

In-class Lab 2

ECON 4223 (Prof. Tyler Ransom, U of Oklahoma)

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The purpose of this lab is to practice using R to conduct hypothesis tests and run a basic OLS regression. The lab should be completed in your group. To get credit, upload your .R script to the appropriate place on Canvas.

For starters

Open up a new R script (named ICL2_XYZ.R, where XYZ are your initials) and add the following to the top:

```
library(tidyverse)
library(skimr)
library(broom)
library(wooldridge)
```

Load the dataset `audit` from the `wooldridge` package, like so:

```
df <- as_tibble(audit)
```

A one-tailed test

The `audit` data set contains three variables: `w`, `b`, and `y`. The variables `b` and `w` respectively denote whether the black or white member of a pair of resumes was offered a job by the same employer. `y` is simply the difference between the two, i.e. `y=b-w`.

We want to test the following hypothesis:

$$H_0 : \mu = 0 \quad H_a : \mu < 0$$

where $\mu = \theta_B - \theta_W$, i.e. the difference in respective job offer rates for blacks and whites.

The `t.test()` function in R

To conduct a t-test in R, simply provide the appropriate information to the `t.test` function.

How do you know what the “appropriate information” is?

- In the RStudio console, type `?t.test` and hit enter.
- A help page should open in the bottom-right of your RStudio screen. The page should say “Student’s t-Test”
- Under **Usage** it says `t.test(x, ...)`.
 - This means that *at minimum* we only have to provide it with is some object `x`. The `...` signals that we can provide it more than just `x`.
- Under **Arguments** it explains what `x` is: “a (non-empty) numeric vector of data values”
 - This means that R is expecting us to pass a column of a data frame to `t.test()`

- The other information in the help explains default settings of `t.test()`. For example:
 - `alternative` is "two.sided" by default
 - `mu` is 0 by default
 - ... other options that we won't worry about right now

Now let's do the hypothesis test written above. Add the following code to your script:

```
t.test(df$y, alternative="less")
```

R automatically computes for us the t-statistic using the formula

$$\frac{\bar{y} - \mu}{SE_{\bar{y}}}$$

All we had to give R was the sample of data (`y`, in our case) and the null value (0, which is the `t.test` default)!

Interpreting the output of `t.test()`

Now that we've conducted the t-test, how do we know the result of our hypothesis test? If you run your script, you should see something like

```
> t.test(df$y, alternative="less")

One Sample t-test

data:  df$y
t = -4.2768, df = 240, p-value = 1.369e-05
alternative hypothesis: true mean is less than 0
95 percent confidence interval:
 -Inf -0.08151529
sample estimates:
mean of x
-0.1327801
```

R reports the value of the t-statistic, how many degrees of freedom, and the p-value associated with the test. R *does not* report the critical value, but the p-value provides the same information.

In this case, our p-value is approximately 0.00001369, which is much lower than 0.05 (our significance level). Thus, we reject H_0 .

A two-tailed test

Now suppose instead we want to test if job offer rates of blacks are *different* from those of whites. We want to test the following hypothesis:

$$H_0 : \theta_b = \theta_w \quad H_a : \theta_b \neq \theta_w$$

This hypothesis test considers the case where there might be *reverse discrimination* (e.g. through affirmative action policies).

The code to conduct this test is similar to the code we used previously. (Add the following code to your script:)

```
t.test(df$b,df$w,alternative="two.sided",paired=TRUE)
```

You'll notice that the t-statistic is the exact same (-4.2768) for both of the tests. But the p-value for the two-tailed test is twice as large (0.00002739). This is because the two-tailed test must allow for the possibility of either direction of the \neq sign. (In other words, that the job offer rate for blacks could be higher or lower than for whites.)

Your first regression (of this class)

Let's load a new data set and run an OLS regression. This data set contains year-by-year statistics about counties in the US. It has counts on number of various crimes committed, as well as demographic characteristics about the county.

```
df <- as_tibble(countymurders)
```

A handy command to get a quick overview of an unfamiliar dataset is `glimpse()`:

```
glimpse(df)
```

`glimpse()` tells you the number of observations, number of variables, and the name and type of each variable (e.g. integer, double).¹

Regression syntax

To run a regression of y on x in R, use the following syntax:

```
est <- lm(y ~ x, data=data.name)
```

Here, `est` is an object where the regression coefficients (and other information about the model) is stored. `lm()` stands for “linear model” and is the function that you call to tell R to compute the OLS coefficients. `y` and `x` are variables names from whatever `tibble` you've stored your data in. The name of the `tibble` is `data.name`.

Regress murder rate on execution rate

Using the `df` data set we created above, let's run a regression where `murders` is the dependent variable and `execs` is the independent variable:

```
est <- lm(murders ~ execs, data=df)
```

To view the output of the regression in a friendly format, type

```
tidy(est)
```

¹“double” means “double precision floating point” and is a computer science-y way of expressing a real number (as opposed to an integer or a rational number).

```
## # A tibble: 2 x 5
##   term      estimate std.error statistic      p.value
##   <chr>      <dbl>    <dbl>    <dbl>      <dbl>
## 1 (Intercept)    6.84    0.242    28.3    3.97e-174
## 2 execs         65.5    2.15    30.5    7.44e-202
```

In the `estimate` column, we can see the estimated coefficients for β_0 —(`Intercept`) in this case—and β_1 (`execs`). `est` also contains other information that we will use later in the course.

You can also look at the R^2 by typing

```
glance(est)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic      p.value    df logLik    AIC
##   *      <dbl>          <dbl> <dbl>    <dbl>      <dbl> <int>  <dbl>  <dbl>
## 1    0.0243         0.0243  46.6     930    7.44e-202     2 -196508 393021
## # ... with 3 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>
```

Again, there's a lot of information here, but for now just focus on the R^2 term reported in the first column.