Multiple Regression Analysis

 $\diamondsuit y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + u$



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Assumptions of the Classical Linear Model (CLM)

- Knowing the expected value and variance of the OLS estimators is useful for describing the location and precision of the OLS estimators.
- However, in order to perform statistical inference, we need more than just the first two moments of $\hat{\beta}_j$'s. We need to know the full sampling distribution of the $\hat{\beta}_j$'s.

Assumptions of the Classical Linear Model (CLM)

Even under the Gauss-Markov assumptions (MLR1-MLR5), the distribution of β_j's can have virtually any shape.

 In order to do classical hypothesis testing, we need to add another assumption, beyond the Gauss-Markov assumptions.

Assume that *u* is independent of $x_1, x_2, ..., x_k$ and *u* is normally distributed with zero mean and variance σ^2 : $u \sim \text{Normal}(0, \sigma^2)$.

Assumptions

• MLR.6: NORMALITY The error *u* is independent of $x_1, x_2, ..., x_k$ and *u* is normally distributed with zero mean and variance σ^2

 $u \sim \text{Normal}(0,\sigma^2)$

If we make MLR.6, then we are necessarily assuming MLR.3 and MLR.5

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CLM Assumptions

Assumptions MLR.1 through MLR.6 are called the classical linear model (CLM) assumptions.

It is best to think of the CLM assumptions as containing all the Gauss-Markov assumptions *plus* the assumption of a normally distributed error term.

CLM Assumptions

- ♦ Under CLM, **OLS** is not only BLUE, but is the minimum variance unbiased estimator.
- This means that OLS has the smallest variance among all unbiased estimators; we no longer have to restrict our comparison to estimators that are linear in the y_i .



• We can summarize the population assumptions of CLM as follows

 $y/\mathbf{x} \sim \text{Normal}(\beta_0 + \beta_1 x_1 + \ldots + \beta_k x_k, \sigma^2)$

Normality

The claim for normality is usually done on the basis of a Central Limit Theorem (CLT), but this is restrictive in some cases. Normality cannot be assumed always. \diamond In any application, whether normality of *u* can be assumed is really an empirical matter. Often, using a transformation, i.e. taking log's, yields a distribution that is closer to normal.



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Normality

- Normality is easy to handle from a mathematical point of view.
- Large samples will allow us to drop normality without affecting to much the results.
- Normality of the error term translates into normal sampling distributions of the OLS estimators.

Normality of OLS **THEOREM 4.1 NORMAL SAMPLING DISTRIBUTIONS** Under the CLM assumptions, MLR.1 through MLR.6, conditional on the sample values of the independent variables, $\hat{\beta}_j \sim Normal \left[\beta_j; Var(\hat{\beta}_j) \right]$ where $Var(\hat{\beta}_i)$ was given in topic 3. Therefore, $\frac{\beta_j - \beta_j}{sd(\hat{\beta}_i)} \sim Normal(0;1)$

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Normality of OLS

The proof of Theorem 4.1 is not difficult, and is based on the fact that $\hat{\beta}_i$ is a linear combination of the errors, that are independent normal variables, and the important fact that a linear combination of normal variables has a normal distribution (Appendix B).

• Previously we showed that $E(\hat{\beta}_j) = \beta_j$ and derived $Var(\hat{\beta}_j)$

Normality of OLS

- The conclusion of Theorem 4.1 can be strengthened.
- In fact, any linear combination of the $\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2, ..., \hat{\beta}_k$
 - is also normally distributed, and any subset of the $\hat{\beta}_j$'s has a joint normal distribution.
- In the next topic we shall show that normality holds as an approximation even without MLR.6.

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- Wypothesis testing entails making a decision, on the basis of sample data, whether to accept that certain restrictions are satisfied by the basic assumed model.
- The restrictions we are going to test are known as the *null hypothesis*, denoted by H_0 .
- We also define an *alternative hypothesis*, denoted by H_1 , which represents our conclusion if the experimental test indicates that H_0 is false.

Hypothesis Testing: Example



$$H_0: \beta_1 = 1$$

versus

$$\mathbf{H}_1: \boldsymbol{\beta}_1 = \mathbf{0}$$

• In order to conclude that H_0 is false and that H_1 is true, we must have evidence "beyond reasonable doubt" against H_0 .

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Hypothesis Testing: Example

- \diamond Usually we are not so specific about H₁, so this is generally stated as
 - H₁: $\beta_1 < 1$ (one side alternative)

or

(two side alternative) $H_1: \beta_1 \neq 1$



• **Important**: We are testing hypothesis about the *population* parameters. We are not testing hypothesis about the estimates from a particular sample.

- In hypothesis testing, we can make two kinds of mistakes.
- 1. First, we can reject H_0 when it is in fact true. This is called **Type I error**.
- 2. Second, we can fail to reject H_0 when it is actually false. This is called **Type II error**.

After we have made the decision of whether or not to reject H_0 , we have either decided correctly or we have committed an error. We shall never know with certainty whether an error was committed.



However, we can compute the *probability* of making either a Type I error or a Type II error.

- Hypothesis testing rules are constructed to make the probability of committing a Type I error fairly small.
- Generally, we define the significance level
 (α) of a test as the probability of a Type I
 error. Symbolically

 $\alpha = \Pr(\text{Reject } H_0 \mid H_0)$

Read as: "The probability of rejecting H_0 given that H_0 is true."

Classical hypothesis testing requires that we initially specify a **significance level** for the test. When we specify a value for α , we are essentially quantifying our tolerance for Type I error.



Common values for α are .10, .05 and .01. If $\alpha = .05$, then the researcher is willing to falsely reject H₀ 5% of the time, in order to detect deviations from H₀.

- Once we have chosen α , we would then like to minimize the probability of a Type II error, Pr(Fail to Reject H₀ | H₁)
- Alternatively, we would like to maximize the power of a test against all relevant alternatives. The power of a test, π(β₁), is
 π(β₁) = 1 Pr(Fail to Reject H₀ | β₁) = Pr(Reject H₀ | β₁) where β₁ denotes the actual value of the parameter.

Naturally, we would like the power function to be 1 under H_1 (a false null) and 0 under H_0 (a true null).



But this is not possible!.



power for a given α .

- In order to test a null hypothesis against an alternative, we need to choose a test statistic and a critical value.
- ۲

The choices for the statistic and the critical value are based on convenience and on the desire to maximize power given a significance level for the test.

A **test statistic**, *T*, is some function of the random sample, so is itself a random variable.

- When we compute the statistic for a particular sample, we obtain an outcome of the test statistic, say t.
- In order to perform an statistical test we should know the distribution of T under the null hypothesis.
 - Given the test statistic and its distribution, we can define a rejection rule that determines when H_0 is rejected in favor of H_1 .

- In this course, all rejection rules are based on comparing the value of the test statistic, *t*, to a **critical value**, *c*.
- ۲
- The set of values of *t* that result in rejection of the null hypothesis are collectively known as the rejection region.
- In order to determine the critical value, we must first decide on a significance level of the test, α .

Then, given α , the critical value associated with α is determined by the distribution of *T*, *assuming* that H₀ is true.



We shall write this critical value as c, but it should be understood that c depends on α .

Hypothesis Testing: CLM

We are now interested testing hypothesis about a single population parameter in the context of the CLM,

 $y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + u$



♦ Even if β_i is unknown, we can hypothesize about the value of β_i and then use statistical inference to test our hypothesis.

The main result we need is the next one.

THEOREM 4.2 t DISTRIBUTION FOR THE STANDARDIZED ESTIMATORS
Under the CLM assumptions MLR.1 through MLR.6,

 $\frac{\hat{\beta}_j - \beta_j}{se(\hat{\beta}_j)} \sim t_{n-k-1}$

where k + 1 is the number of unknown parameters in the population model (*k* slope parameters and the intercept, β_0).

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- Theorem 4.2 is important in that it allows as to test hypothesis involving the β_i .
- Compare this result with Theorem 4.1. The t distribution comes from the fact that the constant σ in $sd(\hat{\beta}_i)$ has been replaced with the random variable $\hat{\sigma}$.



Are the normal and *t* distributions very different?.



Generally not, they are very similar in shape. Both symmetric and centered around zero, but...

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they are quite different at the tails. And these are the important parts of the distributions in hypothesis testing.

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The 2.5% tail of a normal distribution starts 1.96 standard deviations from its mean.

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The 2.5% tail of a *t* distribution with 10 degrees of freedom starts 2.33 standard deviations from its mean.

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Consider the null hypothesis,

 $H_0: \beta_j = 0$

Since β_j measures the partial effect of x_j on y, after controlling for all other independent variables, $H_0: \beta_j = 0$ means that, once $x_1, x_2,$ $\dots, x_{j-1}, x_{j+1}, \dots, x_k$ have been accounted for, x_j has *no effect* on y.

This is called a **significance test**.

• The statistic we use to test $H_0: \beta_j = 0$, against any alternative, is called "the" *t* statistic or "the" *t* ratio of $\hat{\beta}_i$ and is defined as

~

$$t_{\hat{\beta}_j} \equiv \frac{\beta_j}{se(\hat{\beta}_j)}$$

Why is this a good statistic to test this hypothesis?

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- $\text{Since } se(\hat{\beta}_j) > 0, t_{\hat{\beta}_j} \text{ will have the same sign} \\ as \hat{\beta}_j.$
- In order to test H₀: β_j = 0; first, it is natural to look at our unbiased estimator of β_j, β̂_j.
 In a given sample β̂_j will never be zero exactly, but a small value will indicate a true null, whereas a big value will indicate a false null.



- We must recognize that there is a sampling error in our estimate β_j, so the size of β_j must be weighted against its sampling error.
 This is precisely what we do using t_{β_j}, since this statistic measures how many estimated
 - standard deviations $\hat{\beta}_j$ is away from zero.
In order to determine a rule for rejecting H₀, we need to decide on the relevant alternative hypothesis.

First, consider a one-sided alternative of the form

 $\mathrm{H}_1: \beta_j > 0$

How should we choose a rejection rule?

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- First, decide on a significance level, α, or the probability of rejecting H₀ when it is in fact true, i.e. $\alpha = .05$.
- While $t_{\hat{\beta}_j}$ has a *t* distribution under H₀, so it has zero mean, under the alternative $\beta_j > 0$, so the expected value of $t_{\hat{\beta}_j}$ is positive.
- Thus we are looking for a "sufficiently large" positive value of $t_{\hat{\beta}_j}$ in order to reject H_0 : $\beta_j = 0$ in favor of H_1 : $\beta_j > 0$.

- ♦ Negative values of t_{βj} provide no evidence in favor of H₁: β_j > 0.
 ♦ The definition of a "sufficiently large", with α = .05, is the 95th percentile in a t distribution with n k 1 degrees of freedom, say c.
- **Rejection rule**: Reject $H_0: \beta_j = 0$ in favor of $H_1: \beta_j > 0$ at $\alpha = .05$ if $t_{\beta_j} > c$





Example of a rejection rule for 28 degrees of freedom.

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- By our choice of the critical value c, rejection of H₀ will occur for 5% of all random samples when H₀ is true.
- This is an example of a **one-tailed test**.
- In order to obtain c, we only need the significance level and the degrees of freedom.
- You should note a pattern in the critical values of the *t* distribution: as α falls, *c* increases.





Thus, if H_0 is rejected at, say, the 1% level, then it is automatically rejected at the 5% level.

t distribution

t Distribution: Critical values of t

Degrees of								
freedom	One-tailed test	5%	6 2	2.5%	1%	0.5%	0.1%	0.05%
1		6.31	4 12	2.706	31.821	63.657	318.31	636.62
2		2.92	0 4	4.303	6.965	9.925	22.327	31.598
3		2.35	3 3	3.182	4.541	5.841	10.214	12.924
4		2.13	2 2	2.776	3.747	4.604	7.173	8.610
5		2.01	5 2	2.571	3.365	4.032	5.893	6.869
				•				
				•				
18		1.73	4 2	2.101	2.552	2.878	3.610	3.922
19		1.72	9 2	2.093	2.539	2.861	3.579	3.883
20		1.72	5 2	2.086	2.528	2.845	3.552	3.850
		•••	••	•				
		•••	••	•				•••
120		1.65	8 ´	1.980	2.358	2.617	3.160	3.373
00		1.64	5	1.960	2.326	2.576	3.090	3.291
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Normal versus t distributions

As the degrees of freedom (*df*) in the *t* distribution gets large, the *t* distribution approaches the standard normal distribution.



Consider the one sided alternative,



The rejection rule is just the mirror image of the previous case. Now, the critical value comes from the left tail of the *t* distribution.

 $H_1: \beta_i < 0$



In practice, it is easiest to think of the **rejection rule** as: Reject $H_0: \beta_j = 0$ in favor of $H_1: \beta_j < 0$ at $\alpha = .05$ if $t_{\beta_j} < -c$, where *c* is the critical value for $H_1: \beta_j > 0$.

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Example of a rejection rule for 28 degrees of freedom.

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For simplicity, we always assume c is positive, since this is how critical values are reported in t tables, and so -c is a negative number.

To reject H_0 against the alternative $H_1: \beta_j < 0$, we must get a negative *t* statistic. A positive *t* ratio, no matter how large, provides no evidence in favor of $H_1: \beta_i < 0$.

• Consider now the null hypothesis $H_0: \beta_j = 0$ against a two sided-alternative

 $H_1: \beta_i \neq 0$



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- When the alternative is two-sided, we are interested in the *absolute value* of the *t* statistic.
- **♦ Rejection rule**: Reject H₀: β_j = 0 in favor of H₁: β_j ≠ 0 at α = .05 if $|t_{\beta_j}| > c$, where |•| denotes absolute value and *c* is an appropriately chosen critical value.

- Siven α, for a **two-tailed test**, *c* is chosen to make the area in each tail of the *t* distribution equal to $\alpha/2$.
- Hence, for $\alpha = .05$, *c* is chosen to make the area in each tail of the *t* distribution equal to 0.025.
- ♦ In other words, *c* is the 97.5th percentile in the *t* distribution with n k 1 df.







Example of a rejection rule for 28 degrees of freedom and a two-sided alternatives.



As before, if H_0 is rejected at, say, the 1% level, then it is automatically rejected at the 5% level.

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t distribution

t Distribution: Critical values of t

Degrees of	Two-tailed test	10%	5%	2%	1%	0.2%	0.1%
freedom	One-tailed test	5%	2.5%	1%	0.5%	0.1%	0.05%
1		6.314	12.706	31.821	63.657	318.31	636.62
2		2.920	4.303	6.965	9.925	22.327	31.598
3		2.353	3.182	4.541	5.841	10.214	12.924
4		2.132	2 2.776	3.747	4.604	7.173	8.610
5		2.015	5 2.571	3.365	4.032	5.893	6.869
18		1.734	2.101	2.552	2.878	3.610	3.922
19		1.729	2.093	2.539	2.861	3.579	3.883
20		1.725	5 2.086	2.528	2.845	3.552	3.850
120		1.658	3 1.980	2.358	2.617	3.160	3.373
8		1.645	5 1.960	2.326	2.576	3.090	3.291

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- When a specific alternative is not stated, it is usually considered to be two-sided.
- If H_0 is rejected in favor of H_1 at $\alpha = 5\%$, we usually say that " x_j is **statistically significant** at the 5% level".
- ♦ If H_0 is not rejected, we say that " x_j is **statistically insignificant** at the 5% level".

The two-sided significance test we have just seen is calculated routinely by regression software for each variable included in a model.

These tests and associate probability values are reported together with estimates and standard errors.



Other Hypothesis about β_i

The rejection rule, one or two tails, depend on the form of the alternative.

- We have explained the classical approach:
- 1. State H_0 and H_1 , the last one either explicitly or implicitly.
- 2. Choose α , which determines *c* (i.e. the rejection region).
- Compare the value of the *t* statistic with *c*.
 Eventually H₀ is either rejected or nor rejected at the given α.

- To some extend the classical approach is in some sense arbitrary, since we have to choose α in advance, and eventually H_0 is either rejected or not.
- If H_0 is eventually rejected, we don't know if this rejection is strong o weak. And the same is true if H_0 is not rejected.

Instead of testing at a given α, consider de following question: "Given the observed value of the *t* statistic, what is the smallest significance level at which H₀ would be rejected? This level is known as the *p*-value for the test".



That is, the *p*-value is the significance level of the test when we use the value of the test statistic as the critical value for the test.

Example: Assume df = 40 and $t_{\beta_j} = 1.85$. What would be the *p*-value for a two-tailed tests? p-value = Pr(|T| > 1.85) = 2.Pr(T > 1.85) = 2(.0359) = .0718This means that, if the H₀ is true, we would observe an absolute value of the *t* statistic as large as 1.85 about 7.2% of the time. This provides some evidence against H₀, since it

would be rejected at $\alpha = 10\%$, but not at $\alpha = 5\%$. What would be the *p*-value for a positive one-tailed alternative? And for a negative one?





The *p*-value takes as the critical value the observed value of the test statistic, and from this computes the significance level of the test.

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- This example shows that once the *p*-value has been computed, a classical test can be carried out at any desired level.
- If α denotes the significance level of the test,
 then H₀ is rejected if *p*-value < α; otherwise,
 H₀ is not rejected at the 100.α% level.

- The *p*-value nicely summarizes the strength or weakness of the empirical evidence against H_0 .
- A useful interpretation is the following: the *p*-value is the probability of observing a *t* statistic as extreme as we did if the null hypothesis is true.



This means that small *p*-values are evidence against H₀; large *p*-values provide little evidence against H_0 .

- Since a *p*-value is a probability, its value is always between 0 and 1.
- To compute *p*-values we need a very detailed statistical tables or a computer program that computes areas under probability density functions.
- You don't have to worry about because statistical software computes *p*-values for all statistical tests.

A Note on Terminology

- When H_0 is not rejected, we prefer to say: "we fail to reject H_0 at the α % level", rather than " H_0 is accepted at the α % level".
- The reason why the former is preferred is that, if we change the value of H₀ a little bit, we can also "accept" this new hypothesis, which is meaningless. We cannot "accept" both of these hypothesis.
- All we can say is that the data does not allow us to reject either of these hypothesis. So our sample is consistent with both of them.

Economic *versus* Statistical Significance

So far we have emphasized statistical significance. However it is important to remember that we should pay attention to the magnitude of the coefficient estimates in addition to the *t* statistics.

• Statistical significance of a variable x_j is determined entirely by the size of $t_{\hat{\beta}_j}$, whereas the economic significance of a variable is related to the size (and sign) of $\hat{\beta}_j$.

Economic versus **Statistical Significance**

Too much focus on statistical significance can lead to the false conclusion that a variable is "important" for explaining y even though its estimated effect is modest.

So even if a variable is statistically significant, you need to discuss the magnitude of the estimated coefficient to get an idea of its practical or economic importance.

This step requires some care, depending on how the variables appear in the equation.

- ♦ Under the CLM, we can easily construct a **confidence interval** (CI) for the population parameter, $β_i$.
- CI are also called interval estimates, because they provide a range of likely values for β_j, and not just a point estimate.



$$\frac{\hat{\beta}_j - \beta_j}{se(\hat{\beta}_j)} \sim t_{n-k-1}$$

a simple manipulation leads to a CI for the unknown β_j .

• A 95% CI, is given by $\hat{\beta}_j \pm c.se(\hat{\beta}_j)$

where *c* is the 97.5th percentile in a t_{n-k-1} distribution.

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• More precisely, the lower and upper bounds of the confidence interval are given by $\underline{\beta}_{j} \equiv \hat{\beta}_{j} - c.se(\hat{\beta}_{j})$

and

$$\overline{\beta}_j \equiv \hat{\beta}_j + c.se(\hat{\beta}_j)$$

respectively.
Confidence Intervals: Meaning

♦ If random samples were obtained over and over again, with β_j, and β_j computed each time, then the (unknown) population value β_j would lie in the interval (β_j, β_j) for (1 − α)% of the samples.

♦ Unfortunately, for the single sample that we use to construct the CI, we do not know whether $β_i$ is actually contained in the interval.

Confidence Intervals

- Once a CI is constructed, it is easy to carry out two-tailed hypothesis tests.
- ♦ If the null hypothesis is H₀: $β_j = a_j$, then H₀ is rejected against H₁: $β_j ≠ a_j$ at (say) the 5% significance level if, and only if, a_j is *not* in the 95% CI.
- Hence all values contained in the CI are consistent with our data, in the sense that wouldn't be rejected in a two-tailed test.

- In many applications we are interested in testing hypothesis involving more than one of the population parameters.
- **Example:** Cobb-Douglas Production Function $\log(y) = \beta_0 + \beta_1 \log(l) + \beta_2 \log(k) + u$ Hypothesis of interest: Constant Returns

$$\mathbf{H}_0: \boldsymbol{\beta}_1 + \boldsymbol{\beta}_2 = 1$$

Against

$$H_1: \beta_1 + \beta_2 \neq$$

- We cannot simply use the individual *t* statistics for $\hat{\beta}_1$ and $\hat{\beta}_2$ to test H₀.
- ♦ However, it is easy to see that the *t* statistic is now based on whether the estimated sum $\hat{\beta}_1 + \hat{\beta}_2$ is sufficiently different from one to reject H₀ in favor of H₁.

To account for the sampling error in our estimators, we standardize this sum by dividing by the standard error

$t_{\hat{\beta}_1+\hat{\beta}_2} = \frac{\hat{\beta}_1 + \hat{\beta}_2 - 1}{se(\hat{\beta}_1 + \hat{\beta}_2)}$

Once we have the *t* statistic, testing proceeds as before. We choose a significant level for the test, α, and, based on the *df*, obtain a critical value, *c*.

- Or, we compute the *t* statistic and then compute the *p*-value of the test.
- The procedure is the same if H_1 is a one sided alternative, H_1 : $\beta_1 + \beta_2 < 1$ or H_1 : $\beta_1 + \beta_2 > 1$.
- The only tedious part in obtaining $t_{\hat{\beta}_1+\hat{\beta}_2}$ is $se(\hat{\beta}_1+\hat{\beta}_2)$, since you cannot compute it from the individual standard errors of the estimates, that is the information you get from the
 - regression output.



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- Many econometric software packages have an option to display estimates of the covariance terms like $Cov(\hat{\beta}_1, \hat{\beta}_2)$.
- ♦ More generally, we can always restate the problem to get the test we want.
- ♦ So in practice is usually much easier to estimate a different model that directly delivers the standard error of interest.

♦ Lets see our previous example.

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Testing a Linear Combination • Define $\theta = \beta_1 + \beta_2 - 1$, so $H_0: \theta = 0$. From this $\beta_1 = \theta - \beta_2 + 1$, so substitute β_1 in the original equation $\log(y) = \beta_0 + (\theta - \beta_2 + 1) \log(l) + \beta_2 \log(k) + u$ Hence $\log(y/l) = \beta_0 + \theta \log(l) + \beta_2 \log(k/l) + u$ Regress $\log(y/l)$ on a constant, $\log(l)$ and $\log(k/l)$; and get the *t* statistic $t_{\hat{\theta}} = \frac{\hat{\theta}}{se(\hat{\theta})}$ from the regression output.

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- The strategy of rewriting the model, so that it contains the parameter of interest, works in all cases and is usually easy to implement.
- Other examples of hypotheses about a single linear combination of parameters are:

 $\beta_1 = \beta_2; \ \beta_1 = -(1/2)\beta_2; \ \beta_1 = 1 + \beta_2; \ \beta_1 = 5\beta_2;...$

Multiple Linear Restrictions

So far, we have only considered hypothesis involving a *single* restriction. But frequently, we wish to test *multiple* hypothesis about the underlying parameters $\beta_0, \beta_1, \beta_2, \dots, \beta_k$. • We begin with the leading case of testing whether a set of independent variables has no partial effect on the dependent variable, y. These are called **exclusion restrictions**.

Example: Consider the model

- $y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5 + u$
- A typical example of exclusion restrictions is

$$H_0: \beta_3 = \beta_4 = \beta_5 = 0$$

This is an example of a set of **multiple restrictions**, because we are putting more than one restriction on the parameters in the above equation.

- A test of multiple restrictions is called a multiple hypothesis test or a joint hypothesis test.
- As before we need:
- 1. H_1 , either explicitly or implicitly.
- 2. A significance level, α .
- 3. A statistic whose distribution is known under H_0 .
- 4. A critical value, *c*, which determines the rejection region.

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- We do not have the statistical background necessary to cover tests that have more power under multiple one-sided alternatives. \diamond To test H₀ it is temping to use the individual
 - t statistics on x_3 , x_4 and x_5 .
- This option is not appropriate.
- A particular *t* statistic tests a hypothesis that puts no restriction on the other parameters.



We need a way to test exclusion restrictions *jointly*.

- It turns out that the sum of squared residuals, SSR, provide us with a very convenient basis for testing multiple hypothesis.
 Before we go into the details of the statistic to use, we need two more concepts in
 - relation to H₀.
- **1. Unrestricted model**: The model we begin with.



In the above example the restricted model

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + u$$



The restricted model is obtained by imposing H_0 on the original model.

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 ♦ Moreover it is always true that SSR_r ≥ SSR_{ur} where SSR_r is the SSR of the restricted model, and SSR_{ur} is the SSR of the unrestricted model.

To see this, note that imposing restrictions on a model cannot lower the SSR. Remember that, because OLS estimates are chosen to minimize the sum of squared residuals, the SSR never decreases (and generally increases) when some restrictions (like dropping variables) are introduced into the model.



This is an algebraic fact.

Hence, even if the SSR itself tells us nothing about the truth of H_0 . The increase in the SSR when the restrictions are imposed can tell us something about the likely truth of H_0 .



◆ If we get a large increase, this is evidence against H_0 , and this hypothesis will be rejected.



◆ If the increase is small, this is not evidence against H_0 , and this hypothesis will not be rejected.

- The question is then whether the observed increased in the SSR when the restrictions are imposed is large enough, relative to the SSR in the unrestricted model, to warrant rejecting H_0 .
- In others words, what we need to decide is whether the increased in the SSR in going from the unrestricted model to the restricted model is large enough to warrant rejection of H_0 .

 \diamond As with all testing, the answer depends on α . \diamond But we cannot carry out the test at a chosen α until we have a statistic whose distribution is known, and can be tabulated, under H_0 . Thus, we need a way to combine the information in SSR, and SSR, to obtain a test statistic with a known distribution under H_0 .



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Unrestricted model: y = β₀ + β₁x₁ + β₂x₂ + ... + β_kx_k + u We have *q* exclusion restrictions to test, that is, H₀ states that *q* of the variables have zero coefficients.

Assuming that they are the last q variables, H₀ is stated as $H \cdot B = B = -B = 0$

Restricted model:



• Obtained by imposing H_0 on the unrestricted model.



$H_1: H_0$ is **not** true

The *F* statistic, or *F* ratio, is defined by

$$F = \frac{\left(\text{SSR}_r - \text{SSR}_{ur}\right)/q}{\text{SSR}_{ur}/(n-k-1)}$$

where SSR_r is the SSR of the restricted model, and SSR_{ur} is the SSR of the unrestricted model.



$SSR_r \ge SSR_{ur} \implies F \ge 0$

- The easiest way to remember where the SSR's appear is to think of F as measuring the relative increase in SSR when moving from the unrestricted to the restricted model.
- The difference in SSR's in the numerator of *F* is divided by *q*, which is the number of restrictions imposed in moving from the unrestricted to the restricted model.

Note that we can write

q = numerator degrees of freedom = df_r - df_{ur} so q is the difference in the df between the restricted and unrestricted model, df_r > df_{ur}.
♦ The SSR in the denominator of F is divided by df_{ur}.

n-k-1 = **denominator degrees of freedom** $= df_{ur}$

• In fact, the denominator of *F* is just the unbiased estimator of $\sigma^2 = Var(u)$ in the unrestricted model.

 $\hat{\sigma}^2 = \frac{\text{SSR}_{ur}}{n-k-1}$

In order to use the *F* statistic for hypothesis testing, we must know its sampling distribution under H₀ in order to choose *c* for a given α, and determine the rejection rule.

- It can be shown that, under H_0 , and assuming the CLM assumptions hold, the *F* statistic is distributed as an *F* random variable with
 - (q, n-k-1) df.

We write this result as

 $F \sim F_{q,n-k-1}$ on H_0

The $F_{q,n-k-1}$ distribution is readily tabulated and available in statistical tables.

 \clubsuit It is pretty clear from the definition of F that we will reject H_0 in favor of H_1 when F is sufficiently "large".



 \diamond As usual, how large depends on α .

• For $\alpha = .05$, let c be the 95th percentile in the $F_{a.n-k-1}$ distribution. This critical value depends on q, the numerator df, and on n-k-1, the denominator df.

The rejection rule is quite simple.

• **Rejection rule**: Reject H_0 in favor of H_1 at the given α if F > c, where *c* is the corresponding percentile in the $F_{q,n-k-1}$ distribution.



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The F statistic



Example of a rejection rule: Reject H₀ at $\alpha = .05$ if F > c.

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• If H_0 is rejected, then we say that x_{k-q+1} , x_{k-q+2}, \ldots, x_k are jointly statistically significant, or just *jointly significant*, at the appropriate significance level. This tests alone does not allow us to say which of the variables has a partial effect on y; they may all affect y or maybe only one affects y.

• If H_0 is not rejected, then we say that x_{k-q+1} , x_{k-q+2}, \ldots, x_k are **jointly statistically insignificant**, or just *jointly insignificant*, which often justifies dropping them from the model.

The *F* statistic is often useful for testing
 exclusion of a group of variables when the
 variables in the group are highly correlated.

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Relation between F and t Statistics

We have just seen how to use the F statistic to test whether a group of variables should be included in the model.



 \diamond What happens if we apply the *F* statistic to the case of testing significance of a *single* independent variable?



• This is, when q = 1 and H_0 : $\beta_k = 0$?

• We know that the *t* statistic on β_k can be used to test this hypothesis.

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Relation between F and t Statistics

- Do we have two different ways of testing the same H₀: $\beta_k = 0$?
- The answer is **no**.
- It can be shown that the *F* statistic for testing H₀: $\beta_k = 0$, is just equal to the square of the corresponding t statistic.

Hence, the two approaches lead to exactly the same outcome, provided that the alternative is two-sided.

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Relation between F and t Statistics

- It can be shown that $t_{n-k-1}^2 \equiv F_{1,n-k-1}$.
- But, the *t* statistic is more flexible for testing a single hypothesis, because it can be used to test against one-sided alternatives.
- Moreover, since the *t* statistics are also easier to obtain than the *F* statistics, there is really no good reason to use an *F* statistic to test a single hypothesis. Use a *t* test instead.

Relation between F and t Statistics

- **Remember**: The *F* statistic is intended to detect whether any combination of a set of coefficients is jointly different from zero, but it is never the best test for determining whether a single coefficient is different from zero.
- Hence, if we fail to reject H_0 there is always the possibility that a single variable will be significant.
- The *t* test is best suited for testing a single hypothesis.

The *R*-Squared form of the *F* Statistic

• It often convenient to have a form of the Fstatistic that can be computed from the R^2 of the restricted and unrestricted models.

• Using the fact that $SSR_r = SST.(1 - R_r^2)$ and $SSR_{ur} = SST.(1 - R_{ur}^2)$, we can write the *F* as

$$F = \frac{\left(R_{ur}^{2} - R_{r}^{2}\right)/q}{\left(1 - R_{ur}^{2}\right)/(n - k - 1)}$$

since the SST term cancels.

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The R-Squared form of the F Statistic

This is called the *R*-squared form of the *F* statistic.

Warning: Whereas the *R*-squared form of the *F* statistic is very convenient for testing exclusion restrictions, it cannot be applied for testing all kind of linear restrictions.
 More on this later on.

Computing *p*-values for *F* Tests

In the F testing context, the p-value is defined as

$$p$$
-value = $\Pr(\Im > F)$

where \Im denotes an *F* random variable with (q, n-k-1) df, and *F* is the actual value of the test statistic.

Computing *p*-values for *F* Tests

The *p*-value still have the same interpretation as it did for t statistics: It is the probability of observing a value of F at least as large as we did, given that the null hypothesis is true.



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And H₁ is that at least one of the β_j is different from zero,
 H₁: β_i ≠ 0 for some j

The restricted model is

 $y = \beta_0 + u$

• For this model $\hat{\beta}_0 = \overline{y}$, $\hat{u}_i = y_i - \overline{y}$ and $R^2 = 0$

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♦ Therefore, the *F* statistic for testing H₀ can be written as $F = \frac{R^2/k}{(1-R^2)/(n-k-1)}$

where \mathbb{R}^2 is just the usual *R*-squared from the regression of *y* on $x_1, x_2, ..., x_k$.

• Warning: This special form of the F statistic is valid only for testing joint exclusion restriction of all independent variables, excluded the intercept.

This is called testing the overall significance of the regression, and it is usually computed by regression software after OLS estimation.

- Sometimes we are interested in testing multiple joint restrictions, which not all are of the exclusion form.
- For example, in a model with k = 5, H₀: β₁ = β₂, β₃ = 1, β₄ = 0, β₅ = 0
 The important thing we should remember is that the SSR form of the *F* test can always be applied in these situations.

- All we need is the SSR of the restricted and unrestricted models.
- \diamond In order to get SSR, we have to impose the restrictions on the model, to get the restricted model.



Note that this can involve redefining some variables, before the restricted model can be estimated.

♦ In the previous example the restricted model **1**S $y = \beta_0 + \beta_1 x_1 + \beta_1 x_2 + x_3 + u$ but before we can estimate it, we should write the model as $y - x_3 = \beta_0 + \beta_1(x_1 + x_2) + u$ So to get SSR, we regress $y - x_3$ on $x_1 + x_2$.

 Once the restricted and unrestricted model have been estimated, the *F* statistic is computed in the usual way, using SSR from both models.

Warning: We cannot use the *R*-squared form of the *F* statistic in this example because the dependent variable in the restricted and the unrestricted model is different. This means that the SST are different in the two regressions and both formulas are no longer equivalent.

As a general rule, the SSR form of the *F* statistic should be used if a different dependent variable is needed in running the restricted regression.

- Some guidelines on how to report multiple regression results:
- 1. Estimated OLS coefficients should always be reported.
- 2. For the key variables in an analysis, you should *interpret* the estimated coefficients.
 This often requires knowing the units of measurement of the variables.

- 3. The economic or practical importance of the estimates of the key variables should be discussed.
- 4. The standard errors should always be included along with the estimated coefficients.
 - Better standard errors than t statistics.
- 5. The *R*-squared from the regression should always be included.

- 6. Reporting the overall significant *F* test, and its *p*-value, is good practice.
- 7. Reporting SSR and the standard error of the regression is good practice, but it is not crucial.
- 8. The number of observations, *n*, should be reported.
- 9. Reporting can be done in equation form, or in table form for many equations at a time.

- 10. This list will be updated as more material is covered.
 - In particular when we study misspecification tests.