Design of Experiments & Hypothesis Testing

Felipe José Bravo Márquez

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Motivation

In the first lecture we discussed the three major goals of statistics:

1. Describe
2. Decide
3. Predict

- In this lecture we will introduce the ideas behind the use of statistics to make decisions.
- In particular, decisions about whether a particular **hypothesis** is supported by the data. [Poldrack, 2019]

Null Hypothesis Statistical Testing (NHST)

- The specific type of hypothesis testing that we will discuss is known null hypothesis statistical testing (NHST).
- If you pick up almost any scientific research publication, you will see NHST being used to test hypotheses.
- Learning how to use and interpret the results from hypothesis testing is essential to understand the results from many fields of research.
- NHST is usually applied to **experimental** data.
- Thus, we need to introduce basic concepts on the design of experiments.

Experiments and Inference About Cause

- In the previous lecture we studied how to infer characteristics of a population from sample data using surveys or polls.
- A second type of inference is when we want to infer **cause-effect relationships** between two or more variables (e.g, does smoking cause cancer) from experimental data.
- Example [Watkins et al., 2010]: Children who drink more milk have bigger feet than children who drink less milk.

Figure: Image source: `https://www.dreamstime.com`

Experiments and Inference About Cause

- There are three possible explanations for this association:
  1. Drinking more milk causes children's feet to be bigger.

  2. Having bigger feet causes children to drink more milk.

  3. A **confounding variable** is responsible for both.

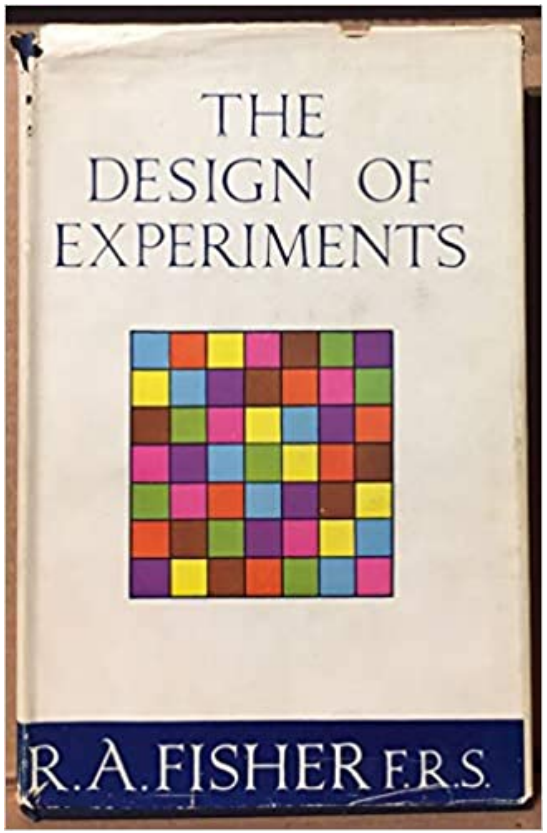
- A confounding variable is a variable that may or may not be apparent at the outset but, once identified, could explain the pattern between the variables.
- We know that bigger children have bigger feet, and they drink more milk because they eat and drink more of everything than do smaller children.

Experiments and Inference About Cause

- The right explanation is the third one: the child's **overall size** is the confounding variable.
- However, suppose we want to prove that explanation 1 is the right reason.
- Approach 1: take a bunch of children, give them milk, and wait to see if their feet grow.
- This won't prove anything, because children's feet will grow whether they drink milk or not.
- Approach 2: take a group of children, divide them randomly into two **groups**: 1) one group that will drink milk and 2) another group that will not, wait and compare the size of the feet of both groups.
- This approach is an **experiment**, and is standard practice in statistics to establish cause and effect relationships.

The Design of Experiments

- The main ideas of the design of experiments were proposed in 1936 in the book "Design of Experiments" by the English statistician Ronald Fisher [Fisher, 1936].



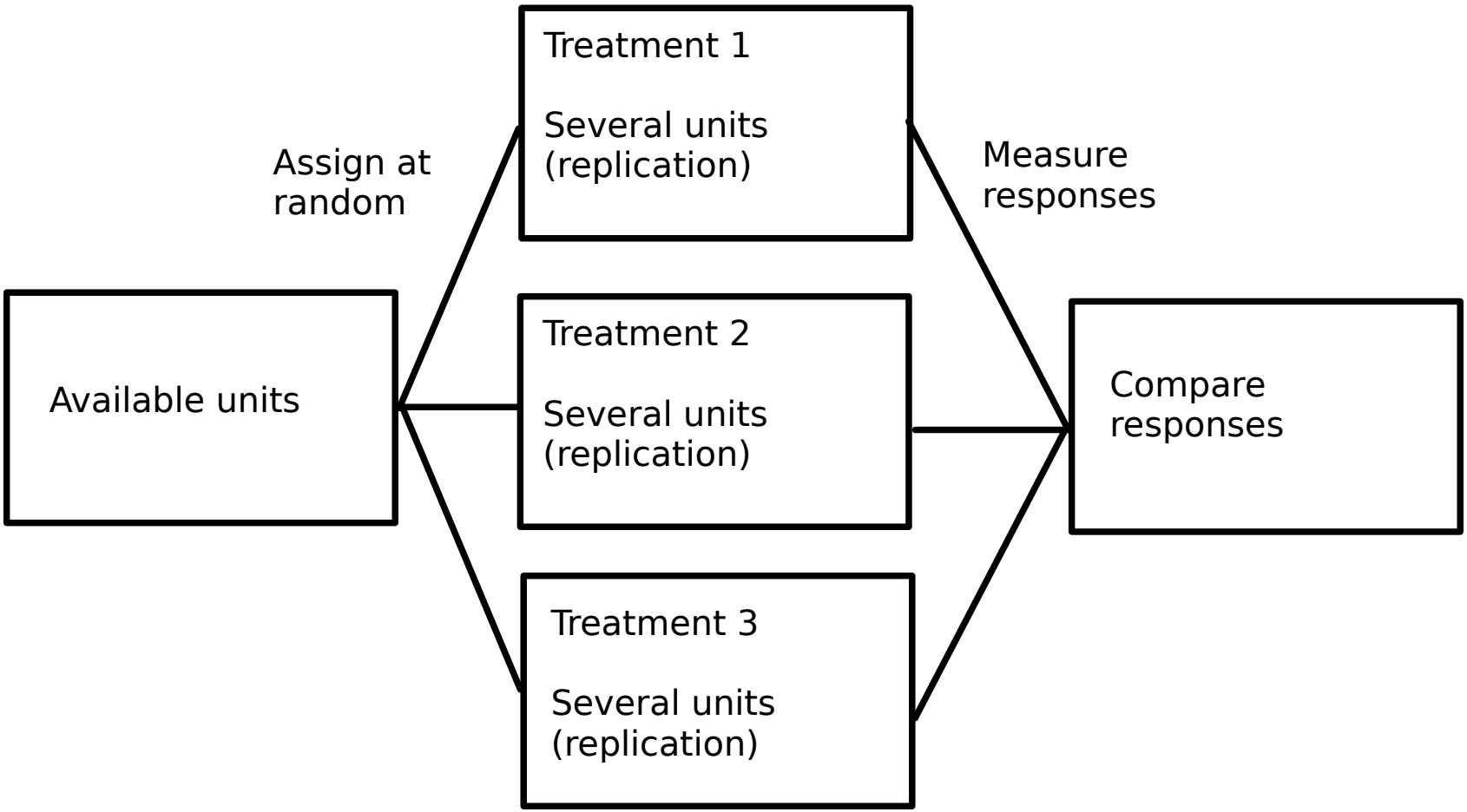
Main Concepts of Experimental Design

- **Experimental units**: the subjects on which we experiment (e.g, patients, users, laboratory animals). When the experiment units are people, we call them **subjects**.
- **Treatments**: the conditions on which we compare different unit groups. Examples: drinking milk vs. not drinking milk, smoking vs. not smoking, taking drug A vs. drug B.
- **Treatment or Experimental group**: a group of units receiving a particular treatment. Example: patients taking a new drug, software users seeing a new layout.
- **Control group**: a group of units used for comparison receiving either a standard treatment or no treatment at all. Example: patients taking a placebo (a fake treatment), software users seeing the standard layout.
- **Response variable**: the variable of interest used to measure the effect of the treatments on the units. Examples: weight, birth rate, antibody levels, click-rate, revenue, etc.

Main Concepts of Experimental Design

- **Randomization**: random assignment of treatments (including the control group) to units. This is very important since not all units are alike (e.g., people have different ages, weights, preferences).
    - Randomization is the most reliable method of creating homogeneous treatment groups, without involving any potential biases or judgments.
- **Replication**: the repetition of an experiment on a large group of subjects. Replication reduces variability in experimental results.
- **Randomized Controlled Trial** (RCT): an experiment in which units are randomly assigned to one of several treatments and one of these groups is a control group.
- **Blind Experiment**: when the units (e.g., patients) don't know the treatment they are receiving.
- **Double-blind Experiment**: when neither the units (e.g., patients) nor the experimenters (e.g., doctors) know who is receiving a particular treatment.

Main Concepts of Experimental Design



Characteristics of a well-designed experiment.

A/B Testing

- Data-driven companies like Amazon, Microsoft, eBay, Facebook, Google and Netflix constantly conduct experiments to make decisions [Kohavi et al., 2012].
- In this context, experiments are called **online controlled experiments** or **A/B tests**.
- The idea is the same, users (experimental units) are randomly exposed to one of two variants of the software: Control (A), or Treatment (B).
- When there is more than one treatment we have an A/B/n test.
- The response variable is called **Overall Evaluation Criterion** (OEC), which is a quantitative measure of the experiment's objective.
- OECs can be revenue, clickthrough-rate, user session duration, etc...

A/B Testing

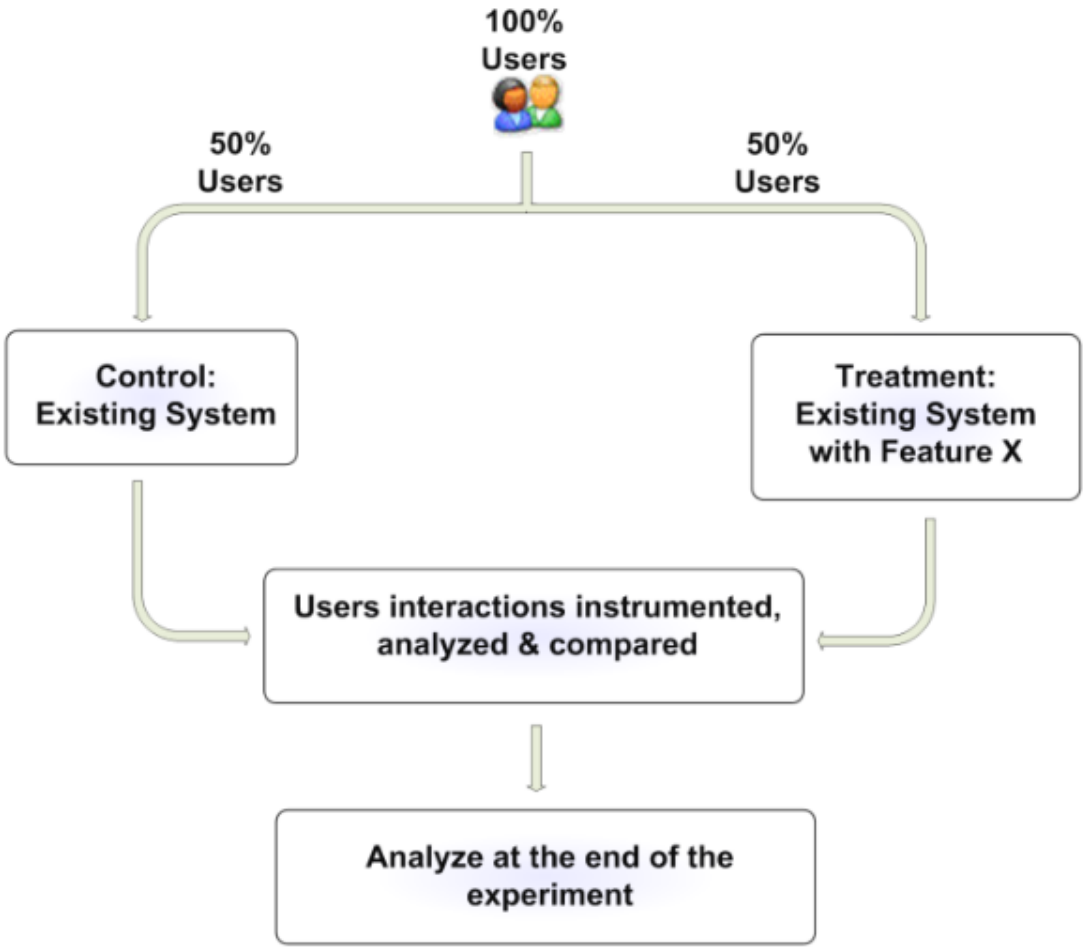


Image source: [Kohavi et al., 2012]

Example: MSN Real Estate

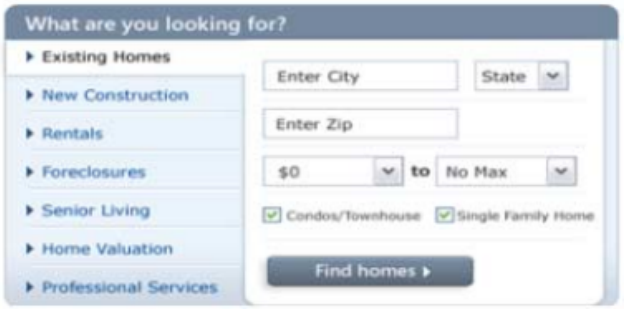
- The team running the MSN Real Estate site wanted to test different designs for the “Find a home” widget [Kohavi et al., 2009].
- Visitors who click on this widget are sent to partner sites, and Microsoft receives a referral fee.
- Six different designs of this widget, including the incumbent (control), were proposed.
- Users were randomly splited between the variants in a persistent manner (a user receives the same experience in multiple visits) during the experiment period.

Example: MSN Real Estate

Control

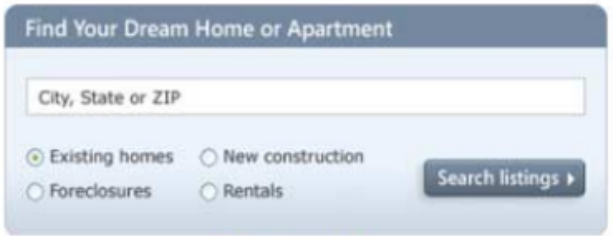
Treatment1

Treatment 2



Treatment 3

Treatment 4



Treatment 5

Example: MSN Real Estate

- Their interactions are instrumented and key metrics computed.
- In this experiment, the Overall Evaluation Criterion (OEC) was average revenue per user.
- The winner, Treatment 5, increased revenues by almost 10% (due to increased clickthrough).
- The Return-On-Investment (ROI) for MSN Real Estate was phenomenal, as this is their main source of revenue, which increased significantly through a simple change.

Observational Studies and Confounding

- Sometimes we can't randomly assign units to the different treatments.
- For example, it would be unethical to design a randomized controlled trial deliberately exposing people to a potentially harmful situation.
- In an **observational study** the conditions of interest are already built into the units being studied.
- Observational studies are almost always worse than controlled experiments for determining cause-effect relationships.
- But sometimes is the only thing we can do.
- A phenomenon called **confounding** is the major treat to observational studies.
- Two possible influences on an observed outcome are **confounded** if they are mixed in a way that makes it impossible to separate their effects on the responses [Watkins et al., 2010].

A Confounded Observational Study

- The thymus, a gland located in our neck, behaves in a peculiar way.
- Unlike other organs of the body, it doesn't get larger as you grow—it actually gets smaller.
- Ignorance of this fact led early 20th-century surgeons to adopt a worthless and dangerous surgical procedure.

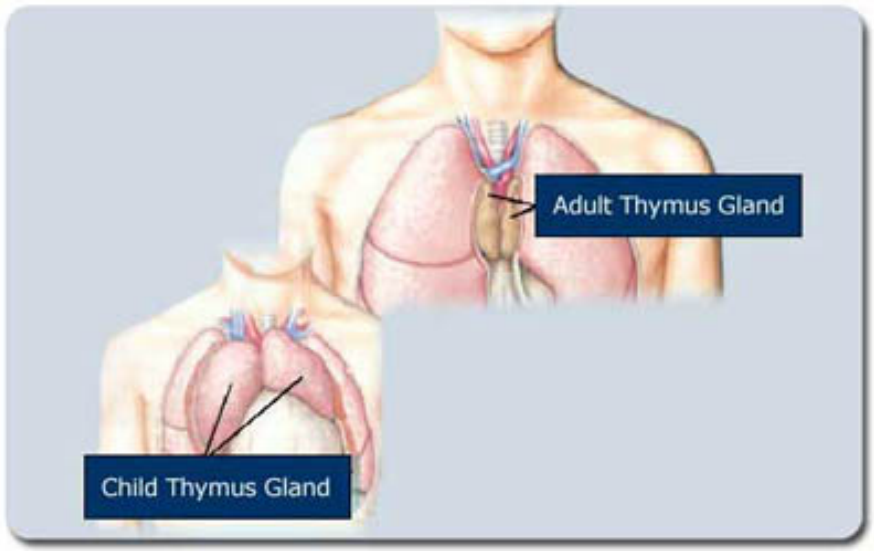


Figure: source: `http://esvc001414.wic005tu.server-web.com/tech_imm_bio_principle.htm`

A Confounded Observational Study

- Many infants were dying of what seemed to be respiratory obstructions.
- Doctors did autopsies on infants who died with respiratory symptoms and compared against autopsies made on adults who died of various causes.
- Most autopsies to infants show big thymus glands compared to adults.
- Doctors concluded that the respiratory problems were caused by an enlarged thymus.
- In 1912, Dr. Charles Mayo published an article recommending removal of the thymus to treat respiratory problems in children.
- This recommendation was made even though a third of the children who were operated on died.
- The doctors could not tell whether children with a large thymus tended to have more respiratory problems because they had no evidence about children with a smaller thymus.

A Confounded Observational Study

- Age and size of thymus were confounded.
- The thymus study is an example of an observational study, not an experiment.

	Age	
	Child	Adult
Thymus size		
Large	Problems	No evidence
Small	No evidence	No problems

- If Dr. Mayo had used a randomized experiment to evaluate surgical removal of the thymus, he would have seen that the treatment was not effective and many lives might have been spared.
- However, at the time, randomized experiments were not often used in the medical profession.
- These days, any new medical treatment (e.g., a COVID vaccine) must prove its value in an RCT.

Another Example of Confounding

- Suppose we want to compare student performance on a standardized tests (e.g., SIMCE, PSU) between public and private schools.
- We know that the socioeconomic distribution of students is different in public and private schools.
- We also suspect that socioeconomic background may influence student performance on these tests.
- The type of school (public or private) and the socioeconomic background are confounded.

Another Example of Confounding

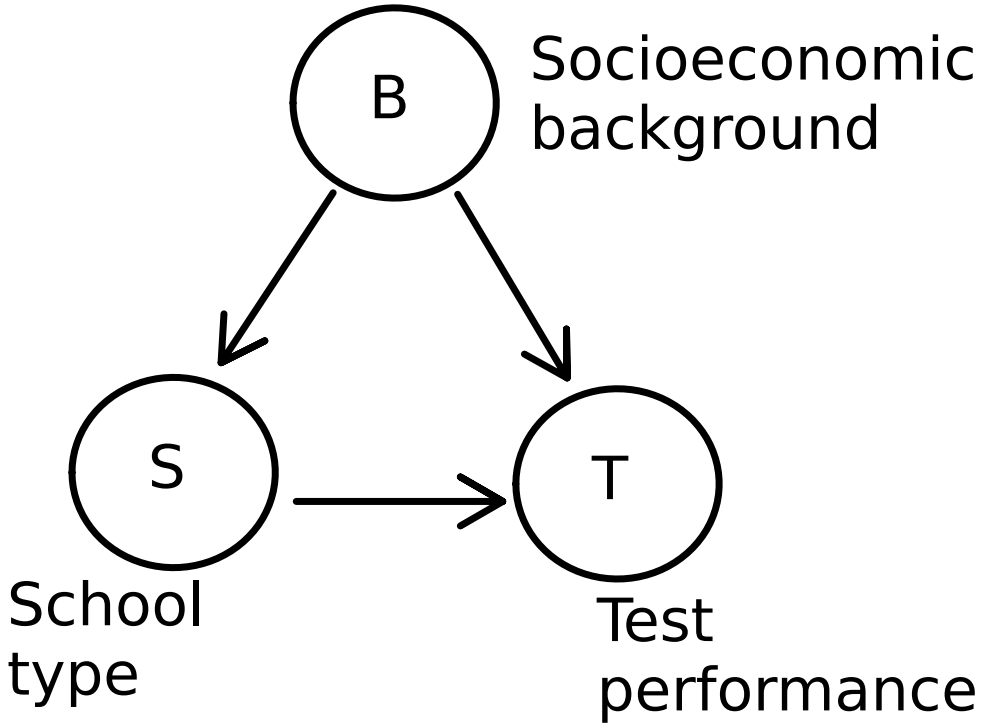


Figure: A possible causal explanation of socioeconomic background, school type, and test performance.

Randomized Paired Comparison (Matched Pairs)

- Randomized Paired Comparison or Matched Pairs is an approach to design experiments **controlling** for confounding variables.
- We sort the experimental units into pairs of similar units (matched pairs or **blocks**), where similarity is measured according to confounding variables.
- The two units in each pair should be enough alike that you expect them to have a similar response to any treatment.
- Randomly decide which unit in each pair is assigned which treatment.
- We are essentially building comparable Control and Treatment populations by segmenting the users by common confounds, similarly to stratified sampling.

Matched Pairs Example

- Suppose we want to study the relation between hypertension and end-stage renal disease (ESRD) [De Graaf et al., 2011].
- Obesity is a potential confounder as obesity is associated with both hypertension and ESRD.
- Matching approach: we ensure that the average body mass index (BMI) is the same in the group of patients exposed to hypertension and another group of patients unexposed to hypertension.
- This could be achieved by searching an obese patient without hypertension for each obese patient with hypertension.
- Other potential confounding variables like age or sex could also be considered in the matching.

Hypothesis Testing

- Now that we understand what experimental data looks like we are in place to introduce Null Hypothesis Statistical Testing (NHST).
- A **hypothesis test** allows us to to measure whether some assumed **property** about a population is contrasted with a statistical sample.
- By hypothesis we refer to a subset of values for our target population parameter θ.
- In the context of experiments, NHST helps us to determine weather observed differences between treatment and control groups are unlikely to have occurred by chance.
- Hypothesis testing can be applied to all kinds of population parameters (e.g., mean, variance, median).
- In the class we will focus on testing the **population mean** μ.

Hypothesis Testing

- We will study the following types of parametric tests to the mean:
  1. **One sample test**: we contrast the sample mean to a pre-specified value.
  2. **Unpaired two sample test**: we compare the sample means of two independent groups (control vs. treatment).
  3. **Paired two sample test**: here we compare the means of two dependent groups where we have two values for the same samples. For example: in matched pairs experiments.
- All these tests can be one-sided or two-sided.
- In the same way as for confidence intervals we will use Normal and T-student distributions for modeling the sampling distribution of sample means.
- Warning: there are many counterintuitive concepts around NHST (e.g., null hypothesis, p-values).
- Thus, we will fist introduce these concepts with two examples taken from [Poldrack, 2019] and [Marchini, 2008].
- Then we will formalize them in more detail.

Example 1: Body-worn Cameras

- Body-worn cameras are thought to reduce the use of force and improve behavior of police officers.
- An RCT of the effectiveness of body-worn cameras was performed by the Washington, DC government and DC Metropolitan Police Department in 2015/2016.
- Officers were randomly assigned to wear a body-worn camera or not.
- Their behavior was then tracked over time to determine whether the cameras resulted in less use of force and fewer civilian complaints about officer behavior.

Figure: source: `https://www.nytimes.com`

Example 1: Body-worn Cameras

- Let's say we want to specifically test the hypothesis of whether the use of force is decreased by the wearing of cameras.
- The RCT provides us with the data to test the hypothesis – namely, the rates of use of force by officers assigned to either the camera or control groups.
- The next obvious step is to look at the data and determine whether they provide convincing evidence for or against this hypothesis.
- That is: What is the likelihood that body-worn cameras reduce the use of force, given the data and everything else we know?
- It turns out that this is **not** how null hypothesis testing works.

Example 1: Body-worn Cameras

- Instead, we first take our hypothesis of interest (i.e. that body-worn cameras reduce use of force), and flip it on its head, creating a **null hypothesis**.
- In this case, the null hypothesis would be that cameras do not reduce use of force.
- Importantly, we then assume that the null hypothesis is true.
- We then look at the data and determine how likely the data would be if the null hypothesis were true.
- If the data are sufficiently unlikely under the null hypothesis that we can reject the null in favor of the **alternative hypothesis** which is our hypothesis of interest.
- If there is not sufficient evidence to reject the null, then we say that we retain (or "fail to reject") the null.
- Then we stick with our initial assumption that the null is true.

Example 2: Babies

- From previous experience we know that the birth weights of babies in England have a mean of 3000g and a standard deviation of 500g.
- We think that maybe babies in Australia have a mean birth weight greater than 3000g and we would like to test this hypothesis.
- We take a sample of babies from Australia, measure their birth weights and see if the sample mean is significantly larger than 3000g.
- The main hypothesis that we are most interested in is the **research hypothesis**, denoted H_1, that the mean birth weight of Australian babies is greater than 3000g.

Example 2: Babies

- The other hypothesis is the null hypothesis, denoted H_0, that the mean birth weight is equal to 3000g.
- We can write this compactly as:

$$H_0: \mu = 3000g^1$$
$$H_1: \mu > 3000g$$

- The null hypothesis is written first followed by the research hypothesis.
- The research hypothesis is often called the **alternative hypothesis** even though it is often the first hypothesis we think of.

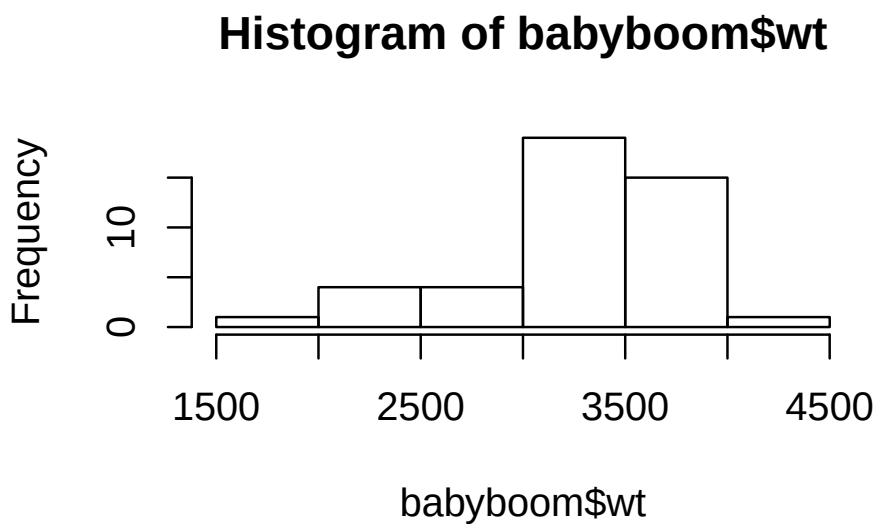
[1] In the strict sense $H_0: \mu \leq 3000$, but this complicates all the following explanations.

Example 2: Babies

- Normally, we start with the research hypothesis and “set up” the null hypothesis to be directly counter to what we hope to show.
- We then try to show that, in the light of our collected data, that the null hypothesis is false.
- We do this by calculating the probability of the data if the null hypothesis is true.
- If this probability is very small, it suggests that the null hypothesis is false.
- Once we have set up our null and alternative hypothesis, we can collect a sample of data.
- For example, we can imagine we collected the birth weights of the 44 babies in the Babyboom dataset.

```
>library(UsingR)
>data(babyboom)
>hist(babyboom$wt)
```

Example 2: Babies



- The sample mean of the dataset $\overline{x}$ is:

```
> xbar<-mean(babyboom$wt)
> xbar
[1] 3275.955
```

Example 2: Babies

- We now want to calculate the probability of obtaining a sample with a mean as large as 3275.955 under the assumption of the null hypothesis H_0.
- From the CLT we know that the sampling distribution of $\overline{X}$ follows as Normal distribution when n is sufficiently large: $\overline{X} \sim N(\mu, \sigma^2/n)$
- If we assume H_0 is true, then $\mu = 3000$.
- The value of n is 44 and the value of σ is known is this case and is equal to 500.
- Let's calculate the standard error $\frac{\sigma}{\sqrt{n}}$:

```
> mu0<-3000
> sd<-500
> n<-nrow(babyboom)
> se<-sd/sqrt(n)
> se
[1] 75.37784
> se^2
[1] 5681.818
```

Example 2: Babies

- Now we can calculate the probability of obtaining a sample with a mean as large as 3275.955:

```
> #pvalue
> 1-pnorm(xbar, mean =mu0, sd =se)
[1] 0.0001256405
> #or
> Z.score<-(xbar-mu0)/se
> Z.score
[1] 3.660951
> p.value<-1-pnorm(Z.score)
> p.value
[1] 0.0001256405
```

Example 2: Babies

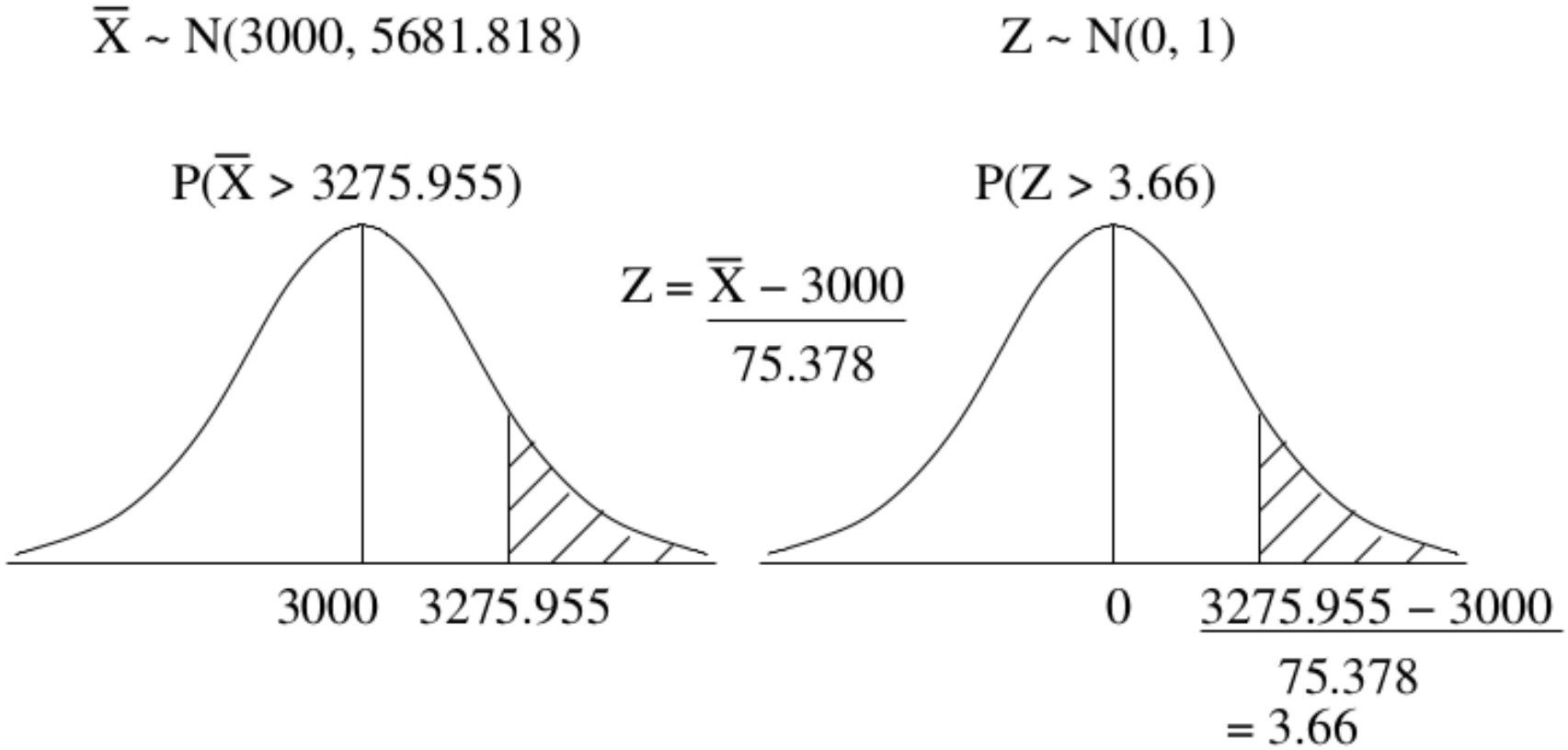


Figure: [Marchini, 2008]

Example 2: Babies

- The probability we calculate is called the **p-value** of the test.
- In this case the p-value is very low.
- This says that the probability of the data is very low if we assume the null hypothesis is true.
- But how low does this probability have to be before we can conclude that the null hypothesis is false.
- The convention within statistics is to choose a **level of significance** α before the experiment that dictates how low the p-value should be before we reject the null hypothesis.
- In practice, many people use a significance level of 5% and conclude that there is significant evidence against the null hypothesis if the p-value is less than or equal to 0.05.
- A more conservative approach uses a 1% significance level and conclude that there is significant evidence against the null hypothesis if the p-value is less than 0.01.

Example 2: Babies

- In our current example, the p-value is 0.00013 which is lower than $\alpha = 0.05$.

```
> alpha<-0.05
> p.value<=alpha
[1] TRUE
```

- In this case, we would conclude that:
  "there is significant evidence against the null hypothesis at the 5% level".
- Another way of saying this is that:
  "we reject the null hypothesis at the 5% level"
- If the p-value for the test much larger, say 0.23, then we would conclude that:
  "the evidence against the null hypothesis is not significant at the 5% level"
- Another way of saying this is that:
  "we cannot reject the null hypothesis at the 5% level"

T-tests

- In the previous example, we assumed that σ was known.
- In many cases σ is unknown and we must estimate it using the unbiased estimator s that we saw in the previous class.
- If the sample size is small and we assume the data to be normal, we can calculate a T statistic $\frac{\overline{X_n} - \mu_o}{\frac{s}{\sqrt{n}}}$:

```
> s<-sd(babyboom$wt)
> s
[1] 528.0325
> se.t<-s/sqrt(n)
> se.t
[1] 79.60389
>
> T.sta<-(xbar-mu0)/se.t
> T.sta
[1] 3.466596
```

T-tests

- From previous class we know that T follows a t-student distribution with $n-1$ degrees of freedom $T \sim t_{n-1}$.
- We can now perform a T-test using the t-student distribution instead of a Gaussian.
- The p-value can be calculated analogously to the previous case now using the t-student distribution.

```
> p.value<-1-pt(T.sta,df = n-1)
> p.value
[1] 0.0006042622
```

- We also reject the null hypothesis in this case with $\alpha = 0.05$.
- But the p-value is larger than before.
- This is because the t-distribution has wider tails than the Normal distribution.
- The wide tails imply that there is more uncertainty because we had to estimate σ and the sample size is relatively small.

T-tests

- We can perform t-tests straightforwardly in R as follows:

```
> t.test(x = babyboom$wt,mu = 3000,
alternative = "greater",conf.level = 1-alpha)

One Sample t-test

data:  babyboom$wt
t = 3.4666, df = 43, p-value = 0.0006043
alternative hypothesis: true mean is greater than 3000
95 percent confidence interval:
 3142.135      Inf
sample estimates:
mean of x
 3275.955
```

Calculating a critical region

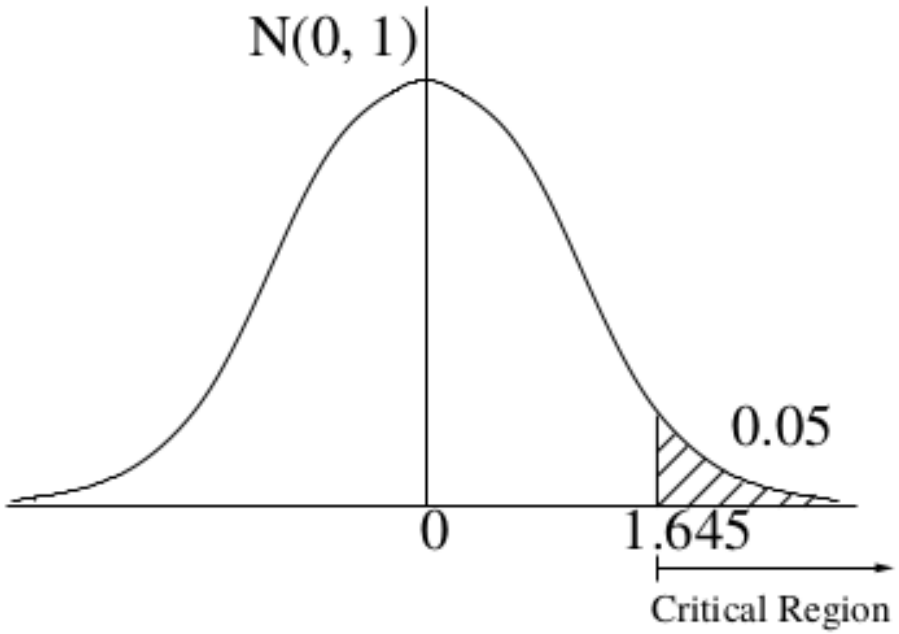
- Another way of thinking about this test is that there is some critical region of values such that if the test statistic lies in this region then we will reject H_0.
- If the test statistic lies outside this region we will not reject H_0.
- In the babies example, using a 5% level of significance this set of values will be the most extreme 5% of values in the right hand tail of the distribution.
- We can calculate that the boundary of this region, called the critical value:

```
> crit<-qnorm(1-alpha)
> crit
[1] 1.644854
```

- The value of our test statistic is 3.66 which lies in the critical region so we reject the null hypothesis at the 5% level.

```
> Z.score>=crit
[1] TRUE
```

Calculating a critical region



- Alternatively, using a T-distribution:

```
 > crit2<-qt(1-alpha, df = n-1)
> crit2
[1] 1.681071
> T.sta>=crit2
[1] TRUE
```

Overview of NHST

The two hypotheses in NHST

- **Null Hypothesis** H_0: what has been considered real up to the present or what would we expect the data to look like if there is no effect.
  - The null hypothesis always involves some kind of equality ($=, \leq, \geq$).
- **Alternative Hypothesis** H_a: it is the alternative model that we want to consider or what we expect if there actually is an effect.
  - The alternative hypothesis always involves some kind of inequality ($\neq$, $>$, or $<$).

- Importantly, null hypothesis testing operates under the assumption that the null hypothesis is true unless the evidence shows otherwise.
- The idea is to find enough **statistical evidence** to reject H_0 and be able to conclude H_a.
- If we do not get enough statistical evidence **we fail to reject** H_0.

Overview of NHST

Methodology to Perform a Hypothesis Test

- Specify a null hypothesis H_0 and alternative H_a.
- Set a test significance level α.
- Collect some data relevant to the hypothesis.
- Fit a model to the data and compute a test statistic T.
  - In parametric tests, T is a standardized value that (e.g., a Z-score).
- Assess the "statistical significance" of T.

The last part can be done with two approaches

- P-value approach: compute the probability of the observed value (or more extreme values) of that statistic assuming that the null hypothesis is true and compare it with α.
- Critical region: Calculate a region of values such that if T lies in this region then we will reject H_0.

More on P-values

- Generally, in addition to knowing whether we reject or fail to reject a null hypothesis we want to quantify the evidence we have against it.
- P-values allow us to quantity this.
- A p-value is defined as the probability of obtaining an outcome **at least as extreme** as that observed in the data given that the null hypothesis is true.
- “Extreme” means far from the null hypothesis and favorable for the alternative hypothesis (larger than the sample mean in previous example).
- We must consider all more extreme values because the probability of any particular value (such as the observed sample mean) is zero for continuous distributions.
- We must recall that we are trying to determine how weird our result would be if the null hypothesis were true.
- Hence, any result that is more extreme will be even more weird.
- So we want to count all of those weirder possibilities when we compute the probability of our result under the null hypothesis.

Two-sided Tests

- In the previous example we wanted to test the research hypothesis that mean birth weight of Australian babies was greater than 3000g.
- This suggests that we had some prior information that the mean birth weight of Australian babies was definitely not lower than 3000g.
- If this were not the case then our research hypothesis would be that the mean birth weight of Australian babies was different from 3000g.
- This allows for the possibility that the mean birth weight could be less than or greater than 3000g.
- This is an example of a **two-sided** test as opposed to the previous example which was a **one-sided** test.
- In this two-sided case we would write our hypotheses as

$$H_0: \mu = 3000g$$
$$H_1: \mu \neq 3000g$$

Two-sided Tests

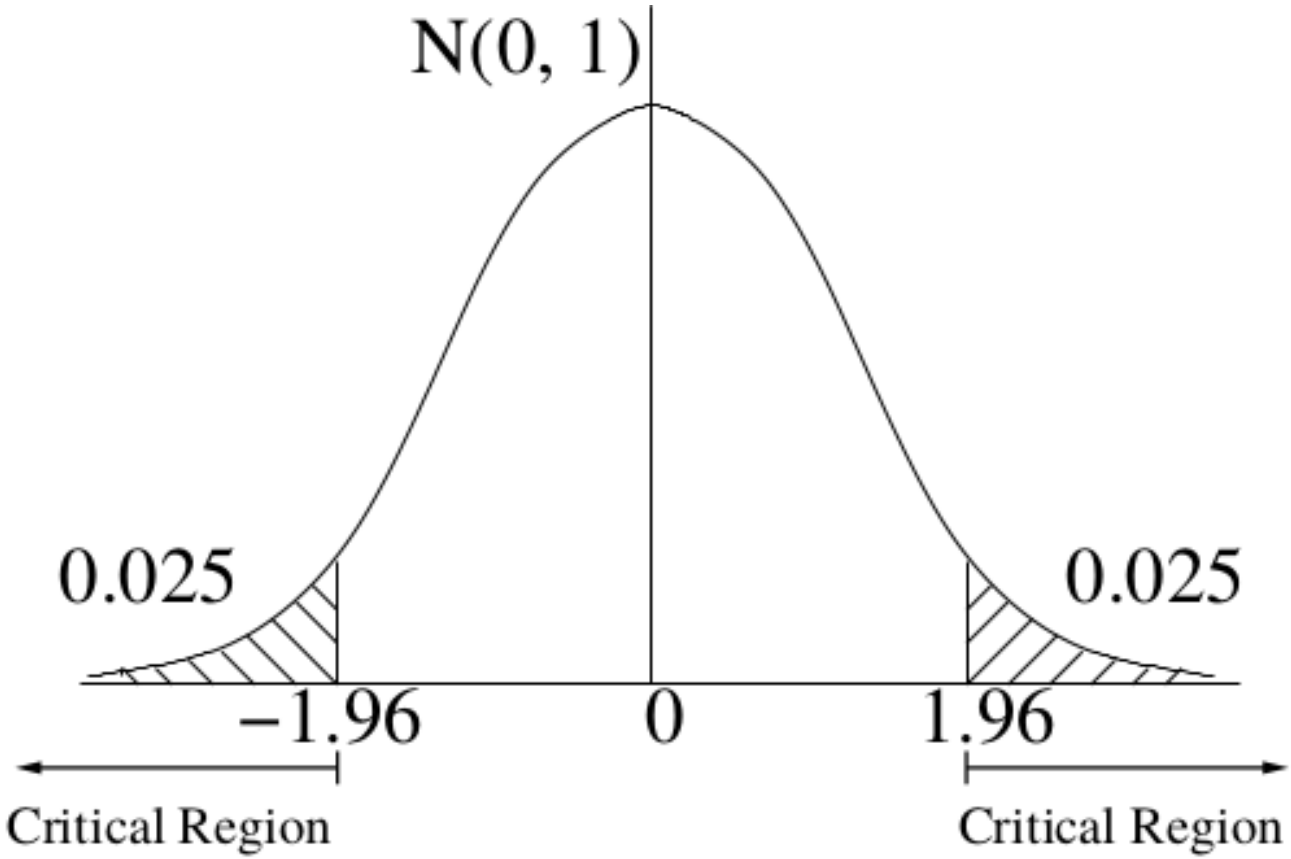
- As before we would calculate our test statistic as 3.66 for the Normal distribution and 3.47 for the T-student.
- In this case we allow for the possibility that the mean value is less than 3000g by setting our critical region to be lowest 2.5% and highest 2.5% of the distribution.
- In this way the total area of the critical region remains 0.05 and so the level of significance α of our test remains 5%.
- The critical values for a Z-test are:

```
> crit.left<-qnorm(alpha/2)
> crit.left
[1] -1.959964
> crit.right<-qnorm(1-alpha/2)
> crit.right
[1] 1.959964
```

- Thus if our test statistic is less than -1.96 or greater than 1.96 we would reject the null hypothesis.
- In this example, the value of test statistic does lie in the critical region so we reject the null hypothesis at the 5% level.

```
> Z.score<=crit.left | Z.score >= crit.right
[1] TRUE
```

Two-sided Tests



Two-sided Tests

- For the case of the T-distribution our critical region is:

```
> crit2.left<-qt(alpha/2,df = n-1)
> crit2.left
[1] -2.016692
> crit2.right<-qt(1-alpha/2,df = n-1)
> crit2.right
[1] 2.016692
>
> T.sta<=crit2.left |T.sta >= crit2.right
[1] TRUE
```

- Since T is in the rejection region, we reject the null hypothesis.

Two-sided Tests

- Alternatively, we could calculate a confidence interval for the sample mean with $(1-\alpha)\%$ confidence.
- The confidence interval becomes the **acceptance region** and we reject H_0 if $\mu_0 = 3000$ is not trapped by the interval.

```
> left.conf<-xbar-qt(p=1-alpha/2,n-1)*se.t
> left.conf
[1] 3115.418
> right.conf<-xbar+qt(p=1-alpha/2,n-1)*se.t
> right.conf
[1] 3436.491
> mu0 >= left.conf | mu0 <= right.conf
[1] TRUE
```

- Since $\mu_0 = 3000$ is not in my acceptance region, we reject the null hypothesis at the 0.05 significance level.
- Confidence intervals and p-values always agree on statistical significance [Editor, 2015].

Two-sided P-value

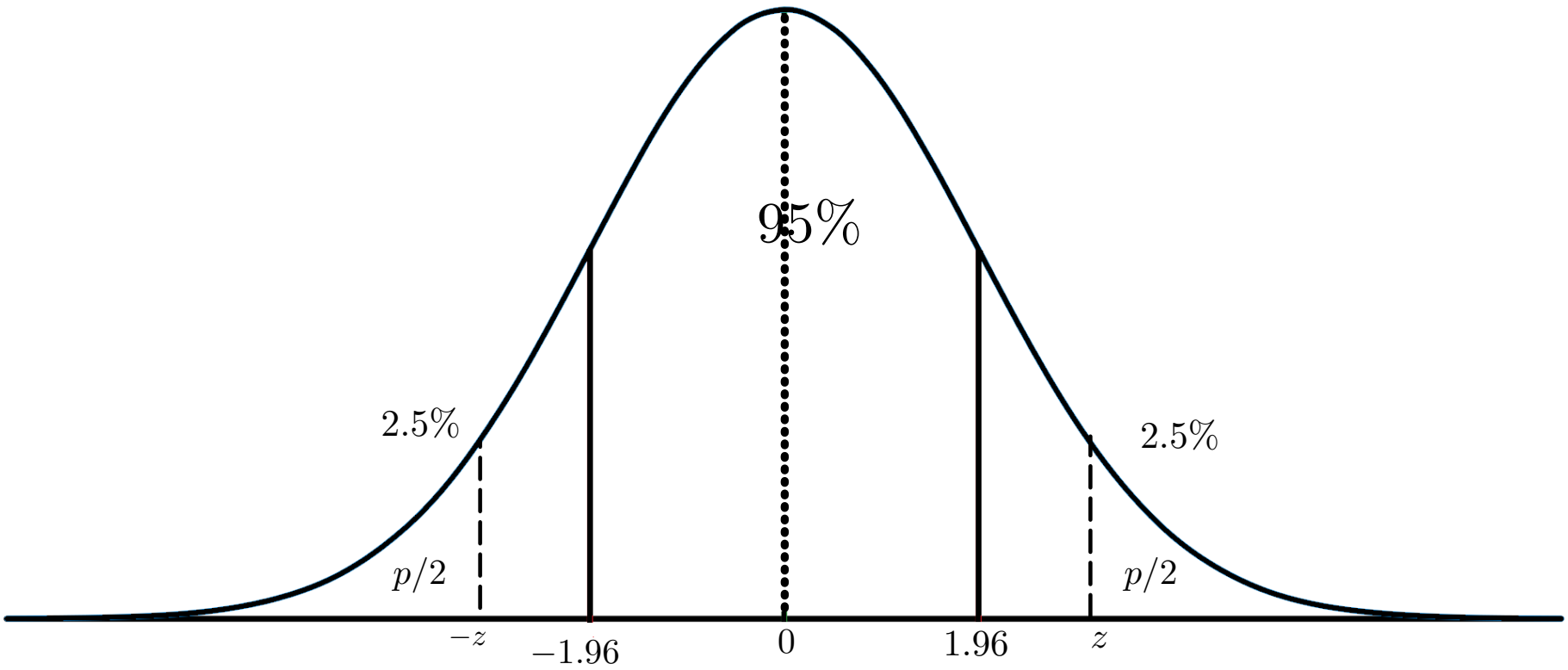
- In order to calculate a p-value in a two-sided test we need to consider both left and right tails:

$$p.value = \Phi(-Z) + (1 - \Phi(Z)) = 2\Phi(-|Z|)$$

```
> pvalue<-pnorm(-Z.score)+(1-pnorm(Z.score))
> pvalue
[1] 0.0002512811
> # or more compactly
> 2*pnorm(-abs(Z.score))
[1] 0.0002512811
```

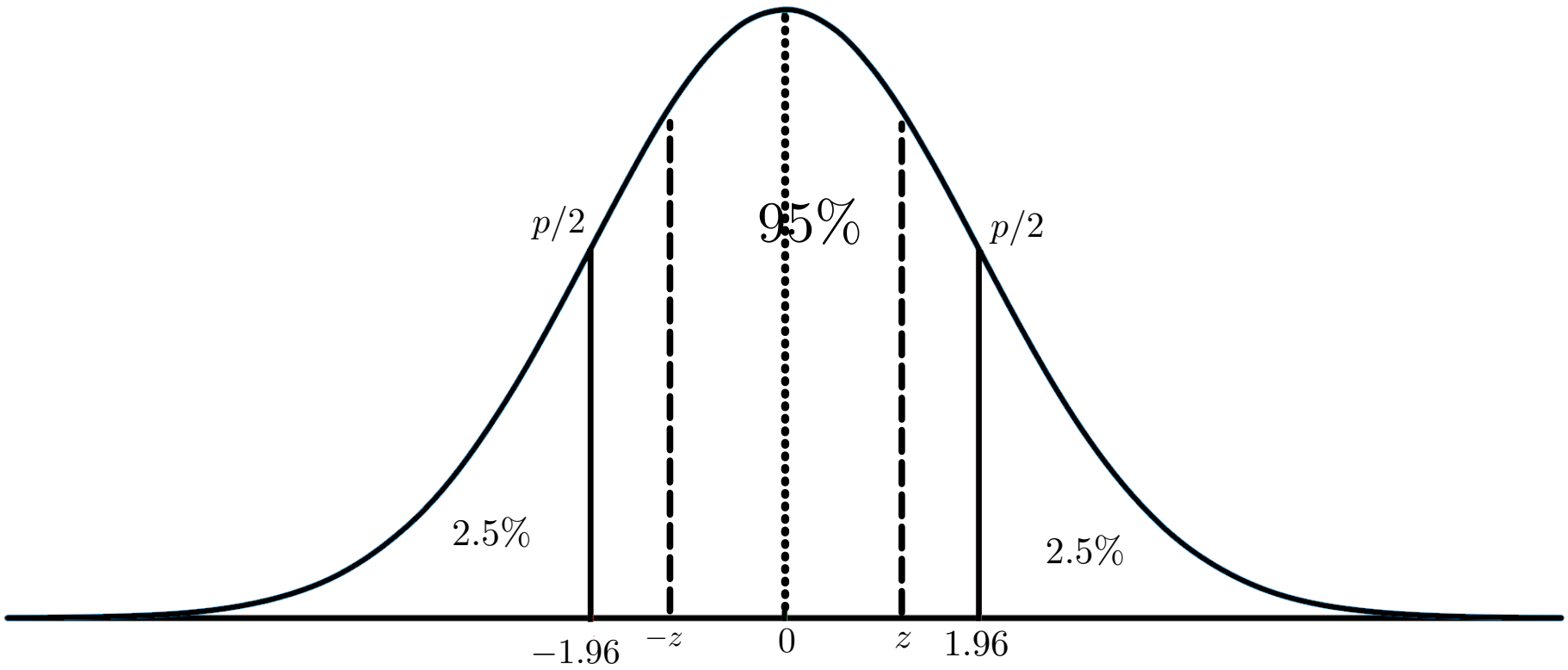
- Notice that this p-value is larger than for the one-sided test.
- This reflects the fact that an extreme value is less surprising since it could have occurred in either direction.

Two-sided P-value



Here *p.value* is less than α so we reject H_0.

Two-sided P-value



Here *p.value* is greater than α so we fail to reject H_0.

Two-sided P-value

- Now, let's calculate the p-value for the T-test:

```
> pvalue<-pt(-T.sta,df=n-1)+(1-pt(T.sta,df=n-1))
> pvalue
[1] 0.001208524
> # or more compactly
> 2*pt(-abs(T.sta),df=n-1)
[1] 0.001208524
```

Two-sided Tests

- We can run a two-sided t-test in R with one single call:

```
> t.test(x=babyboom$wt,mu=3000,
alternative="two.sided",conf.level = 1-alpha)

One Sample t-test

data:  babyboom$wt
t = 3.4666, df = 43, p-value = 0.001209
alternative hypothesis: true mean is not equal to 3000
95 percent confidence interval:
 3115.418 3436.491
sample estimates:
mean of x
 3275.955
```

Unpaired Two Sample Tests

- The babyboom dataset has a column specifying the gender of each baby.

```
> summary(babyboom$gender)
girl  boy
  18   26
```

- Suppose our research hypothesis is that the mean birth weight of boys is different (two-sided) than mean birth weight of girls:

$$H_0: \mu_{boys} = \mu_{girls} \text{ or } \mu_{boys} - \mu_{girls} = 0$$
$$H_1: \mu_{boys} \neq \mu_{girls} \text{ or } \mu_{boys} - \mu_{girls} \neq 0$$

- We call this test a two sample tests (one sample with the births of boys and the other of girls).
- The two samples are independent or unpaired (we have different number of observations for boys and girls).
- This types of tests are very important for experimental data and observational studies (i.e., one sample is the control group and the other is the treatment).

Unpaired Two Sample Tests

- Asymptotic theory tells us that the difference between two sample means (when the sample sizes are sufficiently large) has a Normal sampling distribution:

$$\overline{X}_1 - \overline{X}_2 \sim N\left(0, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right)$$

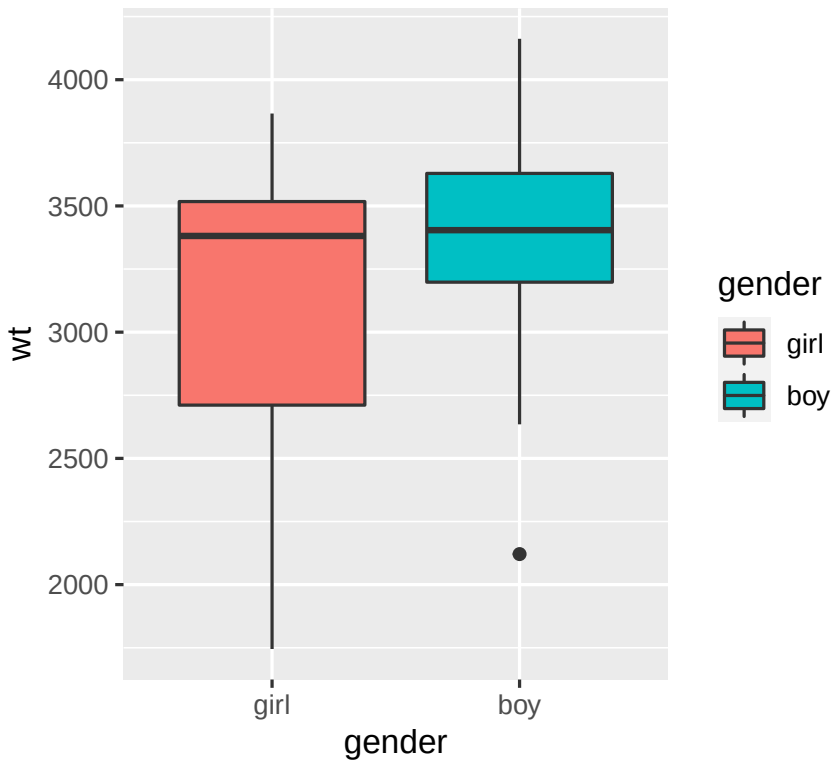
- When the standard deviations of each group are unknown (σ_1, σ_2) we can estimate them as usual (s_1,s_2) and build the following T satistics:

$$T = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

- The T statistic is distributed according to a t-student distribution.

Unpaired Two Sample Tests

- When the groups are the same size and have equal variance, the degrees of freedom for the T test is $n_1 + n_2 - 2$.
- In this case the box plot shows that the “girl” group is more variable than then “boy” group.
- We also know that the number of observations in each group is different.



Unpaired Two Sample Tests

- We need to use a more complex formula for the degrees of freedom, which is often referred to as a “Welch t-test”:

$$d.f. = \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\frac{(s_1^2/n_1)^2}{n_1 - 1} + \frac{(s_2^2/n_2)^2}{n_2 - 1}}$$

- For this example d.f. = 27.631 which is lower than what we would get by subtracting 2 from the sample size.
- Recall that the lower the d.f the wider the tails in the t-student distribution.
- This is essentially, imposing a penalty on the test for differences in sample size or variance.

Unpaired Two Sample Tests

- We can run a Welsh T-test in R as follows:

```
> t.test(babyboom$wt~babyboom$gender)

Welch Two Sample t-test

data:  babyboom$wt by babyboom$gender
t = -1.4211, df = 27.631, p-value = 0.1665
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -593.1538  107.4273
sample estimates:
mean in group girl  mean in group boy
          3132.444           3375.308
```

- In this case, we fail to reject H_0 at the 5% significance level.

Paired Two Sample Tests

- Another very useful type of two sample test is the Paired T-Test.
- This test is used to compare the means between two **related groups** of samples.
- Here we have two values (i.e., pair of values) for the same samples [Kassambara,].
- This type of data arises when we compare a response variable after and before a treatment for each subject.
- It also arises in matched pairs experiments.
- Paired t-test analysis is performed as follow:
  1. Calculate the difference d between each pair of value.
  2. Compute the mean $\overline{d}$ and the standard deviation s_d of these differences.
  3. Compare the $\overline{d}$ to 0 in the same way as previous tests.

Paired Two Sample Tests

- The test statistics T is calculated as follows for the paired test:

$$T = \frac{\overline{d}}{s_d/\sqrt{n}}$$

- The the degrees of freedom (df) are simply $n - 1$.
- As an example of data, 20 mice received a treatment X during 3 months.
- We want to know whether the treatment X has an impact on the weight of the mice.
- The weight of the 20 mice has been measured before and after the treatment.
- Let's test the following hypotheses:

$$H_0 : \overline{d} = 0$$
$$H_1 : \overline{d} \neq 0$$

Paired Two Sample Tests

- We can run a paired t-test in R as follows:

```
> before <-c(200.1, 190.9, 192.7, 213, 241.4, 196.9, 172.2,
+            185.5, 205.2, 193.7)
> # Weight of the mice after treatment
> after <-c(392.9, 393.2, 345.1,393, 434, 427.9, 422,
+           383.9, 392.3, 352.2)
> t.test(after, before, paired = TRUE, alternative = "two.sided")

Paired t-test

data:  after and before
t = 20.883, df = 9, p-value = 6.2e-09
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 173.4219 215.5581
sample estimates:
mean of the differences
                 194.49
```

Errors

- We have two types of errors when we perform a hypothesis test.
- Type I error: it is when we reject the null hypothesis when it was true (also called “false alarm”).
- Type II error: is when the null hypothesis is false but we do not have statistical evidence to reject it (also called a “miss”).

	Retain H_0	Reject H_0
H_0 true	✓	type I error
H_1 true	type II error	✓

Errors

- Jerzy Neyman and Egon Pearson, two very influential statisticians from the 20th century, coined two terms to describe the probability of these two types of errors in the long run:
  - P(Type I error) = α
  - P(Type II error) = β

Figure: Neyman & Pearson

Errors

- If we set α to .05, then in the long run we should make a Type I error 5% of the time.
- The standard value for an acceptable level of β is .2.
- That is, we are willing to accept that 20% of the time we will fail to detect a true effect when it truly exists.
- The concept of **statistical power** is the complement of Type II error:

$$power = 1 - \beta$$

- The power of a test is the likelihood of finding a positive result given that it exists [Poldrack, 2019].
- To mitigate type I errors we generally use smaller values of α.
- To mitigate type II errors (or increase the power of the test) we generally work with larger samples.
- There is a trade-off between type I and type II errors.
- There are tools to analyze the power of a test that go beyond the scope of this course.

What does a significant result mean?

- There is a great deal of confusion about what p-values actually mean.
- Suppose we do an experiment comparing the means between conditions, and we find a difference with a p-value of .01.
- Does it mean that the probability of the null hypothesis being true is .01?
  - No. Remember that in NHST, the p-value is the probability of the data given the null hypothesis: $P(data|H_0)$.
  - It does not warrant conclusions about the probability of the null hypothesis given the data: $P(H_0|data)$.
- Does it mean that the probability that you are making the wrong decision is .01?
  - No. This would be $P(H_0|data)$, but remember as above that p-values are probabilities of data under H_0, not probabilities of hypotheses.

What does a significant result mean?

- Does it mean that you have found a practically important effect?
  - No. There is an essential distinction between statistical significance and practical significance.
  - Suppose we performed an RCT to examine the effect of a particular diet on body weight, and we find a statistically significant effect at $p < .05$.
  - This doesn't tell us how much weight was actually lost.
  - The loss of one ounce (i.e. the weight of a few potato chips) can be statistically significant but not practically significant.
- Many scientist think that NHST is flawed and that is has been the cause of serious problems in science [Poldrack, 2019].
- For example, The American Statistical Association (ASA) released a "Statement on Statistical Significance and P-Values" indicating the proper use and interpretation of the p-value [Wasserstein and Lazar, 2016].

There are many other tests

There are a plethora of other tests that we will not teach in this course

- Proportion tests.
- The Fisher's exact test.
- Analysis of Variance (ANOVA).
- The Chi-square tests of independence.
- The Wilcoxon signed-rank test.
- The Kolmogorov–Smirnov test.

Conclusions

- In this class we have introduced two important statistical concepts: design of experiments and NHST.
- Experiments are a powerful approach to determining cause-effect relationships.
- It is very important to identify and control confounding variables in the design of experiments.
- Hypothesis testing is a family of techniques for testing hypotheses using data.
- NHST must be used with care and we should always remind that p-values do not measure the probability of a given hypothesis.

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