Lesson 15: MLR Model Diagnostics

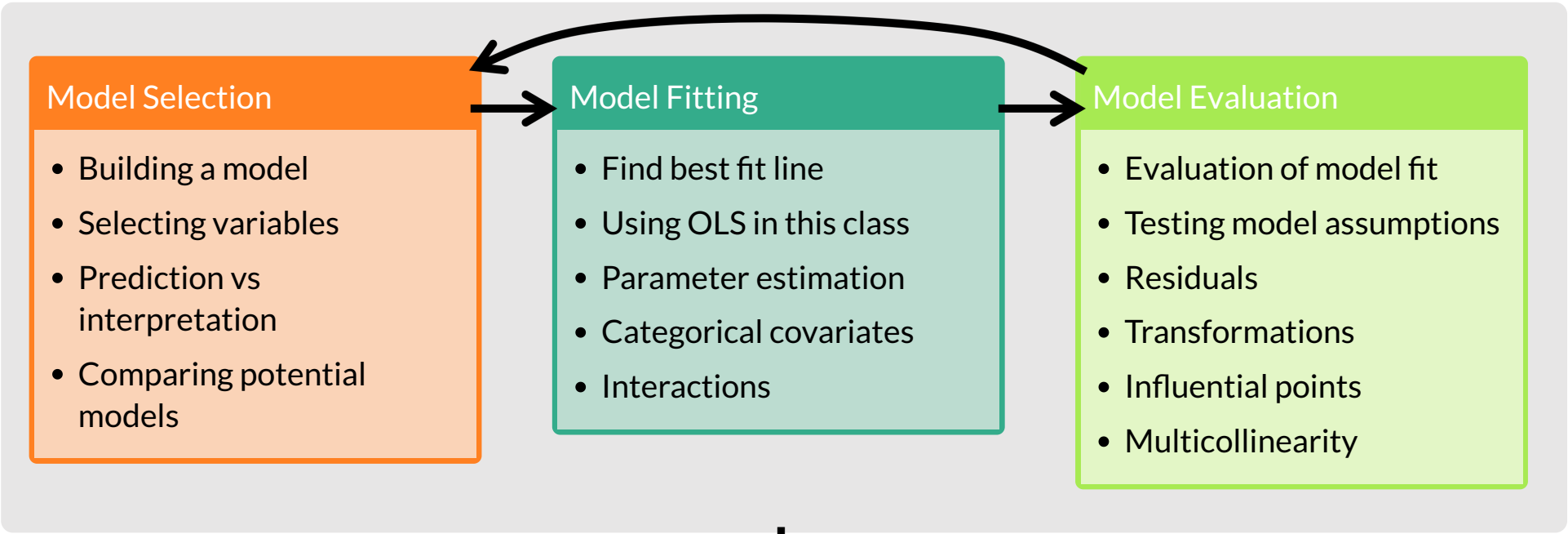
Nicky Wakim

2026-03-04

Learning Objectives

1. Apply tools from SLR (Lesson 6: SLR Diagnostics) in MLR to **evaluate LINE assumptions**, including residual plots and QQ-plots
2. Apply tools involving standardized residuals, leverage, and Cook's distance from SLR (Lesson 7: SLR Diagnostics 2) in MLR to **flag potentially influential points**
3. Use Variance Inflation Factor (VIF) and it's general form to **detect and correct multicollinearity**

Regression analysis process



Let's remind ourselves of the final model

- Our **final model** contains
  - Cell phones per 100 people
  - Basic sanitation (quartiles)
  - Freedom status
  - Income level
  - Vaccination rate
  - Happiness score
  - No interactions

▶ Display regression table for final model

Characteristic	Beta	95% CI	p-value
Cell phones per 100 people	0.01	-0.02, 0.04	0.7
Basic sanitation (%)			
[21.6,61.1]	—	—	
(61.1,92.8]	4.5	2.0, 7.0	<0.001
(92.8,98]	7.0	4.2, 9.8	<0.001
(98,100]	9.0	5.8, 12	<0.001
Freedom status			
NF	—	—	
PF	1.2	-0.72, 3.2	0.2
F	-0.35	-2.9, 2.2	0.8
Income level			
Low income	—	—	
Lower middle income	-0.25	-3.4, 2.9	0.9
Upper middle income	-0.11	-4.2, 4.0	>0.9
High income	3.5	-1.8, 8.8	0.2
Vaccination rate (%)	0.03	-0.08, 0.14	0.6
Happiness score	0.14	0.03, 0.25	0.014

Abbreviation: CI = Confidence Interval

It's a lot to visualize

- Part of the reason why we discussed model diagnostics in SLR was so that we could have accompanying visuals to help us understand

- With 6 variables in our final model, it is hard to scatterplots to visualize linearity, outliers, and influential points

- I highly encourage you revisit the SLR lessons (SLR: Checking model assumptions and SLR: Diagnostics to help understand these notes

Remember our friend `augment()`?

- Run `final_model` through `augment()` (`final_model` is input)
  - So we assigned `final_model` as the output of the `lm()` function
- Will give us values about each observation in the context of the fitted regression model
  - cook's distance (`.cooksd`), $\widehat{Y}_i$ (`.fitted`), leverage (`.hat`), residuals (`.resid`), std residuals (`.std.resid`)

```
1 aug = augment(final_model)
2 head(aug) %>% relocate(.fitted, .resid, .std.resid, .hat, .cooksd, .after = life_exp)
```

```
# A tibble: 6 × 13
  life_exp .fitted .resid .std.resid   .hat   .cooksd cell_phones_100 BS_q
     <dbl>   <dbl>  <dbl>      <dbl>  <dbl>     <dbl>           <dbl> <fct>
1     62.6    62.8 -0.166    -0.0506 0.342  0.000111            56.3 (61.1,92.…
2     76.1    75.1  0.954     0.251  0.110  0.000647            98.4 (98,100]
3     73.4    80.3 -6.88     -1.87   0.166  0.0581             196.  (98,100]
4     75.4    75.1  0.267     0.0700 0.109  0.0000499          131.  (98,100]
5     73.7    75.5 -1.88     -0.486  0.0829 0.00178            131.  (98,100]
6     71.4    71.0  0.374     0.0981 0.108  0.0000971          108.  (92.8,98]
# ℹ 5 more variables: freedom_status <fct>, income_level_4 <fct>,
#   vax_rate <dbl>, happiness_score <dbl>, .sigma <dbl>
```

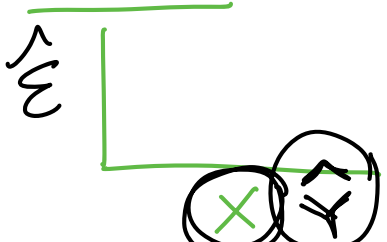
RDocumentation on the `augment()` function.

Learning Objectives

1. Apply tools from SLR (Lesson 6: SLR Diagnostics) in MLR to **evaluate LINE assumptions**, including residual plots and QQ-plots
2. Apply tools involving standardized residuals, leverage, and Cook's distance from SLR (Lesson 7: SLR Diagnostics 2) in MLR to **flag potentially influential points**
3. Use Variance Inflation Factor (VIF) and it's general form to **detect and correct multicollinearity**

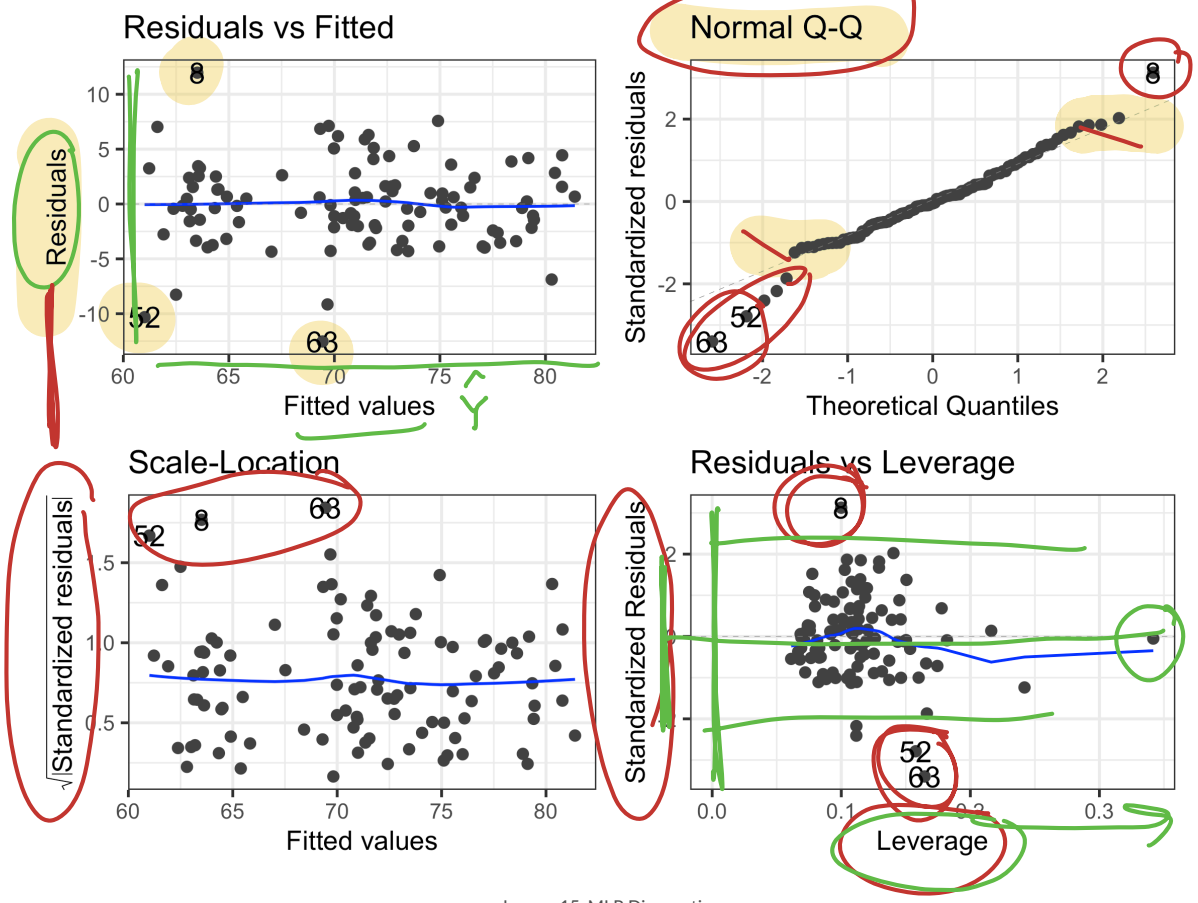
Summary of the assumptions and their diagnostic tool

Assumption	What needs to hold?	Diagnostic tool
Linearity	• Relationship between **each** X and Y is linear	• Scatterplot of Y vs. X
Independence	• Observations are independent from each other	• Study design
Normality	• Residuals (and thus $Y \mid X_1, X_2, \ldots, X_p$) are normally distributed	• QQ plot of residuals • Distribution of residuals
Equality of variance	• Variance of residuals (and thus $Y \mid X_1, X_2, \ldots, X_p$) is same across fitted values (homoscedasticity)	• Residual plot



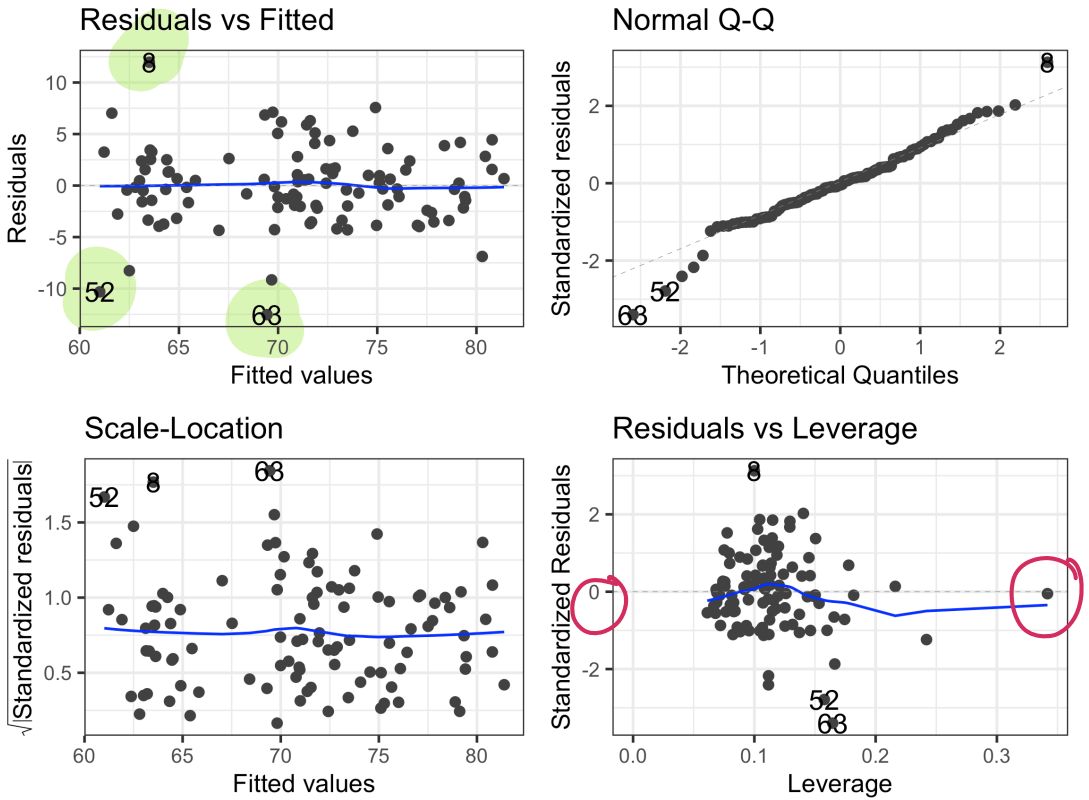
`autoplot()` to examine equality of variance and Normality

```
1 library(ggfortify)
2 autoplot(final_model) + theme(text=element_text(size=20))
```



`autoplot()` to examine equality of variance and Normality

```
1 library(ggfortify)
2 autoplot(final_model) + theme(text=element_text(size=
```



Looks like 2 obs are flagged:

- 8: Bangladesh
- 52: Lesotho
- 66: Malawi

Without them, QQ-plot and residual plot look good

- Points on QQ-plot are close to identity line
- Residuals have pretty consistent spread across fitted values

But don't take them out!!!

- Instead, discuss what may be missing in our regression model that is not capturing the characteristics of these countries

Poll Everywhere Question 1

Learning Objectives

1. Apply tools from SLR (Lesson 6: SLR Diagnostics) in MLR to **evaluate LINE assumptions**, including residual plots and QQ-plots
2. Apply tools involving standardized residuals, leverage, and Cook's distance from SLR (Lesson 7: SLR Diagnostics 2) in MLR to **flag potentially influential points**
3. Use Variance Inflation Factor (VIF) and it's general form to **detect and correct multicollinearity**

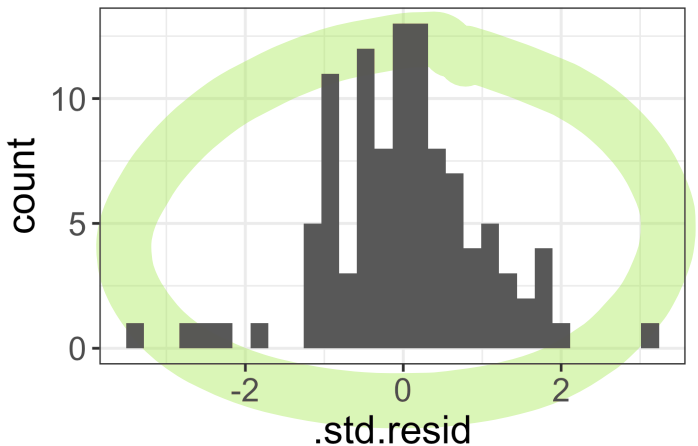
Identifying outliers

Internally standardized residual

$$r_i = \frac{\hat{\epsilon}_i}{\sqrt{\widehat{\sigma}^2(1 - h_{ii})}}$$

- We flag an observation if the standardized residual is "large"
  - Different sources will define "large" differently
  - PennState site uses $|r_i| > 3$
  - `autoplot()` shows the 3 observations with the highest standardized residuals
  - Other sources use $|r_i| > 2$, which is a little more conservative

```
1 ggplot(data = aug) +
2   geom_histogram(aes(x = .std.resid))
```



Countries that are outliers ($|r_i| > 3$)

- We can identify the countries that are outliers

```
aug %>% relocate(.std.resid, .after = territory) %>%
  filter(abs(.std.resid) > 3) %>% arrange(desc(abs(.std.resid)))
```

```
# A tibble: 2 × 14
  territory  .std.resid life_exp cell_phones_100 BS_q        freedom_status
  <chr>           <dbl>    <dbl>           <dbl> <fct>       <fct>
1 Mozambique      -3.40     56.9            45.8 (61.1,92.8] PF
2 Bangladesh       3.13     75.5           110.  [21.6,61.1] PF
# ℹ 8 more variables: income_level_4 <fct>, vax_rate <dbl>,
#   happiness_score <dbl>, .fitted <dbl>, .resid <dbl>, .hat <dbl>,
#   .sigma <dbl>, .cooksd <dbl>
```

Leverage h_i

- Values of leverage are: $0 \leq h_i \leq 1$
- We flag an observation if the leverage is "high"
  - **Only good for SLR:** Some textbooks use $h_i > 4/n$ where n = sample size
  - **Only good for SLR:** Some people suggest $h_i > 6/n$
  - **Works for MLR:** $h_i > 3p/n$ where p = number of regression coefficients

```
1 aug = aug %>% relocate(.hat, .after = cell_phones_100)
2 aug %>% arrange(desc(.hat)) %>% head(5)
```

```
# A tibble: 5 × 14
  territory   life_exp cell_phones_100  .hat BS_q  freedom_status income_level_4
  <chr>          <dbl>           <dbl> <dbl> <fct> <fct>          <fct>
1 Afghanistan     62.6            56.3 0.342 (61.… NF             Low income
2 Botswana        62.7           178.  0.242 (61.… F              Upper middle …
3 Yemen           66.3            46.5 0.216 (61.… NF             Low income
4 Montenegro      75.7           207.  0.182 (98,… PF             Upper middle …
5 Gabon           66.9           123.  0.178 [21.… NF             Upper middle …
# ℹ 7 more variables: vax_rate <dbl>, happiness_score <dbl>, .fitted <dbl>,
#   .resid <dbl>, .sigma <dbl>, .cooksd <dbl>, .std.resid <dbl>
```

Countries with high leverage ($h_i > 3p/n$)

- We can look at the countries that have high leverage: there are NONE

```
n = nrow(gapm2); p = length(final_model$coefficients) - 1
aug %>%
  filter(.hat > 3*p/n) %>%
  arrange(desc(.hat))
```

```
# A tibble: 1 × 14
  territory   life_exp cell_phones_100  .hat BS_q  freedom_status income_level_4
  <chr>          <dbl>           <dbl> <dbl> <fct> <fct>          <fct>
1 Afghanistan     62.6            56.3 0.342 (61.… NF             Low income
# ℹ 7 more variables: vax_rate <dbl>, happiness_score <dbl>, .fitted <dbl>,
#   .resid <dbl>, .sigma <dbl>, .cooksd <dbl>, .std.resid <dbl>
```

Cook's distance

- Measures the overall influence of an observation
- Attempts to measure how much **influence a single observation has** over the fitted model
  - Measures **how coefficient estimates change** when the ith observation is removed from the model
  - Combines leverage and outlier information

The Cook's distance for the i^{th} observation

$$d_i = \frac{h_i}{2(1-h_i)} \cdot r_i^2$$

where h_i is the leverage and r_i is the studentized residual

- Another rule for Cook's distance that is not strict:
  - Investigate observations that have $d_i > 1$
- Cook's distance values are already in the augment tibble: `.cooksd`

Identifying points with high Cook's distance

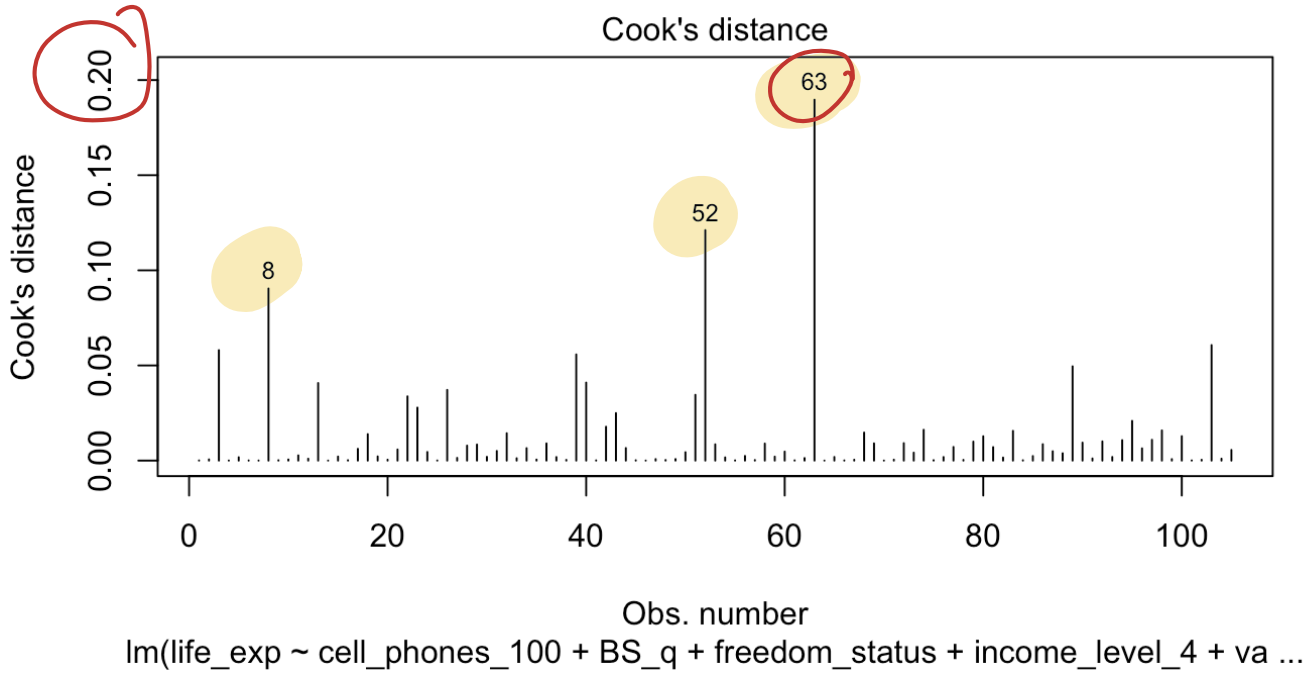
- No countries with high Cook's distance

```
aug = aug %>% relocate(.cooksd, .after = territory)
aug %>% arrange(desc(.cooksd)) %>% filter(.cooksd > 1)
```

```
# A tibble: 0 × 14
# ℹ 14 variables: territory <chr>, .cooksd <dbl>, life_exp <dbl>,
#   cell_phones_100 <dbl>, .hat <dbl>, BS_q <fct>, freedom_status <fct>,
#   income_level_4 <fct>, vax_rate <dbl>, happiness_score <dbl>, .fitted <dbl>,
#   .resid <dbl>, .sigma <dbl>, .std.resid <dbl>
```

Plotting Cook's Distance

```
1 # plot(model) shows figures similar to autoplot() but adds Cook's distance
2 plot(final_model, which = 4)
```



- Identify 3 highest Cook's distance: 8, 52, ~~66~~ 63 (Bangladesh, Lesotho, ~~Malawi~~ Malawi)

How do we deal with influential points?

- If an observation is influential, we can **check data errors**:
  - Was there a data entry or collection problem?
  - If you have reason to believe that the observation does not hold within the population (or gives you cause to redefine your population)
- If an observation is influential, we can **check our model**:
  - Did you leave out any important predictors?
  - Should you consider adding some interaction terms?
  - Is there any nonlinearity that needs to be modeled?
- Basically, deleting an observation should be justified outside of the numbers!
  - If it's an honest data point, then it's giving us important information!
- **Means we will need to discuss the limitations of our model**
  - For example: Think about measurements that might help explain life expectancy that are NOT in our model
- A really well thought out explanation from StackExchange

Poll Everywhere Question 2

When we have detected problems in our model...

- We have talked about influential points
- We have talked about identifying issues with our LINE assumptions

What are our options once we have identified issues in our linear regression model?

- Are we missing a crucial measure in our dataset?
- Try categorization or transformation (or numeric variables) if there is an issue with linearity or normality
  - Addressed in model selection
- Try a weighted least squares approach if unequal variance (oof, not enough time for us to get to)
- Try a robust estimation procedure if we have a lot of outlier issues (outside scope of class)
  - ↳ robust SE's

Learning Objectives

1. Apply tools from SLR (Lesson 6: SLR Diagnostics) in MLR to **evaluate LINE assumptions**, including residual plots and QQ-plots
2. Apply tools involving standardized residuals, leverage, and Cook's distance from SLR (Lesson 7: SLR Diagnostics 2) in MLR to **flag potentially influential points**

3. Use Variance Inflation Factor (VIF) and it's general form to **detect and correct multicollinearity**

What is multicollinearity? (adapted from parts of STAT 501 page)

So far, we've been ignoring something very important: multicollinearity

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \varepsilon$$

highly correlated

Multicollinearity

Two or more covariates in a multivariable regression model are *highly* correlated

- Types of multicollinearity
  - **Structural multicollinearity**
    - Mathematical artifact caused by creating new covariates from other covariates
    - For example: If we have age, and decide to transform age to include age-squared
      - Then we have age and age-squared in the model: age-squared is perfectly predicted by age!

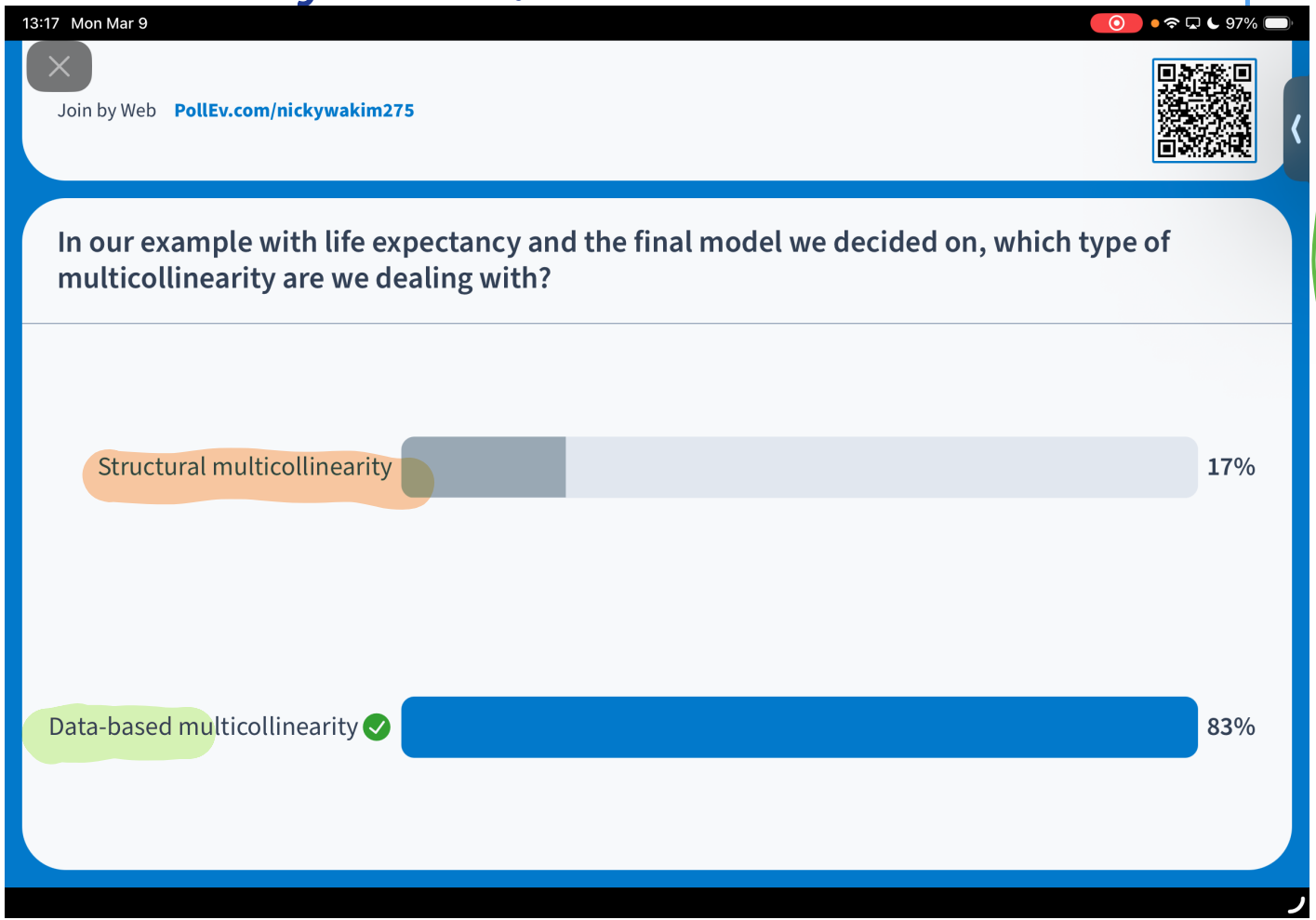
$$Y = \beta_0 + \beta_1 Age + \beta_2 Age^2 + \varepsilon$$

$\hat{\beta}_1$ $\hat{\beta}_2$: their SEs are inflated

center

  - **Data-based multicollinearity**
    - Result of a poorly designed experiment, reliance on purely observational data, or the inability to manipulate the system on which the data are collected
    - Or we are using two variables that are practically measuring the same thing

Poll Everywhere Question 3



- Our **final model** contains
  - Cell phones per 100 people
  - Basic sanitation (quartiles)
  - Freedom status
  - Income level
  - Vaccination rate
  - Happiness score

basic sani (%)
(numeric)

Why is multicollinearity a problem?

In linear regression, **depending on the other predictors in the model**, the following will change:

- Estimated regression coefficient of any one variable
  - Not necessarily bad, but a big change might be an issue
- Hypothesis tests for any coefficient may yield different conclusions → SE for coeff of affected variable will be larger
- Contribution of any one predictor variable in reducing sum of squared errors

When there is multicollinearity in our model:

- **Precision** of the estimated regression coefficients or correlated covariates **decreases a lot** ↑ $SE_{\hat{\beta}}$
  - Basically, **standard error increases and confidence intervals get wider**, which means we're not as confident in our estimate anymore
  - Because highly correlated covariates are not adding much more information, but are constraining our model more

Did you notice anything about all the consequences of multicollinearity?

- All consequences relate to estimating a regression coefficient **precisely**
  - Recall that precision is linked to analysis **goals of association and interpretability**
  - See lesson on Model Selection

talk abt relationship b/w an X & Y

- Multicollinearity is *not really an issue* when our **goal is prediction**
  - Highly correlated covariates/predictors will not hurt our prediction of an outcome

best predicts Y, inc accuracy of $\hat{Y}$ (predicted Y)

How do we detect multicollinearity?

- **Variance inflation factors (VIF):** quantifies how much the variance of the estimated coefficient for covariate k increases
  - Increases: from SLR with only covariate k to MLR with all other covariates

- General rule of thumb
  - $VIF < 4$: Good!
  - $4 < VIF < 10$: Warrent investigation (but most people aren't investigating this...)
  - $VIF > 10$: Requires correction
    - Influencing regression coefficient estimates

VIF

$$VIF = \frac{1}{1 - R_k^2}$$

R_k^2 is the R^2-value obtained by regressing the k^{th} covariate/predictor on the remaining predictors

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \varepsilon$$

$$X_1 = \beta_0 + \beta_1 X_2 + \varepsilon$$

Let's apply it to our final model

- Naive way to calculate this in R:

```
1 library(rms)
2 rms::vif(final_model)
```

output from lm()

```
                cell_phones_100                  BS_q(61.1,92.8]
                       1.903507                         1.920420
                  BS_q(92.8,98]                    BS_q(98,100]
                       2.428357                         3.171019
               freedom_statusPF                 freedom_statusF
                       1.517866                         2.081666
income_level_4Lower middle income income_level_4Upper middle income
                       3.672232                         5.994002
        income_level_4High income                        vax_rate
                       6.812730                         1.428216
               happiness_score
                       2.765792
```

- All $VIF < 10$
- Problem: multi-level covariates (CO2 Emissions and income level) have different VIF's even though they should be considered one variable

Let's apply it to our final model *correctly* (1/2)

- Calculate the GVIF and, more importantly, the $GVIF^{1/(2 \cdot df)}$
- GVIF is the R^2-value for regressing a covariate's group indicators on the remaining covariates
  - Captures the correlation between covariates better
- $GVIF^{1/(2 \cdot df)}$ helps standardize GVIF based on how many levels each categorical covariate has
  - I'll refer to this as df-corrected GVIF or standardized GVIF
  - If continuous covariate, $GVIF^{1/(2 \cdot df)} = \sqrt{GVIF}$

```
1 library(car)
2 car::vif(final_model)
```

```
                    GVIF Df GVIF^(1/(2*Df))
cell_phones_100 1.903507  1        1.379676
BS_q            2.658818  3        1.177013
freedom_status  1.660933  2        1.135241
income_level_4  5.648213  3        1.334500
vax_rate        1.428216  1        1.195080
happiness_score 2.765792  1        1.663067
```

$\rightarrow 5.64^{(1/6)}$

Let's apply it to our final model *correctly* (2/2)

- If continuous covariate, $GVIF^{1/(2 \cdot df)} = \sqrt{GVIF}$
- So we can square $GVIF^{1/(2 \cdot df)}$ and set VIF rules
- OR: we can correct any $GVIF^{1/(2 \cdot df)} > \sqrt{10} = 3.162$

```
1 car::vif(final_model)
```

cutoff for VIF > 10 correct

```
                    GVIF Df GVIF^(1/(2*Df))
cell_phones_100 1.903507  1        1.379676
BS_q            2.658818  3        1.177013
freedom_status  1.660933  2        1.135241
income_level_4  5.648213  3        1.334500
vax_rate        1.428216  1        1.195080
happiness_score 2.765792  1        1.663067
```

> 3.162

- All of these covariates are okay! No multicollinearity to correct in this dataset!

But what if we do need to make corrections for multicollinearity?

- We have been dealing with **data-based multicollinearity** in our example
- If we had issues with multicollinearity, then what are our options?
  - Remove the variable(s) with large VIF
  - Use expert knowledge in the field to decide
- If one variable has a large VIF, then there is usually another one or more variables with large VIFs
  - Basically, all the covariates that are correlated will have large VIFs
- Example: our two largest GVIFs were for world region and income levels
  - Hypothetical: their $GVIF^{1/(2 \cdot df)} > 3.162$
  - Remove one of them
  - I'm no expert, but from more of a data equity lens, there's a lot of generalizations made about world regions
    - I think relying on the income level of a country might give us more information as well

What about structural multicollinearity?

- **Structural multicollinearity**
  - Mathematical artifact caused by creating new covariates from other covariates

- For example: If we have age, and decide to transform age to include age-squared
  - Then we have age and age-squared in the model: age-squared is perfectly predicted by age!
  - By having the untransformed and transformed covariate in the model, they are inherently correlated!

- **Best practice to reduce the correlation: center you covariate**
  - By centering age, we no longer have a one-to-one connection between age and age-squared
  - If centered at 40yo: a 35yo has centered age of -5 and a 45yo centered age of 5, but both have age-squared of 25

35 → 1225
45 → 2025

- Check out the Penn State site for a work through of an example with VIFs

Summary of multicollinearity

- Correlated covariates/predictors will hurt our model's precision and interpretations of coefficients

- We need to check for multicollinearity by using VIFs or GVIFs

- If $VIF > 10$ or $GVIF^{1/(2 \cdot df)} > 3.162$, we need to do something about the covariates
  - Data based: remove one the of correlated variables
  - Structural based: centering usually fixes it

Regression analysis process