# Hypothesis Testing Cheat Sheet

## Basic Idea:

How to decide if it is reasonable to conclude that an underlying true parameter (e.g. $\beta$ in a regression model $y = \beta_0 + \beta x + \epsilon$) is equal to a particular value $h_0$ on the basis of an estimate $\hat{\beta}$?

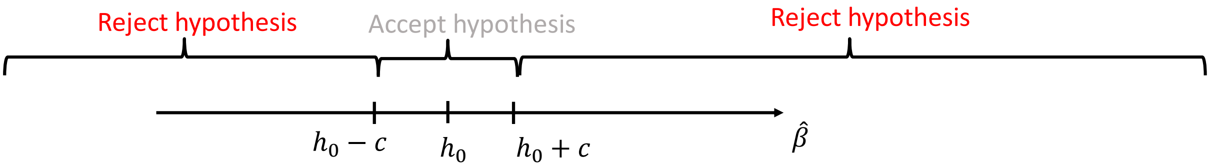
We call this a hypothesis about $\beta$ and call it the Null Hypothesis,

$$\text{H0: } \beta = h_0.$$

We also take note of what must be the case if H0 is not true. This is called the Alternative Hypothesis written as

$$\text{H1: } \beta \neq h_0$$

We will reject H0 (i.e. conclude that $\beta$ is probably not equal to $h_0$) if the estimate $\hat{\beta}$ is quite far away from $h_0$ (i.e. if $\hat{\beta}$ is either much bigger or much smaller than $h_0$).



But how far is *too far* exactly? Or in terms of the figure above: how big is $c$? This depends on the reliability of the estimate $\hat{\beta}$. If we know that the estimate is imprecise – i.e. there is a high likelihood that $\hat{\beta}$ is very far away from $h_0$ even if H0 is true, then we would tolerate higher values for *c*.

With the Monte-Carlo Analysis we have seen that

- $\hat{\beta}$ is (approximately) normally distributed
- The estimate is more precise (i.e. the standard error $\sigma_{\hat{\beta}}$ is smaller) if the variance of the error ($\sigma_\epsilon^2$ ) is smaller or the variance of the explanatory variable x is larger.

After running a regression it is possible to estimate $\sigma_{\hat{\beta}}$ (i.e. we can label this estimate $\hat{\sigma}_{\hat{\beta}}$) and R provides this estimate as part of its regression output. Here is an example:

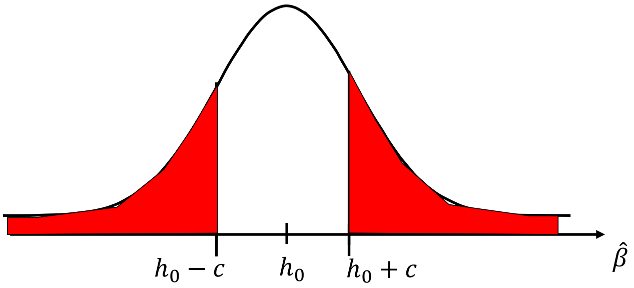
```
df=read_dta("../data/foreigners.dta")

 df['crimesPc']=df$crimes11/df$pop11
 reg1=lm(crimesPc~b_migr11,df)
 summary(reg1)

##
## Call:
## lm(formula = crimesPc ~ b_migr11, data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5886 -0.3789 -0.1038  0.2046 14.0988
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.992957   0.079387  12.508  < 2e-16 ***
## b_migr11    0.037630   0.005088   7.396 1.23e-12 ***
## ---
```

Estimate of standard error for slope parameter

Hence, we can use the bell-shaped normal distribution (with mean $h_0$ and standard error $\hat{\sigma}_{\hat{\beta}}$ ; i.e. $N(h_0, \hat{\sigma}_{\hat{\beta}})$ ) to work out the likelihood is for $\hat{\beta}$ to fall in the rejection area even though it is true; i.e. it is the combined area under the bell curve in the tails of the distribution for a given c.



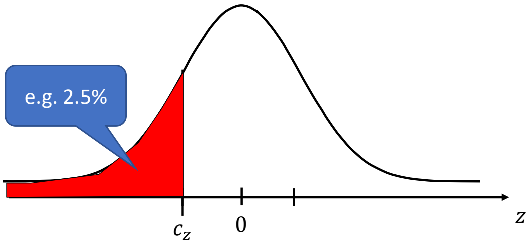
Equally we can work out which $c$ goes along with a given desired probability. This latter approach is what we do in hypothesis testing. We decide first what probability (i.e. risk that we reject the hypothesis even though it is correct) we find acceptable (e.g. 1%, 5% or 10%) and we then work out the relevant c. Those risk levels are also referred to as significance levels.

## Implementation

It turns out that instead of working out the c for a given distribution $N(h_0, \hat{\sigma}_{\hat{\beta}})$ it's sufficient to work out the relevant threshold numbers only once for the Standard Normal Distribution $N(0,1)$. The reason for this that an estimate that is Normally distributed can always be converted into one that is Standard Normally distributed by subtracting its expected value and dividing by its standard error; i.e. by computing

$$z = \frac{\hat{\beta} - h_0}{\sigma_\beta}$$

Thus, we can compare $z$ to the thresholds for the standard normal distribution. To find those in turn we can use the qnorm() R-function which is the inverse of the cumulative density function. You have to provide qnorm with a probability (e.g. 0.025) and it will tell you for which value $c_z$ the left tail of the normal distribution will correspond to that probability



**qnorm(0.025)   =   -1.959964**

Similarly, we can find the thresholds for other possible significance levels

**qnorm(0.005)   =   -2.575829** for 1%

**qnorm(0.05)   =   -1.644854** for 10%

So if we find a $\hat{\beta}$=`0.037630` (as in the example above) and $\sigma_{\hat{\beta}} = 0.005088$ and we are testing the hypothesis that $\beta$ could be zero (H0: $\beta = 0$) we need to check if $\frac{0.037630-0}{0.005008} = 7.513978$ is within the interval implied by those values (i.e. in this case we would reject the hypothesis even if we only allowed for a small significance level).

## What about t-statistics?

The so-called t statistic is like the z value above except that we now allow the standard error to be estimated as well:

$$t = \frac{\hat{\beta} - h_0}{\widehat{\sigma_\beta}}$$

Hence, because in practice we never know $\sigma_\beta$ this is what we compute in practice. As a consequence, rather than being Standard Normally distributed, t is t distributed. Luckily this does not matter much in practice because the t distribution is almost identical to the standard normal distribution, provided our sample is large enough; e.g. at 12 observations the 5% threshold value would be 2.228. However, at 100 observations the threshold is -1.984467; i.e. fairly close to the 1.96 found with the normal distribution. You can work this out with the qt(0.025, 98) command where the second number refers to the degrees of freedom; i.e. the number of observations minus the number of parameters in your model (i.e. 2 in our case: intercept and slope).

## P-values

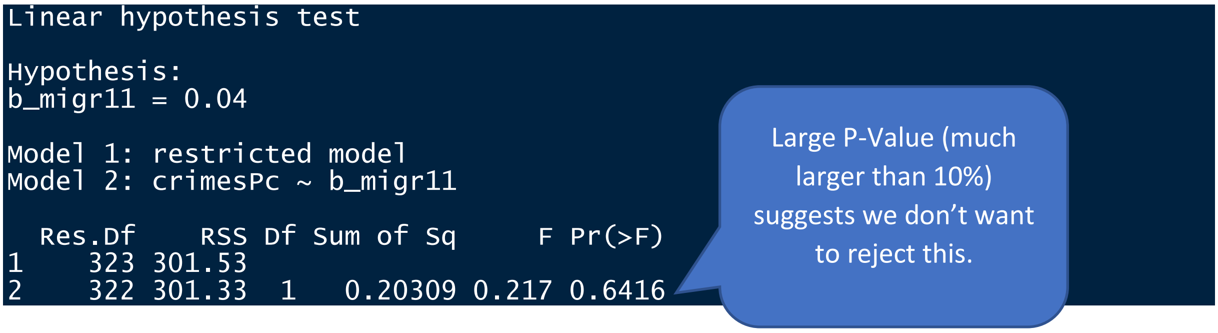
An even simpler way of doing the same thing (i.e. hypothesis test) involves P values. In the past without computers this was hard but now this is easy. P values for the hypothesis test H0: $\beta = 0$ are routinely reported along with regression output; e.g. in R it's the values in the column **`Pr(>|t|)`**.

The P value is the significance level you would have to choose if the value you estimated was equal to the rejection threshold; i.e. $|\hat{\beta} - h_0| = c$. Hence, thus if P is very small (smaller than your desired significance level) then you would reject the hypothesis. If it is rather large (larger than your desired significance level) than you don't reject your hypothesis.

You can get P-values for tests other than H0: $\beta = 0$ using the linearHypothesis command (part of library(“car”)).

For example if you wanted to check if the migration coefficient in the example above is equal to 0.04 you could run the command

```
linearHypothesis(reg1, c( "b_migr11= 0.04") )
```



```
Linear hypothesis test

Hypothesis:
b_migr11 = 0.04

Model 1: restricted model
Model 2: crimesPc ~ b_migr11

  Res.Df    RSS Df Sum of Sq     F Pr(>F)
1    323 301.53
2    322 301.33  1   0.20309 0.217 0.6416
```

Large P-Value (much larger than 10%) suggests we don’t want to reject this.