in visualization of the data, e.g. in boxplots, and transformations are helpful. Transformations can also be helpful for applying parametric tests. They can often allow the parametric t-test to work better for smaller datasets.

If we compare both the permutation test and the t-test on log-transformed data, then even with the smaller sample sizes the permutation distribution looks much closer to the t-distribution.




```
## pvalue permutation= 0.4446
## pvalue t.test= 0.3261271
```

Why didn't the p-value for the permutation test change?

What does it mean for my null hypothesis to transform to the log-scale? Does this make sense?

3.7 Why parametric models?

We do the comparison of the permutation test to the parametric t-test not to encourage the use of the the t-test in this setting – the data, even after transformation, is pretty skewed and there's no reason to not use the permutation test instead. The permutation test will give pretty similar answers regardless of the transformation[5] and is clearly indicated here.

This exercise was to show the use and limits of using the parametric tests, and particularly transformations of the data, in an easy setting. Historically, parametric t-tests were necessary in statistics because there were not computers to run permutation

[5]In fact, if we were working with the difference in the means, rather than the t-statistics, which estimates the variance, the permutation test would give exactly the same answer since the log is a monotone transformation.

tests. That's clearly not compelling now! However, it remains that parametric tests are often easier to implement (one-line commands in R, versus writing a function); you will see parametric tests frequently (even when resampling methods like permutation tests and bootstrap would be more justifiable).

The take-home lesson here regarding parametric tests is that when there are large sample sizes, parametric tests can overcome violations of their assumptions[6] so don't automatically assume parametric tests are completely wrong to use. But a permutation test is the better all-round tool for this question: it is has more minimal assumptions, and can look at how many different statistics we can use.

There are also some important reasons to learn about t-tests, however, beyond a history lesson. They are the easiest example of a parameteric test, where you make assumptions about the distribution your data (i.e. $X_1, \ldots, X_{n_1}$ and $Y_1, \ldots, Y_{n_2}$ are normally distributed). Parametric tests generally are very important, even with computers. Parametric models are particularly helpful for researchers in data science for the development of new methods, particularly in defining good test statistics, like T.

Parametric models are also useful in trying to understand the limitations of a method, mathematically. We can simulate data under different models to understand how a statistical method behaves.

There are also applications where the ideas of bootstrap and permutation tests are difficult to apply. Permutation tests, in particular, are quite specific. Bootstrap methods, which we'll review in a moment, are more general, but still are not always easy to apply in more complicated settings. A goal of this class is to make you comfortable with parametric models (and their accompanying tests), in addition to the resampling methods you've learned.

4 Digging into Hypothesis tests

Let's break down some important concepts as to what makes a test. Note that all of these concepts will apply for *any* hypothesis test.

1. A null hypothesis regarding a particular feature of the data
2. A test statistic for which extreme values indicates less correspondence with the null hypothesis
3. An assumption of how the data was generated under the null hypothesis

[6] At least those tests based on the central limit theorem!

4. The distribution of the test statistic under the null hypothesis.

As we've seen, different tests can be used to answer the same basic "null" hypothesis – are the two groups "different"? – but the specifics of how that null is defined can be quite different. For any test, you should be clear as to what the answer is to each of these points.

4.1 Significance & Type I Error

The term significance refers to measuring how incompatible the data is with the null hypothesis. There are two importnat terminologies that go along with assessing significance.

p-values You often report a p-value to demonstrate how unlikely the data is under the null.

Q: Does the p-value give you the probability that the null is true?

Decision: Reject/Not reject We can just report the p-value, but it is common to also make an assessment of the p-value and give a final decision as to whether the null hypothesis was too unlikely to have reasonably created the data we've seen. This is a decision approach – either reject the null hypothesis or not. In this case we pick a cutoff, e.g. p-value of 0.05, and report that we reject the null.

You might see sentences like "We reject the null at level 0.05." The **level** chosen for a test is an important concept in hypothesis testing and is the cutoff value for a test to be significant. In principle, the idea of setting a level is that it is a standard you can require before declaring significance; in this way it can keep researchers from creeping toward declaring significance once they see the data and see they have a p-value of 0.07, rather than 0.05. However, in practice it can have the negative result of encouraging researchers to fish in their data until they find *something* that has a p-value less than 0.05.

Commonly accepted cutoffs for unlikely events are 0.05 or 0.01, but these values are too often considered as magical and set in stone. Reporting the actual p-value is more informative than just saying yes/no whether you reject (rejecting with a p-value of 0.04 versus 0.0001 tells you something about your data).

The deeper concept about the level of the test is that it defines a repeatable procedure ("reject if p-value is $< \alpha$"). Then the level actually reports the uncertainity in this procedure. Specifically, with any test, you can make two kinds of mistakes:

- Reject the null when the null is true (**Type I error**)
- Not reject the null when the null is in fact not true (**Type II error**)

Then the **level** of a decision is the probability of this procedure making a type I error: if you always reject at 0.05, then 5% of such tests will wrongly reject the null hypothesis when in fact the null is true is true.

Note that this is no different in concept that our previous statement saying that a p-value is the likelihood under the null of an event as extreme as what we observed. However, it does a quantify how willing you are to making Type I Error in setting your cutoff value for decision making.

4.2 Type I Error & All Pairwise Tests

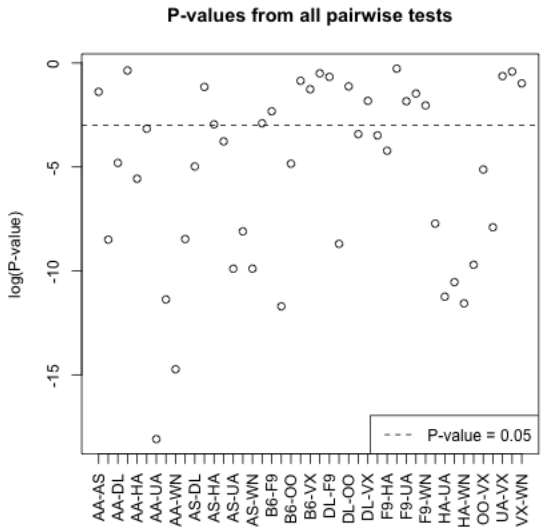
Let's make the importance of accounting and measuring Type I error more concrete. We have been considering only comparing the carriers United and American. But in fact there are 10 airlines. What if we want to compare all of them? What might we do?

```
## number of pairs: 45
```

For speed purposes in class, I'll use the t-test to illustrate this idea and calculate the t-statistic and its p-value for every pair of airline carriers (with our transformed data):

```
## [1]  2 45
##       statistic.t      p.value
## AA-AS   1.1514752 0.2501337691
## AA-B6  -3.7413418 0.0002038769
## AA-DL  -2.6480549 0.0081705864
## AA-F9  -0.3894014 0.6974223534
## AA-HA   3.1016459 0.0038249362
## AA-OO  -2.0305868 0.0424142975
##       statistic.t      p.value
```

```
## AA-AS   1.1514752 0.2501337691
## AA-B6  -3.7413418 0.0002038769
## AA-DL  -2.6480549 0.0081705864
## AA-F9  -0.3894014 0.6974223534
## AA-HA   3.1016459 0.0038249362
## AA-OO  -2.0305868 0.0424142975
## Number found with p-value < 0.05:  26 ( 0.58  proportion of tests)
```



What does this actually mean? Is this a lot to find significant?

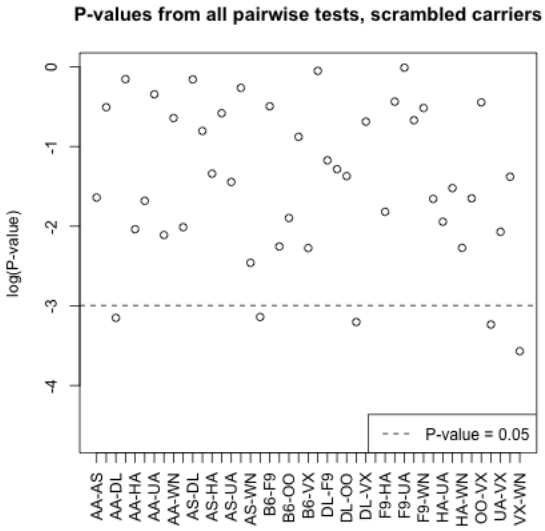
Roughly, if each of these tests has level 0.05, then even if *none* of the pairs are truly different from each other, I might expect on average around 2 to be rejected at level 0.05 just because of variation in sampling.[7] This is the danger in asking many questions from your data – something is likely to come up just by chance. [8]

We can consider this by imagining what if I scramble up the carrier labels – randomly assign a carrier to a flight. Then I know there shouldn't be any true difference amongst the carriers. I can do all the pairwise tests and see how many are significant.

```
## Number found with p-value < 0.05:  6 ( 0.13  proportion)
```

[7]In fact, this is not an accurate statement because these tests are reusing the same data, so the data in each test are not independent, and the probabilities don't work out like that. But it is reasonable for understanding the concepts here.

[8]Indeed this true of all of science, which relies on hypothesis testing, so one always has to remember the importance of the iterative process of science to re-examine past experiments.



What does this suggest to you about the actual data?

Multiple Testing Intuitively, we consider that if we are going to do all of these tests, we should have a stricter criteria for rejecting the null so that we do not routinely find pairwise differences when there are none. Does this mean the level should be higher or lower to get a 'stricter' test? What about the p-value?

Making such a change to account for the number of tests considered falls under the category of **multiple testing adjustments**, and there are many different flavors beyond the scope of the class. Let's consider the most widely known correction: the **Bonferroni correction**.

Specifically, say we will quantify our notion of 'stricter' to require "of all the tests I ran, there's only a 5% chance of a type I error". Let's make this a precise statement. Suppose that of the K tests we are considering, there are $V \leq K$ tests that are type I errors, i.e. the null is true but we rejected. We will define our cummulate error rate across the set of K tests as

$$P(V \geq 1)$$

So we if we can guarantee that our testing procedure for the set of K tests has $P(V \geq 1) \leq \gamma$ we have controlled the **family-wise error rate** to level γ.

How to control the family-wise error rate? We can do a simple correction to our K individual tests to ensure $P(V \geq 1) \leq \gamma$. If we lower the level α we require in order to reject H_0, we will lower our chance of a single type I error, and thus also lowered our family-wise error rate. Specifically, if we run the K tests and set the individual level of *each individualtest* to be $\alpha = \gamma/K$, then we will guarantee that the family-wise error rate is no more than γ.

In the example of comparing the different airline carriers, the number of tests is 45. So if we want to control our family-wise error rate to be no more than 0.05, we need each individual tests to reject only with $\alpha = 0.0011$.

```
## Number found significant after Bonferonni:  16
## Number of shuffled differences found significant after Bonferonni:  0
```

If we reject each tests only if

$$p - value \leq \alpha = \gamma/K$$

, then we can equivalently say we only reject if

$$K\frac{p - value}{\leq}\gamma$$

We can therefore instead think only about γ (e.g. 0.05), and create **adjusted p-values**, so that we can just compare our adjusted p-values directly to γ. In this case if our standard (single test) p-value is p, we have

$$\text{Bonferroni adjusted p-values} = p \times K$$

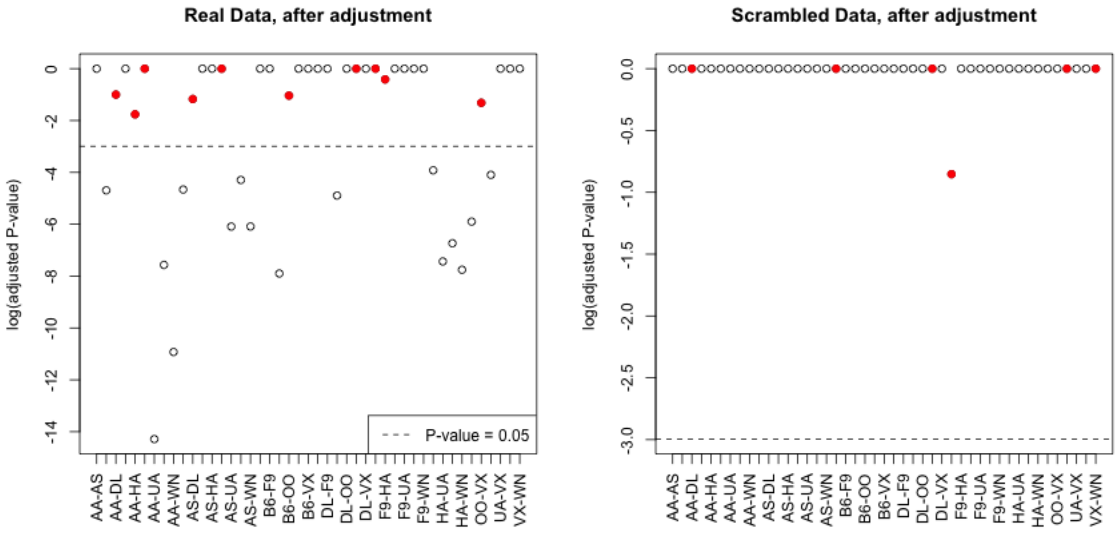
```
##       statistic.t      p.value  p.value.adj
## AA-AS   1.1514752 0.2501337691 11.256019611
## AA-B6  -3.7413418 0.0002038769  0.009174458
## AA-DL  -2.6480549 0.0081705864  0.367676386
## AA-F9  -0.3894014 0.6974223534 31.384005904
## AA-HA   3.1016459 0.0038249362  0.172122129
## AA-OO  -2.0305868 0.0424142975  1.908643388
##       statistic.t    p.value p.value.adj
## AA-AS  -1.3008280 0.19388985    8.725043
## AA-B6   0.5208849 0.60264423   27.118990
## AA-DL  -2.0270773 0.04281676    1.926754
## AA-F9  -0.1804245 0.85698355   38.564260
## AA-HA  -1.5553127 0.13030058    5.863526
## AA-OO  -1.3227495 0.18607903    8.373556
```

Notice some of these p-values are greater than 1! So in fact, we want to multiply by K, unless the value is greater than 1, in which case we set the p-value to be 1.

$$\text{Bonferroni adjusted p-values} = min(p \times K, 1)$$

```
##        statistic.t      p.value  p.value.adj p.value.adj.final
## AA-AS    1.1514752 0.2501337691 11.256019611       1.000000000
## AA-B6   -3.7413418 0.0002038769  0.009174458       0.009174458
## AA-DL   -2.6480549 0.0081705864  0.367676386       0.367676386
## AA-F9   -0.3894014 0.6974223534 31.384005904       1.000000000
## AA-HA    3.1016459 0.0038249362  0.172122129       0.172122129
## AA-OO   -2.0305868 0.0424142975  1.908643388       1.000000000
```

Now we plot these adjusted values, for both the real data and the data I created by randomly scrambling the labels. I've colored in red those tests that become non-significant after the multiple testing correction.



5 Confidence Intervals

Another approach to inference is with confidence intervals. Confidence intervals give a range of values (based on the data) that are most likely to overlap the true parameter. This means confidence intervals are only appropriate when we are focused on estimation of a specific numeric feature of a distribution (a parameter of the distribution), though they do *not* have to require parametric models to do so.[9]

[9]We can test a null hypothesis without having a specific parameter of interest that we are estimating. For example, the Chi-squared test that you may have seen in an introductory statistic class

Form of a confidence interval Confidence intervals also do not rely on a specific null hypothesis; instead they give a range of values (based on the data) that are most likely to overlap the true parameter. Confidence intervals take the form of an interval, and are paired with a confidence, like 95% confidence intervals, or 99% confidence intervals.

Which should should result in wider intervals, a 95% or 99% interval?

General definition of a Confidence interval A 95% confidence interval for a parameter θ is a interval (V_1, V_2) so that

$$P(V_1 \leq \theta \leq V_2) = 0.95.$$

Notice that this equation *looks* like θ should be the random quantity, but θ is a fixed (and unknown) value. The random values in this equation are actually the V_1 and V_2 – those are the numbers we estimate from the data. It can be useful to consider this equation as actually,

$$P(V_1 \leq \theta \text{ and } V_2 \geq \theta) = 0.95,$$

to emphasize that V_1 and V_2 are the random variables in this equation.

5.1 Quantiles

Without even going further, it's clear we're going to be inverting our probability calculations, i.e. finding values that give us specific probabilities. For example, you should know that for X distributed as a normal distribution, the probability of X being within about 2 standard deviations of the mean is 0.95 – more precisely 1.96 standard deviations.

Figuring out what number will give you a certain probability of being less than (or greater than) that value is a question of finding a **quantile** of the distribution. Specifically, quantiles tell you at what point you will have a particular probability of being less than that value. Precisely, if z is the α quantile of a distribution, then

$$P(X \leq z) = \alpha.$$

We will often write z_α for the α quantile of a distribution.

tests whether two discrete distributions are independent, but there is no single parameter that we are estimating.

So if X is distributed as a normal distribution and z is a 0.25 quantile of a normal distribution,

$$P(X \leq z) = 0.25.$$

z is a 0.90 quantile of a normal if $P(X \leq z) = 0.90$, and so forth

These numbers can be looked up easily in R for standard distributions.

```
qnorm(0.2, mean = 0, sd = 1)
```

```
## [1] -0.8416212
```

```
qnorm(0.9, mean = 0, sd = 1)
```

```
## [1] 1.281552
```

```
qnorm(0.0275, mean = 0, sd = 1)
```

```
## [1] -1.918876
```

What is the probability of being between -0.84 and 1.2815516 in a $N(0, 1)$?

6 Parametric Confidence Intervals

This time we will start with using parametric models to create confidence intervals. We will start with how to construct a parametric CI for the mean of single group.

6.1 Confidence Interval for Mean of One group

As we've discussed many times, a SRS will have a sampling distribution that is roughly a normal distribution (the Central Limit Theorem). Namely, that if $X_1, \ldots, X_n$ are a SRS from a distribution with mean μ and variance σ^2, then $\hat{\mu} = \bar{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$

will have a roughly normal distribution

$$N(\mu, \frac{\sigma^2}{n}).$$

Let's assume we know σ^2 for now. Then a 95% confidence interval can be constructed by

$$\bar{X} \pm 1.96\frac{\sigma}{\sqrt{n}}$$

More generally, we can write this as

$$\bar{X} \pm zSD(\bar{X})$$

Where did $z = 1.96$ come from? Note for a r.v. $Y \sim N(\mu, \sigma^2)$ distribution, the value $\mu - 1.96\sqrt{\sigma^2}$ is the 0.025 quantile of the distribution, and $\mu + 1.96\sqrt{\sigma^2}$ is the 0.975 quantile of the distribution, so the probability of Y being between these two values is 0.95. By the CLT we'll assume $\bar{X} \sim N(\mu, \frac{\sigma^2}{n})$, so the the probability that $\bar{X}$ is within

$$\mu \pm 1.96\sqrt{\sigma^2}$$

is 95%. So it looks like we are just estimating μ with $\bar{X}$.

That isn't quite accurate. What we are saying is that

$$P(\mu - 1.96\sqrt{\frac{\sigma^2}{n}} \leq \bar{X} \leq \mu + 1.96\sqrt{\frac{\sigma^2}{n}}) = 0.95$$

and we really need is to show that

$$P(\bar{X} - 1.96\sqrt{\frac{\sigma^2}{n}} \leq \mu \leq \bar{X} + 1.96\sqrt{\frac{\sigma^2}{n}}) = 0.95$$

to have a true 0.95 confidence interval. But we're almost there.

We can invert our equation above, to get

$$\begin{aligned}
0.95 &= P(\mu - 1.96\sqrt{\frac{\sigma^2}{n}} \leq \bar{X} \leq \mu + 1.96\sqrt{\frac{\sigma^2}{n}}) \\
&= P(-1.96\sqrt{\frac{\sigma^2}{n}} \leq \bar{X} - \mu \leq 1.96\sqrt{\frac{\sigma^2}{n}}) \\
&= P(-1.96\sqrt{\frac{\sigma^2}{n}} - \bar{X} \leq -\mu \leq 1.96\sqrt{\frac{\sigma^2}{n}} - \bar{X}) \\
&= P(1.96\sqrt{\frac{\sigma^2}{n}} + \bar{X} \geq \mu \geq -1.96\sqrt{\frac{\sigma^2}{n}} + \bar{X}) \\
&= P(\bar{X} - 1.96\sqrt{\frac{\sigma^2}{n}} \leq \mu \leq \bar{X} + 1.96\sqrt{\frac{\sigma^2}{n}})
\end{aligned}$$

General equation for CI Of course, we can do the same thing for any confidence level we want. If we want a $(1-\alpha)$ level confidence interval, then we take

$$\bar{X} \pm z_{\alpha/2} SD(\bar{X})$$

Where $z_{\alpha/2}$ is the $\alpha/2$ quantile of the $N(0,1)$.

In practice, we do not know σ so we don't know $SD(\bar{X})$ and have to use $\hat{\sigma}$, which mean that we need to use the quantiles of a t-distribution with $n-1$ degrees of freedom for smaller sample sizes.

Example in R For the flight data, we can get a confidence interval for the mean of the United flights using the function `t.test` again. We will work on the log-scale, since we've already seen that makes more sense for parametric tests because our data is skewed:

```
t.test(log(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "UA"] + addValue))
```

```
##
##  One Sample t-test
##
## data:  log(flightSFOSRS$DepDelay[flightSFOSRS$Carrier == "UA"] + addValue)
## t = 289.15, df = 2964, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  3.236722 3.280920
```

```
## sample estimates:
## mean of x
##  3.258821
```

Notice the result is on the (shifted) log scale! Because this is a monotonic function, we can invert this to see what this implies on the original scale:

```
logT <- t.test(log(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "UA"] + addValue))
exp(logT$conf.int) - addValue
```

```
## [1] 3.450158 4.600224
## attr(,"conf.level")
## [1] 0.95
```

6.2 Confidence Interval for Difference in the Means of Two Groups

Now lets consider the average delay time between the two airlines. Then the parameter of interest is the difference in the means:

$$\delta = \mu_{United} - \mu_{American}.$$

Using the central limit theorem again,

$$\bar{X} - \bar{Y} \sim N(\mu_1 - \mu_2, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2})$$

You can do the same thing for two groups in terms of finding the confidence interval:

$$P((\bar{X} - \bar{Y}) - 1.96\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}} \leq \mu_1 - \mu_2 \leq (\bar{X} - \bar{Y}) + 1.96\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}) = 0.95$$

Then a 95% confidence interval for $\mu_1 - \mu_2$ if we knew σ_1^2 and σ_2^2 is

$$\bar{X} \pm 1.96\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

Estimating the variance Of course, we don't know σ_1^2 and σ_2^2, so we will estimate them, as with the t-statistic. We know from our t-test that if $X_1, \ldots, X_{n_1}$ and $Y_1, \ldots, Y_{n_2}$ are normally distributed, then our t-statistic,

$$T = \frac{|\bar{X} - \bar{Y}|}{\sqrt{\frac{\hat{\sigma_1}^2}{n_1} + \frac{\hat{\sigma_2}^2}{n_2}}}.$$

has actually a t-distribution.

How does this get a confidence interval (T is not an estimate of δ)? We can use the same logic of inverting the equations, only with the quantiles of the t-distribution to get a confidence interval for the difference.

Let $t_{0.025}$ and $t_{0.975}$ be the quantiles of the t distribution. Then,

$$P((\bar{X} - \bar{Y}) - t_{0.975}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}} \leq \mu_1 - \mu_2 \leq (\bar{X} - \bar{Y}) - t_{0.025}\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}) = 0.95$$

Of course, since the t distribution is symmetric, $-t_{0.025} = t_{0.975}$. Why?

We've already seen that for reasonably moderate sample sizes, the difference between the normal and the t-distribution is not that great, so that in most cases it is reasonable to use the normal-based confidence intervals only with $\hat{\sigma}_1^2$ and $\hat{\sigma}_2^2$. This is why ± 2 standard errors is such a common mantra for reporting estimates.

2-group test in R We can get the confidence interval for the difference in our groups using `t.test` as well.

```
logUA <- log(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "UA"] + addValue)
logAA <- log(flightSFOSRS$DepDelay[flightSFOSRS$Carrier ==
    "AA"] + addValue)
t.test(logUA, logAA)
```

```
##
##  Welch Two Sample t-test
##
## data:  logUA and logAA
## t = 5.7011, df = 1800.7, p-value = 1.389e-08
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
##  0.07952358 0.16293414
## sample estimates:
## mean of x mean of y
##  3.258821  3.137592
```

What is the problem from this confidence interval on the log-scale that we didn't have before when we were looking at a single group?

7 Bootstrap Confidence Intervals

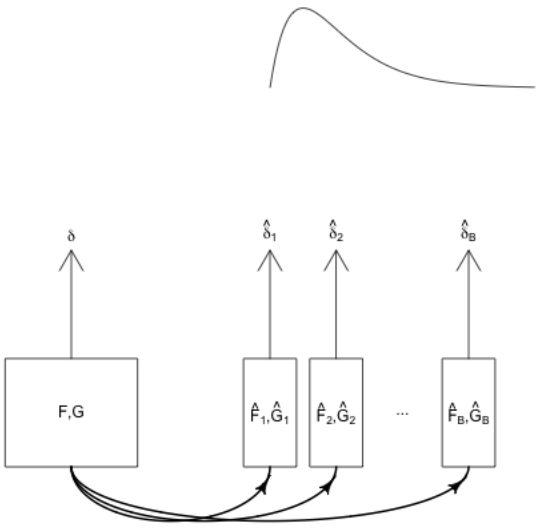
Suppose we are interested instead in whether the median of the two groups is the same. Why might that be a better idea than the mean?

As we saw, perhaps a more relevant statistic than either would be the difference in the proportion greater than 15 minutes late. Let θ_{United}, and $\theta_{American}$ be the true proportions of the two groups, and now

$$\delta = \theta_{United} - \theta_{American}.$$

The sample statistic estimating δ would be what?

What we would like to be able to do is collect multiple data samples for any particular δ.



Since we only see one $\hat{\delta}$, of course this isn't an option. What are our options?

With normal-based confidence intervals (for the mean!), we used the central limit theorem that tells us the mean is approximately normal. For other statistics, like the difference in the median, we also can rely on CLT-like theorems to mathematically determine the distribution of $\hat{\delta}$ (and the proportion is actually a type of mean).

This can be very difficult to do mathematically for complicated statistics. More importantly, when you go with statistics that are beyond the mean, the mathematics often require more assumptions about the data-generating distribution – the central limit theorem for the mean works for most any distribution you can imagine (with large enough sample size), but that's a special property of the mean.

Rather than try to analyze this process mathematically, the bootstrap tries to estimate this process by recreating it with the computer. Namely, we don't know F, G, but we estimate them with our data; that's what we've done in the first module is use SRS as an estimate of the unknown true distribution. So we know we can get estimates $\hat{F}, \hat{G}$.

So while what we need is the distribution of $\hat{\delta}$ from many samples from F, G, instead we will create many samples from $\hat{F}, \hat{G}$ as an approximation.

Specifically, assume we get a SRS from F and G. The observed sample gives us an estimated distribution (also called the **empirical distribution**) $\hat{F}$ and $\hat{G}$, along with an estimate $\hat{\delta}$, of the unknown quantities F, and G (and δ).

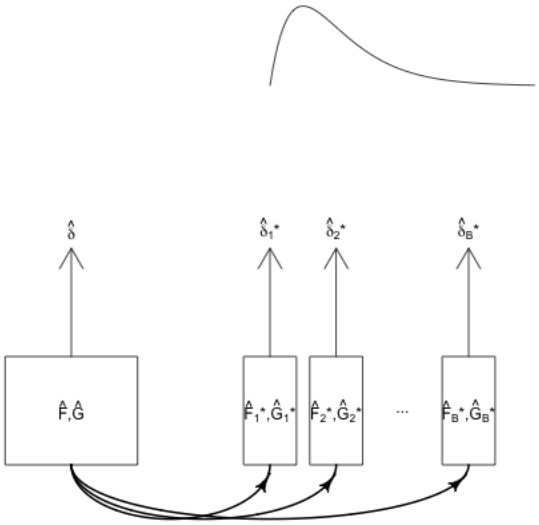
But it's important to understand that our estimate of the distribution is itself a probability distribution. So I can make a SRS from my sample data; this is called a

bootstrap sample.

How would you make a SRS from your data?

My bootstrap sample itself defines an distribution, call it $\hat{F}^*, \hat{G}^*$ and δ^*. So the distribution of my bootstrap sample is an estimate of the population it was drawn from, $\hat{F}, \hat{G}$, and δ^* is an estimate of $\hat{\delta}$.

Here is a visual of how we are trying to replicate the process with our bootstrap samples:

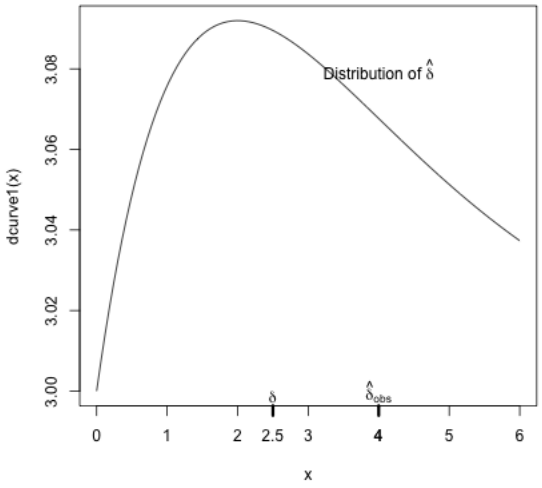


Of course I don't need to estimate $\hat{F}, \hat{G}$ or $\hat{\delta}$ – I know them from my data! But my bootstrap sample can give me an idea of how good of an estimate I can expect $\hat{\delta}$ to be.

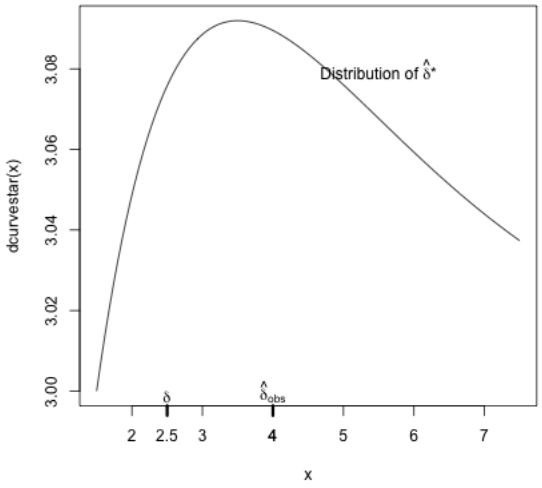
For example, for a confidence interval, I would like to have v_1 and v_2 so that

$$0.95 = P(\delta - v_1 \leq \hat{\delta} \leq \delta + v_2)$$

so that I could invert the equation and get a confidence interval for δ. In other words, I'd like to know the following distribution, but I only get to see a single value, $\hat{delta}_{obs}$.



But if draw a bootstrap sample, I can get the following distribution of $\hat{\delta}^*$ (centered now at $\hat{\delta}$!):



So $\hat{\delta}^*$ is not a direct estimate of the distribution of $\hat{\delta}$! But if the distribution of $\hat{\delta}^*$ around $\hat{\delta}$ is like that of $\hat{\delta}$ around δ, then that gives me useful information about how likely it is that my $\hat{\delta}$ is far away from the true δ, e.g.

$$P(|\hat{\delta} - \delta| > 1) \approx P(|\hat{\delta}^* - \hat{\delta}| > 1)$$

Or more relevant, for a confidence interval, I could find v_1 and v_2 so that

$$0.95 = P(\hat{\delta} - v_1 \leq \hat{\delta}^* \leq \hat{\delta} + v_2)$$

and then use the same v_1, v_2 to approximate that

$$0.95 = P(\delta - v_1 \leq \hat{\delta} \leq \delta + v_2)$$

In short, we don't need that $\hat{\delta}^*$ approximates the distribution of $\hat{\delta}$. We just want that the distance of $\hat{\delta}^*$ from it's true generating value $\hat{\delta}$ replicate the distance of $\hat{\delta}$ from the (unknown) true generating value δ.

7.1 Implementing the bootstrap confidence intervals

What does it actually mean to resample from $\hat{F}$? It means to take a sample from $\hat{F}$ just like the kind of sample we took from the actual data generating process, F.

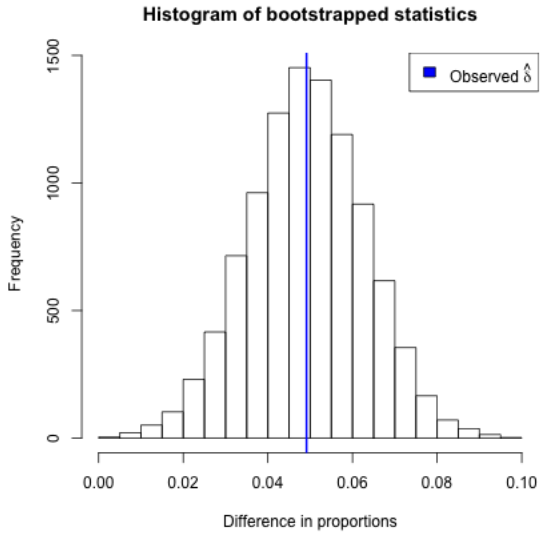
Specifically in our two group setting, say we assume we have a SRS $X_1, \ldots, X_{n_1}, Y_1, \ldots, Y_{n_2}$ from an unknown distributions F and G. What does this actually mean? Consider our airline data; if we took the full population of airline data, what are we doing to create a SRS?

Then to recreate this we need to do *the exact same thing*, only from our sample. Specifically, we resample *with replacement* to get a single bootstrap sample *of the same size* consisting of new set of samples, $X_1^*, \ldots, X_{n_1}^*$ and $Y_1^*, \ldots, Y_{n_2}^*$. Every value of X_i^* and Y_i^* that I see in the bootstrap sample will be a value in my original data. Moreover, some values I will see more than once, why?

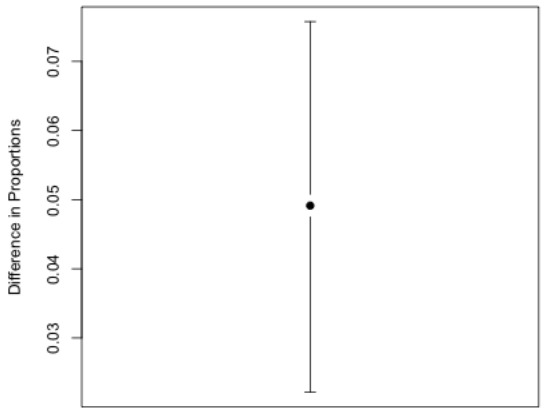
From this single bootstrap sample, we can recalculate the difference of the medians on this sample to get $\hat{\delta}^*$.

We do this repeatedly, and get a distribution of $\hat{\delta}^*$; specifically if we repeat this B times, we will get $\hat{\delta}_1^*, \ldots, \hat{\delta}_B^*$. So we will now have a distribution of values for $\hat{\delta}^*$.

We can apply this function to the flight data, and examine our distribution of $\hat{\delta}^*$.



To construct a confidence interval, we use the 0.025 and 0.975 quantiles as the limits of the 95% confidence interval.[10] We apply it to our flight data set to get a confidence interval for the difference in proportion of late or cancelled flights.



How do you interpret this confidence interval?

[10]There are many different strategies for calculating a bootstrap CI from the distribution of $\hat{\delta}^*$; this method called the percentile method and is the most common and widespread. It doesn't exactly correspond to the v_1, v_2 strategy from above – known as using a pivotal statistic. If it looks like the v_1, v_2 method is backward compared to the percentile method, it pretty much is! But both methods are legitimate methods for creating bootstrap intervals and we focus on the percentile method because of it's simplicity and wider applicability.

7.2 Assumptions: Bootstrap

Assumption: Good estimates of $\hat{F}$, $\hat{G}$ A big assumption of the bootstrap is that our sample distribution $\hat{F}, \hat{G}$ is a good estimate of F and G. We've already seen that will not necessarily the case. Here are some examples of why that might fail:

- Sample size n_1/n_2 is too small
- The data is not a SRS

Assumption: Data generation process Another assumption is that our method of generating our data X_i^*, and Y_i^* matches the way X_i and Y_i were generated from F, G. In particular, in the bootstrap procedure above, we are assuming that X_i and Y_i are i.i.d from F and G (i.e. a SRS with replacement).

Assumption: Well-behaved test statistic We also need that the parameter θ and the estimate $\hat{\theta}$ to be well behaved in certain ways

- $\hat{\theta}$ needs to be an **unbiased** estimate of θ, meaning across many samples, the average of the $\hat{\theta}$ is equal to the true parameter θ [11]
- θ is a function of F and G, and we need that the value of θ changes smoothly as we change F and G. In other words if we changed from F to F', then θ would change to θ'; we want if our new F' is very "close" to F, then our new θ' would be very close to θ. This is a pretty mathematical requirement, and requires a precise definition of "close" for two distributions that is not too important for this class to understand. But here's an example to make it somewhat concrete: if the parameter θ you are interested in is the maximum possible value of a distribution F, then θ does NOT change smoothly with F. Why? because you can choose distributions F' that are very close to F in every reasonable way to compare two distributions, but their maximum values θ and θ' are very far apart.[12]

[11] There are methods for accounting for a small amount of bias with the bootstrap, but if the statistic is wildly biased away from the truth, then the bootstrap will not work.

[12] This clearly assumes what is a "reasonable" definition of "close" between distributions that we won't go into right now.

8 Thinking about confidence intervals

Suppose you have a 95% confidence interval for δ given by $(.02, .07)$. What is wrong with the following statements regarding this confidence interval?

1. δ has a 0.95 probability of being between $(.02, .07)$

2. If you repeatedly resampled the data, the difference δ would be within $(.02, .07)$ 95% of the time.

Confidence Intervals or Hypothesis Testing? Bootstrap inference via confidence intervals is more widely applicable than permutation tests we described above. The permutation test relied on being able to simulate from the null hypothesis, by using the fact that if you detach the data from their labels you can use resampling techniques to generate a null distribution. In settings that are more complicated than comparing groups, it can be difficult to find this kind of trick.

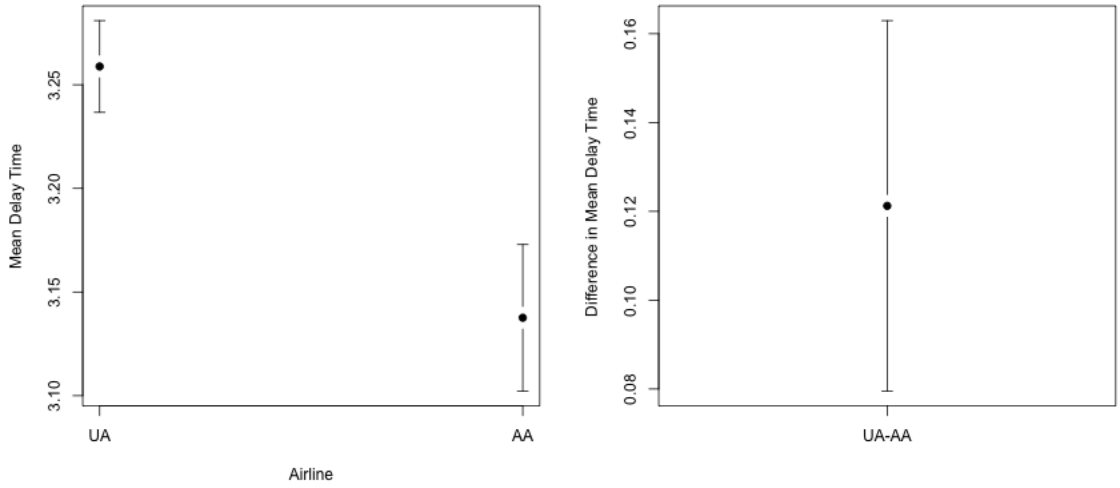
More generally, confidence intervals and hypothesis testing are actually closely intertwined. For example, for the parametric test and the parametric confidence interval, they both relied on the distribution of the same statistics, the t-statistic. If you create a 95% confidence interval, and then decide to reject a specific null hypothesis (e.g. $H_0 : \delta = 0$) only when it does not fall within the confidence interval, then this will exactly correspond to a test with level 0.05. So the same notions of level, and type I error, also apply to confidence intervals

Confidence intervals, on the other hand, give much greater interpretation and understanding about the parameter.

8.1 Comparing Means: CI of means vs CI of difference

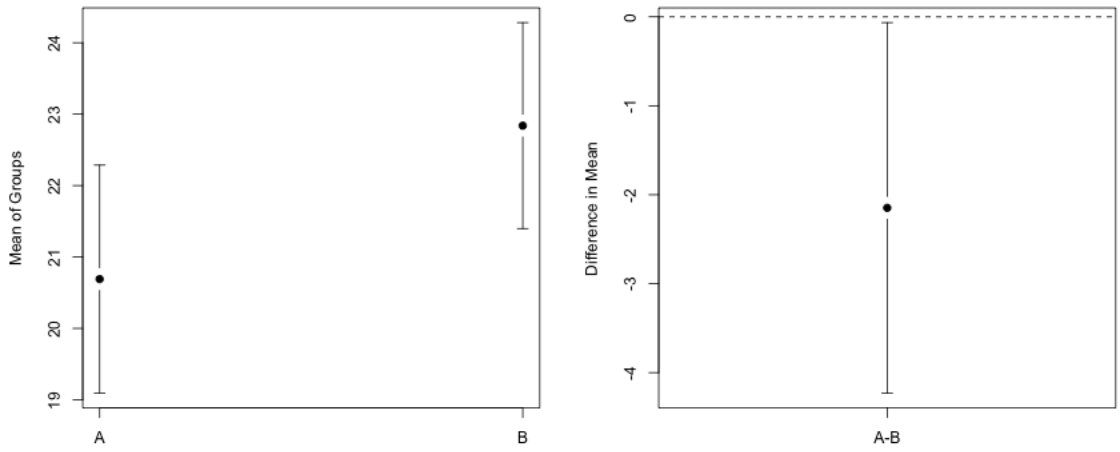
We have focused on creating a confidence interval of the difference (δ). Another common strategy is to do a confidence interval of each mean, and compare them.

We can compare these two options using the t-statistic:



We see that their confidence intervals don't overlap, and that the CI for the difference in the means doesn't overlap zero, so we draw the same conclusion in our comparison, namely that the means are different.

However, this doesn't have to be the case. Here's some made-up data[13]:



What to think here? What is the right conclusion? The confidence interval for the difference for the means corresponds to the test for the difference of the means, which means that if the CI for δ doesn't cover zero, then the corresponding p-value from the t-test will be < 0.05. So this is the "right" confidence interval for determining statistical significance.

[13]From https://statisticsbyjim.com/hypothesis-testing/confidence-intervals-compare-means/

Why does this happen? Basically, with the t-test-based CI, we can examine this analytically (a big advantage of parametric models).

In the first case, for a CI of the difference δ to be significantly larger than zero, it means that the lower end of the CI for delta is greater than zero:

$$\bar{X} - \bar{Y} > 1.96\sqrt{\frac{\hat{\sigma}_1^2}{n_1} + \frac{\hat{\sigma}_2^2}{n_2}}$$

Alternatively, if we create the two confidence intervals for $\bar{X}$ and $\bar{Y}$, separately, to have them not overlap, we need that the lower end of the CI for X be greater than the upper end of the CI of Y:

$$\bar{X} - 1.96\sqrt{\frac{\hat{\sigma}_1^2}{n_1}} > \bar{Y} + 1.96\sqrt{\frac{\hat{\sigma}_2^2}{n_2}}$$

$$\bar{X} - \bar{Y} > 1.96\left(\sqrt{\frac{\hat{\sigma}_2^2}{n_2}} + \sqrt{\frac{\hat{\sigma}_1^2}{n_1}}\right)$$

Note that these are not the same requirements. In particular,

$$\sqrt{\frac{\hat{\sigma}_1^2}{n_1} + \frac{\hat{\sigma}_2^2}{n_2}} < \left(\sqrt{\frac{\hat{\sigma}_2^2}{n_2}} + \sqrt{\frac{\hat{\sigma}_1^2}{n_1}}\right)$$

(take the square of both sides...).

So that means that the difference of the means doesn't have to be as big for CI based for δ to see the difference as for comparing the individual mean's CI. We know that the CI for δ is equivalent to a hypothesis test, so that means that IF there is a difference between the individual CI means there is a significant difference between the groups, but the converse is NOT true: there could be significant differences between the means of the groups but the CI of the individual means are overlapping.

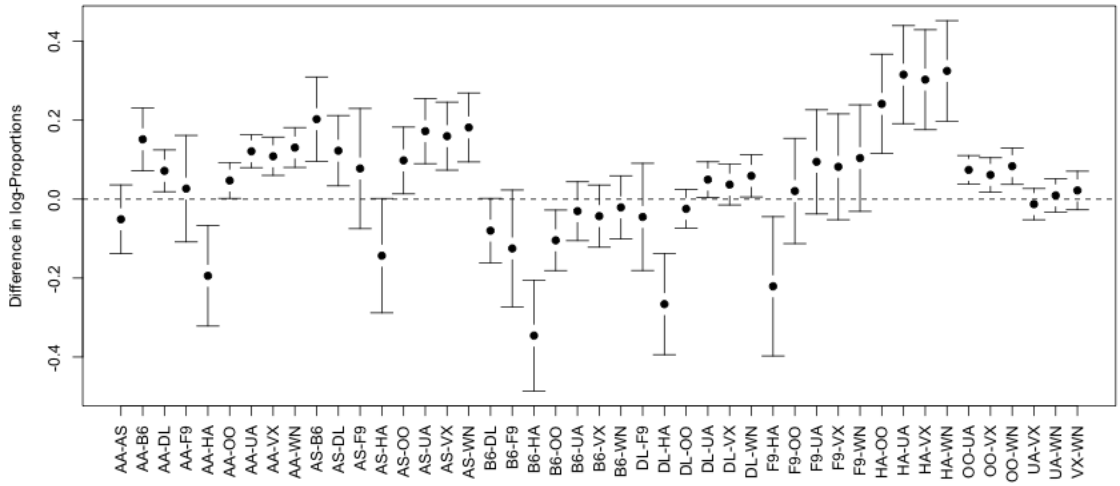
Reality Check However, note that the actual difference between the two groups in our toy example is pretty small and our significance is pretty marginal. So it's not such a big difference in our conclusions after all.

9 Revisiting pairwise comparisons

Just as with hypothesis testing, you can have multiple comparison problems with confidence intervals. Consider our pairwise comparisons of the different carriers. We

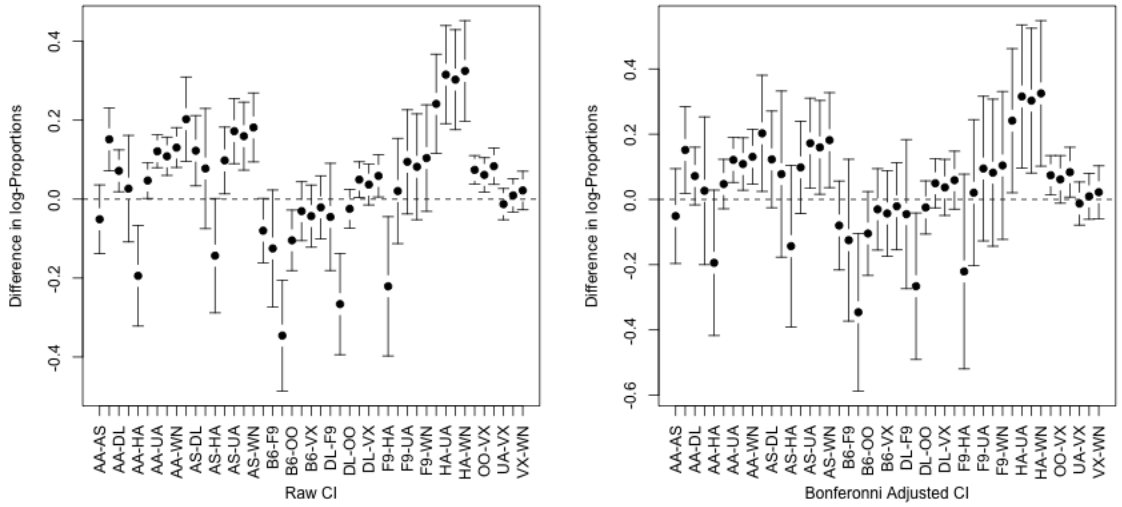
can also create confidence intervals for them all. Again, we will use the t-test on the log-differences to make this go quickly.

```
##       mean.of.x mean.of.y        lower       upper
## AA-AS  3.086589  3.137592 -0.138045593  0.03603950
## AA-B6  3.289174  3.137592  0.071983930  0.23118020
## AA-DL  3.209319  3.137592  0.018600177  0.12485342
## AA-F9  3.164201  3.137592 -0.108192832  0.16141032
## AA-HA  2.943335  3.137592 -0.321473062 -0.06704092
## AA-OO  3.184732  3.137592  0.001615038  0.09266604
```



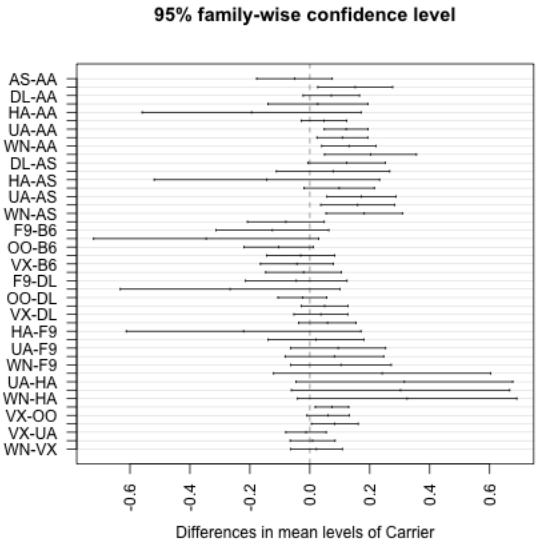
These confidence intervals suffer from the same problem as the p-values: even if the null value (0) is true in every test, roughly 5% of them will happen to not cover 0 just by chance.

So we can do bonferonni corrections to the confidence intervals. Since a 95% confidence interval corresponds to a level 0.05 test, if we go to a $0.05/K$ level, which is the bonferonni correction, that corresponds to a $100 * (1 - 0.05/K)\%$ confidence interval.

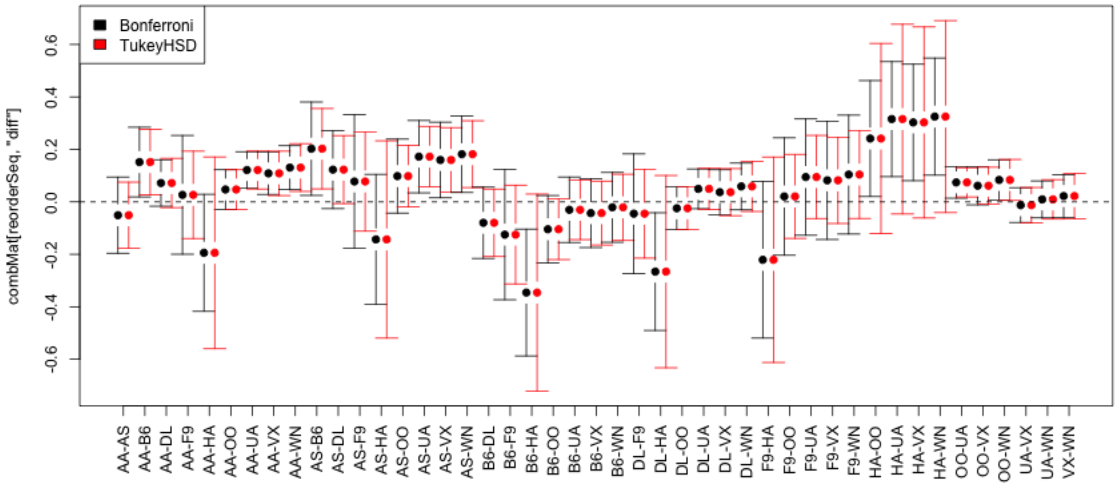


TukeyHSD In fact, as mentioned, there are many ways to do multiple testing corrections, and Bonferonni is the simplest, yet often most crude correction. There is a multiple testing correction just for pairwise comparisons that use the t-test, called the Tukey HSD test.

```
tukeyCI <- TukeyHSD(aov(logDepDelay ~ Carrier, data = flightSFOSRS))
plot(tukeyCI, las = 2)
```



Let's compare them side-by-side.



What differences do you see?

Which to use? The TukeyHSD is a very specific correction – it is only valid for doing pairwise comparisons with the t-test. Bonferonni, on the other hand, can be used with any set of p-values from any test, e.g. permutation, and even if not all of the tests are pairwise comparisons.