Linear Regression

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STAT 3150—Statistical Computing

Lecture Objectives

- Fit linear regression models using **R**.
- · Understand the output.
- · Compare and contrast with t-tests and ANOVA.

Motivation

- In the last module, we discussed how bootstrap can be used to approximate the sampling distribution.
 - The general idea is based on replacing the true CDF by the empirical CDF (i.e. sampling with replacement).
- If we make assumptions about the data-generating mechanism, we can sometimes improve on the general bootstrap.
- We will explore this idea using linear regression.
 - · But first, we will review it!

General notation

- Linear regression estimates the relationship between a single variable Y, called the *outcome variable*, and a series of variables X_1, \ldots, X_p , called *covariates*.
 - · Machine learning uses target and features, respectively.
- \cdot The outcome Y is typically a continuous variable.
 - Eg. Height, income, blood pressure, etc.
- The covariates X_1, \ldots, X_p can be anything.
- We want to collect all variables Y, X_1, \ldots, X_p on the same unit of observation (e.g. person, school, animal, olive oil).

Simplest linear regression

- The simplest linear regression only has an outcome variable Y, no covariates.
 - · It's equivalent to a one-sample t-test.
- · The linear regression equation can be written as

$$E(Y) = \beta_0.$$

- In other words, we are saying the population mean of Y (i.e. E(Y)) is equal to a parameter β_0 .
 - This notation is a bit overkill, but it will make more sense soon...

Example i

```
library(readr)
dataset <- read_csv("heart.csv")

# Use function lm
fit <- lm(age ~ 1, data = dataset)
fit</pre>
```

Example ii

```
##
## Call:
## lm(formula = age ~ 1, data = dataset)
##
## Coefficients:
## (Intercept)
##
         54.37
# To compute confidence interval
# use confint
confint(fit)
```

Example iii

```
## 2.5 % 97.5 %
## (Intercept) 53.3396 55.39307
```

One binary covariate i

- The next simplest linear regression has a single covariate X which can take only two values: 0 or 1.
- The idea is that it encodes a binary variable.
 - Eg. Male: 1; Female 0. CS Major: 1; Non-CS Major: 0.
- The linear regression equation for this situation can be written as

$$E(Y|X) = \beta_0 + \beta_1 X.$$

- · Let's unpack this:
 - · When X=0, the RHS simplifies to eta_0 , and we get

$$E(Y|X=0) = \beta_0.$$

a

One binary covariate ii

 \cdot When X=1, we get

$$E(Y|X=1) = \beta_0 + \beta_1.$$

- In other words, β_0 represents the population mean of Y when X=0, but β_1 represents the difference in population means between the two subgroups.
 - If β_1 is significantly different from 0, then we have evidence of a difference in means between the two groups!

Example i

```
fit <- lm(age ~ sex, data = dataset)</pre>
fit
##
## Call:
## lm(formula = age ~ sex, data = dataset)
##
## Coefficients:
## (Intercept)
                        sex
## 55.677 -1.919
```

Example ii

```
confint(fit)
##
                   2.5 % 97.5 %
## (Intercept) 53.858832 57.4953350
              -4.118464 0.2812059
## sex
# What if we change the coding 0/1 to female/male?
dataset <- transform(dataset, sex = ifelse(sex == 1,</pre>
                                            "male".
                                            "female"))
```

Example iii

```
fit <- lm(age ~ sex, data = dataset)</pre>
fit
##
## Call:
## lm(formula = age ~ sex, data = dataset)
##
## Coefficients:
## (Intercept) sexmale
## 55.677 -1.919
```

Summary so far

- We saw how linear regression connects the average value of an outcome variable with covariates.
- Important: the regression coefficient β_1 measures a difference in means.
- With a single binary covariate, we recover the two-sample t-test.

Exercise

Using the heart dataset, determine whether average cholesterol levels are different between men and women.

Solution i

One continuous covariate i

- \cdot Next we look at the case of a single continuous covariate X
- The linear regression equation for this situation can also be written as

$$E(Y|X) = \beta_0 + \beta_1 X.$$

- · Let's unpack this:
 - · When X=0, the RHS still simplifies to eta_0 , and we get

$$E(Y|X=0)=\beta_0.$$

- Let's compare two values of X that differ by 1 unit, e.g. x and x+1. We have

One continuous covariate ii

$$E(Y|X = x) = \beta_0 + \beta_1 x$$

$$E(Y|X = x + 1) = \beta_0 + \beta_1 (x + 1)$$

$$= (\beta_0 + \beta_1 x) + \beta_1$$

$$= E(Y|X = x) + \beta_1.$$

- Rearranging, we get

$$\beta_1 = E(Y|X = x + 1) - E(Y|X = x).$$

One continuous covariate iii

- In other words, β_1 represents the **difference** in population means between two subgroups that differ by 1 unit in their value of the covariate X.
- β_0 still represents the population mean of Y when X=0.
 - But depending on what X represent (e.g. age, cholesterol), X=0 may not be possible!

Example i

```
fit <- lm(age ~ chol, data = dataset)</pre>
fit
##
## Call:
## lm(formula = age ~ chol, data = dataset)
##
## Coefficients:
## (Intercept)
                       chol
## 45,14573 0,03744
```

Example ii

```
confint(fit)
```

```
## 2.5 % 97.5 %
## (Intercept) 40.25979148 50.03166732
## chol 0.01802571 0.05685821
```

• Interpretation: the estimated value of β_1 is 0.04, which means that two groups of people from the study who differ in their cholesterol levels by 1 unit on average differ in their age by 0.04 year (i.e. about two weeks), with a higher cholesterol level being associated with being older.

Exercise

It is perhaps more natural to think of the difference in cholesterol levels for groups of different ages. Using the heart dataset, determine the average difference in cholesterol levels for people in the study whose age differ by one year.

Solution i

```
fit <- lm(chol ~ age, data = dataset)</pre>
fit
##
## Call:
## lm(formula = chol ~ age, data = dataset)
##
## Coefficients:
## (Intercept)
                         age
## 179.967
                       1,219
```

Solution ii

confint(fit)

```
## 2.5 % 97.5 %
## (Intercept) 145.1132605 214.821681
## age 0.5870764 1.851806
```

• Interpretation: the estimated value of β_1 is 1.22, which means that two groups of people from the study who differ in their age by 1 year on average differ in their cholesterol levels by 1.22 mg/dl, with being older being associated with higher cholesterol level.

Inspecting the model fit i

- We can use a scatter plot to investigate the model fit,
 i.e. whether the regression equation is a good description of the data.
 - But only really helpful when both Y and the single covariate X are continuous.

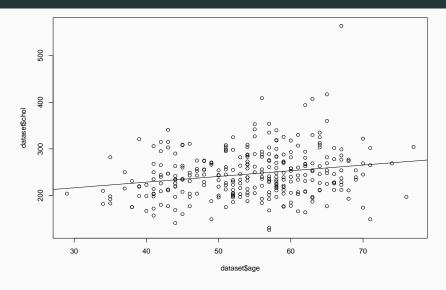
```
fit <- lm(chol ~ age, data = dataset)
# Extract coefficient estimates with coef
coef(fit)</pre>
```

Inspecting the model fit ii

```
## (Intercept) age
## 179.967471 1.219441

plot(dataset$age, dataset$chol)
abline(a = coef(fit)[1],
    b = coef(fit)[2])
```

Inspecting the model fit iii



Categorical covariate i

- \cdot Now, let's assume we measured a continuous outcome variable Y across different subgroups.
 - For simplicity, we'll assume only three subgroups, but this can easily be generalized.
- \cdot Let Z keep track of which subgroup an observation is from.
 - \cdot Eg. Z=1 for CS major, Z=2 for Psych Major, and Z=0 for non-CS, non-Psych major.
- \cdot We want to compare the average value of Y between all subgroups.
 - · How can we fit this into linear regression?

Categorical covariate ii

- · Solution: we introduce dummy variables X_1 and X_2 .
 - $\cdot X_1 = 1$ if Z = 1, and $X_1 = 0$ otherwise.
 - $\cdot X_2 = 1$ if Z = 2, and $X_2 = 0$ otherwise.

\overline{Z}	X_1	X_2
0	0	0
1	1	0
2	0	1

Categorical covariate iii

 The linear regression equation for this situation can then be written as

$$E(Y|X) = \beta_0 + \beta_1 X_1 + \beta_2 X_2.$$

- · Let's unpack this:
 - . When Z=0, both $X_1=0$ and $X_2=0$, and so the RHS simplifies to β_0 :

$$E(Y|Z=0) = \beta_0.$$

. When Z=1, we have $X_1=1$ and $X_2=0$, and so the RHS simplifies to $\beta_0+\beta_1$:

$$E(Y|Z=1) = \beta_0 + \beta_1.$$

Categorical covariate iv

· When Z=2, we have $X_1=0$ and $X_2=1$, and so the RHS simplifies to $\beta_0+\beta_2$:

$$E(Y|Z=2) = \beta_0 + \beta_2.$$

- · In other words, β_1 represents the difference in population means between the two subgroups Z=0 and Z=1, and β_2 represents the difference between the two subgroups Z=0 and Z=2
- \cdot β_0 still represents the population mean of Y when Z=0.

Example i

fit

```
library(dslabs)
table(olive$region)
##
                          Sardinia Southern Italy
## Northern Italy
##
               151
                                98
                                                323
fit <- lm(oleic ~ region, data = olive)</pre>
```

Example ii

```
##
## Call:
## lm(formula = oleic ~ region, data = olive)
##
## Coefficients:
## (Intercept) regionSardinia regionSouthern Italy
## 77.93 -5.25 -6.93
confint(fit)
```

Example iii

```
## 2.5 % 97.5 %

## (Intercept) 77.484107 78.37695

## regionSardinia -5.961921 -4.53873

## regionSouthern Italy -7.471234 -6.38964
```

Example iv

Interpretation

- The average level of oleic acid for olive oils in Northern Italy (i.e. the reference category) is $\beta_0=$ 77.9.
- The average level of oleic acid for olive oils in Sardinia is $\beta_0+\beta_1=$ 72.7.
- The average level of oleic acid for olive oils in Southern Italy is $\beta_0+\beta_2=$ 71.
- The average level of oleic acid is highest in Northern Italy, and it's significantly different from that of other regions.
 - But these confidence intervals can't tell us whether the average levels are different between Sardinia and Southern Italy.

Summary

- We introduced linear regression as a general framework for comparing means between subgroups.
- We saw how one-sample and two-sample t-tests are special cases.
- By introducing dummy variables, we can also get ANOVA as a special case.
- Next lecture: we will discuss the assumptions behind linear regression.