

Design of Experiments & Hypothesis Testing

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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. [?]

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 [?]: 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.



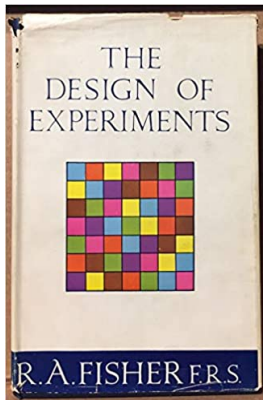
- A confounding variable is a variable that may or may not be apparent at the outset but, once identified, could explain the pattern between the variables.
- We know that bigger children have bigger feet, and they drink more milk because they eat and drink more of everything than do smaller children.

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 [?].



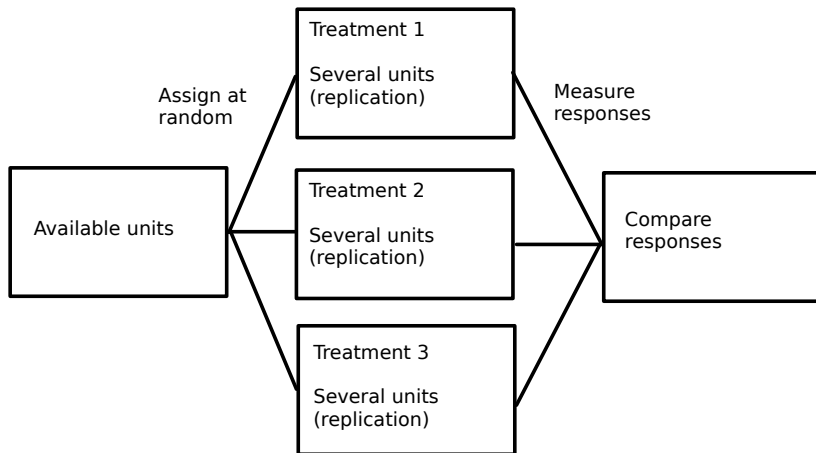
Main Concepts of Experimental Design

- **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 [?].
- 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

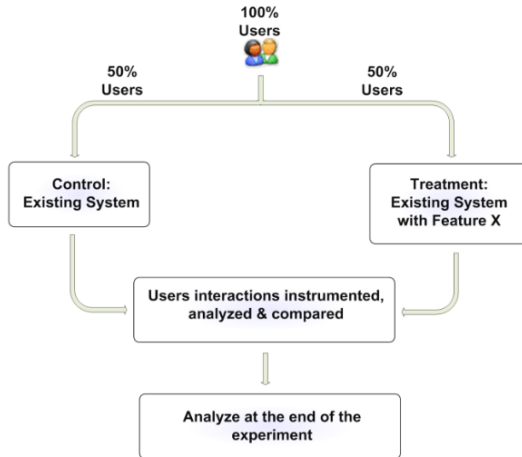


Image source: [?]

Example: MSN Real Estate

- The team running the MSN Real Estate site wanted to test different designs for the “Find a home” widget [?].
- 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 split between the variants in a persistent manner (a user receives the same experience in multiple visits) during the experiment period.

Example: MSN Real Estate

Find a new home or apartment

☒ Existing Homes
from REALTOR.com®
 ☐ New Homes
from Move.com™
 ☐ Foreclosures
from RealtyTrac.com™
 ☐ Rentals
from Move.com™

Price Range: \$0 — No Maximum

Enter City

Select a State

Or Enter ZIP

Go

• Senior Living • Home Plans

Control

Existing Homes Foreclosures New Construction Rentals

Find Existing Homes for Sale


 Enter City
 State
 or
 Enter Zip
 Find homes

Treatment1

Existing Homes Foreclosures New Construction Rentals

Find Existing Homes for Sale


 Enter City
 State
 or
 Enter Zip
 Find homes

Treatment 2

What are you looking for?

☒ Existing Homes
 Enter City
 State
 ☒ New Construction
 Enter Zip
 ☐ Rentals
 \$0 to No Max
 ☒ Senior Living
 ☒ Home Valuation
 ☒ Foreclosures
 ☒ Professional Services
 Find homes

Treatment 3

Find a new Home or Apartment

 Existing Homes
  New Construction
  Foreclosures
  Rentals

Enter Zip or Enter City State Search listings

Treatment 4

Find Your Dream Home or Apartment

City, State or ZIP

☒ Existing homes
 ☐ New construction
 ☐ Foreclosures
 ☐ Rentals
 Search listings

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 [?].

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.

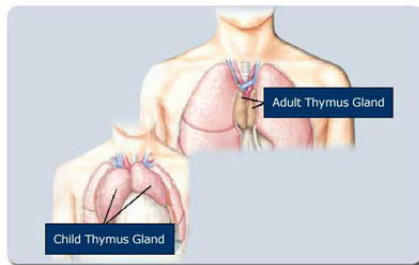


Figure: source: http://esvc001414.wic005tu.server-web.com/tech_imm_bio_principle.htm

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

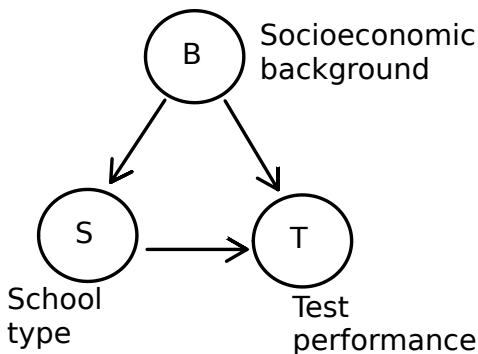


Figure: A possible causal explanation of socioeconomic background, school type, and test performance.

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) [?].
- 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 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 whether 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 first introduce these concepts with two examples taken from [?] and [?].
- 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:

$$\begin{aligned}H_0: \mu &= 3000g^1 \\ H_1: \mu &> 3000g\end{aligned}$$

- 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.

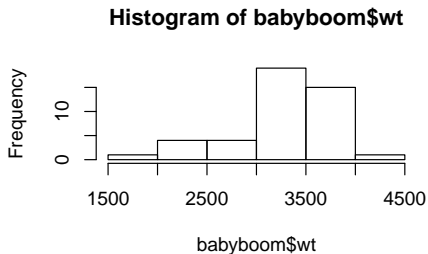
¹ In the strict sense $H_0: \mu \leq 3000$, but this complicates all the following explanations.

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 \bar{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 \bar{X} follows as Normal distribution when n is sufficiently large: $\bar{X} \sim N(\mu, \sigma^2/n)$
- If we assume H_0 is true, then $\mu = 3000$.
- The value of n is 44 and the value of σ is known in 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:

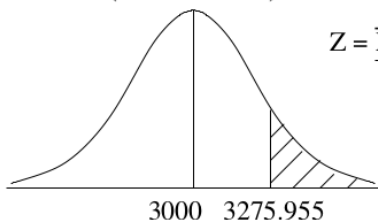
```
> #pvalue
> 1-pnorm(xbar, mean =mu0, sd =se)
[1] 0.0001256405
> #or
> Z.score<-(xbar-mu0)/se
> Z.score
[1] 3.660951
> p.value<-1-pnorm(Z.score)
> p.value
[1] 0.0001256405
```

Example 2: Babies

$$\bar{X} \sim N(3000, 5681.818)$$

$$Z \sim N(0, 1)$$

$$P(\bar{X} > 3275.955)$$



$$Z = \frac{\bar{X} - 3000}{75.378}$$

$$P(Z > 3.66)$$

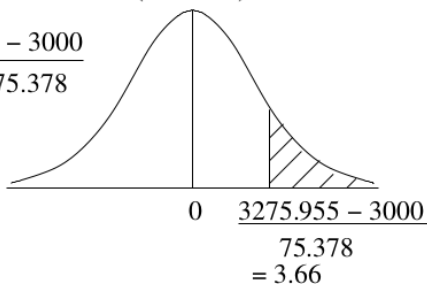


Figure: [?]

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 $\frac{\bar{X}_n - \mu_0}{\frac{s}{\sqrt{n}}}$:

```
> 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

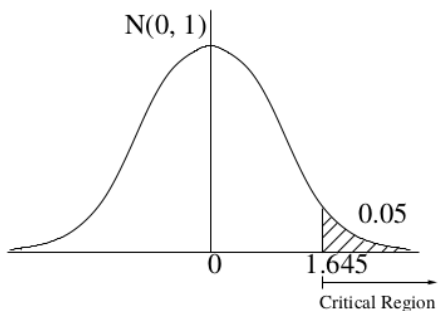
- Another way of thinking about this test is that there is some critical region of values such that if the test statistic lies in this region then we will reject H_0 .
- If the test statistic lies outside this region we will not reject H_0 .
- In the babies example, using a 5% level of significance this 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 ($\neq, >, <$).
- 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 quantify 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

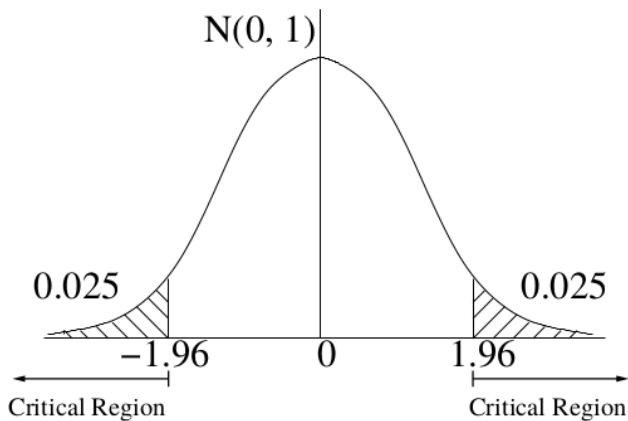
- As before we would calculate our test statistic as 3.66 for the Normal distribution and 3.47 for the T-student.
- In this case we allow for the possibility that the mean value is less than 3000g by setting our critical region to be lowest 2.5% and highest 2.5% of the distribution.
- In this way the 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 [?].

Two-sided P-value

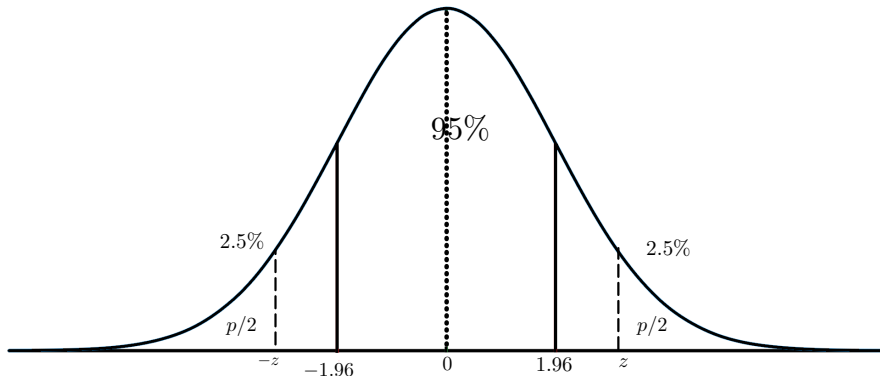
- In order to calculate a p-value in a two-sided test we need to consider both left and right tails:

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

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

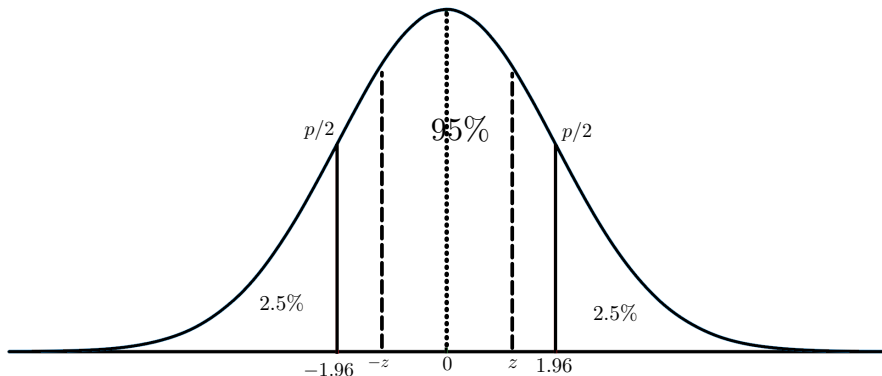
- Notice that this p-value is larger than for the one-sided test.
- This reflects the fact that an extreme value is less surprising since it could have occurred in either direction.

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:

$$\bar{X}_1 - \bar{X}_2 \sim N\left(\mu_1 - \mu_2, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right)$$

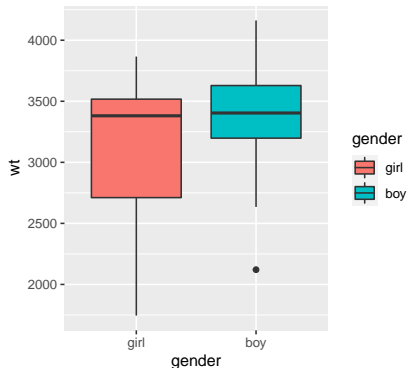
- When the standard deviations of each group are unknown (σ_1, σ_2) we can estimate them as usual (s_1, s_2) and build the following T statistics:

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

- 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 the “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 Welch 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 [?].
- 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 \bar{d} and the standard deviation s_d of these differences.
 - 3 Compare the \bar{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:

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

- 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:

$$H_0: \bar{d} = 0$$

$$H_1: \bar{d} \neq 0$$

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:
 - $P(\text{Type I error}) = \alpha$
 - $P(\text{Type II error}) = \beta$



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 [?].
- 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 [?].
- 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 [?].

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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