# Stats 401 Lab 13 (w/ Solutions) 

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## Outline

- Interpreting Coefficients
- Collinearity
- Interactions


## Interpretation: Simple Linear Regression

- Let's first consider the case with 1 predictor
- Suppose we've fit a linear model

$$
y_{i}=b_{0}+b_{1} x_{i 1}+e_{i}
$$

where, $i=1, \ldots, n$

- What is the interpretation of the sample coefficient $b_{1}$ ?


## Interpretation: Simple Linear Regression

- Recall: we interpret $b_{1}$ as the expected change in our response variable for every 1 unit increase in our explanatory variable


## Example

We consider pitching data for 2015, which we have obtained using the $R$ package Lahman:
matrix(names(pitchers), nrow $=3$, byrow $=T$ )

| \#\# | [,1] | [,2] | [,3] | [,4] |
| :--- | :--- | :--- | :--- | :--- |
| \#\# | $[1]$, | "playerID" | "teamID" | "W" |
| \#\# | "L" |  |  |  |
| \#\# [2,] | "G" | "GS" | "BB" | "SO" |
| "ERA" | "Kp9" | "IPpG" | "starter" |  |

For this lab, we will be interested in the last 3 variables: strikeouts per 9 innings (Kp9), innings pitched per game (IPpG), and a dummy variable for starter (starter), which is 1 if the pitcher is a starter and 0 if the pitcher is a reliever.

## Example

We fit a model to predict strikeouts per 9 innings (Kp9) using innings pitched per game (IPpG)
lm_simple $=\operatorname{lm}(\mathrm{Kp} 9 \sim$ IPpG, data $=$ pitchers $)$
round(summary(lm_simple)\$coefficients,4)

| \#\# | Estimate | Std. Error $t$ value $\operatorname{Pr}(>\|t\|)$ |  |  |
| :--- | ---: | ---: | ---: | ---: |
| \#\# (Intercept) | 8.3912 | 0.1880 | 44.6283 | $0 \mathrm{e}+00$ |
| \#\# IPpG | -0.1937 | 0.0483 | -4.0104 | $1 \mathrm{e}-04$ |

How can we interpret the coefficient for IPpG?

## Interpretation: Multiple Regression

- Now suppose we include a second predictor, $x_{i 2}$, and instead fit the model

$$
y_{i}=b_{0}+b_{1} x_{i 1}+b_{2} x_{i 2}+e_{i}
$$

for $i=1, \ldots, n$

- Is our interpretation of $b_{1}$ the same?


## Interpretation: Multiple Regression

- The interpretation is different!
- When we include additional predictors, the value of $b_{1}$ will change
- We can think of $b_{1}$ as the expected change in our response variable for every 1 unit increase in $x_{1}$ for a fixed value of $x_{2}$


## Example (Continued)

Suppose we now predict strikeouts per 9 innings using innings pitched per game and an indicator of whether the pitcher is a starting pitcher

```
lm_mult = lm(Kp9 ~ IPpG + starter, data = pitchers)
round(summary(lm_mult)$coefficients,4)
```

| \#\# | Estimate | Std. Error | t value | $\operatorname{Pr}(>\|t\|)$ |
| :--- | ---: | ---: | ---: | ---: |
| \#\# (Intercept) | 7.6043 | 0.2395 | 31.7452 | 0 |
| \#\# IPpG | 0.9099 | 0.2210 | 4.1169 | 0 |
| \#\# starterStarter | -5.4789 | 1.0720 | -5.1109 | 0 |

## Collinearity

- Collinearity (or Multicollinearity) occurs when explanatory variables are linearly related to each other
- If we can write one variable as a linear combination of the other variables, then we have collinearity
- For example, suppose we have the vectors of predictors $\mathbf{w}, \mathbf{x}$, and $\mathbf{z}$, and that $\mathbf{w}=2 \mathbf{x}-3 \mathbf{z}$. Then the predictors in this case are collinear


## Why is this a problem?

- When we have collinear variables, it becomes impossible to distinguish between the effects of the variables
- Suppose $\mathbf{x}_{1}$ and $\mathbf{x}_{2}$ are collinear, and that they both have an effect on $\mathbf{y}$
- When we try to fit the model $y_{i}=b_{0}+b_{1} x_{i 1}+b_{2} x_{i 2}+e_{i}$, it is impossible to tell which value to assign to $b_{1}$ and which to assign to $b_{2}$
- This is exactly the problem we saw when we discussed over-specified models with factor variables


## Example

Recall our baseball pitchers example, where we fit a model predicting strikeouts per 9 innings using innings pitched per game:

| \#\# | Estimate | Std. Error |
| :--- | ---: | ---: |
| \#\# (Intercept) | 8.39 | 0.19 |
| \#\# IPpG | -0.19 | 0.05 |

Suppose in our data set, we also have a variable "outs per game" and that we accidentally include it in our model. Since outs are equal to innings times 3 , outs per game and innings per game are collinear.

## Example

- Our sample model is $y_{i}=8.39-0.19 x_{i 1}+e_{i}$ where $y_{i}$ is strikeouts per 9 innings and $x_{i 1}$ is innings pitched per game for pitcher $i$.
- These coefficients are the unique least squares solution and minimize the sum of square residuals
- Let $x_{i 2}$ be outs per game. Because the predictors are collinear $\left(\mathbf{x}_{2}=3 \mathbf{x}_{1}\right)$, the model $y_{i}=b_{0}+b_{1} x_{i 1}+b_{2} x_{i 2}+e_{i}$ does not have a unique solution!
- There are infinitely many solutions, each of which is just as "correct" as the others - we can't tell which value to assign to $b_{1}$ and which to $b_{2}$


## Lab Activity (Part 1)

We are interested in studying the weights of grapefruit by type:

| \#\# | weight | type | circumference |
| :--- | ---: | ---: | ---: |
| \#\# | 1 | 8.3 | red |$\quad 11.0$

Let $\mathbf{x}_{1}$ be a dummy variable for red grapefruits, $\mathbf{x}_{2}$ be a dummy variable for pink grapefruits, and $\mathbf{x}_{3}=(11,10,10.6,10.2,7)$ be circumference. Let $\mathbf{y}=(8.3,7,7.5,9,6)$ be the weights of the grapefruits. For which model(s) would the explanatory variables be collinear?

$$
\begin{aligned}
& \text { 1. } y_{i}=b_{0}+b_{2} x_{i 2}+b_{3} x_{i 3}+e_{i} \\
& \text { 2. } y_{i}=b_{0}+b_{1} x_{i 1}+b_{2} x_{i 2}+b_{3} x_{i 3}+e_{i} \\
& \text { 3. } y_{i}=b_{1} x_{i 1}+b_{2} x_{i 2}+b_{3} x_{i 3}+e_{i} \\
& \text { 4. } y_{i}=b_{0}+b_{1} x_{i 1}+b_{3} x_{i 3}+b_{4} x_{i 3}^{2}+e_{i}
\end{aligned}
$$

## Lab Activity (Part 1) - Solutions

Only the second model will have collinear variables. For the second model the design matrix is:

| \#\# | (Intercept) | typered | typepink | circumference |
| :--- | ---: | ---: | ---: | ---: |
| \#\# | 1 | 1 | 0 | 11.0 |
| \#\# 2 | 1 | 1 | 0 | 10.0 |
| \#\# 3 | 1 | 0 | 1 | 10.6 |
| \#\# 4 | 1 | 1 | 0 | 10.2 |
| \#\# 5 | 1 | 0 | 1 | 7.0 |

However, the second plus the third column equals the column of 1's corresponding to the intercept. For model $4, \mathbf{x}_{3}$ and $\mathbf{x}_{3}^{2}$ are directly related but not it is a quadratic, rather than a linear relationship.

## Approximate Collinearity

- It is also an issue when variables are close to collinear
- When predictors are approximately collinear, it becomes difficult to disentangle the associations of the variables with the outcome variable


## Another Way to Think of Collinearity

- Exact collinearity causes the variance of $\hat{\beta}_{i}$ to be infinite (because there are infinitely many least squares solutions)
- When variables are close to collinear, the variance is not infinite, but very high


## Why do we care?

- The sample coefficients are the estimates for the true coefficients
- If the estimates are unreliable, it is difficult to make good inferences
- For example, with a high variance, we would have large confidence intervals and it would be hard to tell if the observed coefficient is statistically significant


## Collinearity in R

- When we attempt to fit a model with exact collinearity, R will recognize that the variables are collinear and drop one of the variables

```
pitchers$OpG = 3*pitchers$IPpG
lm_mult = lm(Kp9 ~ IPpG + starter + OpG, data = pitchers)
coef(lm_mult)
```

\#\# (Intercept)
\#\# 7.6043474
$0.9098721 \quad$-5.4789241

- If the variables are only approximately collinear, then R will still fit the model with all variables - we need to be aware that our coefficient estimates could be unreliable


## Example

Almost collinear variables often show up in data sets (especially when there are many predictors). Let's examine the data set from homework 11:

```
senic = read.table("https://ionides.github.io/401f18/hw/hw
matrix(names(senic),ncol = 3)
```

| \#\# | [.1] | [,2] | [,3] |
| :--- | :--- | :--- | :--- |
| \#\# [1,] "Hospital" | "Culture" | "Region" |  |
| \#\# [2,] "Length.of.stay" "X.ray" | "Patients" |  |  |
| \#\# [3,] "Age" | "Beds" | "Nurses" |  |
| \#\# [4,] "Infection.risk" "Med.school" "Facilities" |  |  |  |

We can see there are some variables that appear to measure similar things. Specifically, patients, beds, and nurses are all measuring the number of patients in some way.

## Example

Using the cor() function, we can obtain the pairwise correlations for a matrix or data frame. We can use this to verify our hypothesis above.
$\operatorname{cor}(\operatorname{senic}[, c(7,10,11)])$

| \#\# | Beds | Patients | Nurses |
| :--- | ---: | ---: | ---: |
| \#\# Beds | 1.0000000 | 0.9809977 | 0.9155042 |
| \#\# Patients | 0.9809977 | 1.0000000 | 0.9078970 |
| \#\# Nurses | 0.9155042 | 0.9078970 | 1.0000000 |

We can see that these 3 variables are highly correlated. We will examine how this approximate collinearity affects the model fit in the lab ticket.

Note: it is often a good idea to examine the full correlation matrix to see if there are potential collinearity issues (i.e., using 'cor(senic)' will give all the pairwise correlations in the data set).

## Interaction Terms

- So far, we've examined the effects of 1 predictor at a time on the outcome
- For example, we could answer the question: is the linear association between strike outs per 9 innings and innings pitched per game different from 0 ?
- What if we wanted to examine the effects of 2 predictors simultaneously?
- For example, we might want to know if the effect of innings pitched per game on strikeouts per 9 innings is different for starting and relief pitchers


## Interaction Terms

- To accomplish this we use interaction terms: interaction terms are the product of predictors
- Suppose we have the following model:

$$
y_{i}=b_{0}+b_{1} x_{i 1}+b_{2} x_{i 2}+b_{3} x_{i 1} \times x_{i 2}+e_{i}
$$

where for each $i, y_{i}$ is the strikeouts per 9 innings, $x_{i 1}$ is the innings pitched per game, $x_{i 2}$ is a dummy variable for a starting pitcher

- Recall that by including the dummy variable for pitcher type, we have two different intercepts
- By including the interaction term $x_{i 1} \times x_{i 2}$, we have two different slopes
- How should we interpret $b_{3}$ ?


## Interaction Terms

- The example above included the interaction between a continuous and categorical variable
- Interactions can also be done between 2 continuous variables, as well as 2 categorical variables


## Lab Ticket

1. Read in the SENIC data using the following command:
```
file = "https://ionides.github.io/401f18/hw/hw11/senic.txt'
senic = read.table(file,header = T)
```

2. Fit two models in R. In both cases, use Infection.risk as outcome

- Predictors: Beds and Patients
- Predictor: Beds

3. How do coefficients for Beds differ between the two models? What about the standard errors, t statistics, and p-values?
4. Explain how what you observed in (3) is related to the approximate collinearity between Beds and Patients

## Lab Ticket - Solutions

2. 

lm1 $=\operatorname{lm}$ (Infection.risk $\sim$ Beds + Patients, senic)
lm2 $=\operatorname{lm}($ Infection.risk $\sim$ Beds, senic)

## Lab Ticket - Solutions

3. Beds has a negative estimated coefficient for the first model and a positive estimated coefficient for the second. In the first model, the standard error is higher. The coefficient is not statistically different from zero, while it is in the second model. The inflated standard error has resulted in a lower t-statistic and higher p -value for the first model.
round (summary(lm1)\$coefficients,3)

| \#\# | Estimate Std. Error | $t$ value $\operatorname{Pr}(>\|t\|)$ |  |  |
| :--- | ---: | ---: | ---: | ---: |
| \#\# (Intercept) | 3.763 | 0.195 | 19.297 | 0.000 |
| \#\# Beds | -0.003 | 0.003 | -0.844 | 0.400 |
| \#\# Patients | 0.007 | 0.004 | 1.671 | 0.098 |

## Lab Ticket - Solutions

3. (cont)
round (summary (lm2) \$coefficients, 3)

| \#\# | Estimate | Std. Error | t value | $\operatorname{Pr}(>\|t\|)$ |
| :--- | ---: | ---: | ---: | ---: |
| \#\# (Intercept) | 3.724 | 0.195 | 19.081 | 0 |
| \#\# Beds | 0.003 | 0.001 | 4.062 | 0 |

4. Collinearity results in a higher variance for the coefficients. Because of this, our estimates are less reliable (hence, a value in lm1 that's very different from the value in 1 m 2 ). In addition, we can see the standard error of the sample coefficient is higher for $\operatorname{lm} 1$. This results in a lower t -statistic and higher p -value.
