Statistical inferences

Lucie Lu

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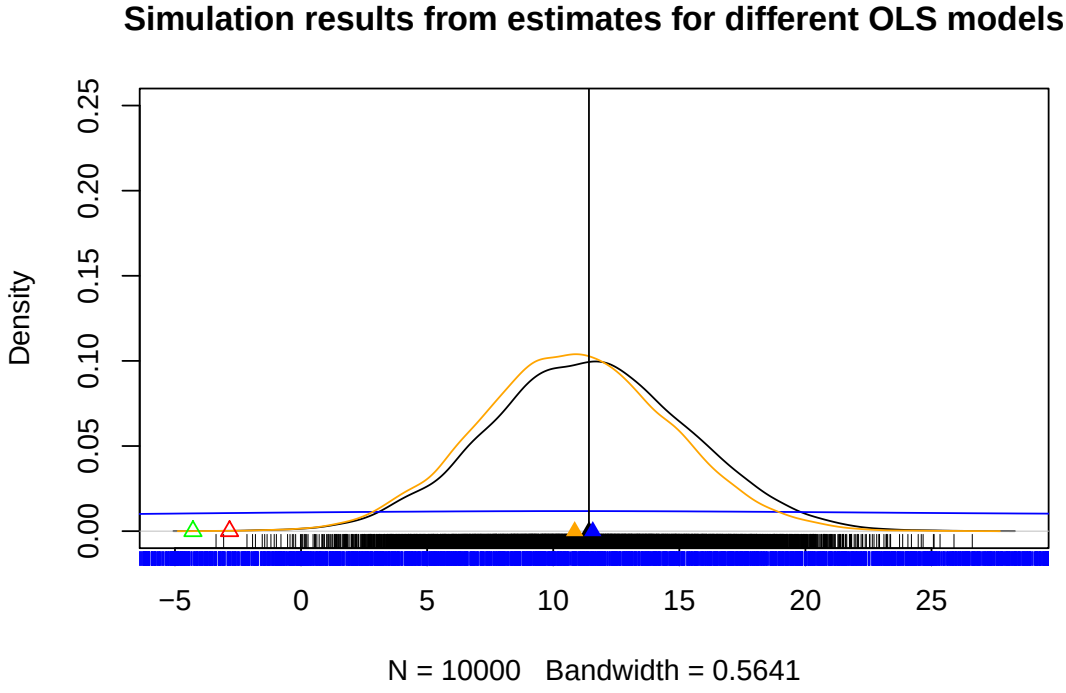
Checking unbiasedness and consistency of the estimates in the OLS model

	bestATE	unbiasedATE	bestATE2
trueATE	11.42	11.42	11.42
sampmeans	11.42	11.57	10.85
bias	0.00	0.15	0.57
sd	3.96	31.82	3.78
MSE	15.64	1012.36	14.58

Table 1: Simulation results from different estimates for OLS model



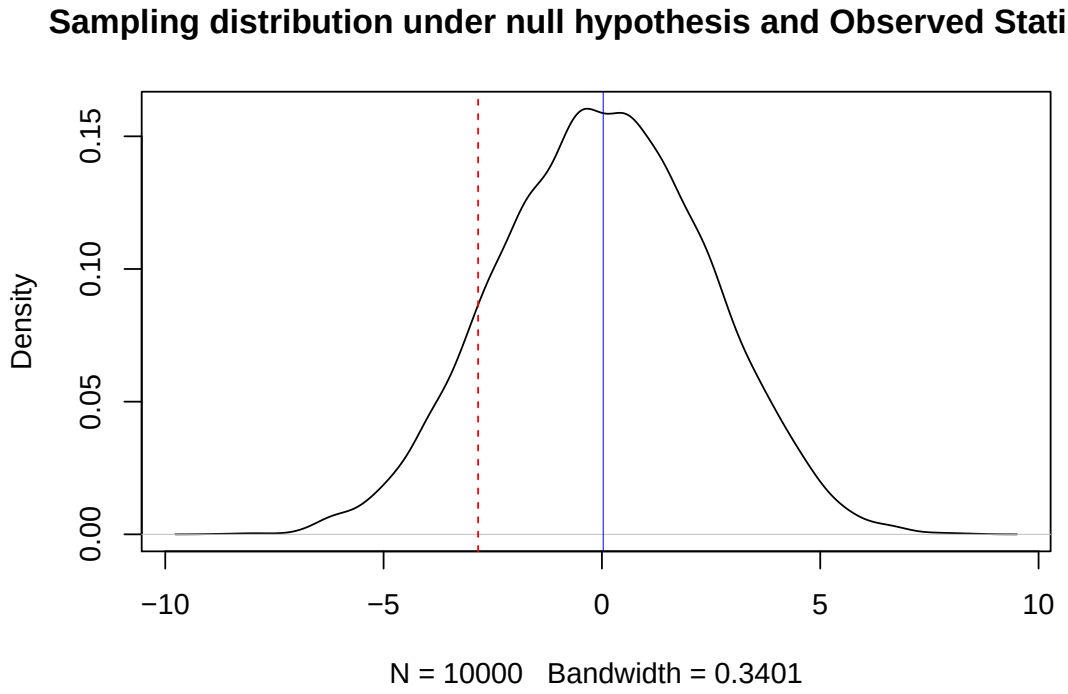
The *bestATE* is the estimaor in a *lm* function with all the relevant covariates in the model. The *unbiasedATE* is the estimaor in a *lm* function with no covariates in the model at all. The *bestATE2* is the estimaor in a residual-based function.

To assess biasedness, I compare sample means of the estimators with the true mean I created in the simulation test. In a simple way, I can compare the third row, the values of bias for each estimator, and choose the smallest one (bias is denoted as the absoluate positive values: the differences between trueATE and the means of the estimates). All of the three estimators are close to the true mean (11.416) I created in the simulation test. This suggest all three of them are (pretty much) unbiased. In fact, the *bestATE* has the lowest bias out of the three. Its absolute distance to the true mean is the smallest one, with bias equals to 0.0025. The *bestATE2* is slightly biased (with biase equalling to 0.5661).

To assess consistency or efficiency, the MSEs for bestATE and bestATE2 are relatively the same, but the bestATE2 behave slightly better ($14.575 < 15.6409$). The estimators *bestATE* and *bestATE2* are efficient, compared to the *unbiasedATE*. The standard error for *unbiasedATE* is very high (31.8188), suggesting that this estimate is very inefficient and inconsistent. It does not converge to the true mean at all. From this simulation test, because the bestATE has the lowest bias and is the most efficient one, this estimate is preferred.

P-values from the permutation test

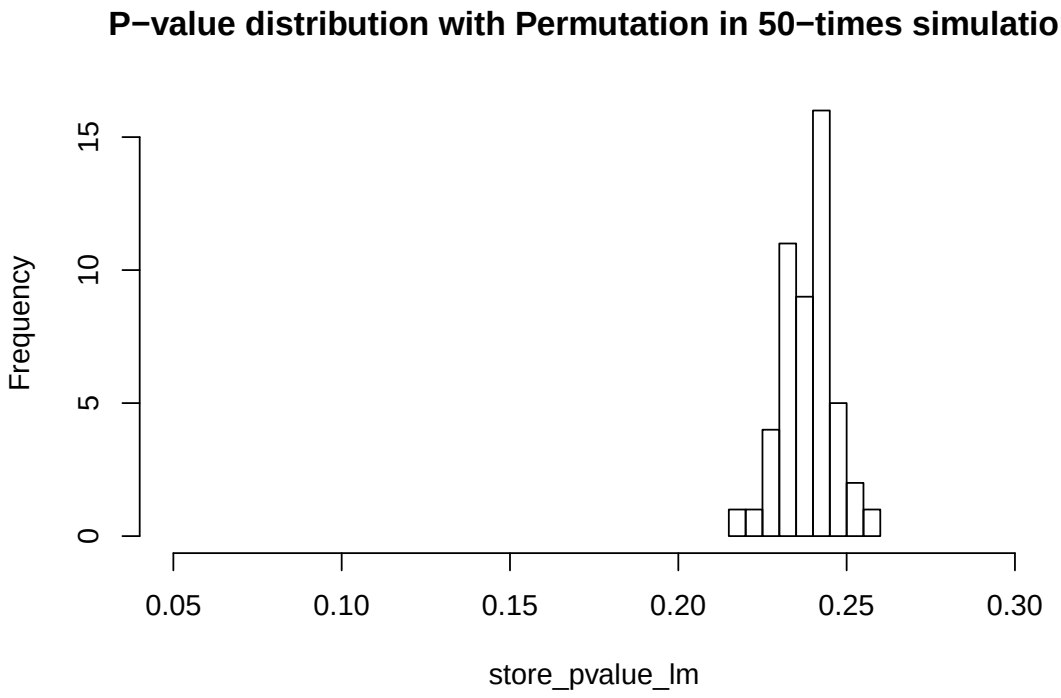
P-value tells us how likely I can get the observed treatment effect from my experiment under the no treatment effect null hypothesis. After I have done the hypothetical experiment, I would do a hypothesis testing. Here, in this study, the hypothetical experiment is that countries are "randomly assigned" to be democratic or non-democratic on average over 1980s and 1990s. The worrisome is the Fisher's sharp null hypothesis: there is a possibility of no effect for all the units in this hypothetical experiment. Instead, I just observe the differences in means by chance. My null hypothesis is there is no treatment effect between the treated and control groups for each unit. In other words, the null hypothesis is there are no differences in the tariff rates between democratic and non-democratic countries.



First, I use a test statistic to summarize my observed data from the experiment: -2.8357 is my test statistic of mean difference in tariff rates. Second, I set the null hypothesis of no effects: I create a new experiment and shuffle the labels of countries. Here, I break the relatioships existing in the data structure to create an experiment of no effect. Then, by using the computing power, I replicate the experiments of no effect in the testing on the computer as if I run the experiments 10000 times. Then I observe the differences-in-means 0.0295 under the null hypotehsis, and we compare how likely it is to get the differences-in-means greater than or equal to the observed data. This probability is the p-value 0.235. It means we have 0.235 (around 1 in 5 replications of the no effect experiment) to produce the values as large as or greater than the estimators in the *lm* function. The p-value here is the probability that a value as extreme or more extreme will be observed under the null hypothesis. This probability gives me the information that I may not have many evidence to against the null effect hypothesis.

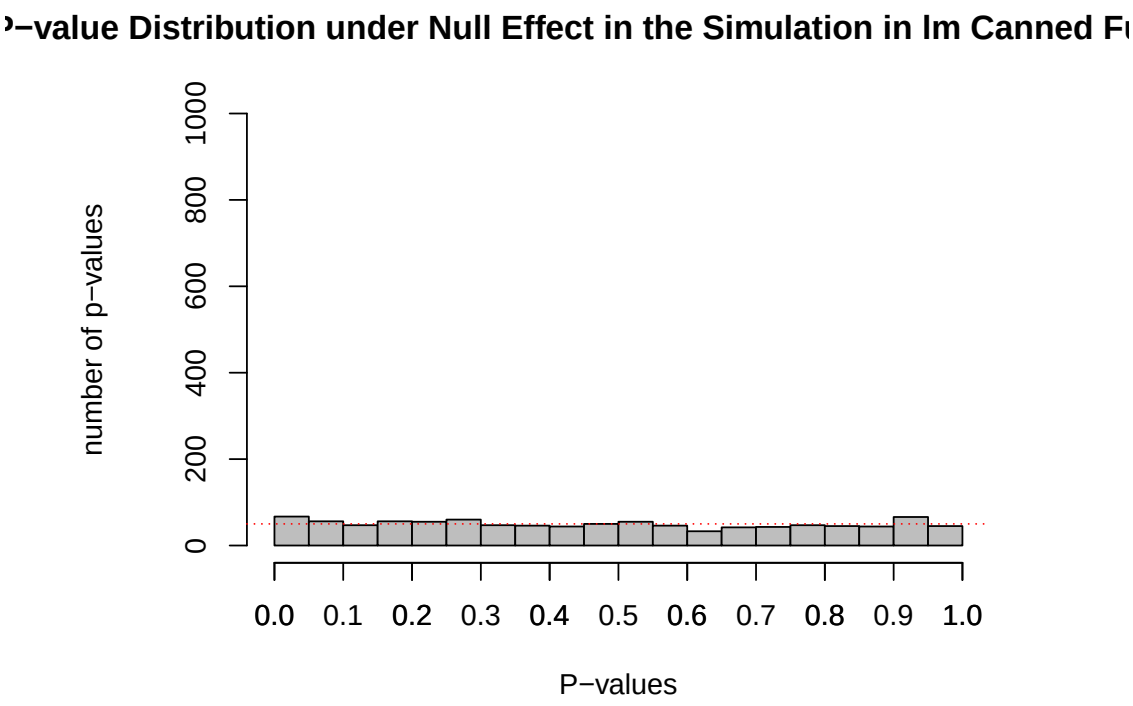
I use the permutation test to obtatin p-value where the relationships between the treatment and outcome variables are shuffled and the test statistic is calculated based on the data. The key advantage of this test does not rely on any assumptions of the distribution. In the canned lm function, the standard assumption that the statistic follows a t-distribution gives a p-value of 0.23 (by default). This is in quite good agreement with the p-value I obtained in the permutation test 0.235. But I would not necessarily know beforehand that the two p-values would agree. The following figure shows the null distribution obtained from using the data itself is close to a t-distribution. This can explain why the p-value from the CLT+IID justified test and the p-value from the permutation test is similar.

[1] 0.2268



After I calculated the p-value 0.235 from a permutation test, I replicated this process for 50 times and calculated 50 different p-values generated from the same process. From this histogram, we can see that the p-values are distributed around from 0.22 to 0.26.

To check the error rate of the *lm function*, I create a null effect in the error rate test knowing that my null hypothesis is true. If the false positive rate is 0.05, this means 5 out of 100 times, the test faslely reject the nulls (knowing the null is true but I still reject it). If the false positive rate is close to 0.05, it means the test fulfills its promises. The false positive rate is 0.046. If we run it a couple of times, the false positive rates are slightly different, but they are around 0.05. The p-value from the built-in lm function has a similar false positive rate to the nominal false positive rate (0.05).



In this plot, we know that when there is no true effect, p-values are what is called 'uniformly distributed under the null'. The p-value distribution is basically flat. Every p-value is equally likely when the null hypothesis is true, and every bar in the graph will contain 5% of all the p-values (as indicated by the dotted red line). The first bar is the false positive rate, which is slightly higher than but it is very close to 0.05.

I also followed the same procedures to calculate the p-value and false positive rates of the *lm rob* function. I summarize the results in the following table.

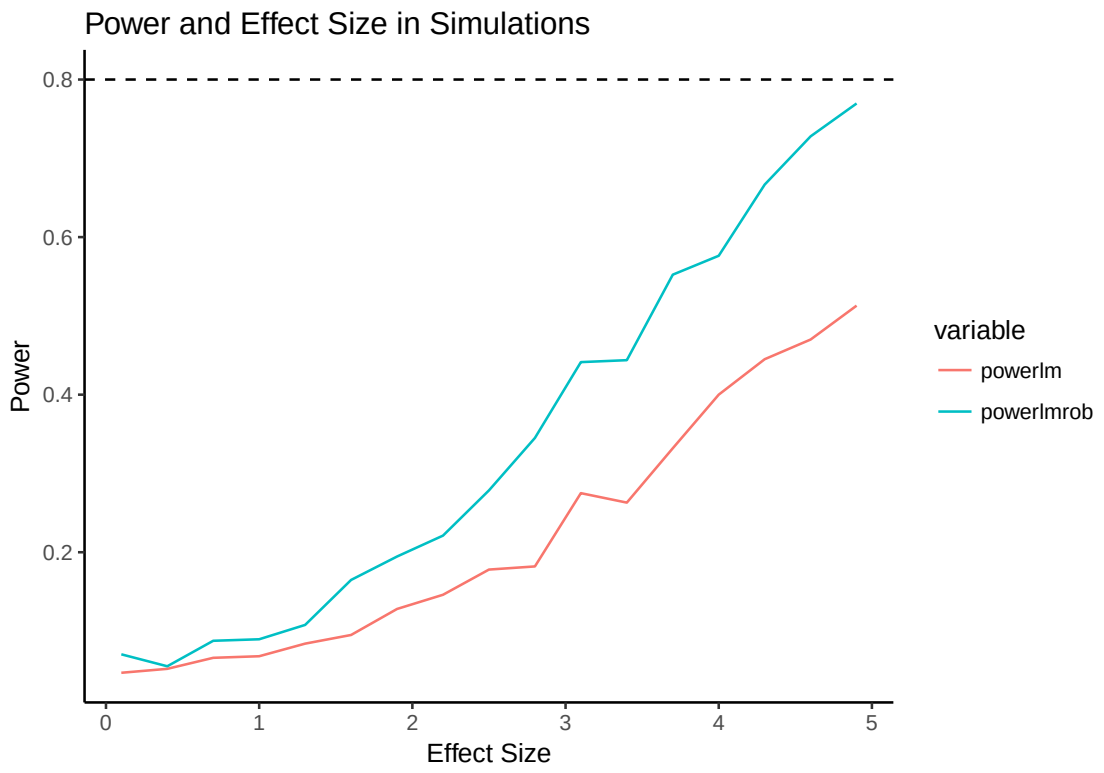
	Permutation	t-distritbuion	False Positive Rate
lmp	0.24	0.28	0.05
lmrobp	0.06	0.04	0.06

Table 2: P-values obtained from simulation, t-distribution and their error rates

Power and effect size

When our study has effects, we hope that our test has the power to detect the true effect when the null hypothesis is false. Increasing the power of the test requires bigger sample sizes, or studying larger effects. Here, my sample size is 81, and I want to check which test (of *lm* or *lmrob*) has higher power for different effect sizes.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
effectsize	0.10	0.40	0.70	1.00	1.30	1.60	1.90	2.20	2.50	2.80	3.10	3.40	3.70	4.00	4.30
somepower	0.05	0.05	0.07	0.07	0.08	0.10	0.13	0.15	0.18	0.18	0.28	0.26	0.33	0.40	0.44
somepower_lmrob	0.07	0.06	0.09	0.09	0.11	0.16	0.19	0.22	0.28	0.35	0.44	0.44	0.55	0.58	0.67



Power

analysis of two models:

We can use simulations to estimate the statistical power of a model. The statistical power is the probability of observing a statistically significant result, if there is a true effect. When there is an effect, I hope that my statistical test is able to detect it. This denotes to high power in my study.

Cohen describes effect size as "the degree to which the null hypothesis is false." In this simulation test, I generate different hypothetical effect sizes (from 0.1 to 5), and I calculate the number of p-values that are are lower than 0.05 ("reject the null") when I know there is a true effect (the null is false). When the effect size increases, the powers in both functions also increase.

For a given sample size, the *lmrob* model has larger statistical power given an effect size. As effect size increases, the power of the *lmrob* model is also increasing faster than that of the *lm* model. To achieve an ideal 80% statistical power, the *lmrob* model requires an effect size larger than 5. 80% statistical power essentially means when there is a true effect, there is 80 percent that I will observe a signifiant effect. For this *lm* model, I need a bigger effect size to achieve the same level of power as *lmrob* model requires. This is probably due to a relatively small sample size in this study (81 countries).