Math 300 NTI Lesson 12

Simple Linear Regression - Discrete x

Professor Bradley Warner

June, 2022

Contents

Objectives	
Reading	
Lesson	
Documenting software	{

Objectives

- 1. Explore the relationship between 2 variables, one numerical and one categorical, using summary statistics and visualizations in R.
- 2. Fit a linear regression model to two variables, one numerical and one categorical, using the lm() function and interpret the output. This includes the interpretation of baseline mean and offsets.
- 3. Generate a table of observations, fitted values, and residuals from a linear regression object.

Reading

Chapter 5.2

Lesson

Remember that you will be running this more like a lab than a lecture. You want them using R and answering questions. Have them open the notes rmd and work through it together.

Work through the learning checks LC5.4 - LC5.7.

- The response y is the numeric variable. Math 378 discusses cases where the response is categorical. Understanding the regression output here is important. There is no line just a baseline average and offsets from that.
- The regression output will still predict the **mean** value of the response variable.
- The baseline is an average and is the first level of the factor based on alphabetic order.

Setup

```
library(tidyverse)
library(moderndive)
library(skimr)
library(gapminder)
```

Create the data needed for the exercises.

```
gapminder2007 <- gapminder %>%
filter(year == 2007) %>%
select(country, lifeExp, continent, gdpPercap)
```

Let's look at 5 random rows of data.

```
set.seed(1234)
gapminder2007 %>%
sample_n(size = 5)
```

```
## # A tibble: 5 x 4
##
     country
                     lifeExp continent gdpPercap
     <fct>
                       <dbl> <fct>
## 1 Congo, Dem. Rep.
                         46.5 Africa
                                             278.
## 2 Mali
                         54.5 Africa
                                            1043.
## 3 Peru
                                            7409.
                         71.4 Americas
## 4 Senegal
                         63.1 Africa
                                            1712.
## 5 Venezuela
                         73.7 Americas
                                           11416.
```

LC 5.4 (Objective 1)

(LC5.4) Conduct a new exploratory data analysis with the same explanatory variable x being continent but with gdpPercap as the new outcome variable y. Remember, this involves three things:

- Most crucially: Looking at the raw data values.
- Computing summary statistics, such as means, medians, and interquartile ranges.
- Creating data visualizations.

What can you say about the differences in GDP per capita between continents based on this exploration?

Solution:

• Looking at the raw data values:

glimpse(gapminder2007)

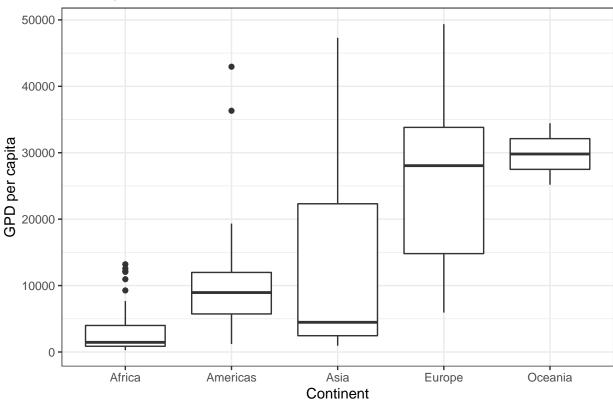
• Computing summary statistics, such as means, medians, and interquartile ranges:

```
gapminder2007 %>%
 select(gdpPercap, continent) %>%
 my_skim() %>%
 print()
## -- Data Summary -----
##
                       Values
## Name
                       Piped data
## Number of rows
                       142
## Number of columns
## _____
## Column type frequency:
##
   factor
                       1
##
   numeric
## Group variables
                      None
##
## -- Variable type: factor ------
## skim_variable n_missing complete_rate ordered n_unique
## 1 continent
                    0 1 FALSE
  top counts
## 1 Afr: 52, Asi: 33, Eur: 30, Ame: 25
## -- Variable type: numeric -----
  skim_variable n_missing complete_rate mean
                                        sd p0 p25 p50
                   0 1 11680. 12860. 278. 1625. 6124. 18009.
## 1 gdpPercap
     p100
##
## 1 49357.
## $factor
##
skim_variable n_missing complete_rate ordered n_unique top_counts
                        1 FALSE
## 1 continent
                    0
                                       5 Afr: 52, Asi: 33, Eur:~
##
## $numeric
##
## -- Variable type: numeric -------
  skim_variable n_missing complete_rate mean sd p0 p25 p50
## 1 gdpPercap
                   0
                               1 11680. 12860. 278. 1625. 6124. 18009.
## # ... with 1 more variable: p100 <dbl>
  • Creating data visualizations:
ggplot(gapminder2007, aes(x = continent, y = gdpPercap)) +
 geom_boxplot() +
 labs(
  x = "Continent", y = "GPD per capita",
```

title = "GDP by continent") +

theme_bw()

GDP by continent



Based on this exploration, it seems that GDP's are very different among different continents, in terms of medians, variation, and symmetry. At a minimum this means that continent might be an important predictor for an area's mean GDP.

LC 5.5 (Objective 2)

(LC5.5) Fit a new linear regression using lm(gdpPercap ~ continent, data = gapminder2007) where gdpPercap is the new outcome variable y. Get information about the "best-fitting" line from the regression table by applying the get_regression_table() function. How do the regression results match up with the results from your previous exploratory data analysis?

Solution:

```
# Fit regression model:
gdp_model <- lm(gdpPercap ~ continent, data = gapminder2007)</pre>
# Get regression table:
get_regression_table(gdp_model)
## # A tibble: 5 x 7
##
     term
                          estimate std_error statistic p_value lower_ci upper_ci
##
     <chr>
                              <dbl>
                                        <dbl>
                                                   <dbl>
                                                           <dbl>
                                                                     <dbl>
                                                                               <dbl>
                              3089.
                                        1373.
                                                    2.25
                                                           0.026
                                                                               5804.
## 1 intercept
                                                                      375.
## 2 continent: Americas
                             7914.
                                        2409.
                                                    3.28
                                                           0.001
                                                                     3150.
                                                                              12678.
## 3 continent: Asia
```

4.26

5027.

13741.

2203.

9384.

```
## 4 continent: Europe 21965. 2270. 9.68 0 17478. 26453. ## 5 continent: Oceania 26721. 7133. 3.75 0 12616. 40826.
```

$$\widehat{y} = \widehat{\text{gdpPercap}} = b_0 + b_{\text{Amer}} \cdot \mathbb{1}_{\text{Amer}}(x) + b_{\text{Asia}} \cdot \mathbb{1}_{\text{Asia}}(x) + b_{\text{Euro}} \cdot \mathbb{1}_{\text{Euro}}(x) + b_{\text{Ocean}}(x)$$

$$= 3089 + 7914 \cdot \mathbb{1}_{\text{Amer}}(x) + 9384 \cdot \mathbb{1}_{\text{Asia}}(x) + 21965 \cdot \mathbb{1}_{\text{Euro}}(x) + 26721 \cdot \mathbb{1}_{\text{Ocean}}(x)$$

In our previous exploratory data analysis, it seemed that continent is a statistically significant predictor for an area's mean GDP. Here, by fitting a new linear regression using $lm(gdpPercap \sim continent, data = gapminder2007)$ where gdpPercap is the new outcome variable y, we are able to write an equation to predict average gdpPercap using the continent as a predictor. Therefore, the regression results matches with the results from your previous exploratory data analysis.

LC 5.6 (Objective 3)

(LC5.6) Using either the sorting functionality of RStudio's spreadsheet viewer or using the data wrangling tools you learned in Chapter @ref(wrangling), identify the five countries with the five smallest (most negative) residuals? What do these negative residuals say about their life expectancy relative to their continents?

Solution:

We switched by to life expectancy. We need the model.

```
lifeExp_model <- lm(lifeExp ~ continent, data = gapminder2007)</pre>
```

Let's use R.

```
get_regression_points(lifeExp_model, ID = "country") %>%
  arrange(residual) %>%
  slice_head(n=5)
```

```
## # A tibble: 5 x 5
##
     country
                  lifeExp continent lifeExp_hat residual
                    <dbl> <fct>
                                           <dbl>
##
     <fct>
                                                     <dbl>
                                                     -26.9
## 1 Afghanistan
                     43.8 Asia
                                             70.7
                                                     -15.2
## 2 Swaziland
                     39.6 Africa
                                            54.8
                                                     -12.7
## 3 Mozambique
                     42.1 Africa
                                            54.8
                                            73.6
                                                     -12.7
## 4 Haiti
                     60.9 Americas
## 5 Zambia
                     42.4 Africa
                                             54.8
                                                     -12.4
```

We can identify that the five countries with the five smallest (most negative) residuals are: Afghanistan, Swaziland, Mozambique, Haiti, and Zambia.

These negative residuals indicate that these data points have the biggest negative deviations from their group means. This means that these five countries' average life expectancies are the lowest compared to their respective continents' average life expectancies. For example, the residual for Afghanistan is -26.9 and it is the smallest residual. This means that the average life expectancy of Afghanistan is 26.9 years lower than the average life expectancy of its continent, Asia.

LC 5.7 (Objective 3)

(LC5.7) Repeat this process, but identify the five countries with the five largest (most positive) residuals. What do these positive residuals say about their life expectancy relative to their continents?

Solution:

Using R.

```
get_regression_points(lifeExp_model, ID = "country") %>%
  arrange(desc(residual)) %>%
  slice_head(n=5)
```

```
## # A tibble: 5 x 5
##
     country
               lifeExp continent lifeExp_hat residual
##
     <fct>
                  <dbl> <fct>
                                         <dbl>
                                                   <dbl>
## 1 Reunion
                   76.4 Africa
                                          54.8
                                                    21.6
## 2 Libya
                                          54.8
                                                    19.1
                   74.0 Africa
## 3 Tunisia
                   73.9 Africa
                                          54.8
                                                    19.1
## 4 Mauritius
                   72.8 Africa
                                          54.8
                                                    18.0
## 5 Algeria
                   72.3 Africa
                                          54.8
                                                    17.5
```

We can identify that the five countries with the five largest (most positive) residuals are: Reunion, Libya, Tunisia, Mauritius, and Algeria.

These positive residuals indicate that the data points are above the regression line with the longest distance. This means that these five countries' average life expectancies are the highest comparing to their respective continents' average life expectancies. For example, the residual for Reunion is 21.636 and it is the largest residual. This means that the average life expectancy of Reunion is 21.636 years higher than the average life expectancy of its continent, Africa.

Documenting software

File creation date: 2022-06-04
R version 4.1.3 (2022-03-10)
tidyverse package version: 1.3.1
skimr package version: 2.1.4
gapminder package version: 0.3.0

• moderndive package version: 0.5.4