Econometric Methods for Political Analysis

Volume I: Causal Inference and Regression

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Preface

This book is the 1st book in a sequence on **Econometric Methods for Political Analysis**.

1. Volume I: Causal Inference and Regression (this book) introduces causal inference, randomised experiments, and the tool of regression in estimating causal effects.
2. Volume II: Causal Estimation for Observational Studies expands on the first book by discusses modern causal inference techniques, such as instrumental variables and quasi-experimental techniques, which are useful when regression or randomised experiments are not feasible.
3. Volume III: Measurement and Prediction discusses topics in latent variable measurement, prediction and classification methods, and measurement of textual data for statistical analysis.

This series is designed to be both an approachable, but also rigorous, introduction to Econometrics and the use of statistical methods for the analysis of political institutions and actors.

I assume a solid understanding of basic probability and statistics, including the topics of conditional probabilities, random variables and distributions, expectation/mean and variance, and correlation.

I also assume a solid understanding of mathematics, including algebra, single variable calculus, and some linear algebra. While you will be able to still learn from this book without a solid mathematical background, you will gain much more from understanding the mathematics behind the methods.

To see what mathematics is specifically required, or to refresh on the mathematics needed, consult the **Quantitative Methods** sequence (particularly the 1st volume and some topics in the 2nd volume).

I will also add some reference code for the R-programming language and Stata in case you are interested in implementing these methods on your own.

If you have completed this book, or already have a strong understanding of potential outcomes, causal effects, and regression, you can move on to the later books in this series, which build on this first book.

Part I

Econometrics and Causal Inference

Chapter 1

Causal Inference

1.1 Introduction to Econometrics

Econometrics is the field of applying statistical methods to analyse real-world economic and social science data. While econometrics was initially pioneered by economics, the techniques econometricians developed have been adopted by most of the social sciences, including Political Science. Econometrics has two primary goals:

1. **Causal Inference**: Establishing how one feature directly causes another feature. This is essential to understanding the world around us and designing better policies. Key point: correlation causation.
2. **Predictive Inference/Forecasting**: Given data we have, how can we predict the values of data we do not have? For example, what will sales be next year? GDP? Who will win the next election? What are the likely costs/effects of a policy?

This book focuses mostly on Causal Inference, which is generally the more important and commonly used part of econometrics for political science. The later book in the series, *Advanced Econometrics for Political Analysis*, dives more into the predictive side of things.

The most important thing about econometrics and causal inference is that **correlation does not equal causation**.

For example, *Ice Cream Sales* and *Number of Fatal Shark Attacks* are two highly correlated variables in the United States. Does this mean that selling ice cream causes fatal shark attacks? No!

The reason this relationship exists is because of another variable - the *weather*. The weather, when it is sunny, causes both ice cream sales and more people to go to the beach, which causes more fatal shark attacks. However, there is no direct link between ice cream sales and the number of fatal shark attacks.

The goal of econometrics is to distinguish between correlation and causation. We want to "partial out" the effect of confounding variables (like the sunny weather in the above example), and isolate the causal effects.

We will then discuss Randomised Controlled Trials, the best way of estimating causal effects. However, these randomised trials are often impossible to do in Economics and Political Science, so we will spend the remainder of this series finding different methods and techniques to approximate the true causal effects.

1.2 Potential Outcomes Framework

A **causal effect** is a change in some feature of the world Y, that would directly result from a change in some other feature D. Essentially, change in D causes change in Y.

> Key Definition: Potential Outcomes
>
> Causal effect implies that there are **potential outcomes**. Imagine that there are 2 worlds, that are exactly the same until treatment D occurs. In one world, you get the treatment D, and the other world, you do not get this treatment. Since these 2 worlds are identical besides the treatment D, the difference between the world's Y outcomes are the effect of our treatment D.
>
> In the real world, we only observe one of these realities - either a unit i gets, or does not get, the treatment. The other world that we do not observe is called a **counterfactual**.

Thus, there are two states of the world in the potential outcomes framework:

- The control state $D = 0$ is the world where a unit does not receive the treatment D. Y_{1i} is the potential outcome for unit i, given it is in the treatment state $D_i = 1$.
- The treatment state $D = 1$ is identical to the control state, with the only exception that a unit receives the treatment D. Y_{0i} is the potential outcome for unit i, given it is in the control state $D_i = 0$.

The **individual causal effect** τ of the treatment D for any unit i is $\tau_i = Y_{1i} - Y_{0i}$. Since the two states are identical except for treatment D, the resulting difference must be as a result of treatment D. However, in the real world, we do not have parallel worlds (unfortunately) - we only observe one outcome: either unit i gets the treatment $D_i = 1$, or does not get the treatment $D_i = 0$.

> Key Definition: Observed Outcomes
>
> The **observed Y outcome** (in the real world) of any unit i is given by the equation:
>
> $$Y_i = D_i \times Y_{1i} + (1 - D_i) \times Y_{0i}$$

This equation might be a little abstract, however, it is easy to understand by plugging D_i in:

$$[Y_i | D_i = 0] = 0 \times Y_{1i} + (1 - 0) \times Y_{0i} = Y_{0i}$$
$$[Y_i | D_i = 1] = 1 \times Y_{1i} + (1 - 1) \times Y_{0i} = Y_{1i}$$

Intuitively, if the observation is in the control state $D_i = 0$, we observe potential outcome Y_{0i}. When an observation is in the treatment state $D_i = 1$, we observe potential outcome Y_{1i}.

Stable Unit Treatment Value Assumption

Take two units i and j. The Stable Unit Treatment Value Assumption (SUTVA) is the assumption that unit j getting the treatment D, does not affect the outcomes of unit i.

This is important - because if this assumption were to be violated, we would have more than two potential outcomes. If unit i were affected by j's treatment status, we would not only have the potential outcomes of unit i being in treatment or control, but also would have to consider unit j being in treatment or control.

1.3 Estimands and Estimator Properties

Causal Estimands

An **estimand** is the quantity we are trying to estimate (i.e. what we are interested in). The fundamental problem of causal inference is that we only can observe one of 2 potential outcomes. For example, if you get treatment D, we cannot observe the world where you do not get treatment D. Thus, we cannot estimate individual effects of the causal treatment. However, there are other estimands we can use.

One of the estimands is the Average Treatment Effect:

> Key Definition: Average Treatment Effect
>
> **Average treatment effect (ATE)** is the average of all individual treatment effects:
>
> $$\tau_{ATE} = \mathbb{E}[\tau_i] = \mathbb{E}[Y_{1i} - Y_{0i}] = \frac{1}{n}\left(\sum Y_{1i} - \sum Y_{0i}\right)$$

There are also other treatment effects we can use to estimate. The **average treatment effect on the treated (ATT)** is the treatment effect of only units who recieved the treatment $D_i = 1$

$$\tau_{ATT} = \mathbb{E}[Y_{1i} - Y_{0i}|D_i = 1]$$

The **average treatment effect on the controls (ATC)** is the treatment effect of units who only did not recieve the treatment $D_i = 0$

$$\tau_{ATC} = \mathbb{E}[Y_{1i} - Y_{0i}|D_i = 0]$$

The **conditional average treatment effect (CATE)** is the treatment effect of units, given they have some other variable X value. For example, if X is gender, the CATE could be the treatment effect on only females.

$$\tau_{CATE} = \mathbb{E}[Y_{1i} - Y_{0i}|X = x]$$

Estimator Bias and Variance

The above causal estimands are not directly calculable, and we to estimate them with an **estimator**.

Bias is when an estimator consistently and systematically poorly estimates the estimand.

Or in other words, the estimator's average estimate of our estimand (over many tries of estimation), is not actually the true value of the estimand. That means something is consistently off with our estimator - we might be consistently overestimating by 5%, or underestimating, etc. Mathematically:

$$\mathbb{E}[\hat{\theta}_i] = \mathbb{E}[\theta], \text{ where } \hat{\theta} \text{ is the estimate}$$

- Or more intuitively, imagine you are trying to hit a bullseye in archery. Bias is when you might be very accurate, but aiming in the wrong place, thus not hitting the bullseye. A biased estimator is essentially that - we are consistently and systematically making a mistake when estimating the quantity in question.

Variance is the difference between our estimations derived from our estimator - i.e. the consistency.

- For example, you might have an unbiased estimator, where our average estimate is the actual causal estimand. However, while the average is correct, the variance of our estimates is very wide.
- Or more intuitively, in the archery example, we are aiming correctly at the bullseye, however, the wind and our muscles are unpredictable, so each shot might be slightly off in different directions. If we average all our shots, we are hitting the middle, but not each individual shot is in the bullseye.

Ideally, we want an unbiased estimator that has low variance. We will explore many different types of estimators for causal effects throughout this book, each with its own bias and variance.

1.4 Correlation is not Causation: Naive Estimator

The **naive estimator** is an estimator that only compares our observed outcomes, without any comparison to the counterfactual potential outcomes:

$$\mathbb{E}[Y_{1i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$$

Or more intuitively, the average observed outcome Y of those in the treatment group, minus the average observed outcome Y of those in the control group.

This is often what many people initially do when trying to find a causal effect. Essentially, we are comparing units that are assigned to treatment, and the units that are not assigned to treatment, and their observed outcomes.

- In other words, the naive estimator is looking at the correlation between the treatment D and the observed outcomes of Y, without considering the counterfactual.

The naive estimator is a bad idea. Remember, our treatment effects are supposed to be comparing to two potential outcomes of the same unit. We are supposed to compare Y_{1i} to Y_{0i}.

- However, in this scenario, we are not comparing the potential outcomes of the same individual. We are comparing the outcome of some observation A in treatment Y_{1A} and the outcome of some other observation B in control Y_{0B}.
- But what if observation A and B are different? There outcomes may not be due to the treatment D, but because of the differences between A and B. This is why counterfactual comparison is important - when we compare the potential outcomes of the same unit in control and treatment groups, we can be confident of the affect of the treatment, since it is the same unit of observation for both groups.

We can prove this mathematically. We start with the naive estimator:

$$\mathbb{E}[Y_{1i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$$

Then, we do a little algebra trick - we add a new term to this equation, and then subtract the same term. The two new terms thus cancel each other out to 0.

$$= \mathbb{E}[Y_{1i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0] + \mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i - 1]$$

Then, we rearrange the terms, then simplify, getting the result:

$$= \mathbb{E}[Y_{1i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 1] + \mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$$
$$= \mathbb{E}[Y_{1i} - Y_{0i}|D_i = 1] + \mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$$

If we look at the final result, we can divide it into 2 parts:

1. The first part, $\mathbb{E}[Y_{1i} - Y_{0i}|D_i = 1]$, is the average treatment effect of the treated τ_{ATT} that we introduced previously.
2. The second part $\mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$ is what we call the **selection bias**. Intuitively, it is the difference between the treatment and control groups prior to the treatment taking place (hence the potential outcome being Y_{0i}).

1.5 Selection Bias and Confounding Variables

Selection Bias

The differences between the treatment and control groups prior to treatment is captured in our naive estimator, which is why our results with the naive estimator are **biased**.

For example, if we are measuring the question *does going to the hospital make you more healthy*, and we simply measured the outcomes of people who went to the hospital and did not go to the hospital, we might see that in general, people who did not go to the hospital are healthier!

- Does this mean that going to the hospital makes you unhealthier? No! It is because more unhealthy people choose to go to the hospital in the first place. Thus, the hospital has generally more unhealthy individuals in it. The hospital might perform miracles on these people, but they are still not as healthy as the healthy people who did not need to go to the hospital.
- The differences between the people who chose to go to the hospital versus the people who did not go to the hospital explains the differences in our outcome, not the actual treatment that the hospital provided.

This is selection bias - when our treatment and control groups are fundamentally different and unequal even prior to treatment.

Confounding Variables

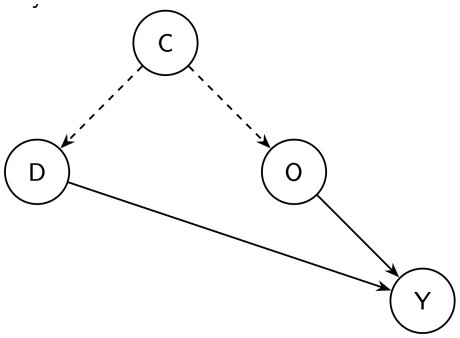
Key Definition: Confounders

A **confounder** is a variable that is explaining the differences in the treatment and control groups.

- For example, smoking might be a confounding variable in the example above - people who smoke more often will go to the hospital, and will have worse outcomes than people who did not smoke and did not go to the hospital. Confounders are often the cause of selection bias.

Confounding variables result in selection bias, and are why correlation does not equal causation. In order to accurately calculate causal effects, we need to find some way to eliminate the effect of confounding variables.

For example, look at the figure below:



In the figure above, D is the treatment group, and O is the observed group. C is some confounding variable correlated with D, that affects whether an observation i gets the treatment D or control C.

When we calculate the naive estimate (or correlation), our causal estimate captures both the effect of $D \to Y$, but also the effect of $D \leftrightarrow C \to O \to Y$, since D and C are correlated.

- This second effect through the correlation of D and C is called the **backdoor path**.
- Both the direct $D \to Y$ and the backdoor path are included in the naive estimator (and correlation).

However, the actual causal effect of treatment D on Y is only the section of $D \to Y$, which does not include the backdoor path.

- So, we need to find some way to only look at $D \to Y$, and eliminate/partial out the effect of the backdoor path.

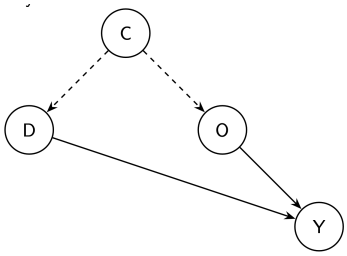
To make an accurate causal effect estimate, we must get rid of confounding variables, selection bias, and the backdoor path. How do we do this? The best method is randomisation, which we will cover next.

Chapter 2

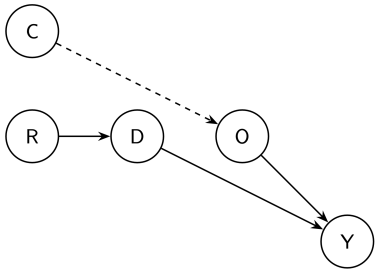
Randomised Controlled Trials

2.1 Random Assignment and Estimation

The **assignment mechanism** is how we decide which observations receive treatment D. In the last chapter, we discussed how confounder C affects which observations get the treatment, introducing selection bias.



We can address this confounder C and eliminate the backdoor path $D \leftrightarrow C \rightarrow O \rightarrow Y$ by randomly assigning units into either the treatment or control group:



With random assignment mechanism R, now units are assigned to control randomly, not based on the confounder variable C. Thus, C and D should no longer be correlated, thus removing the backdoor effect, selection bias, and the influence of confounder C.

Key Definition: Random Assignment

With random assignment, selection bias and the influence of confounder C is eliminated, thus the control group and treatment group should be very similar. Thus, the potential outcomes are independent of treatment/control status:

$$\mathbb{E}[Y_{1i}|D_i = 1] \approx \mathbb{E}[Y_{1i}|D_i = 0] \quad \text{and} \quad \mathbb{E}[Y_{0i}|D_i = 1] \approx \mathbb{E}[Y_{0i}|D_i = 0]$$

If this assumption of random assignment is met, then we can use the naive estimator to estimate the treatment effect. This is because we have eliminated the confounders that cause selection bias.

Mathematically, we can prove this. Recall the naive estimator:

$$\mathbb{E}[Y_{1i} - Y_{0i}|D_i = 1] + \mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0]$$

The selection bias term $\mathbb{E}[Y_{0i}|D_i = 1] - \mathbb{E}[Y_{0i}|D_i = 0] = 0$ under the above assumptions of randomisation. Thus, there is no longer selection bias, and confounding variables will have been accounted for.

Our observed potential outcomes in our randomised experiments are Y_{1i} and Y_{0i}. We know that the treatment group D_i does not affect our potential outcomes. Thus we know that:

$$\mathbb{E}[Y_{1i}|D_i = 1] = \mathbb{E}[Y_{1i}]$$
$$\mathbb{E}[Y_{0i}|D_i = 0] = \mathbb{E}[Y_{0i}]$$

Now that we have $\mathbb{E}[Y_{1i}]$ and $\mathbb{E}[Y_{0i}]$, we can calculate the average treatment effect.

Key Definition: ATE Estimate of a Randomised Experiment

The estimate of the average treatment effect of a randomised controlled trial is:

$$\hat{\tau}_{ATE} = \mathbb{E}[\tau_i] = \mathbb{E}[Y_{1i}] - \mathbb{E}[Y_{0i}] = \bar{Y}_t - \bar{Y}_c$$

Where $\bar{Y}_t$ is the average Y value of the treatment group, and $\bar{Y}_c$ is the average Y value of the control group. Thus, the causal effect is simply a **difference of means** between the treatment and control group.

For this estimate of the ATE to be true, there must be random assignment of treatment, and the treatment and control groups must be similar to each other.

2.2 Uncertainty and Standard Errors

Intuition of Uncertainty

Remember how we randomly assigned units to treatment or control? What if we ran the experiment again? The treatment and control groups would very likely not be exactly the same, and thus, we would get a slightly different causal effect. Thus, we have some uncertainty with our causal estimate - re-running the experiment might result in a different answer.

The ATE we have calculated is only our specific sample average treatment effect (SATE), often notated $\hat{\tau}_{ATE}$ or $\hat{ATE}$.

- Why sample? Well, through random assignment, you are basically "randomly sampling" potential outcomes - since randomly choosing one unit to be in treatment/control means not seeing the other counterfactual potential outcome.

Thus, we need some mechanism to account for sampling variability and how rerunning the experiment might result in slightly different results. We do this with sampling distributions and standard errors.

Sampling Distributions and Standard Error

Imagine that we take a sample from a population (or some random assignment mechanism). Then, we find the average treatment effect of the sample $\hat{\tau}_{ATE}$. That is a **sample estimate**, which is often notated $\hat{\theta}$. (I use θ, since this idea of uncertainty can be applied to any estimate, not just average treatment effect).

Then, let us take another sample from the same population (or do another random assignment), and find the sample estimate. This will be slightly different than the first sample, since we are randomly sampling. That is another sample estimate. We keep taking samples from the same population (more random assignments), and getting more and more sample estimates.

Let us plot all our sample estimates $\hat{\theta}$ (different $\hat{\tau}_{ATE}$ values) into a "histogram" or density plot. The x axis labels the possible $\hat{\tau}_{ATE}$ values, and the y axis is how frequently a specific sample estimate occurs. We get a distribution, just like a random variable distribution. That distribution is the **sampling distribution**

Key Definition: Standard Error

A **sampling distribution** is the imaginary distribution of estimates, if we repeated the sampling and estimation process many, many times.
The **standard error** is the standard deviation of the sampling distribution. It is often notated $SE(\hat{\theta})$. The computer/software we use will calculate this for us.

2.3 Confidence Intervals and Hypothesis Testing

Confidence Intervals

Since there is variability of estimates between samples, we have to create an interval around our sample estimate $\hat{\theta}_j$ to account for this uncertainty. We assume our estimated $\hat{\theta}_j$ is the centre of this distribution, then add some "buffer" to both sides.

Key Definition: Confidence Intervals

A **confidence interval**'s lower and upper bounds are defined as, given a confidence level of 95% (the standard confidence level):

$$\hat{\theta}_j \pm 1.96 \times \hat{se}(\hat{\theta}_j)$$

Where $\hat{se}(\hat{\theta}_j)$ is the standard error of our estimate of how precisely we have estimated the true value of θ_j, introduced in the previous section.

Confidence intervals say that if we repeated the sampling and estimation process many many times (like we did for our sampling distribution), 95% of the confidence intervals we construct from our samples, would correctly contain the true θ_j.

Why 1.96? It is because in a normal distribution, 95% of the data is contained within 1.96 standard deviations, and Central Limit Theorem states that sampling distributions are normally distributed.

Every value in a given confidence interval is a plausible value of the true θ_j in the population. The most important thing is if 0 is included within the confidence interval. $\theta = 0$ means that there is no causal effect.

Hypothesis Testing

In academia, we do not claim we have found a new theory, unless we are quite confident that the old theory was not true. The old theory is called our **null hypothesis**, often notated H_0. This is the old theory that we are trying to disprove.

- Most often, the "old theory" we are trying to disprove is that *there is no causal effect of* D on Y (since it is rare to study something that has already been proven). No relationship means that $\theta_j = 0$

The new theory we have come up with, and are trying to prove, is called the **alternate hypothesis**, often notated H_1 or H_a.

- In general, our new hypothesis is that t*here is a causal effect of* D on Y, or $\theta_j \neq 0$

We assume that the null hypothesis is true, unless we are 95% confident that we can reject the null hypothesis, and only then, can we accept the alternative hypothesis. How do we actually test these hypotheses? First, we have to calculate a t-test statistic:

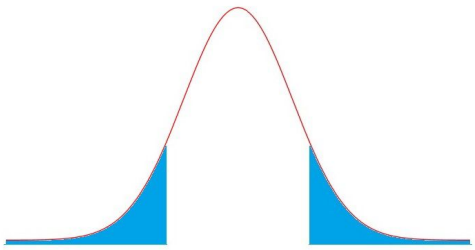
Key Definition: T-test Statistic

The t-test statistic basically tells us how far the parameter we tested is from 0, in terms of standard errors of the parameter:

$$t = \frac{\hat{\theta}_j}{\hat{se}(\hat{\theta}_j)}$$

Then, we calculate degrees of freedom:number of observations n, minus the number of variables k, then minus 1: $DF = n-k-1$. With the degrees of freedom, we can find the corresponding t-distribution, labeled t_{n-k-1}. Then, we start from the middle of that t distribution, and go the *number of standard errors* away based on the t-test statistic. We do this on both sides from the middle of the t-distribution.

Once we have found that point, we find the probability (area under the distribution) of a t-test statistic of ours, or more extreme, could occur. The figure below, with its blue highlighted area, shows this probability (called the p-value):



Key Definition: P-value

Essentially, a p-value is how likely we are to get a test statistic at or more extreme than the one we got for our estimated θ_j, given the null hypothesis is true.

- So if the p-value is very high, there is a high chance that the null hypothesis is true.
- If the p-value is very low, then there is a low chance that the null hypothesis is true

Generally, in the social sciences, if the p-value is less that 0.05 (5%), we can **reject the null hypothesis**, and conclude the alternate hypothesis.

2.4 Balance Table and Stratified Experiments

Balance Tables

As previously discussed, in order to use the difference of means estimator for the ATE, we must be confident that the control and treatment groups are similar to each other. This is because of the assumption:

$$\mathbb{E}[Y_{1i}|D_i = 1] \approx \mathbb{E}[Y_{1i}|D_i = 0] \quad \text{and} \quad \mathbb{E}[Y_{0i}|D_i = 1] \approx \mathbb{E}[Y_{0i}|D_i = 0]$$

If the treatment and control groups are not similar (especially in regard to key confounding variable values), this assumption will not hold.

To confirm this assumption is met, researchers will often show a **balance** table before or their estimation process. A balance table is essentially a table that shows the average difference in values of confounders in both treatment and control groups. This is to ensure that neither the treatment or control group differ too much in key confounding variables.

For example, below is a balance table:

	Confounder 1	Confounder 2	Confounder 3	Confounder 4
Control Group Values	11.503***	1.474***	0.405***	81.983***
	(0.196)	(0.060)	(0.015)	(2.980)
Treatment - Control	−0.069	−0.062	0.009	−1.760
	(0.241)	(0.074)	(0.019)	(4.179)
Num. obs.	562	565	560	565

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

The key row to look at is the *treatment-control* row. The numbers not in parentheses the difference between treatment and control for the corresponding confounder. The numbers in parentheses are the standard errors of the estimated difference. Starts (see legend below the table) show significance levels of a t-test.

Notice how not a single value in the *treatment-control* row is statistically significant (no stars). That is good! We want our treatment and control to be similar, so we do not want them to be significantly different.

If no *treatment-control* for key confounders is significantly different, then randomisation has suceeded, and indeed, our control and treatment group are similar. Thus, we can estimate the ATE as explained previously.

Blocking and Stratified Experiments

Blocking, also called stratified experiments, is an extension of the random experiment to deal with some common issues.

Imagine that you have four units in your experiment that you have to assign to treatment/control. Their pre-treatment outcomes are $Y_{0i} = \{2, 2, 8, 8\}$. This means that you have a 1/3 chance to end up with the random assignment of $\{2, 2\}$ in one group and $\{8, 8\}$ in the other group.

This is a major issue! After all, the core assumption of random experiments is that randomisation makes the treatment and control group similar, eliminating selection bias.

With blocking, you can prevent this from happening.

1. Before randomisation, you separate your sample of N units into J subgroups.
2. Within each group, randomly assign units to treatment and control group (essentially, smaller randomised experiments within a bigger experiment).

For example, we could divide our prior example into 2 subgroups: $\{2, 2\}$ and $\{8, 8\}$. Then, within each group, randomly assign one observation to treatment, and one to control. Thus, we are guaranteed to get units from both subgroups in both our treatment and control groups.

To estimate our effects for blocking experiments, we will have to take the weighted average of each subgroup's average treatment effect (ATE), with the weights being the proportion of units each group accounts for:

$$\tau_{ATE} = \sum_{j=1}^{J} \frac{N_j}{N} \tau_j$$

Where N is the total number of observations, J is the total number of subgroups, j is one of the subgroups, N_j is the number of units within subgroup j, and τ_j is the ATE of the subgroup j.

2.5 Validity and Limitations of Randomised Experiments

There are two types of validity in Randomised Experiments: Internal and External validity.

Internal validity is about if our experiment accurately captures the average causal effect of our units in our experiment. Essentially - did we estimate the causal effect correctly? Some things that can cause lack of internal validity include:

1. Failure of randomisation: if treatment and control groups are not similar, we violate assumptions of random experiments and that will include selection bias in our estimates.
2. Non-Compliance: Sometimes, our subjects that are assigned to treatment, refuse to comply with the treatment (we cannot force them to). This will mess up the average treatment effect, since some units did not properly undergo the treatment.
3. Attrition: Sometimes, outcomes cannot be measured for some study participants, for example, if they drop out or refuse to answer. This is concerning - because the people who drop out might have some common characteristic (confounding variable), and we will miss this entirely in our estimation.

External Validity is about the generalisation of our conclusions - we know the effect on our experimental subjects, but does this causal effect apply to other units across the world?

- For example, if we do a study in Japan, can we assume that the same effects are applicable in the US? South Africa?
- Generally to obtain this, you want the units included in your observation to be representative of the larger units you want to apply your results to. For example, if you are measuring the causal effect of some treatment on Americans, you want your subjects to be representative of Americans as a whole.

Finally, Randomised Experiments have some **limitations**.

1. Ethical limitations: sometimes, it is unethical to have units take potentially dangerous treatments, or have some units not undergo potential benefits of treatment. We are essentially randomly selecting what happens to people's lives.
2. Practical limitations: often, running experiments is just not possible. For example, let us say you want to see if democracy increases economic growth. To do this, you would need to randomly assign countries to democracy or autocracy (control) groups. But let us be honest, you can't force Canada to be a dictatorship against their will. Often, we will have to use **observational studies** - where we do not control assignment of treatment.

Part II

Multiple Linear Regression

Chapter 3

Linear Model and Interpreation

3.1 The Linear Regression Model

In the social sciences, randomisation is often not possible. Linear regression allows us to estimate a model with both our treatment and outcome variables, as well as a series of **control** variables. By including all confounding variables as control variables in our regression model, we can (in theory), isolate the effect of our explanatory variable on our outcome variable.

- In reality, since it is nearly impossible to include every possible confounding variable, we will need alternative strategies to estimate causal effects (discussed in volume II of the series).

The **response variable** (outcome variable) is notated Y. The **explanatory variable** (independent variable) is notated X. There is often more than one explanatory variable, so we denote them with subscripts $X_1, X_2, ..., X_k$. We sometimes also denote all explanatory variables as the vector $\overrightarrow{X}$

- Note: our treatment variable (for causal inference) D is considered one of the explanatory variables $\overrightarrow{X}$. We typically define the first of these explanatory variables X_1 as the treatment variable.

A linear regression model is the specification of the conditional distribution of Y, given $\overrightarrow{X}$. The linear regression model focuses on the **expected value** of the conditional distribution of Y given $\overrightarrow{X}$.

- I say **distribution** because there are often a range of Y outcomes, each with their own probabilities, for any given X. For example, if X was age and Y was income, at age $X = 30$, not every single 30 year old makes the same amount of money. There is some distribution of incomes Y at age $X = 30$.

Key Definition: Linear Regression Model

Take a set of observed data, with response variable Y, and a number of X variables for n number of observations. Thus, we will have n number of pairs of (X_i, Y_i) observations. The linear model takes the following form:

$$\mathbb{E}[Y_i|\overrightarrow{X}_i] = \alpha + \beta_1 X_{1i} + ... + \beta_k X_{ki}$$

- Where $\mathbb{E}[Y_i|\overrightarrow{X}_i]$ is the expected value of the conditional distribution $Y_i|\overrightarrow{X}_i$.
- Where the distribution of $Y_i|\overrightarrow{X}_i$ has a variance $Var(Y_i|\overrightarrow{X}_i) = \sigma^2$.
- Where the parameters of the model are the denoted by the vector $\overrightarrow{\beta}$, and contain $\alpha, \beta_1, ..., \beta_k$.

Key Definition: Linear Regression Model

We can also write the linear model for the value of any point Y_i in our data:

$$Y_i = \alpha + \beta_1 X_{1i} + ... + \beta_k X_{ki} + \epsilon_i$$

- Where ϵ_i is the error term function - that determines the error for each unit i.
- Essentially, ϵ_i is another way to think about the conditional distribution of $Y_i|\overrightarrow{X_i}$, and how not every 30 year old makes the exact same income - there is some variation (and error).

In our model, we have parameters $\alpha, \beta_1, ..., \beta_k$ that need to be estimated (based on our data) in order to create a best-fit line we can actually use.

We estimate the parameters and fit the model by using our observed data points $(Y_i, \overrightarrow{X_i})$, and fitting a best fit line to these points. Our resulting model, called the **fitted values**, should take the following form:

$$\hat{Y}_i = \hat{\alpha} + \hat{\beta}_1 X_{1i} + ... + \hat{\beta}_k X_{ki}$$

- Where $\hat{Y}_i$ is our prediction of the value of Y, given any set of $\overrightarrow{X}$ values.
- Notice the error term ϵ_i is not present. This is the expected value of ϵ_i is $\mathbb{E}[\epsilon_i] = 0$.

We will discuss how parameters $\alpha, \beta_1, ..., \beta_k$ are estimated, and how the best-fit line is created, in the next chapter on the ordinary least squares estimator (OLS).

3.2 Interpretations of Coefficients

When there are multiple explanatory variables $X_1, X_2, ..., X_k$, how do we interpret parameters $\hat{\alpha}$ and $\hat{\beta}_1, \hat{\beta}_2, ..., \hat{\beta}_k$?

- I will define $\hat{\beta}_j$ as any one of $\hat{\beta}_1, ..., \hat{\beta}_k$, multiplied to explanatory variable X_j.

First, what does $\hat{\beta}_j$ mean. Consider the regression equation $\hat{Y}_i = \hat{\alpha} + \hat{\beta}_1 X_{1i} + ... + \hat{\beta}_j X_{ji} + ... + \hat{\beta}_k X_{ki}$.

If we find the partial derivative in respect to X_{ji} of the above equation, we get:

$$\begin{aligned}
\frac{\partial \hat{Y}_i}{\partial X_{ji}} &= \frac{\partial \hat{Y}_i}{\partial X_{ji}} \left[\hat{\alpha} + \hat{\beta}_1 X_{1i} + ... + \hat{\beta}_j X_{ji} + ... + \hat{\beta}_k X_{ki}\right] \\
&= 0 + 0 + ... + \hat{\beta}_j + .. + 0 \\
&= \hat{\beta}_j
\end{aligned}$$

This shows that $\hat{\beta}_j$ is the rate of change between X_{ij} and $\hat{Y}_i$, holding other explanatory variables $X_{1i}...X_{ki}$ constant. This is the case with any $\hat{\beta}_j$ parameter $j = 1, ..., k$.

Interpretation of $\hat{\beta}_j$

When X_j increases by one unit, there is an expected $\hat{\beta}_j$ unit change in Y, holding all other explanatory variables constant.

Second, what does intercept $\hat{\alpha}$ mean? Let us take a regression equation, and input $\overrightarrow{X} = 0$:

$$\begin{aligned}\mathbb{E}[\hat{Y}_i|\overrightarrow{X} = 0] &= \hat{\alpha} + \hat{\beta}_1 X_{1i} + ... + \hat{\beta}_j X_{ji} + ... + \hat{\beta}_k X_{ki} \\ &= \hat{\alpha} + \hat{\beta}_1(0) + ... + \hat{\beta}_j(0) + ... + \hat{\beta}_k(0) \\ &= \hat{\alpha}\end{aligned}$$

This shows that $\hat{\alpha} = \hat{Y}_i$ when $\overrightarrow{X} = 0$.

> **Interpretation of $\hat{\alpha}$**
>
> When all explanatory variables equal 0, the expected value of Y is $\hat{\alpha}$

Interpreting in Terms of Standard Deviation

Sometimes, it is hard to understand what changes in Y and X mean in terms of units.

- For example, if we are measuring "democracy", what does a 5 unit change in democracy mean? Is that a lot?

We can add more relevant detail by expressing the change of Y and X in standard deviations.

How do we calculate this? Well, let us solve for the change in $\hat{Y}$ given $X = x$ and $X = x + \sigma_X$. This will tell us how much $\hat{Y}$ changes by given a increase of one standard deviation in X.

$$\begin{aligned}\mathbb{E}[\hat{Y}_i|X = x + \sigma_X] - \mathbb{E}[\hat{Y}_i|X = x] &= [\hat{\alpha} + \hat{\beta}(x + \sigma_X)] - [\hat{\alpha} + \hat{\beta}(x)] \\ &= \hat{\alpha} + \hat{\beta}x + \hat{\beta}\sigma_X - \hat{\alpha} - \hat{\beta}x \\ &= \hat{\beta}\sigma_X\end{aligned}$$

To get the change in $\hat{Y}$ in terms of standard deviations of Y, we just divide $\hat{\beta}\sigma_X$ by σ_Y.

> **Interpretation in Terms of Standard Deviation**
>
> For a one-std. deviation increase in X_j, there is an expected $\hat{\beta}\sigma_X/\sigma_Y$-std. deviation change in Y.

Binary Y Variable Interpretation

If our response variable is binary, (i.e. Y only has two values, 0 and 1), then our interpretation differs slightly.

We treat Y as a variable of two categories, $Y = 0$ and $Y = 1$. The output $\hat{Y}_i$ indicates the probability of a specific observation i of being in the $Y = 1$ category - we can also interpret probability in percentages by multiplying by 100.

> **Interpretation with Binary Y Variable**
>
> For a one-unit increase in X_j, there is an expected $\hat{\beta}_j \times 100$ percentage point change in the probability of being in category $Y = 1$.
>
> $\hat{\alpha}$ is the expected probability of being in category $Y = 1$ when all explanatory variables equal 0.

This model with binary Y is also called the **linear probability model**.

Binary Explanatory Variables

Binary explanatory variables are variables with 2 values, 0 and 1.

- These are extremely common in econometrics - as our treatment variable D often takes two states: $D = 1$ is the treatment group, and $D = 0$ is the control group. We know that in a regression, D is included as an explanatory variable X.

Binary explanatory variables will change the interpretations of our coefficients. We can "solve" for these interpretations given the standard linear model $E[Y] = \alpha + \beta X$, given X has two categories $X = 0, X = 1$:

$$E[Y|X = 0] = \alpha + \beta(0) = \alpha$$
$$E[Y|X = 1] = \alpha + \beta(1) = \alpha + \beta$$
$$E[Y|X = 1] - E[Y|X = 0] = (\alpha + \beta) - \alpha = \beta$$

Thus, we can interpret the coefficients α and β as follows:

> **Intepretation of Binary Explanatory Variables**
>
> - α is the expected value of Y given an observation in category $X = 0$
> - $\alpha + \beta$ is the expected value of Y given an observation in category $X = 1$
> - β is the expected difference in Y between the categories $X = 1$ and $X = 0$

We can see that β is measuring the difference between the two categories.

- In fact, β actually becomes a **difference-in-means** test, meaning that if β is statistically significant, we can conclude a significant difference in the mean Y between the two categories.

Remember that our ATE in our randomised experiment was estimated with a difference in means. Thus, if we include all possible confounding variables, the β coefficient of D will estimate the ATE.

3.3 Model Summary Statistics

Aside from coefficients, the Linear Regression model also has a few summary statistics that can help us interpret the effectiveness and fit of our model.

Estimated Residual Standard Deviation

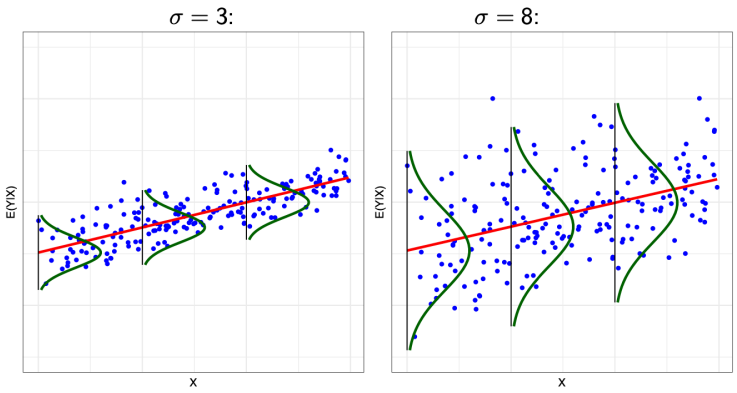
We can derive the estimate of the **residual variance** σ^2 with this formula:

$$\hat{\sigma}^2 = \frac{\sum(Y_i - \hat{Y}_i)^2}{n - k - 1}$$

But what is the residual variance? Recall our regression model: $Y_i = \alpha + \beta_1 X_{1i} + ... + \beta_k X_{ki} + \epsilon_i$

We know that $\epsilon_i \sim \mathcal{N}(0, \sigma^2)$. Our estimate of the residual variance $\hat{\sigma}^2$ is our estimate of the variance of the error term ϵ_i's variance. More intuitively, it explains how spread out observed values of Y are from our prediction value $\hat{Y} = E(Y|X)$.

The figure below better showcases this in 2 different models. The red lines are our predicted regression line, and the green lines represent the distribution of our error term ϵ_i:



The residual standard deviation $\hat{\sigma}$ (square root of variance) is consistent throughout a model. This is one of the assumptions of the linear regression model - that errors are consistently distributed, no matter the value of X. This assumption is called **homoscedasticity**.

If $\hat{\sigma}$ varies depending on the value of X, then that is called **heteroscedasticity**. When this occurs, it is often a suggestion that our relationship may not be linear - and we perhaps need to try a few transformations. We will get into transformations in a later chapter.

Total Sum of Squares

The total sum of squares is the total amount of sample variation in Y:

$$\begin{aligned} TSS &= \sum (Y_i - \bar{Y})^2 \\ &= \sum (\hat{Y}_i - \bar{Y})^2 + \sum (Y_i - \hat{Y}_i)^2 \end{aligned}$$

Where TSS is the total sum of squares, SSM $\sum (\hat{Y}_i - \bar{Y})^2$ is the model sum of squares, and SSE $\sum (Y_i - \hat{Y}_i)^2$ is the sum of squared errors (that we used to fit the model).

SSM (model sum of squares) represents the part of the variation of Y that is explained by the model, while SSE (sum of squared errors) represents the part of the variation of Y that is not explained by the model (hence, why it is called error).

R-Squared Statistic

R-squared is one of the key summary statistics of our model.

Key Definition: R-Squared

R-squared R^2 is a measure of the percentage of variation in Y, that is explained by our model (with our chosen explanatory variables). The percentage of variation in Y explained by our model would be:

$$R^2 = \frac{SSM}{TSS} = \frac{\sum (\hat{Y}_i - \bar{Y})^2}{\sum (Y_i - \bar{Y})^2}$$

Since R^2 shows how much of the variation in Y our model explains, it is often used as a metric for how good our model is - however, don't overly focus on R^2, it is just one metric with its benefits and drawbacks.

3.4 Hypothesis Testing

Robust Standard Errors

So far, we have focused on using standard errors of parameter estimates that were introduced in section 2.2.

However, these "default" standard errors rely on the assumption of **homoscedasticity** (see section 3.4). However, homoscedasticity is frequently violated.

When homoscedasticity is violated, we have to use an alternative estimation of the standard error: **heteroscedasticity-robust standard errors**.

- These robust standard errors are typically larger than the homoscedastic "default" standard errors.
- Because homoscedasticity is frequently violated, and that robust standard errors are more "conservative", we typically use robust standard errors as the "default" in econometrics.

The calculation of robust-standard errors will be done with calculators, and it is not important to know how the mathematics work.

Confidence Intervals

We previously discussed confidence intervals in section 2.4. The mechanics are practically the same, but we replace the sample average treatment effect with $\hat{\beta}_j$ as our sample estimate.

$$\hat{\beta}_j \pm 1.96 \times \hat{se}(\hat{\beta}_j)$$

Hypothesis Testing of Parameters

We previously discussed hypothesis testing in section 2.5. The mechanics are practically the same, but we replace the sample average treatment effect with $\hat{\beta}_j$ as our sample estimate. Generally, for regressions, our hypotheses that we test are:

- $H_0 : \beta_j = 0$ - i.e. there is no relationship between X_j and Y
- $H_1 : \beta_j \neq 0$ - i.e. there is a relationship between X_j and Y

Just like previously discussed in section 2.5, we calculate a t-statistic:

$$t = \frac{\hat{\beta}_j}{\hat{se}(\hat{\beta}_j)}$$

The t-test statistic tells us how far the estimate is from 0, in terms of standard errors of the estimate.

Then, we have to consult a t-distribution (see section 2.5). We find the probability (area under the distribution) of a t-test statistic of ours, or more extreme, could occur. This is the p-value: how likely we are to get a test statistic at or more extreme than the one we got for our estimated β_j, given the null hypothesis is true.

- So if the p-value is very high, there is a high chance that the null hypothesis is true.
- If the p-value is very low, then there is a low chance that the null hypothesis is true

Generally, in the social sciences, if the p-value is less that 0.05 (5%), we can **reject the null hypothesis**, and conclude the alternate hypothesis.

F-Tests of Nested Models

The **F-test of Nested Models** allows us to compare different regression models. We use a smaller model as our null hypothesis, and a larger model (containing the smaller model) as our alternative hypothesis. More mathematically:

$$M_0 : E[Y] = \alpha + \beta_1 X_1 + ... + \beta_g X_g$$
$$M_a : E[Y] = \alpha + \beta_1 X_1 + ... + \beta_g X_g + \beta_{g+1} X_{g+1} + ... + \beta_k X_k$$

Importantly, all explanatory variables in model M_0 must also be in M_a (hence "nested").

The F-test uses the F-test statistic. This statistic compared the R^2 values of the two models. Let us say the R^2 value of M_0 is notated R_0^2, and the R^2 value of M_a is notated as R_a^2. The F-test statistic essentially measures the difference $R_a^2 - R_0^2$. If the difference is sufficiently large, that means the M_a model has significantly more explanatory power than M_0.

Mathematically, the F-test statistic is as follows, with k_a being the number of explanatory variables in the alternate hypothesis:

$$F = \frac{R^2_{\text{change}}/df_{\text{change}}}{(1 - R_a^2)/[n - (k_a + 1)]}$$

The sampling distribution of the F-statistic is the F distribution with parameters $k - a - k_0$ and $n - (k_a + 1)$ degrees of freedom. We then obtain the p-value from this distribution. The p-values of the F-statistic show the following:

- If the p-value is very small, that means R_a^2 is significantly larger than R_0^2. This is evidence against model M_0, and in favour of the larger model M_a
- If the p-value is large, that means R_a^2 is not much larger than R_0^2. This means there is no evidence against M_0, and M_a is not the statistically significantly better model.

F-tests of nested models can help us determine if we should include certain extra explanatory variables. If our model with more variables is statistically significant, it is an indication that we should include those extra variables.

3.5 Interpreting Regression Tables

In most research papers, regression results will be presented in a table. A typical regression table will look like this:

	Education	Mosques per 1,000	Prop.in Poverty	Total Budget
Intercept	11.503***	1.474***	0.405***	81.983***
	(0.196)	(0.060)	(0.015)	(2.980)
Treatment	−0.069	−0.062	0.009	−1.760
	(0.241)	(0.074)	(0.019)	(4.179)
Num. obs.	562	565	560	565
R^2 (full model)	0.000	0.001	0.000	0.000
Adj. R^2 (full model)	−0.002	−0.001	−0.001	−0.002

$^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$

Table 3.1: Coefficients estimated with OLS estimator. Robust standard errors provided in Parentheses

Each column in the table represents a different model. In this table, *Education*, *Mosques per 1,000*, *Prop in Poverty*, and *Total budget* are the different models.

- If the models have different outcome variables (the paper should make this clear), the column names are typically the outcome variable names. This table is a case of that.
- However, often, the outcome variables are the same between all columns, and each is a slightly different model that indicates how coefficients change with different control variables.

In the table, we can see the rows *Intercept* and *Treatment.*

- The *Intercept* row represents the intercept $\hat{\alpha}$. The main number is the coefficient estimate, and the parentheses include the robust standard errors.
- The *Treatment* row represents the $\hat{\beta}$ coefficient that is multiplied to the variable *Treatment*. The main number is the coefficient estimate, and the parentheses include the robust standard errors.
- If there are more explanatory variables, they will be included in further rows, each indicated by the name of the variable in question.
- The stars (***) represent significance level (as indicated in the legend at the bottom of the table).

Below, we have some model summary statistics, including the number of observations, R^2, and adjusted R^2 numbers.

This table is a good example of how a typical regression table is made - so if you ever run a regression for a research paper, this is how you would report your results.

Implementation in R

We will first need the *fixest* package. If you have never used it before, install it as follows:

```
install.packages("fixest")
```

Once you have installed it (or previously installed it), load it every time you open R as follows:

```
library(fixest)
```

Regression

We use the *feols()* function to run a **regression**: The general syntax is as follows:

```
model_name <- lm(Y ~ X1 + X2 + X3, data = mydata, se = "hetero")
summary(model_name)
```

- Replace *model_name* with your model name, *Y* with the name of your response variable, *X1, X2…* with the name of your explanatory variable, and *mydata* with the name of your dataset.
- Add additional explanatory variables with more + signs, and you can remove down to one *X*.
- The final argument, *se = "hetero"*, tells R to calculate heteroscedasticity-robust standard errors, which are standard in econometrics. However, if you can prove homoscedasticity, you can remove this argument for default standard errors.

We can also use the base-R *lm()* function, however, this function is unable to calculate robust standard errors. The syntax for *lm()* is the same, just without the *se = "hetero"* argument.

Confidence Intervals

To calculate confidence intervals, we can use the *confint()* command, and simply input the name of our model within:

```
confint(model)
```

F-Tests of Nested Models

If we want an **F-test** between two models, we can use the *anova()* function, replacing *model1* with the name of the null hypothesis model M_0, and replacing *model2* with the name of the alternative hypothesis model M_a.

```
anova(model1, model2)
```

Implementation in STATA

Regression

To run **regression** in Stata, use the *regress* function:

```
regress Y X1 X2 X3, robust
```

- Replace *Y* with the name of your response variable, *X1, X2…* with the name of your explanatory variable.
- Add additional explanatory variables by simply adding more seperated by a space, and you can remove down to one explanatory variable.
- The final argument, *robust*, tells Stata to calculate heteroscedasticity-robust standard errors, which are standard in econometrics. However, if you can prove homoscedasticity, you can remove this argument for default standard errors.

Confidence Intervals

To calculate **confidence intervals**, we first use the *collect* function to create a collection, *collect* prefix to store our coefficients from our regression, then *collect layout* to display the results:

```
collect create confidence
collect _r_b _r_ci: regress Y X1 X2 X3, robust
collect layout (colname) (result)
```

Chapter 4

Ordinary Least Squares Estimator

4.1 Simple Linear Regression Estimation

How do we estimate our parameters $\alpha, \beta_1, ..., \beta_k$? Obviously, we want our model to be accurate - so we can estimate it through reducing the errors of models (more specifically, the sum of squared errors).

Key Definition: Sum of Squared Errors

The **sum of squared errors** is as follows:

$$SSE = \sum (Y_i - \hat{Y}_i)^2 = \sum (Y_i - \hat{\alpha} - \hat{\beta} X_{1i} - ... - \hat{\beta}_k X_{ki})$$

Or more intuitively, it is exactly as it sounds - find the error of our prediction $Y_i - \hat{Y}$, square that difference, then sum up for all units i in our data.

- Why squared? Well, because we do not care about the direction of our errors (positive or negative), just the size of them. Thus, squaring removes the negative signs so we are only concerned with magnitude.
- Then why not absolute value? There are a few reasons, but generally the primary reason is estimation is much more difficult with absolute value since an absolute value function is not differentiable at its vertex.

The **Ordinary Least Squares (OLS) Estimator** estimates our parameters $\alpha, \beta_1, ..., \beta_k$ through finding the values of $\alpha, \beta_1, ..., \beta_k$ that minimizes the sum of squared errors for our predictions.

A bivariate regression is a regression model with one explanatory variable X, and a fitted simple linear regression takes the form $\hat{Y}_i = \hat{\alpha} + \hat{\beta} X_i$.

Let us define the sum of squared errors as function S:

$$S(\hat{\alpha}, \hat{\beta}) = \sum_{i=1}^{n} (Y_i - \hat{\alpha} - \hat{\beta} X_i)^2$$

The OLS estimator wants to find the parameters that **minimise the sum of squared errors**:

$$(\hat{\alpha}, \hat{\beta}) = \arg\min_{\hat{\alpha}, \hat{\beta}} \sum_{i=1}^{n} (Y_i - \hat{\alpha} - \hat{\beta} X_i)^2 = \arg\min_{\hat{\alpha}, \hat{\beta}} S(\hat{\alpha}, \hat{\beta})$$

Parameter $\hat{\alpha}$

Let us first look at the parameter $\hat{\alpha}$. How do we find what value $\hat{\alpha}$ minimises the sum of squared errors? We know through calculus, that deriving the function to find the first order condition can accomplish this:

$$\frac{\partial S(\hat{\alpha},\hat{\beta})}{\partial \hat{\alpha}} = \frac{\partial S(\hat{\alpha},\hat{\beta})}{\partial \hat{\alpha}} \left[\sum_{i=1}^{n}(Y_i - \hat{\alpha} - \hat{\beta}X_i)^2\right]$$

First, ignore the summation. The partial derivative of the internal section, using chain rule, is the following:

$$\frac{\partial}{\partial \hat{\alpha}}\left[(Y_i - \hat{\alpha} - \hat{\beta}X_i)^2\right] = -2(Y_i - \hat{\alpha} - \hat{\beta}X_i)$$

But how do we deal with the summation? We know that there is the sum rule of derivatives $[f(x)+g(x)]' = f'(x) + g'(x)$. Thus, we know we just sum up the derivatives:

$$\frac{\partial S(\hat{\alpha},\hat{\beta})}{\partial \hat{\alpha}} = \sum_{-i=1}^{n}\left[-2(Y_i - \hat{\alpha} - \hat{\beta}X_i)\right] = -2\sum_{i=1}^{n}(Y_i - \hat{\alpha} - \hat{\beta}X_i)$$

To find the value of $\hat{\alpha}$ that creates the minimum value of the SSE, we set the first order derivative equal to 0. We can ignore the -2, since if the sum is equal to 0, then the -2 will have no effect. Now, using properties of summation, isolate $\hat{\alpha}$ as follows:

$$\begin{aligned}
\sum_{i=1}^{n}(Y_i - \hat{\alpha} - \hat{\beta}X_i) &= 0 \\
\sum_{i=1}^{n}Y_i - n\hat{\alpha} - \hat{\beta}\sum_{i=1}^{n}X_i &= 0 \\
-n\hat{\alpha} &= -\sum_{i=1}^{n}Y_i + \hat{\beta}\sum_{i=1}^{n}X_i \\
\hat{\alpha} &= \frac{1}{n}\sum_{i=1}^{n}Y_i - \frac{1}{n}\hat{\beta}\sum_{i=1}^{n}X_i \\
\hat{\alpha} &= \bar{Y} - \hat{\beta}\bar{X}
\end{aligned}$$

The final step converting to $\bar{Y}$ and $\bar{X}$ is because of the mathematical definition of average. We will plug this $\hat{\alpha}$ equation into our solution for $\hat{\beta}$ to solve that. Once we solve $\hat{\beta}$, we will come back and calculate $\hat{\alpha}$'s value.

Parameter $\hat{\beta}$

Let us find the $\hat{\beta}$ that minimises S by taking the partial derivative of S in respect to $\hat{\beta}$ and setting it equal to 0. This is almost the same as before - use chain rule, then use sum rule to get the deriative:

$$\frac{\partial S(\hat{\alpha},\hat{\beta})}{\partial \hat{\beta}} = \sum_{i=1}^{n}\left[-2X_i(Y_i - \hat{\alpha} - \hat{\beta}X_i)\right] = -2\sum_{i=1}^{n}X_i(Y_i - \hat{\alpha} - \hat{\beta}X_i)$$

Now, let us plug in our previously solved $\hat{\alpha} = \bar{Y} - \hat{\beta}\bar{X}$, and we get:

$$\frac{\partial S(\hat{\alpha},\hat{\beta})}{\partial \hat{\beta}} = -2\sum_{i=1}^{n}\left[X_i(Y_i - [\bar{Y} - \hat{\beta}\bar{X}] - \hat{\beta}X_i)\right]$$

Once again, the -2 does not matter as same reason as before. Set equal to 0 to solve for the value of $\hat{\beta}$ that minimises SSE:

$$0 = \sum_{i=1}^{n} \left[X_i (Y_i - [\bar{Y} - \hat{\beta}\bar{X}] - \hat{\beta} X_i) \right]$$
$$0 = \sum_{i=1}^{n} \left[X_i (Y_i - \bar{Y} - \hat{\beta}(X_i - \bar{X})) \right]$$
$$0 = \sum_{i=1}^{n} \left[X_i (Y_i - \bar{Y}) - X_i \hat{\beta}(X_i - \bar{X}) \right]$$
$$0 = \sum_{i=1}^{n} X_i (Y_i - \bar{Y}) - \hat{\beta}_1 \sum_{i=1}^{n} X_i (X_i - \bar{X})$$

Here are a few properties on summation that will help us solve this equation:

$$\sum_{i=1}^{n} (X_i - \bar{X}) = 0$$
$$\sum_{i=1}^{n} X_i (Y_i - \bar{Y}) = \sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})$$
$$\sum_{i=1}^{n} X_i (X_i - \bar{X}) = \sum_{i=1}^{n} (X_i - \bar{X})^2$$

With these rules, we can transform what we had before into:

$$0 = \sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y}) - \hat{\beta} \sum_{i=1}^{n} (X_i - \bar{X})^2$$

Key Definition

Then solve for $\hat{\beta}$ to get the **OLS estimator** for bivariate regression:

$$\hat{\beta} = \frac{\sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})}{\sum_{i=1}^{n} (X_i - \bar{X})^2} = \frac{Cov(X, Y)}{Var(X)} = \frac{\sigma_{XY}}{\sigma_x^2}$$

If we want $\hat{\alpha}$, we just plug back into $\hat{\alpha} = \bar{Y} - \hat{\beta}\bar{X}$ that we calculated earlier. With this, we now have all parameters estimated and a best fit line ready to use!

4.2 Multiple Regression Estimation

Multiple regression, as introduced previously, allows us to add additional control variables. Similar to our bivariate regression (but with additional variables), our minimisation condition is:

$$(\hat{\alpha}, \hat{\beta}_1, \hat{\beta}_2, ...) = \arg \min_{(\hat{\alpha}, \hat{\beta}_1, \hat{\beta}_2, ...)} (Y_i - \hat{\alpha} - \hat{\beta}_1 X_{1i} - \hat{\beta}_2 X_{2i} ...)^2$$
$$= \arg \min_{(\hat{\alpha}, \hat{\beta}_1, \hat{\beta}_2, ...)} S(\hat{\alpha}, \hat{\beta}_1, \hat{\beta}_2, ...)$$

Taking the partial derivatives of each parameter as before, and setting them equal to 0, we get these first order conditions::

$$-2\sum_{i=1}^{n}(Y_i - \hat{\alpha} - \hat{\beta}_1 X_{1i} - \hat{\beta}_2 X_{2i}...) = 0$$
$$-2\sum_{i=1}^{n} X_{1i}(Y_i - \hat{\alpha} - \hat{\beta}_1 X_{1i} - \hat{\beta}_2 X_{2i}...) = 0$$
$$-2\sum_{i=1}^{n} X_{2i}(Y_i - \hat{\alpha} - \hat{\beta}_1 X_{1i} - \hat{\beta}_2 X_{2i}...) = 0$$
and so on for $X_{3i}, ..., X_{ki}$

The difficulty is that this is essentially a system of equations with $k+1$ variables and equations, with a bunch of summation notation, which is nearly impossible to solve. However, we have another method to solve this: Linear Algebra.

Regression With Linear Algebra

We start with the linear model:

$$Y_i = \alpha + \beta_1 X_{1i} + \beta_2 X_{2i} + ... + \beta_k X_{ki} + \epsilon_i$$

The ith observation can be written in vector form as following:

$$Y = X_i'\beta + \epsilon_i, \text{ where } \beta = \begin{bmatrix} \alpha \\ \beta_1 \\ \vdots \\ \beta_k \end{bmatrix} \text{ and } X_i = \begin{bmatrix} 1 \\ X_{1i} \\ \vdots \\ X_{ki} \end{bmatrix}$$

- The X_i' in the equation is the transpose of X_i, to make matrix multiplication possible.
- The first element of the X_i matrix is 1, since $1 \times \alpha$ gives us the first parameter in the linear model.

Since our model has n different observations of i, we can express this into vector form, with the X_i' and β being vectors within a vector.

$$\begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix} = \begin{pmatrix} X_1'\beta + \epsilon_1 \\ X_2'\beta + \epsilon_2 \\ \vdots \\ X_n'\beta + \epsilon_n \end{pmatrix} = \begin{pmatrix} X_1'\beta \\ X_2'\beta \\ \vdots \\ X_n'\beta \end{pmatrix} + \begin{pmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{pmatrix}$$

Since β vector appears as a common factor for all observations $i = 1, ..., n$, we can factor it out and have an equation:

$$\begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix} = \begin{pmatrix} X_1' \\ X_2' \\ \vdots \\ X_n' \end{pmatrix} \beta + \begin{pmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{pmatrix}$$

We can expand the $X_1', ..., X_n'$ vector into a matrix. Remember that each $X_1', ..., X_n'$ is already a vector of different explanatory variables. Thus, we have a model in the form:

$$Y = X\beta + \epsilon, \text{ where } X = \begin{bmatrix} 1 & x_{21} & ... & x_{k1} \\ 1 & x_{22} & ... & x_{k2} \\ \vdots & \vdots & \vdots & \vdots \\ 1 & x_{2n} & ... & x_{kn} \end{bmatrix}$$

- Where the notation for elements of X is X_{ki}, with i being the unit of observation $i = 1, ...n$, and k being the explanatory variables index.
- Where Y and ϵ are $n \times 1$ vectors (as seen above), and β is a $k \times 1$ vector.
- The first row of X is a vector of 1, which exists because these 1's are multiplied with α in our model.

OLS Estimator with Linear Algebra

Let us define our estimation vector $\hat{\beta}$ as:

$$\hat{\beta} = \arg\min_b (Y - Xb)'(Y - Xb) = \arg\min_b S(b)$$

We can expand $S(b)$ as follows:

$$S(b) = Y'Y - b'X'Y - Y'Xb + b'X'Xb$$
$$Y'Y - 2b'X'Y + b'X'Xb$$

Taking the partial derivative in respect to b, then setting equal to 0, we get:

$$\frac{\partial S(b)}{\partial b}\bigg|_{\hat{\beta}} = \begin{pmatrix} \frac{\partial S(b)}{\partial b_1} \\ \vdots \\ \frac{\partial S(b)}{\partial b_k} \end{pmatrix}\bigg|_{\hat{\beta}} = 0$$

Differentiating with the vector b yields:

$$\frac{\partial S(b)}{\partial b} = -2X'Y + 2X'Xb$$

Evaluted at $\hat{\beta}$, the derivatives should equal zero (since first order condition of finding minimums):

$$\frac{\partial S(b)}{\partial b}\bigg|_{\hat{\beta}} = -2X'Y + DX'X\hat{\beta} = 0$$

Key Definition

When assuming $X'X$ is invertable, our OLS estimator solution for $\hat{\beta}$ is:

$$\hat{\beta} = (X'X)^{-1}X'Y$$

Once we have estimates of $\hat{\beta}$, we can plug them into our linear model to obtain fitted values:

$$\hat{Y} = X\beta = X(X'X)^{-1}X'Y$$

4.3 OLS and Difference-in-Means Estimator

In the previous chapter, we dicussed how a linear regression with binary X variable results in coefficient β being a difference-in-means test.

Let us prove that the bivariate OLS estimator with binary X is equivalent to a difference in means. In section 4.1, we proved the OLS estimator produces the following $\hat{\beta}$ solution for simple linear regression:

$$\hat{\beta} = \frac{\sum_{i=1}^{N}(X_i - \bar{X})(Y_i - \bar{Y})}{\sum_{i=1}^{N}(X_i - \bar{X})^2}$$

Let us focus on the numerator of the $\hat{\beta}$ OLS solution. Let us expand out the numerator as follows:

$$\begin{aligned}\sum_{i=1}^{N}(X_i - \bar{X})(Y_i - \bar{Y}) &= \sum_{i=1}^{N}[X_iY_i - X_i\bar{Y} - X_i\bar{Y} + \bar{X}\bar{Y}] \\ &= \sum_{i=1}^{N} X_iY_i - \sum_{i=1}^{N} X_i\bar{Y} - \sum_{i=1}^{N} \bar{X}Y_i + \sum_{i=1}^{N} \bar{X}\bar{Y}\end{aligned}$$

We know that X is a binary variable with $X = 1$ being the treatment state t, and $X = 0$ being the control state c. N indicates the number of observations, and N_t indicates number of observations in treatment group. We can evaluate the 4 summations we have found from expanding, and simplify further:

$$\begin{aligned}\sum_{i=1}^{N} X_iY_i - \sum_{i=1}^{N} X_i\bar{Y} - \sum_{i=1}^{N} \bar{X}Y_i + \sum_{i=1}^{N} \bar{X}\bar{Y} &= N_t\bar{Y}_t - N_t\bar{Y} - N\left(\frac{N_t}{N}\right)\bar{Y} + N\left(\frac{N_t}{N}\right)\bar{Y} \\ &= N_t\bar{Y}_t - N_t\bar{Y} - N_t\bar{Y} + N_t\bar{Y} \\ &= N_t\bar{Y}_t - N_t\bar{Y} \\ &= N_t(\bar{Y}_t - \bar{Y})\end{aligned}$$

A weighted average formula means $\bar{Y} = \frac{1}{N}(N_t\bar{Y}_t + N_c\bar{Y}_c)$. We can substitute $\bar{Y}$ in our numerator with that as follows:

$$\begin{aligned}N_t(\bar{Y}_t - \bar{Y}) &= N_t\left(Y_t - \frac{1}{N}(N_t\bar{Y}_t + N_c\bar{Y}_c)\right) \\ &= N_t\bar{Y}_t - \frac{N_t}{N}(N_t\bar{Y}_t + N_c\bar{Y}_c) \\ &= N_t\bar{Y}_t - \frac{N_t^2\bar{Y}_t}{N} - \frac{N_tN_c\bar{Y}_c}{N} \\ &= \bar{Y}_t\left(N_t - \frac{N_t^2}{N}\right) - \bar{Y}_c\left(\frac{N_tN_c}{N}\right)\end{aligned}$$

We know that $N_c = N - N_t$, thus $\frac{N_tN_c}{N} = \frac{N_t(N-N_t)}{N} = N_t - \frac{N_t^2}{N}$. Plugging that in to the numerator, and simplifying, we get:

$$\begin{aligned}\bar{Y}_t\left(N_t - \frac{N_t^2}{N}\right) - \bar{Y}_c\left(\frac{N_tN_c}{N}\right) &= \bar{Y}_t\left(N_t - \frac{N_t^2}{N}\right) - \bar{Y}_c\left(N_t - \frac{N_t^2}{N}\right) \\ &= \left(N_t - \frac{N_t^2}{N}\right)(\bar{Y}_t - \bar{Y}_c)\end{aligned}$$

Thus, our $\hat{\beta}$ now looks like (putting in the changes we did to the numerator):

$$\hat{\beta} = \frac{\left(N_t - \frac{N_t^2}{N}\right)(\bar{Y}_t - \bar{Y}_c)}{\sum_{i=1}^{N}(X_i - \bar{X})^2}$$

Now, let us expand the denominator:

$$\sum_{i=1}^{N}(X_i - \bar{X})^2 = \sum_{i=1}^{N} X_i^2 - \sum_{i=1}^{N} X_i\bar{X} - \sum_{i=1}^{N} X_i\bar{X} + \sum_{i=1}^{N} \bar{X}^2$$

Using the same ideas as previously in the numerator, we can solve the 4 separate sums here, and simplify the denominator further:

$$\begin{aligned}\sum_{i=1}^{N} X_i^2 - \sum_{i=1}^{N} X_i\bar{X} - \sum_{i=1}^{N} X_i\bar{X} + \sum_{i=1}^{N} \bar{X}^2 &= N_t - N_t\frac{N_t}{N} - N_t\frac{N_t}{N} + N\left(\frac{N_t}{N}\right)^2 \\ &= N_t - \frac{N_t^2}{N} - \frac{N_t^2}{N} + \frac{N_t^2}{N} \\ &= N_t - \frac{N_t^2}{N}\end{aligned}$$

Thus, putting our simplified denominator in, our $\hat{\beta}$ now looks like:

$$\hat{\beta} = \frac{\left(N_t - \frac{N_t^2}{N}\right)(\bar{Y}_t - \bar{Y}_c)}{\left(N_t - \frac{N_t^2}{N}\right)}$$

Then simplifying and cancelling out:

$$\hat{\beta} = \bar{Y}_t - \bar{Y}_c$$

Our final estimate of $\hat{\beta}$ with OLS is thus equivalent to difference of means.

4.4 Gauss-Markov Theorem, Exogeniety, and Homoscedasticity

The OLS estimator is used because of key properties given by the Gauss-Markov Theorem.

Key Definition: Gauss-Markov Theorem

The Gauss-Markov Theorem states that the OLS esimator is the best linear unbiased estimate (BLUE) with the lowest sampling variance of any linear estimator, given 5 conditions are met:

1. Linearity of Parameters
2. Random sampling from the population
3. Non-perfect collinearity
4. Exogeniety
5. Homoscedasticity

Or in other words, the OLS estimator under these conditions is both:

- Unbiased: The expected value of the estimator over multiple estimations, is the true parameter value (the proof of this is beyond the scope of this book).
- The linear unbiased estimator with the lowest sampling variance - i.e. each estimate will be the least spread out, in comparison to any other linear unbaised estimator.

As discussed previously (section 1.3), we want a causal estimator that is low-bias and low-variance, and OLS, under these assumptions, is exactly that!

- Thus, if we can meet all the Gauss-Markov assumptions, and we control for all possible confounding variables, OLS produces an accurate estimate of causal effects (in fact, just as good as randomisation)!

Assumption 1: Linearity of Parameters.

This essentially means that the coefficients of the model $\alpha, \beta_1, ..., \beta_k$ are always added/subtracted from each other, and never multiplied together.

- Note: the actual explanatory variables $X_1, ..., X_k$ can be multiplied together (as we will show in the next chapter). The key thing is that the parameters are linear, not the explanatory variables.

Assumption 2: Random Sampling from the Population.

This assumption is met when we do random assignment, which is essentially random sampling of potential outcomes.

- This is probably the biggest roadblock for causal estimation, as we frequently do not meet this requirement
- However, just because no random assignment is present, if we do control for all possible confounding variables (we will discuss this part in the next section), the OLS estimator will still produce a relatively good estimate. However, it will not be the best linear unbiased estimator.

Assumption 3: No Perfect Multicollinearity.

This means no two explanatory variables can have correlation coefficient of -1 or 1, which only occurs if the two variables have the same exact values. Mathematically, $X_{ai} \neq X_{ai}, \forall i, \forall X_a, X_b \in \overrightarrow{X}$.

- The matrix $X'X$ is invertable only when these two conditions are met, so if this assumption is violated, we cannot even calculate the OLS estimate.

Assumption 4: Exogeniety

Key Definition

Exogeniety is when the error term and regressors are uncorrelated. In other words, the change in X should not affect the expected value of the error. Mathematically:

$$\mathbb{E}[\epsilon_i | \overrightarrow{X_i}] = 0, \forall i$$

The opposite is **Endogeniety**, when an explanatory variable is correlated with the error term.

We prove this with the OLS estimator. First, let us recall the first-order conditions to maximise our sum of squared errors, for both $\hat{\alpha}$ and $\hat{\beta}$. We also know that the error/residual is $\epsilon_i = Y_i - \hat{\alpha} - \hat{\beta}$. substituting in, we get:

$$\sum_{i=1}^{n}(Y_i - \hat{\alpha} - \hat{\beta}_1 X_i) = \sum_{i=1}^{n}\epsilon_i = 0 \quad \text{sum of residuals is 0}$$
$$\sum_{i=1}^{n}X_i(Y_i - \hat{\alpha} - \hat{\beta}_1 X_i) = \sum_{i=1}^{n}X_i\epsilon_i = 0 \quad \text{no covariance between } X \text{ and } \epsilon$$

Thus, naturally, if the average residuals are 0, and they are uncorrelated with any X, then the residuals conditional on X should also be 0.

When we have some X that is **endogenous**, i.e. some X is correlated with the error term, we violate the assumption.

- Violating this assumption is a huge issue. Endogeneity means that the OLS estimator is not unbiased. If we have endogeneity (any X that is endogenous), we will need other methods to estimate causal effects.
- We will discuss the Instrumental Variable Estimator in Volume II of the series, which is one of the more popular ways to deal with endogenous regressors.

Assumption 5: Homoscedasticity

Key Definition: Homoscedasticity

Homoscedasticity is the assumption that the variance of the error term is consistent and constant for all values of the explanatory variables. Mathematically:

$$Var(\epsilon|\overrightarrow{X}) = \sigma^2$$

If this assumption is violated, we have **heteroscedasticity**.

The simplest way to identify heteroscedasticity is to look at the residual plots - a plot with explanatory variables on the x-axis, and residuals on the y-axis.

- If the residuals show no pattern, then there is no heteroscedasticity. If there is a pattern, for example, if the residuals are very small when X is small, and very big when X is big, then we have heteroscedasticity.
- There are also more formal tests for this, but they take more effort than it is worth. Thus, we will not delve into these heteroscedasticity tests.

OLS is still unbiased as long as the first 4 assumptions are met. Heteroscedasticity does not cause bias or inconsistency in the estimates of coefficients.

- However, heteroscedasticity does have some implications for causal inference and hypothesis testing. This is because the typical standard error formula is based on the assumption of homoscedasticity. This is why we introduced **robust standard errors** in the last chapter, which account for heteroscedasticity.
- In econometrics today, we typically assume heteroscedasticity exists in our data (since it is so common), and default to robust standard errors. We need to prove that homoscedasticity is true if we want to drop robust standard errors.

4.5 Omitted Variable Bias

As mentioned multiple times, to get an accurate causal estimate with OLS, we must account for every possible confounding variable.

But why is this? Let us mathematically show this. Consider two regressions (replaced α with β_0 for simplicity of the next section):

$$Y_i = \beta_0^S + \beta_1^S D_i + \epsilon_i^S \quad \text{"short" regression}$$
$$Y_i = \beta_0 + \beta_1 D_i + \beta_2 X_i + \epsilon_i \quad \text{"long" regression}$$

Essentially, the "long" regression contains the "short" regression, with one additional explanatory variable X. This additional variable X is **omitted** in the "short" regression.

Now consider an auxiliary regression, where the omitted variable X is the outcome variable, and D_i is the explanatory variable:

$$X_i = \delta_0 + \delta_1 D_i + u_i \quad \text{where } u_i \text{ is error and } \delta_0, \delta_1 \text{ are coefficients}$$

Now we have that, let us plug X_i into our long regression:

$$Y_i = \beta_0 + \beta_1 D_i + \beta_2 X_i + \epsilon_i$$
$$Y_i = \beta_0 + \beta_1 D_i + \beta_2(\delta_0 + \delta_1 D_i + u_i) + \epsilon_i$$
$$Y_i = \beta_0 + \beta_1 D_i + \beta_2\delta_0 + \beta_2\delta_1 D_i + \beta_2 u_i + \epsilon_i$$
$$Y_i = \beta_0 + \beta_2\delta_0 + (\beta_1 + \beta_2\delta_1) D_i + \beta_2 u_i + \epsilon_i$$

Notice the last equation only has one dependent variable D_i: this is in the same form as the "short" regression. The coefficient of D_i in the short regression was β_1^S, and now in our final equation $\beta_1 + \beta_2\delta_1$. Thus:

$$\beta_1^S = \beta_1 + \beta_2\delta_1$$

Or in other words, the difference between the coefficient of D_i in the "short" regression β_1^S, and the coefficient of D_i in the long regression β_1, the difference is $\beta_2\delta_1$. Essentially, our "short" regression's coefficient estimate was incorrect/biased by $\beta_2\delta_1$.

Omitted Variable Bias

Omitted Variable Bias is the difference between the β coefficients of our treatment D_i, between a model a certain control variable X, and a model without that variable. By omitting that control variable X, our causal estimate changes by $\beta_2\delta_1$, or in other words, our causal estimate is off by $\beta_2\delta_1$.

Thus, in order to use regression for accurate causal estimation, we must be confident all confounders are included as control variables.

Of course, this is easier said than done. For many social science relationships, there are thousands of confounders, many not measurable or observable. We will introduce more techniques in Volume II to deal with this issue.

Chapter 5

Further Topics in Linear Regression

5.1 Categorical Explanatory Variable

A **categorical polytomous** variable is one with 3 or more categories that are unranked. A classic example is the variable *country*, which is a categorical variable with all the different countries included in a dataset such as Argentina, France, Mexico, etc.

How do we run a regression with polytomous explanatory variables? What happens is that we divide the variables into a set of dummy binary variables (see how dummy variables are interpreted in section 3.2).

- Dummy binary variables are created for all except one of the categories in our variable. Each dummy variable has two values - 1 meaning the observation is in the category, and 0 meaning the observation is not in that category.
- The category without a dummy variable is the **reference/baseline** category. Essentially, when all other dummy variables are equal to 0, that is referring to the reference/baseline category (the intercept)

Key Definition

Thus, a **polytomous explanatory variable** with n number of categories in X, we would create $n-1$ dummy variables, and input it into a regression equation as follows:

$$E[Y] = \alpha + \beta_{x=1}X_{x=1} + ... + \beta_{x=n-1}X_{x=n-1}$$

Where α is the mean of the reference category n, and the other categories $1, ..., n-1$ get their own dummy variable.

For example, take the following polytomous variable: *company*, which contains the categories *microsoft, google,* and *apple*. Let us create dummy variables for 2 of the 3 categories:

- *Google* will become the first dummy variable X_g. When $X_g = 1$, that observation is part of the *google* category. When $X_g = 0$, that observation is NOT a part of the *google* category.
- *Apple* will become the second dummy variable X_a. When $X_a = 1$, that observation is part of the *apple* category. When $X_a = 0$, that observation is NOT a part of the *apple* category.
- *Microsoft* will not get its own dummy variable. This is because when both *apple* and *microsoft* $X_g = X_a = 0$ that is referring to the *microsoft* category (observations not a part of either previous category).

Mathematically, this is how it would be represented in a regression equation:

$$E[Y] = \alpha + \beta_g X_g + \beta_a X_a$$

To find the expected value of each category, we would do the following:

$$\begin{aligned} E[Y|X = \text{Google}] &= E[Y|X_g = 1, X_a = 0] = \alpha + \beta_g(1) + \beta_a(0) = \alpha + \beta_g \\ E[Y|X = \text{Apple}] &= E[Y|X_g = 0, X_a = 1] = \alpha + \beta_g(0) + \beta_a(1) = \alpha + \beta_a \\ E[Y|X = \text{Microsoft}] &= E[Y|X_g = 0, X_a = 0] = \alpha + \beta_g(0) + \beta_a(0) = \alpha \end{aligned}$$

Thus, from these above equations, we can see the interpretation of the coefficients:

- α is the expected value of the reference category, in this case, *microsoft*.
- β_g is the expected Y difference between the *google* category and the reference category *microsoft*. The statistical significance of this coefficient would be a difference of means test between the two categories.
- β_a is the expected Y difference between the *apple* category and the reference category *microsoft*. The statistical significance of this coefficient would be a difference of means test between the two categories.

Interpretation of Polytomous Explanatory Variables

β_j is the expected difference in Y values between category j and the baseline category.
α is the expected value of Y of the baseline category.

The coefficient p-values of β_j are a difference-of-means test between two categories, and not a statistical significance test of the entire categorical variable.

5.2 Interaction Effects

Interactions, also called moderating effects, means that the effect of some X_j on Y is not constant, and depends on some third variable X_k. Essentially, X_k's value changes the relationship between X_j and Y.

For example, Y could be the chance of a civil war occurring, X_1 is the severity of an economic crash, and X_2 is the development level of a country. We could quite reasonably expect that in the effect of a economic crash on a chance of civil war would be significantly higher in developing nations rather than developed.

Or in other words, the chance that a civil war occurs due to a economic crash is higher in countries like Venezuela, North Korea and Eritrea, compared to the relationship in Norway, Switzerland, and Denmark. Essentially, X_1's effect on Y is affected by the value of X_2.

Key Definition: Interaction Effect Regression

Interaction effects are represented by two variables being multiplied together in a regression equation. In the model below, X_1 and X_2 are interacting with each other:

$$\mathbb{E}[Y|\vec{X}] = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_1 X_2 + \text{other explanatory variables}$$

Note: you can see in the above equation, X_1 and X_2 both are interacted, as well as have their own separate coefficients. We should always include both variables independently along with the interaction effect.

We can mathematically show that the effect of X_1 on Y is not constant - and varies due to the value of X_2:

$$\begin{aligned}\hat{Y} &= \hat{\alpha} + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2 + \hat{\beta}_3 X_1 X_2 \\ \frac{\partial \hat{Y}}{\partial X_1} &= 0 + \hat{\beta}_1 + 0 + \hat{\beta}_3 X_2 \\ \frac{\partial \hat{Y}}{\partial X_1} &= \hat{\beta}_1 + \hat{\beta}_3 X_2\end{aligned}$$

As you can see, the relationship between X_1 and Y here depends on the value of X_2. In more intuitive words, given a one unit increase in X_1, there is an expected $\hat{\beta}_1 + \hat{\beta}_3 X_2$ increase in Y.

We can also find the effect of X_2 on Y:

$$\begin{aligned}\hat{Y} &= \hat{\alpha} + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2 + \hat{\beta}_3 X_1 X_2 \\ \frac{\partial \hat{Y}}{\partial X_2} &= \hat{\beta}_2 + \hat{\beta}_3 X_1\end{aligned}$$

With these equations, we can interpret the coefficients of our model more generally.

Interpretation of Interaction Effects

The coefficients in a regression with interaction effects are interpreted as:

- $\hat{\beta}_1$ is the relationship between X_1 and Y, given $X_2 = 0$.
- $\hat{\beta}_2$ is the relationship between X_2 and Y, given $X_1 = 0$.
- $\hat{\beta}_3$ represents two things. For every one unit increase of X_2, the magnitude of the relationship between X_1 and Y changes by $\hat{\beta}_3$. Similarly, for every one unit increase of X_1, the magnitude of the relationship between X_2 and Y changes by $\hat{\beta}_3$.
- α is still the expected value of Y when all explanatory variables equal 0.

The coefficient β_3's significance level tells us if there is a statistically significant interaction.

- If β_3 is not statistically significant, we can often remove the interaction term.
- However, if β_3 is statistically significant, that means we have found two terms that interact.

5.3 Panel Data and Fixed Effects

Hierarchical and Panel Data

Hierarchical data is data that comes in different "clusters" or "levels". For example, if we have data on individuals from multiple different countries, that means our individual observations are clustered at the country-level.

Hierarchical data can also be clustered over time. For example, we might have GDP data for all countries in the world from 1960-2024. Each year (ex. 2024) will have GDP data for all countries, thus, the data is clustered by year. Data clustered over years is often referred to as **panel data** or **longitudinal** data.

Hiearchical data can be clustered over country and year at the same time. The previous example of GDP data can be clustered by year (ex. 2023, 2022, etc.) and clustered by country (ex. USA, UK, etc.).

Why do we care about clusters? Well - this is because one cluster might be very different than another cluster. For example, if we were explaining individual voting turnout between countries, different electoral and cultural factors in each country might explain some of the differences. Another example is the 2008 financial crisis, which may mean 2008 values will be different from 2015 because of circumstances surrounding each particular year.

These differences between clusters affect our regression results. For example, if we want to explain the outcome variable individual voter turnout with the explanatory variable individual education level, some of the effect of different countries and years may be captured in our regression. That means our regression is not accurately measuring the size of effects.

Thus, we need some way to control for these clusters in our data to isolate the effect of our treatment D and accurately assess the causal impact.

Fixed Effects

Fixed Effects are a way to control for the issue of differences between clusters.

Let us assume that we have m number of clusters in our data. Thus, we have a specific cluster $i \in \{1, ..., m\}$. Each cluster i will have n number of observations, so we will have observation $t \in \{1, ..., n\}$ within cluster i.

Using this framework, every observation can be defined as Y_{it}, which essentially means the Y value of the ith cluster's tth observation. The corresponding explanatory variable values will be notated $\overrightarrow{X}_{it}$.

Key Definition: Fixed Effects Model

A fixed effects model will take the following form:

$$Y_{it} = \alpha_i + \beta_1 X_{1it} + ... + \beta_k X_{kit} + \epsilon_{it}$$

Where α_i is the fixed effect for cluster i, defined as:

$$\alpha_i = \beta_{00} + \beta_{02} D)i2 + ... + \beta_{0m} D_{im}$$

Where $D_{i2}, ..., D_{im}$ are dummy variables for the clusters $2, ..., m$. Cluster 1 is the reference category (like a categorical explanatory variable). β_{00} is the average Y of the reference cluster category (cluster 1), when $\overrightarrow{X} = 0$. β_{0j} is the difference between the average Y of cluster j, and the reference category (cluster 1), when all $\overrightarrow{X} = 0$.

Or in other words, including fixed effects for clusters i means using the clusters as an additional categorical variable in our regression. We can demonstrating this by writing out α_i in our above linear model to get:

$$Y_{it} = \beta_{00} + \beta_1 X_{1it} + ... + \beta_k X_{kit} + \beta_{02} D_{i2} + ... + \beta_{0m} D_{im} + \epsilon_{it}$$

The fixed effect α_i captures the predictors of Y that are shared by all observations within their cluster i. For example, if our fixed effects were by countries, α_i would capture all the predictors of Y that are shared by all observations from that same country. To interpret our coefficients β_j, we would do the same as we previously would, but adding the line - controlling for levels of Y we would expect for that cluster in general.

Two-Way Fixed Effects

Often in Political Economics, we will have 2-way clustered data by both country and year. For example, if you have data on GDP and Democracy level from all countries between 2006-2024, you will have two types of clusters - clusters by country, and clusters by year.

Key Definition: Two-Way Fixed Effects

We can combine these two for two-way fixed effects of both country and year. Two-way fixed effects takes the following form:

$$Y_{it} = \alpha_i + \gamma_t + \beta_1 X_{1it} + ... + \beta_k X_{kit} + \epsilon_{it}$$

α_i represents country fixed effects, exactly as we described in the previous section.
γ_t represents year fixed effects. Why does it have the subscript t? Well, in panel data, for each country, you will have many different years of data (ex. USA will have data between 2006-2024). Thus, within cluster i of the country, each observation t is a different year. Thus, t is the year of the data.

To interpret our coefficients β_j, we would do the same as we previously would, but adding the line - controlling for levels of Y we would expect for that country in that year in general.

This allows us to account for differences in countries and differences in years, and is very very common in Political Economics. You will also sometimes see different variations of this, including State-Year, Country-Decade, District-5Years, or any Geographic-Time clustering.

5.4 Polynomial Transformations

Sometimes, a linear (straight-line) best-fit line is a poor description of a relationship. We can model more flexible relationships that are not straight lines, by including a transformation of the variable X that we are interested in.

Quadratic Transformations

Key Definition: Quadratic Transformation

Quadratic transformations of X_j take the following form:

$$\mathbb{E}[Y_i|\overrightarrow{X}] = \alpha + \beta_1 X_{ji} + \beta_2 X_{ji}^2 + \text{other explanatory variables}$$

If you recall from high-school algebra, an equation that takes the form of $y = ax^2 + bx + c$ creates a *parabola*.

- A true parabola has a domain of $(-\infty, \infty)$. However, our model often does not need to do this. The best-fit parabola is only used for the range of plausible X values, given the nature of our explanatory variable.
- For example, if X was age, a negative number would make no sense. Because the parabola's domain often exceeds our plausible range of X values, the vertex of the parabola (where it changes directions) may not be in our data.

We always include lower degree terms in our model. For example, in this quadratic (power 2) model, we also include the X term without the square. To fit a model like this, we simply do the same process of minimising the sum of squared errors. How do we interpret the coefficients β_1 and β_2?

> **Interpretation of Quadratic Transformations**
>
> β_1's value is no longer directly interpretable. This is because we cannot "hold all other coefficients constant", since β_2 also contains the same X variable.
>
> β_2's value also cannot be directly interpreted. If the coefficient of β_2 is statistically significant, we can conclude that there is a non-linear relationship between X and Y. If β_2 is negative, the best-fit parabola will open downwards, and if β_2 is positive, the best-fit parabola will open upwards.

If we want to interpret the magnitude of the model, we are best off using predicted values of Y (obtained using the model equation above).

There is one more thing we can interpret with the quadratic transformation: the **vertex** of the best-fit parabola. The vertex, if we remember our algebra, is either the maximum or minimum point of a parabola.

If we remember from calculus and optimisation, we can find the maximum and minimums through setting the derivative equal to 0. For the quadratic model, this is as follows - we first find the derivative, then set the derivative equal to 0:

$$\begin{aligned}
\hat{Y} &= \hat{\alpha} + \hat{\beta}_1 X + \hat{\beta}_2 X^2 \\
\frac{d\hat{Y}}{dX} &= 0 + \hat{\beta}_1 + 2\hat{\beta}_2 X \\
0 &= \hat{\beta}_1 + 2\hat{\beta}_2 X \\
-\hat{\beta}_1 &= 2\hat{\beta}_2 X \\
X &= \frac{-\hat{\beta}_1}{2\hat{\beta}_2}
\end{aligned}$$

This point is useful, as it is either the maximum or minimum of our best-fit parabola. This means that at the X value we calculate from this equation, we will either see the highest or lowest expected Y value.

General Polynomial Models

While quadratic models are the most common polynomial transformation, we do not have to stop there. We can continue to add further polynomials (although anything beyond cubic is exceedingly rare):

- Cubic: $E[Y] = \alpha + \beta_1 X + \beta_2 X^2 + \beta_3 X^3$
- Quartic: $E[Y] = \alpha + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \beta_4 x^4$

Each higher order coefficient, if statistically significant, indicates that the relationship between X and Y, is not of the previous highest power.

- For example, if the cubic term β_3 is statistically significant, we can reject a quadratic relationship between X and Y

Remember to always include the lower power monomials within our polynomial model. For example, if you have a quartic transformation, you must also have the linear, quadratic, and cubic terms.

5.5 Logarithmic Transformations

Logarithmic transformations are another form of non-linear transformations. These are commonly used for heavily skewed variables, such as when the explanatory variable is income, wealth, and so on.

In situations with heavily skewed variables, we often replace X in our models with $\log(X)$. Note that in statistics, when we refer to logarithms, we are referring to natural logarithms, such that $\log(X) = \ln(X)$.

Key Definition: Logarithmic Transformation

The logarithmic transformation of explanatory variable X_j takes the following form:

$$\mathbb{E}[Y_i|\overrightarrow{X}] = \alpha + \beta_j \log(X_j) + \text{other explanatory variables}$$

Interpretation of the β coefficient can be a little bit trickier for logarithmic transformations.

We could interpret it in the same way we interpret linear regressions: given a one unit increase in the log of X, there is an expected β change in Y.

However, this issue is that this does not really say much - I mean, who knows what a *one unit increase in the log of* X even means?

With some properties of logarithms, we can actually create a more useful interpretation. Based on logarithm rules, we know the following to be true:

$$\begin{aligned} \log(X) + A &= \log(X) + \log(e^A) \\ &= \log(e^A \times X) \end{aligned}$$

Now, let us plug this into our original regression model:

$$\begin{aligned} E[Y|X] &= \alpha + \beta \log(X) \\ E[Y|e^A \times X] &= \alpha + \beta \log(e^A \times X) \\ &= \alpha + \beta[\log(X) + A] \\ &= \alpha + \beta A + \beta \log(X) \end{aligned}$$

Now find the difference between $E[Y|e^A \times X]$ and $E[Y|X]$:

$$\begin{aligned} E[Y|e^A \times X] - E[Y|X] &= [\alpha + \beta A + \beta \log(X)] - [\alpha + \beta \log(X)] \\ E[Y|e^A \times X] - E[Y|X] &= \beta A \end{aligned}$$

Thus, we can seen that when we multiply X by e^A, we get an expected βA change in Y. We can make this interpretation more useful by purposely choosing some value A that makes e^A make more sense. For example, if $A = 0.095$, then $e^A = 1.1$, and multiplying by 1.1 is a 10% increase.

Interpreation: Logarithmic Transformation

When X_j increases by 10%, there is a expected $0.095\beta_j$ unit change in Y

Implementation in R

For R, we will need the package *fixest*.

```
library(fixest)
```

Categorical Explanatory Variables

R automatically treats character/string and boolean/logical data types as categorical variables, so we can just include them in the regression like any other variable.

For variables that are numeric (but need to be represented as categorical variables), we use the as.factor() function in the linear regression. For example, below, X2 is being coerced into a factor variable:

```
model <- feols(Y ~ X1 + as.factor(X2) + X3, data = mydata, se = "hetero")
summary(model)
```

We can also do this before even entering the linear regression by modifying the variable.

```
mydata$X2 <- as.factor(mydata$X2)
```

If we want to change the reference category of the categorical variable, we can use the *relevel()* function (for numeric or logical factor variables, there is no need for the quotation marks).

```
mydata$X2 <- as.factor(mydata$X2)
mydata$X2 <- relevel(mydata$X2, ref = "category name")
```

Interaction Effect

To do an interaction effect, we simply use a asterisk between the two variables we want to interact:

```
model <- feols(Y ~ X1*X2 + X3, data = mydata, se = "hetero")
summary(model)
```

Polynomial Transformations

To do a polynomial regression, we use the *I()* function within our regression model, with the first argument being the variable, and 2nd argument being the polynomial degree. For example, let us make a model with X1 with a cubic polynomial:

```
model <- feols(Y ~ I(X1, 3) + X2 + X3, data = mydata, se = "hetero")
summary(model)
```

Logarithmic Transformations

To do a logarithmic transformation, we put the variable in question in the *log()* function. Note: if you have any 0's in the variable, this may create an error.

```
model <- feols(Y ~ log(X1) + X2 + X3, data = mydata, se = "hetero")
```

Fixed Effects

One way fixed effects: The syntax is very similar to standard linear regression, we just add fixed effects after a bar "|". In the example below, *fix1* is the variable we are using as fixed effects:

```
model <- feols(Y ~ X1 + X2 | fix1, data = mydata)
summary(model)
```

Two way fixed effects: just add another fixed effect variable after *fix1* with a "+" sign:

```
model <- feols(Y ~ X1 + X2 | fix1 + fix2, data = mydata)
summary(model)
```

Important note: Often, the variable *year* is encoded as numeric, but we want it to be a categorical variable for fixed effects, so use the *as.factor()* function to coerce the variable *year*.

Also, you can do this in base-r with the *lm()* function as shown throughout the regression examples, just by including the cluster variable as a categorical explanatory variable, however, the output is not as nice.

Implementation in STATA

Categorical Explanatory Variables

In Stata, we simply put an *i.* in front of the variable to make STATA treat it as a categorical variable:

```
regress Y X1 i.X2 X3, robust
```

Interaction Effects

In Stata, to do an interaction effect, we add two hashtags ## between the two variables we want to interact:

```
regress Y X1##X2 X3, robust
```

Part III

Discrete Regression Models

Chapter 6

Binomial Logistic Regression

Chapter 7

Maximum Likelihood Estimation

Chapter 8

Multinomial and Ordinal Logistic Regression

Chapter 9

Regression for Counts