Lesson 14: Purposeful model selection

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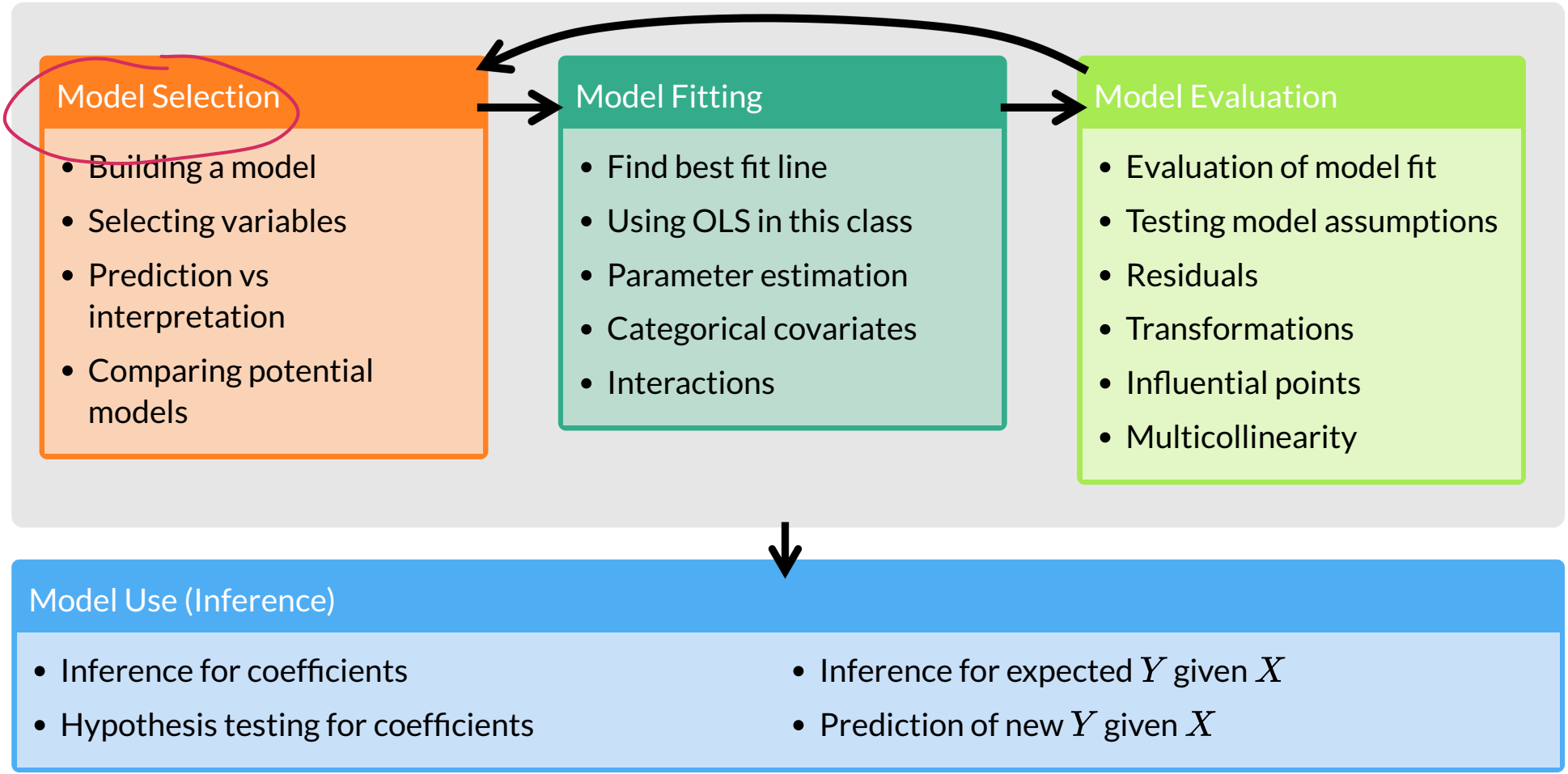
Learning Objectives

1. Understand the overall steps for purposeful selection as a model building strategy
2. Apply purposeful selection to a dataset using R
3. Use different approaches to assess the linear scale of continuous variables in linear regression

Regression analysis process



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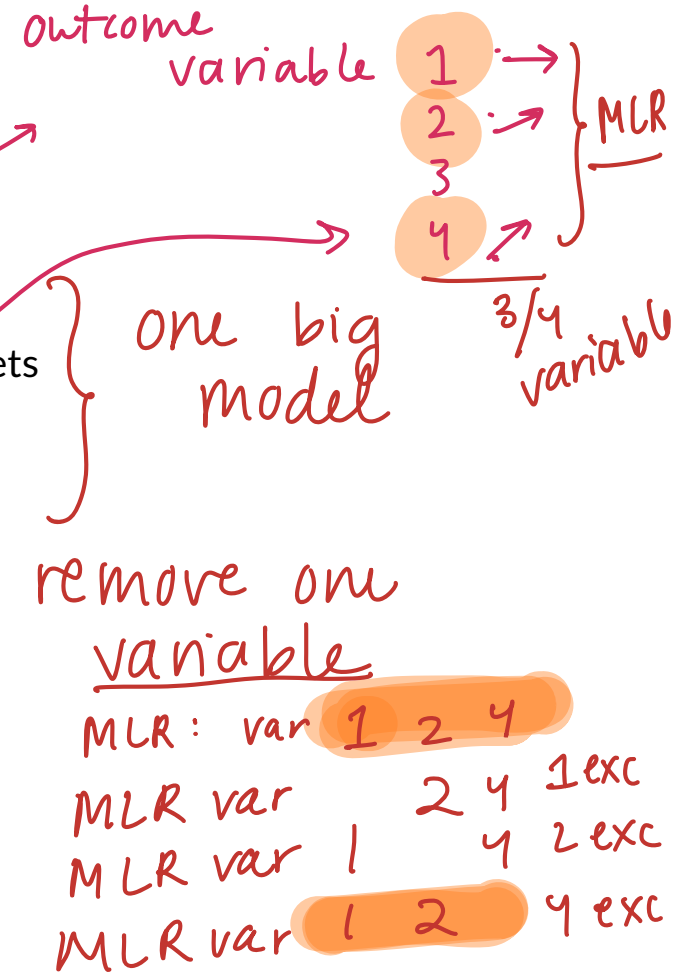
"Successful modeling of a complex data set is part science, part statistical methods, and part experience and common sense."

Hosmer, Lemeshow, and Sturdivant Textbook, pg. 101

Overall Process

0. Exploratory data analysis
1. Check unadjusted associations in simple linear regression
2. Enter all covariates in model that meet some threshold
   - One textbook suggest $p < 0.2$ or $p < 0.25$: great for modest sized datasets
   - PLEASE keep in mind sample size in your study
   - Can also use magnitude of association rather than, or along with, p-value
3. Remove those that no longer reach some threshold
   - Compare magnitude of associations to unadjusted version (univariable)
4. Check scaling of continuous and coding of categorical covariates
5. Check for interactions
6. Assess model fit
   - Model assumptions, diagnostics, overall fit



Process with snappier step names

Pre-step: Exploratory data analysis (EDA)

Step 1: Simple linear regressions / analysis

Step 2: Preliminary variable selection

Step 3: Assess change in coefficients

Step 4: Assess scale for continuous variables

Step 5: Check for interactions

Step 6: Assess model fit

Learning Objectives

1. Understand the overall steps for purposeful selection as a model building strategy

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Pre-step: Exploratory data analysis

- The following slides are all reference until we get to Step 1
- We have covered exploratory data analysis in other classes and have completed it in our previous labs

Pre-step: Exploratory data analysis

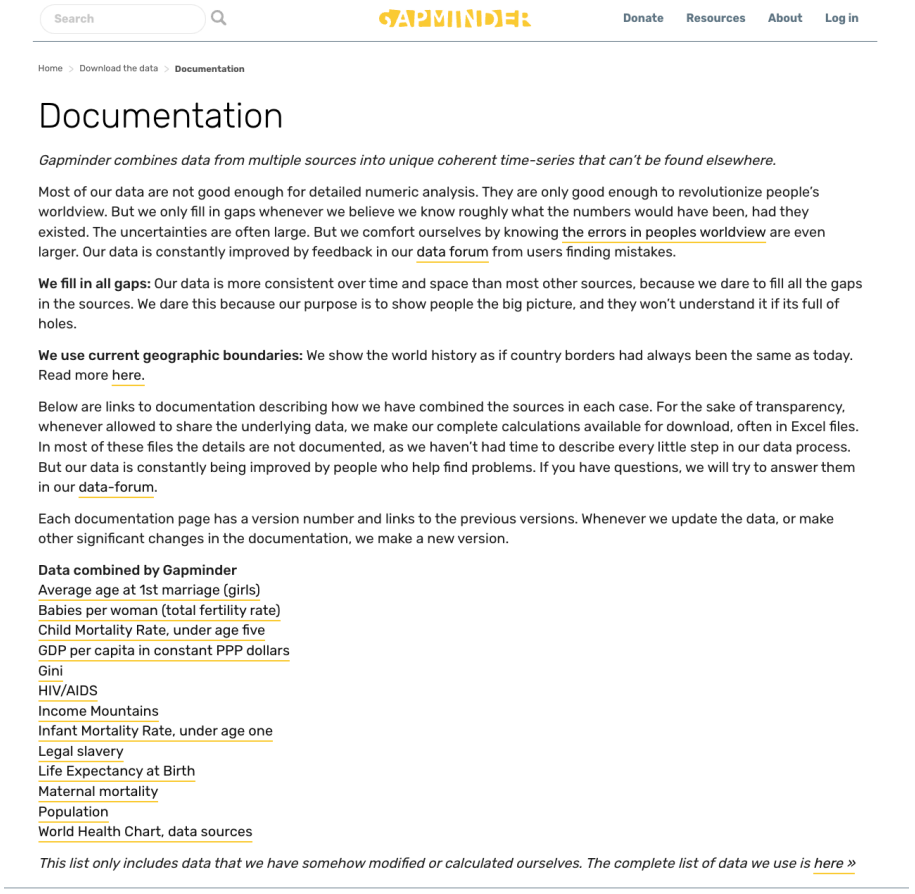
- Things we have been doing over the quarter in class and in our project
- I will not discuss some of the methods mentioned in our lab and data management class
  - I am only going to introduce additional exploratory functions

A few things we can do:

- Check the data
- Study your variables
- Missing data?
- Explore simple relationships and assumptions

Pre-step: Exploratory data analysis: Check the data

- Get to know the potential values for the data
  - Categories
  - Units
- Make yourself a codebook for reference
- Then make sure the summary of values makes sense
  - If minimum or maximum look outside appropriate range
  - For example: a negative value for a measurement that is inherently positive (like population or income)



https://www.gapminder.org/data/documentation/

Pre-step: Exploratory data analysis: Check the data

- Look at a summary for the raw data
- Typical use:

```
1 library(skimr)
2 skim(gapm)
```

- Some `skim()` help

Pre-step: Exploratory data analysis: Check the data

- Look at a summary for the raw data
- Typical use:

```
1 library(skimr)
2 skim(gapm2)
```

- Some `skim()` help
- Note that `skim(gapm)` looks different because I had to create factors
- I am breaking down the `skim()` function into the categorical and continuous variables only because I want to show them on the slides

```
1 skim(gapm2) %>% yank("factor")
```

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
freedom_status	0	1	FALSE	3	PF: 46, NF: 31, F: 28
income_level_4	0	1	FALSE	4	Low: 37, Upp: 34, Hig: 19, Low: 15

Pre-step: Exploratory data analysis: Check the data

```
1 skim(gapm2) %>% yank("numeric")
```

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
cell_phones_100	0	1	116.52	34.56	32.06	99.13	116.68	137.18	207.28	
life_exp	0	1	70.97	6.76	50.69	66.11	71.52	75.67	85.23	
vax_rate	0	1	91.45	8.78	63.00	89.00	95.00	98.00	99.00	
basic_sani	0	1	79.76	23.75	21.64	61.11	92.80	97.99	100.00	
co2_emissions	0	1	5356.04	12822.92	17.67	285.50	871.27	4881.84	102490.55	
happiness_score	0	1	52.35	11.65	12.81	43.59	53.78	60.44	77.29	

Poll Everywhere Question 1

In the following skim() output, what summaries might you flag?

```
1 skim(gapm_sub1) %>% yank("numeric")
```

Variable type: numeric

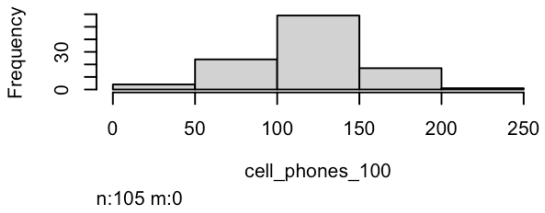
skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
CO2emissions	4	0.98	4.55	6.10	0.03	0.64	2.41	6.22	41.20	
ElectricityUsePP	58	0.70	4220.92	5964.07	31.10	699.00	2410.00	5600.00	52400.00	
FoodSupplykcPPD	27	0.86	2825.06	443.59	1910.00	2490.00	2775.00	3172.50	3740.00	
IncomePP	2	0.99	16704.45	19098.61	614.00	3370.00	10100.00	22700.00	129000.00	
LifeExpectancyYrs	8	0.96	70.66	8.44	47.50	64.30	72.70	76.90	82.90	
FemaleLiteracyRate	115	0.41	81.65	21.95	13.00	70.97	91.60	98.03	99.80	
WaterSourcePrct	1	0.99	84.84	18.64	18.30	74.90	93.50	99.07	100.00	
Latitude	0	1.00	19.11	23.93	-42.00	4.00	17.33	40.00	65.00	
Longitude	0	1.00	21.98	66.52	-175.00	-5.75	21.00	49.27	179.14	
population_mill	0	1.00	35.95	136.87	0.00	1.73	7.57	24.50	1370.00	

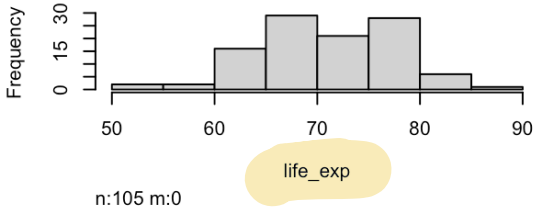
Pre-step: Exploratory data analysis: Study your variables

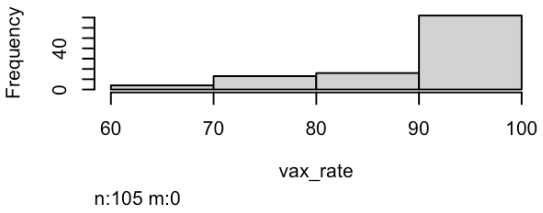
- Started this a little bit in previous slide (`skim()`), but you may want to look at things like:
  - Sample size
  - Counts of missing data
  - Means and standard deviations
  - IQRs
  - Medians
  - Minimums and maximums
- Can also look at visuals
  - Continuous variables: histograms (in `skimr() a little)
  - Categorical variables: frequency plots

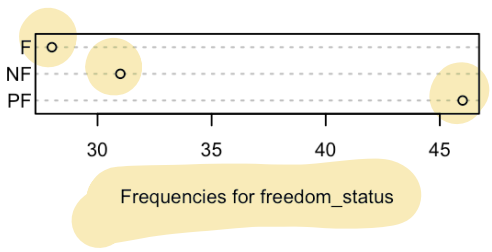
Pre-step: Exploratory data analysis: Study your variables

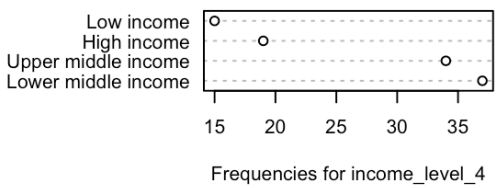
```
1 library(Hmisc)
2 hist.data.frame(gapm2)
```

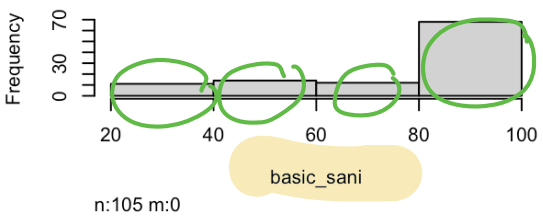


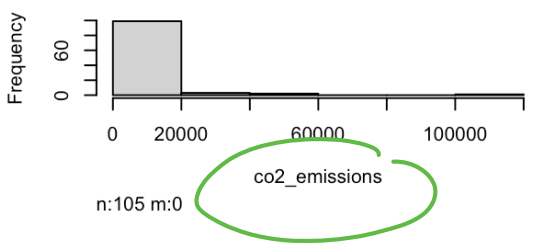


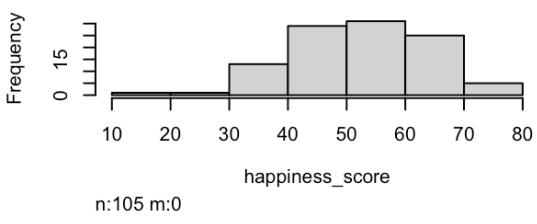












Poll Everywhere Question 2

Pre-step: Exploratory data analysis: Missing data

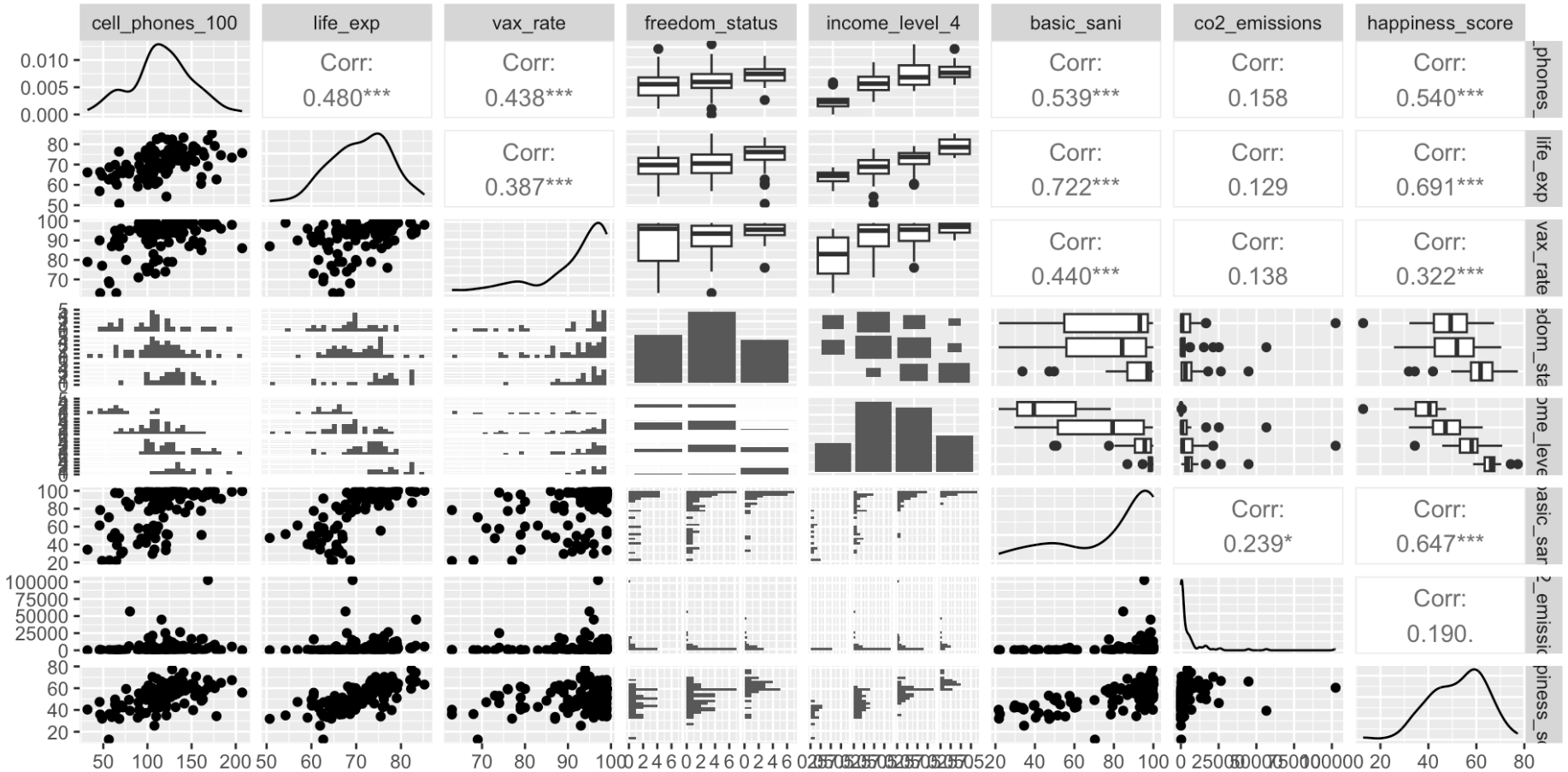
- Why are there missing data?
- Which variables and observations should be excluded because of missing data?
- Will I impute missing data?

- Unfortunately, we don't have time to discuss missing data more thoroughly
- I will try to cover this topic more thoroughly in BSTA 513

- For the Gapminder dataset, we chose to use complete cases

Pre-step / Step 1 : Explore simple relationships and assumptions

```
1 gapm2 %>% ggpairs() # gapm2 is a new dataset with some variables selected
```



Step 1: Simple linear regressions / analysis

- For each covariate, we want to see how it relates to the outcome (without adjusting for other covariates)
- We can partially do this with **visualizations**
  - Helps us see the data we throw it into regression that makes assumptions (like our LINE assumptions)
  - `ggpairs()` can be a quick way to do it
  - `ggplot()` can make each plot
    - `+ geom_boxplot()` to make boxplots by groups for categorical covariates
    - `+ geom_jitter() + stat_summary()` to make non-overlaping points with group means for categorical covariates
    - `+ geom_point()` to make scatterplots for continuous covariates
- We need to run **simple linear regression**
  - We're calling regression with multi-level categories "simple" even though there are multiple coefficients

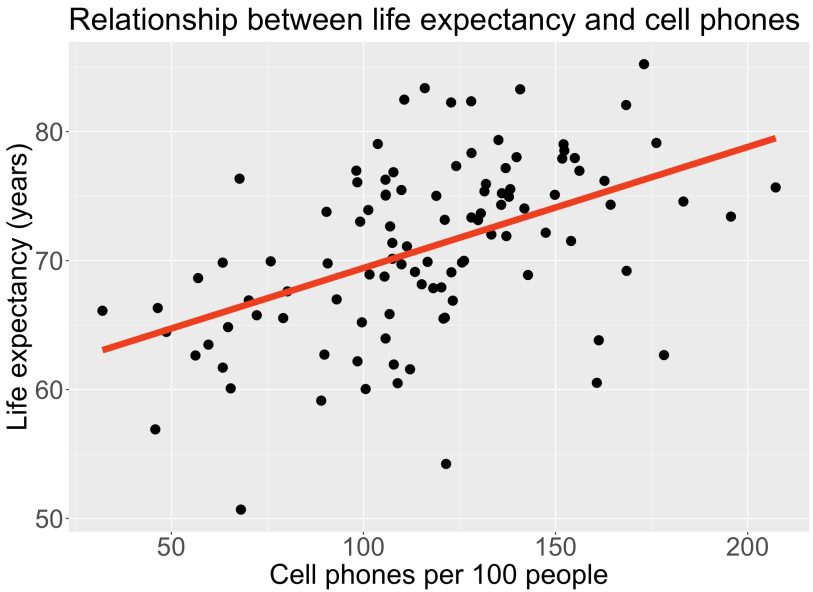
$$Y = \beta_0 + \_\_\_\_$$

Step 1: Simple linear regressions / analysis

- Let's think back to our Gapminder dataset
- Always good to start with our main relationship: life expectancy vs. cell phones
  - *Throwback to Lesson 3 SLR when we first visualized and ran `lm()` for this relationship*

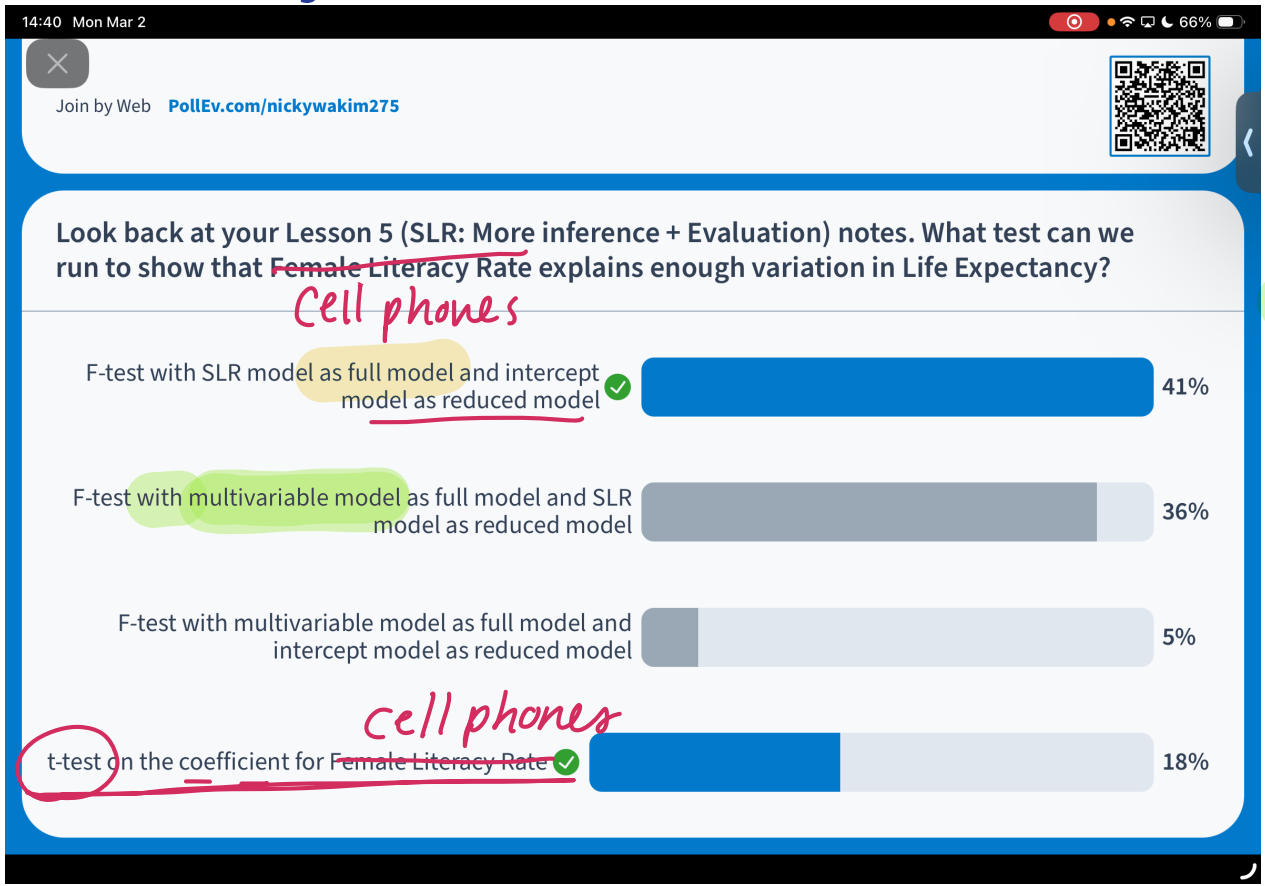
```
1 model_CP = gapm2 %>% lm(formula = life_exp ~ cell_phones_100)
```

$\widehat{LE} = \hat{\beta}_0 + \hat{\beta}_1 CP$



term	estimate	std.error	statistic	p.value
(Intercept)	60.04	2.06	29.21	0.00
cell_phones_100	0.09	0.02	5.55	0.00

Poll Everywhere Question 3



Null (red)

$LE = \beta_0 + \varepsilon$

$\beta_1 = 0$

Alt (full)

$LE = \beta_0 + \beta_1 CP + \varepsilon$

$\beta_1 \neq 0$

b/c only one coef, t-test is same as F-test

Step 1: Simple linear regressions / analysis

- Let's do this with one other variable before I show you a streamlined version of SLR

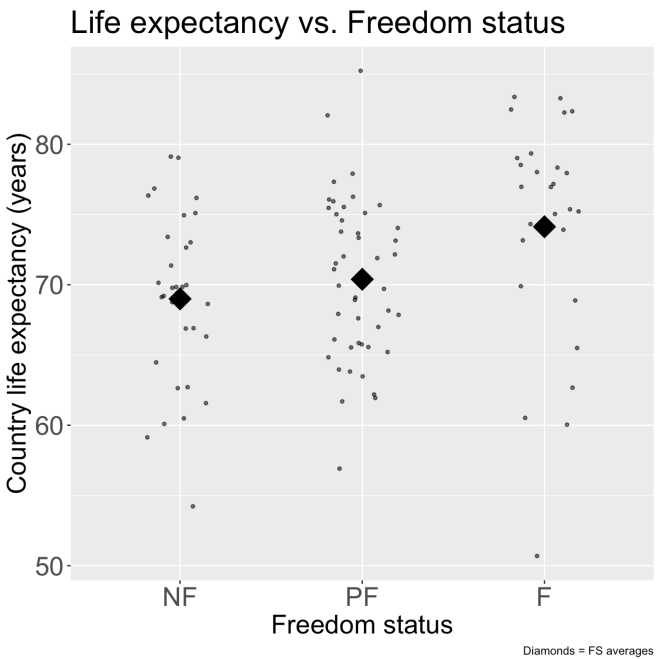
no t-test in this case

```
model_FS = gapm2 %>% lm(formula = life_exp ~ freedom_status)
```

▶ Code

```
anova(model_FS) %>% tidy() %>% gt() %>%
  tab_options(table.font.size = 40) %>%
  fmt_number(decimals = 2)
```

term	df	sumsq	meansq	statistic	p.value
freedom_status	2.00	415.94	207.97	4.89	0.01
Residuals	102.00	4,341.91	42.57	NA	NA



- Recall from Lesson 5 (and Lesson 10):
  - `anova()` with one model name will compare the model (`model_FS`) to the intercept model

Step 1: Simple linear regressions / analysis

- If we do a good job visualizing the relationship between our outcome and each covariate, then we can proceed to a streamlined version of the F-test for each relationship
- Run `add1()` to add each variable one at a time and separately
- Output will include hypothesis test (using F-test) if coefficient(s) is 0 or not
  - Null: intercept model
  - Alternative: model with single variable

for specific variable

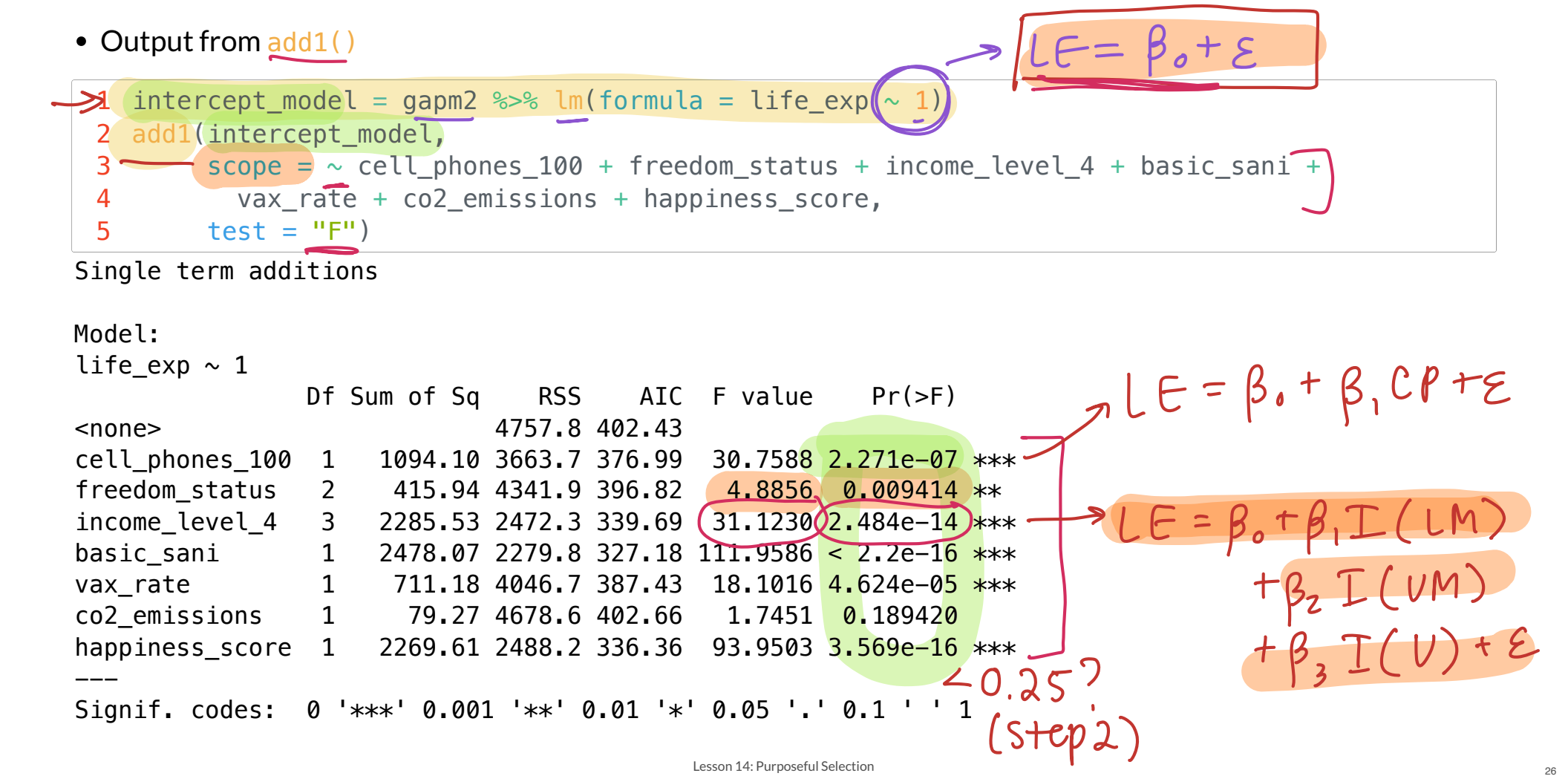
Step 1: Simple linear regressions / analysis

- Output from `add1()`

```
intercept_model = gapm2 %>% lm(formula = life_exp ~ 1)
add1(intercept_model,
     scope = ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani +
       vax_rate + co2_emissions + happiness_score,
     test = "F")
```

```
Single term additions

Model:
life_exp ~ 1
                Df Sum of Sq    RSS    AIC  F value    Pr(>F)
<none>                      4757.8 402.43
cell_phones_100  1   1094.10 3663.7 376.99  30.7588 2.271e-07 ***
freedom_status   2    415.94 4341.9 396.82   4.8856  0.009414 **
income_level_4   3   2285.53 2472.3 339.69  31.1230 2.484e-14 ***
basic_sani       1   2478.07 2279.8 327.18 111.9586 < 2.2e-16 ***
vax_rate         1    711.18 4046.7 387.43  18.1016 4.624e-05 ***
co2_emissions    1     79.27 4678.6 402.66   1.7451  0.189420
happiness_score  1   2269.61 2488.2 336.36  93.9503 3.569e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Step 2: Preliminary variable selection

- Identify candidates for your first multivariable model by performing an F-test on each covariate's SLR
  - Using p-values from previous slide
  - If the p-value of the test is less than 0.25, then consider the variable a candidate

- Candidates for first multivariable model
  - All clinically important variables (regardless of p-value)
  - Variables with univariate test with p-value < 0.25

- With more experience, you won't need to rely on these strict rules as much

Step 2: Preliminary variable selection

- From the previous p-values from the F-test on each covariate's SLR
  - Decision: we keep all the covariates since they all have a p-value < 0.25

```
add1(intercept_model,
     scope = ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + vax_rate +
     test = "F")
```

```
Single term additions

Model:
life_exp ~ 1
                Df Sum of Sq    RSS    AIC  F value    Pr(>F)
<none>                      4757.8 402.43
cell_phones_100  1   1094.10 3663.7 376.99  30.7588 2.271e-07 ***
freedom_status   2    415.94 4341.9 396.82   4.8856  0.009414 **
income_level_4   3   2285.53 2472.3 339.69  31.1230 2.484e-14 ***
basic_sani       1   2478.07 2279.8 327.18 111.9586 < 2.2e-16 ***
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co2_emissions    1     79.27 4678.6 402.66   1.7451  0.189420
happiness_score  1   2269.61 2488.2 336.36  93.9503 3.569e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Step 2: Preliminary variable selection

- Fit an **initial model** including any independent variable with p-value < 0.25 and clinically important variables

```
init_model = gapm2 %>%
  lm(formula =
       life_exp ~ cell_phones_100 +
       freedom_status +
       income_level_4 +
       basic_sani +
       vax_rate +
       co2_emissions +
       happiness_score)
tbl_regression(
  init_model,
  label = list(
    cell_phones_100 ~ "Cell phones per 100
    freedom_status ~ "Freedom status",
    income_level_4 ~ "Income level",
    basic_sani ~ "Basic sanitation (%)",
    vax_rate ~ "Vaccination rate (%)",
    co2_emissions ~ "CO2 emissions",
    happiness_score ~ "Happiness score"
```

Characteristic	Beta	95% CI	p-value
Cell phones per 100 people	0.00	-0.03, 0.04	0.8
Freedom status			
NF	—	—	
PF	0.88	-1.1, 2.8	0.4
F	-0.61	-3.2, 2.0	0.6
Income level			
Low income	—	—	
Lower middle income	-1.3	-4.6, 2.0	0.4
Upper middle income	-0.76	-5.1, 3.6	0.7
High income	3.7	-1.8, 9.1	0.2
Basic sanitation (%)	0.14	0.08, 0.19	<0.001
Vaccination rate (%)	0.04	-0.07, 0.15	0.5
CO2 emissions	0.00	0.00, 0.00	0.3
Happiness score	0.15	0.04, 0.26	0.011

Abbreviation: CI = Confidence Interval

Step 3: Assess change in coefficient

- We have our initial model with all the covariates that we want to consider
  - We want to see if we can remove any of the covariates without changing the coefficient of our main explanatory variable (cell phones) by more than 10%

- One variable at a time, we run the multivariable model with and without a variable
  - We look at the p-value of the F-test for the coefficients of said variable
  - We look at the percent change for the coefficient ($\Delta\%$) of our **explanatory variable** (CP in our example)

- General rule: We can remove a variable if…
  - p-value > 0.05 for the F-test of its own coefficients
  - AND change in coefficient ($\Delta\%$) of our explanatory variable is < 10%

initial model

initial dropping that variable

] not significant / not explaining enough variance

not changing effect of main relationship

Step 3: F-test on dropping each covariate

- Function `drop1()`: If we put in our initial model, the function will remove each covariate and perform the respective F-test to test if the coefficients are 0 (null) or not (alternative).

```
1 drop1(init_model, test="F")
```

```
Single term deletions

Model:
life_exp ~ cell_phones_100 + freedom_status + income_level_4 +
    basic_sani + vax_rate + co2_emissions + happiness_score
                Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                      1604.5 308.29
cell_phones_100  1      1.06 1605.5 306.36  0.0618  0.804149
freedom_status   2     32.94 1637.4 306.43  0.9650  0.384708
income_level_4   3    220.87 1825.3 315.83  4.3134  0.006769 **
basic_sani       1    441.50 2046.0 331.81 25.8660 1.864e-06 ***
vax_rate         1      9.30 1613.8 306.90  0.5451  0.462149
co2_emissions    1     15.46 1619.9 307.30  0.9057  0.343700
happiness_score  1    115.99 1720.5 313.62  6.7952  0.010629 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

initial model (post step 2)

pval > 0.05 so we want to check Δ% in coef estimate for CP

Step 3: F-test on dropping each covariate

Let's consider an example of a hypothesis test from `drop1()` for `income_level_4`

Null H_0

$\beta_8 = \beta_9 = \beta_{10} = 0$

Alternative H_1

$\beta_8 \neq 0$ and/or $\beta_9 \neq 0$ and/or $\beta_{10} \neq 0$

Null / Smaller / Reduced model

$$\begin{aligned} LE = &\beta_0 + \beta_1 \text{CP} + \beta_2 I(\text{FS} = \text{PF}) + \\ &\beta_3 I(\text{FS} = \text{F}) + \beta_4 \text{BS} + \beta_5 \text{VR} + \\ &\beta_6 \text{CO2} + \beta_7 \text{HS} + \epsilon \end{aligned}$$

removing income level from model

Alternative / Larger / Full model INITAL MODEL

$$\begin{aligned} LE = &\beta_0 + \beta_1 \text{CP} + \beta_2 I(\text{FS} = \text{PF}) + \\ &\beta_3 I(\text{FS} = \text{F}) + \beta_4 \text{BS} + \beta_5 \text{VR} + \\ &\beta_6 \text{CO2} + \beta_7 \text{HS} + \beta_8 I(\text{IL} = \text{lower middle}) + \\ &\beta_9 I(\text{IL} = \text{upper middle}) + \beta_{10} I(\text{IL} = \text{upper}) + \epsilon \end{aligned}$$

- From the output of `drop1()`, we can see that the p-value for dropping `income_level_4` is 0.003, which is < 0.05, so there is sufficient evidence that the coefficients are not 0

income level (while adjusted for other vars) explains significant variation

Step 3: Testing for percent change ($\Delta\%$) in a coefficient

main research q

- Our F-test in `drop1()` concluded that we should drop a variable (e.g. freedom status)
  - We then need to check if the change in coefficient for the main variable is less than 10% or not
- Generic form: If we are only considering X_1 and X_2, then we need to run the following two models:
  - Fitted model 1 / reduced model (`mod1`): $\widehat{Y} = \widehat{\beta}_0 + \widehat{\beta}_1 X_1$
    - We call the above $\widehat{\beta}_1$ the reduced model coefficient: $\widehat{\beta}_{1,\text{mod1}}$ or $\widehat{\beta}_{1,\text{red}}$
  - Fitted model 2 / Full model (`mod2`): $\widehat{Y} = \widehat{\beta}_0 + \widehat{\beta}_1 X_1 + \widehat{\beta}_2 X_2$
    - We call this $\widehat{\beta}_1$ the full model coefficient: $\widehat{\beta}_{1,\text{mod2}}$ or $\widehat{\beta}_{1,\text{full}}$

Calculation for % change in coefficient

$$\Delta\% = 100\% \cdot \frac{|\widehat{\beta}_{1,\text{mod1}} - \widehat{\beta}_{1,\text{mod2}}|}{\widehat{\beta}_{1,\text{mod2}}} = 100\% \cdot \frac{|\widehat{\beta}_{1,\text{red}} - \widehat{\beta}_{1,\text{full}}|}{\widehat{\beta}_{1,\text{full}}}$$

Step 3: Assess change in coefficient

- Let's try this out on freedom status

▶ Display the ANOVA table with F-statistic and p-value

term	df.residual	rss	df	sumsq	statistic	p.value
life_exp ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + vax_rate + co2_emissions + happiness_score	94.000	1,604.465	NA	NA	NA	NA
life_exp ~ cell_phones_100 + basic_sani + vax_rate + co2_emissions + happiness_score + income_level_4	96.000	1,637.409	−2.000	−32.944	0.965	0.385

- $\widehat{\beta}_{CP,full} = 0.004, \widehat{\beta}_{CP,red} = 0.0057$

$$\Delta\% = 100\% \cdot \frac{|\widehat{\beta}_{CP,full} - \widehat{\beta}_{CP,red}|}{\widehat{\beta}_{CP,full}} = 100\% \cdot \frac{|0.004 - 0.0057|}{0.004} = 41.97\%$$

- Based off the percent change, I would keep this in the model

freedom status in model

Step 3: Assess change in coefficient (Reference only)

- Let's try this out on vaccination rate

▶ Display the ANOVA table with F-statistic and p-value

term	df.residual	rss	df	sumsq	statistic	p.value
life_exp ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + vax_rate + co2_emissions + happiness_score	94.000	1,604.465	NA	NA	NA	NA
life_exp ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + co2_emissions + happiness_score	95.000	1,613.770	−1.000	−9.305	0.545	0.462

- $\widehat{\beta}_{CP,full} = 0.004, \widehat{\beta}_{CP,red} = 0.006$

$$\Delta\% = 100\% \cdot \frac{|\widehat{\beta}_{CP,full} - \widehat{\beta}_{CP,red}|}{\widehat{\beta}_{CP,full}} = 100\% \cdot \frac{|0.004 - 0.006|}{0.004} = 49.72\%$$

- Based off the percent change, I would keep this in the model

Step 3: Assess change in coefficient (Reference only)

- Let's try this out on CO2 emissions

▶ Display the ANOVA table with F-statistic and p-value

term	df.residual	rss	df	sumsq	statistic	p.value
life_exp ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + vax_rate + co2_emissions + happiness_score	94.000	1,604.465	NA	NA	NA	NA
life_exp ~ cell_phones_100 + freedom_status + income_level_4 + basic_sani + vax_rate + happiness_score	95.000	1,619.924	−1.000	−15.459	0.906	0.344

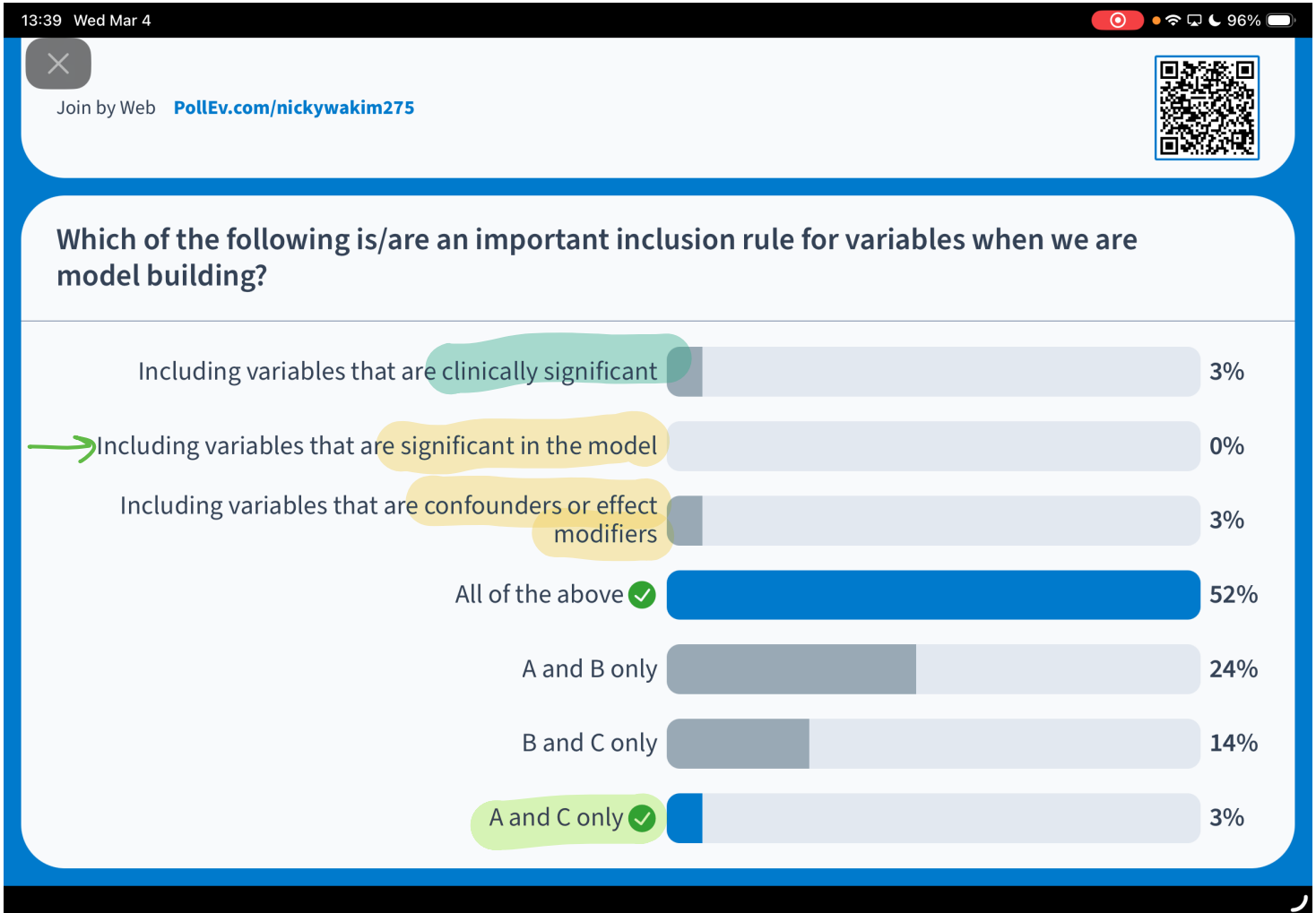
> 0.05

- $\widehat{\beta}_{CP,full} = 0.004, \widehat{\beta}_{CP,red} = 0.0039$

$$\Delta\% = 100\% \cdot \frac{|\widehat{\beta}_{CP,full} - \widehat{\beta}_{CP,red}|}{\widehat{\beta}_{CP,full}} = 100\% \cdot \frac{|0.004 - 0.0039|}{0.004} = 3.35\%$$

- Based off the percent change, I would remove CO2 emissions from the model

Poll Everywhere Question 4



Step 3: Assess change in coefficient: Summary

- At the end of this step, we have a **preliminary main effects model**
- Where the variables are excluded that met the following criteria:
  - P-value > 0.05 for the F-test of its own coefficients
  - Change in coefficient ($\Delta\%$) of our explanatory variable is < 10%
- In our example, the **preliminary main effects model** (end of Step 3) has one less variable than the **initial model** (end of Step 2)
- Preliminary main effects model includes:
  - `cell_phones_100`
  - `freedom_status`
  - `income_level_4`
  - `basic_sani`
  - `vax_rate`
  - `happiness_score`

Recap of Steps 1-3

- Pre-step: Exploratory data analysis
- Step 1: Simple linear regressions / analysis
  - Look at each covariate with outcome
  - Perform SLR for each covariate
- Step 2: Preliminary variable selection
  - From SLR, decide which variables go into the initial model
  - Use F-test to see if each covariate (on its own) explains enough variation in outcome
  - End with **initial model**
- Step 3: Assess change in coefficients
  - From the initial model at end of step 2, we take a variable out of the model if:
    - P-value > 0.05 for the F-test of its own coefficients
    - Change in coefficient ($\Delta\%$) of our explanatory variable is < 10%
  - End with **preliminary main effects model**

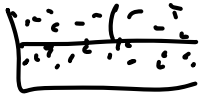
Learning Objectives

1. Understand the overall steps for purposeful selection as a model building strategy
2. Apply purposeful selection to a dataset using R

3. Use different approaches to assess the linear scale of continuous variables in linear regression

Step 4: Assess scale for continuous variables

- We assume the linear regression model is linear for **each continuous variable**
- We need to assess linearity for continuous variables in the model
  - Do this through smoothed scatterplots that we introduced in Lesson 6 (SLR Diagnostics)
  - Residual plots (can be used in SLR) does not help us in MLR
  - Each term in MLR model needs to have linearity with outcome



- Three methods/approaches to address the violation of linearity assumption:
  - **Approach 1:** Categorize continuous variable
  - **Approach 2:** Transformation of variable
  - **Approach 3:** Spline functions
- Approach will depend on the covariate!!
- For our class, only implement **Approach 1 or 2**
- Model at the end of Step 4 is the **main effects model**

Step 4: Assess scale for continuous variables: Smoothed scatterplots

- Smoother scatterplots **only check linearity**, not addressing linearity issues

- Can also identify extreme observations
  - Again, just want to flag these values
  - Can influence the assessment of linearity when using fractional polynomials or spline functions

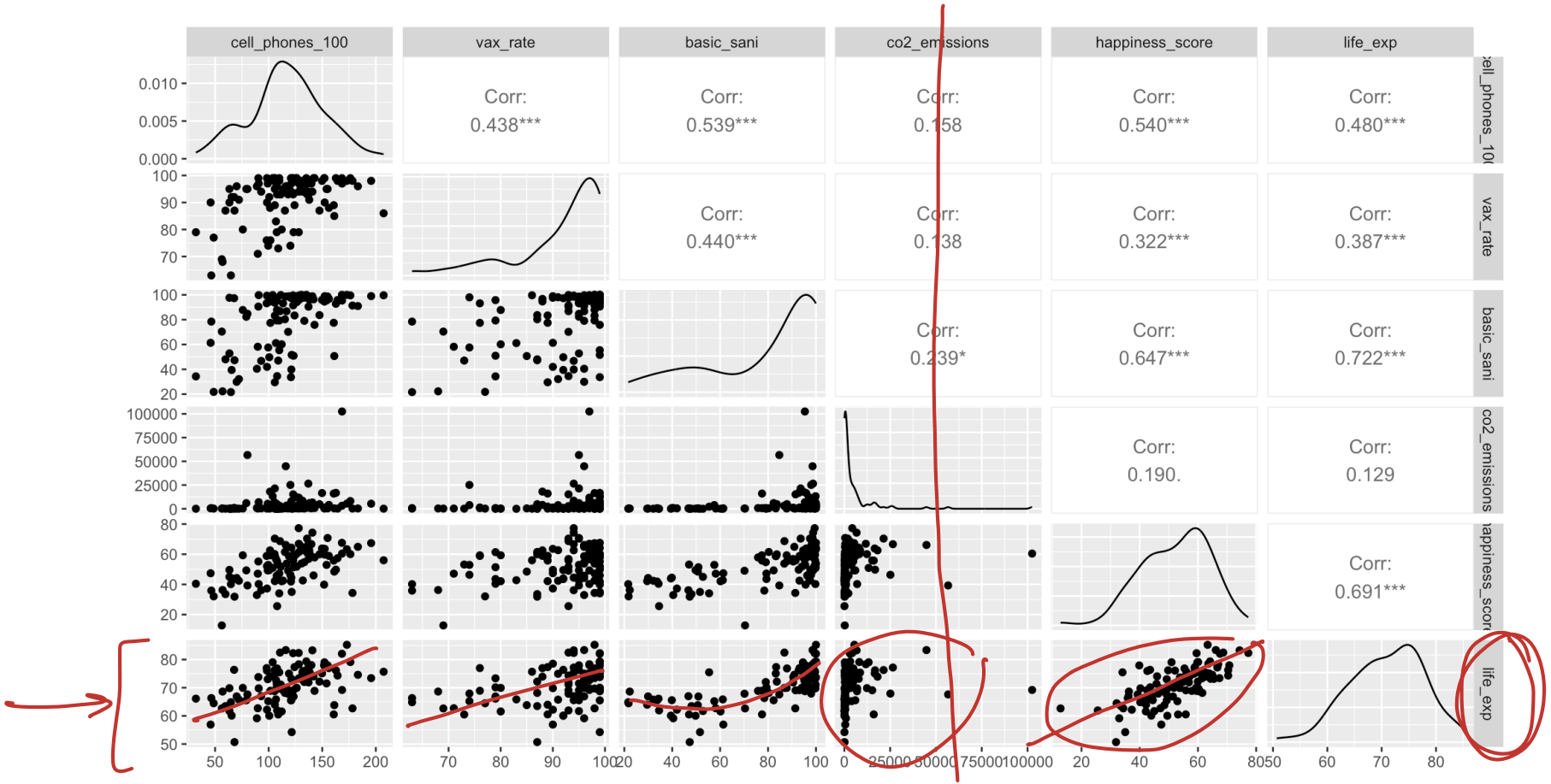
- Helps us decide if the continuous variable can stay **as is** in the model
  - **Problem:** if not linear, then we need to represent the variable in a new way (Approaches 1-3)

Step 4: Assess scale for continuous variables: Smoothed scatterplots

- In Gapminder dataset, we have 5 continuous variables:
  - Cell phones
  - Basic sanitation
  - Vaccination rate
  - ~~CO2 emissions~~
  - Happiness score
- Plot each of these agains the outcome, life expectancy

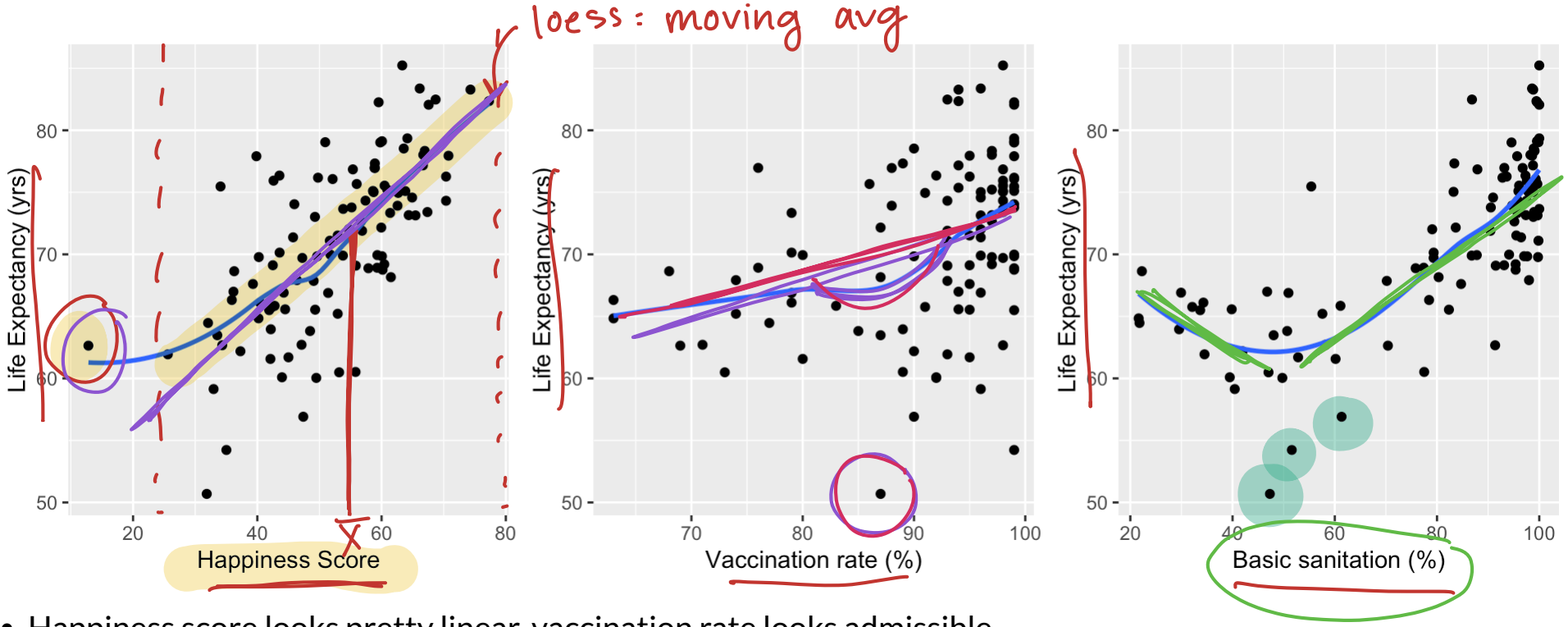
Step 4: Assess scale for continuous variables: Smoothed scatterplots

- We can quickly look at ggpairs() to identify variables



Step 4: Assess scale for continuous variables: Smoothed scatterplots

- Take a look at happiness score, vaccination rate, and basic sanitation



- Happiness score looks pretty linear, vaccination rate looks admissible
- Basic sanitation looks non-linear

Step 4: Assess scale for continuous variables

- Three methods/approaches to address the violation of linearity assumption:
  - **Approach 1:** Categorize continuous variable
  - **Approach 2:** Transformation of variable
  - **Approach 3:** Spline functions

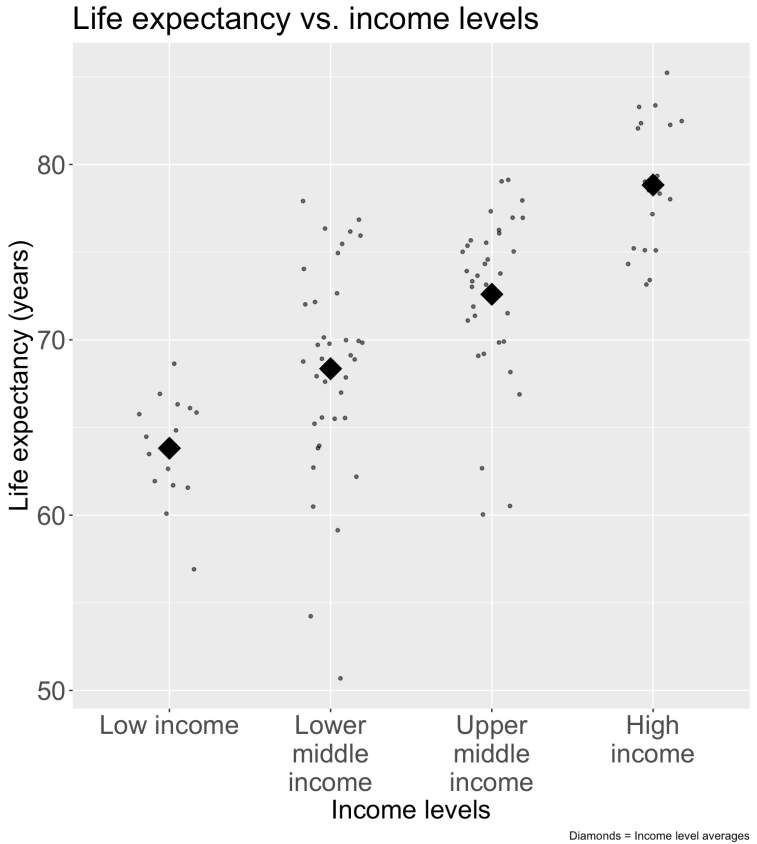
Step 4: Approach 1: Categorize continuous variable

- Categorize continuous variables
  - Percentiles, quartiles, quantiles
    - Create indicator variables corresponding to each quartile
  - Meaningful thresholds
    - Example: income level groups discussed by Gapminder
- Disadvantages:
  - Takes some time to create new variables, especially with multiple continuous covariates
  - Start with quartiles, but might be more appropriate to use different splits
    - No set rules on this
- Advantage: graphical and visually helps

Step 4: Approach 1: Categorize continuous variable

- For income, I would use Gapminder's income level groups
  - Discussed in Lesson 10 Categorical Covariates (slide 43)

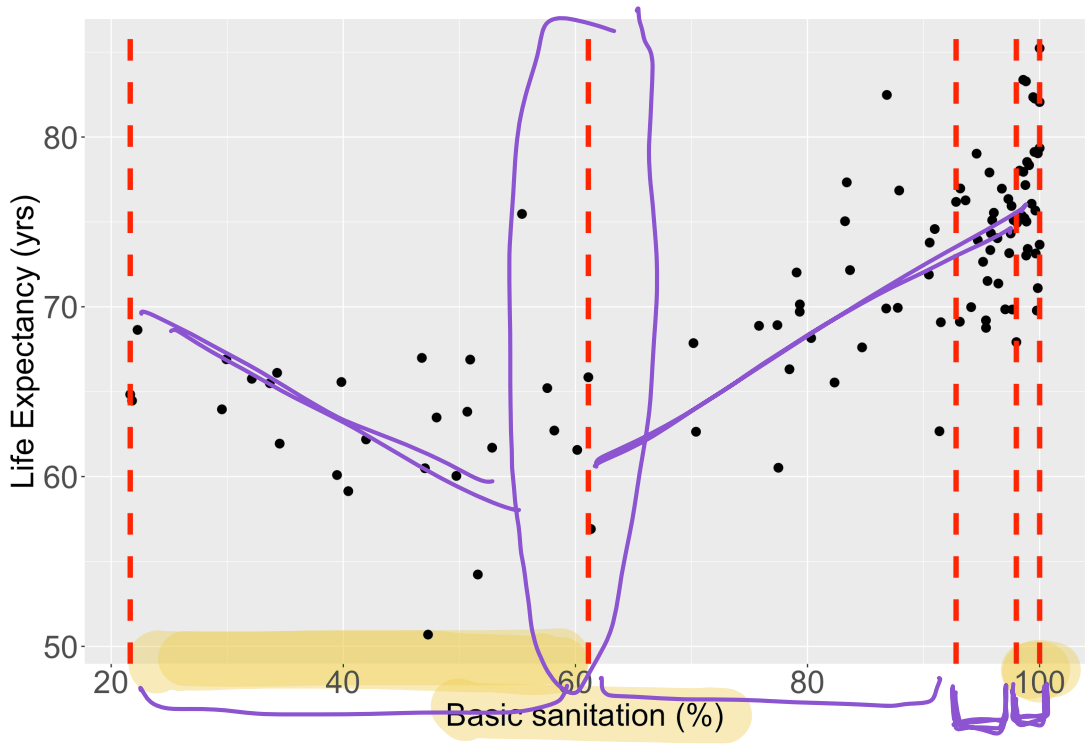
- Experts in the field have developed these income groups
  - I think this is best solution for income (that was not meeting linearity as a continuous variable)



Step 4: Approach 1: Categorize continuous variable

- Let's still try it out with basic sanitation
- I have plotted the quartile lines of basic sanitation with red lines

▶ Take a look at the quartiles within the scatterplot

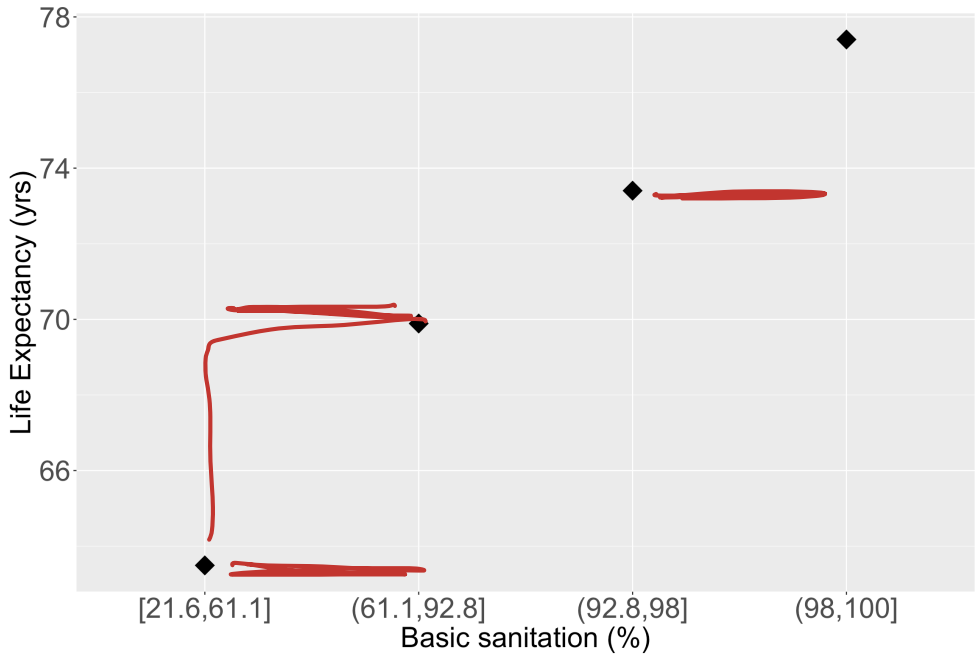


Step 4: Approach 1: Categorize continuous variable

- Let's make the quartiles for basic sanitation:

```
1  library(dvmisc)
2  gapm2 = gapm2 %>%
3    mutate(BS_q = quant_groups(basic_sani, groups = 4) %>% factor())
```

▶ Take a look at the quartile means within the scatterplot



Step 4: Approach 1: Categorize continuous variable

- Let's fit a new model with new representation for basic sanitation

- Remember, this is the **main effects model** if we decide to make basic sanitation into quartiles

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] Quartile 1	—	—	
(61.1,92.8] Quartile 2	4.5	2.0, 7.0	<0.001
(92.8,98] 3	7.0	4.2, 9.8	<0.001
(98,100] 4	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

Step 4: Approach 2: Transformation of variable

- Main concepts and transformations presented in Lesson 7 SLR: Model Evaluation and Diagnostics (slide 33 on)
- Idea: test many transformations of a continuous covariate
  - Based on Royston and Altman, Applied Statistics, 1994

- Recall Tukey's transformation (power) ladder
  - And can use R's `gladder()` to see the transformations

Power p	-3	-2	-1	-1/2	0	1/2	1	2	3
	$\frac{1}{x^3}$	$\frac{1}{x^2}$	$\frac{1}{x}$	$\frac{1}{\sqrt{x}}$	$\log(x)$	$\sqrt{x}$	x	x^2	x^3

- We can run through each and test different models, or use the approach from Lesson 7
- There is also a package we can use!
  - mfp package in R contains the fp() function

↳ polynomials

Step 4: Approach 2: Transformation of variable

```
1 library(mfp)
2
3 model_fp_BS = mfp(life_exp ~ cell_phones_100 + freedom_status + income_level_4 +
4                     vax_rate + happiness_score + fp(basic_sani, df = 4),
5                   data = gapm2, family = "gaussian")
6
7 model_fp_BS$fptable %>% gt(rownames_to_stub = T) %>% tab_options(table.font.size = 24)
```

replaces lm()

$Y \sim N(\mu, \sigma^2) \Rightarrow$ lm()

	df.initial	select	alpha	df.final	power1	power2
basic_sani	4	1	0.05	4	0	0.5
income_level_4Lower middle income	1	1	0.05	1	1	.
income_level_4Upper middle income	1	1	0.05	1	1	.
income_level_4High income	1	1	0.05	1	1	.
happiness_score	1	1	0.05	1	1	.
freedom_statusPF	1	1	0.05	1	1	.
freedom_statusF	1	1	0.05	1	1	.
vax_rate	1	1	0.05	1	1	.
cell_phones_100	1	1	0.05	1	1	.

x^2

x & x^2

$\sqrt{x}$

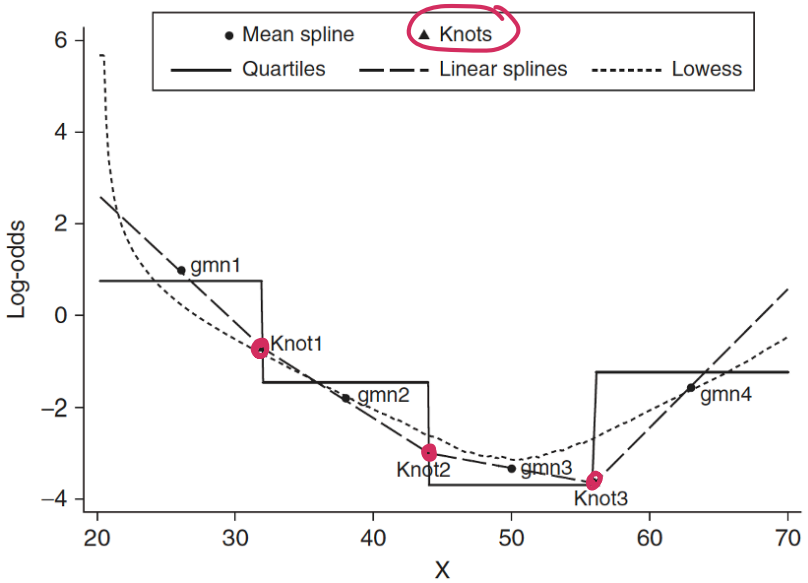
Step 4: Approach 2: Transformation of variable

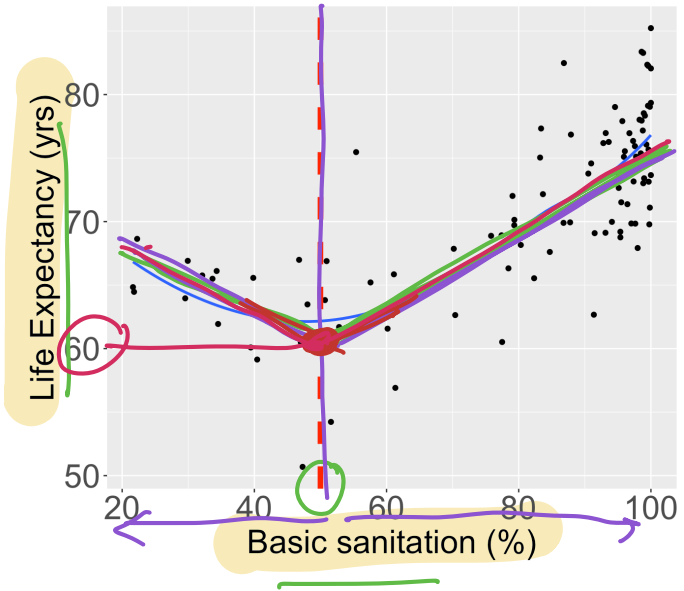
	df.initial	select	alpha	df.final	power1	power2
basic_sani	4	1	0.05	4	0	0.5
income_level_4Lower middle income	1	1	0.05	1	1	.
income_level_4Upper middle income	1	1	0.05	1	1	.
income_level_4High income	1	1	0.05	1	1	.
happiness_score	1	1	0.05	1	1	.
freedom_statusPF	1	1	0.05	1	1	.
freedom_statusF	1	1	0.05	1	1	.
vax_rate	1	1	0.05	1	1	.
cell_phones_100	1	1	0.05	1	1	.

- Conclusion from fractional polynomial is that basic sanitation needs to be transformed
  - Use square root transformation for basic sanitation
- `fp()` does NOT test for linearity assumption, just tells you best fit
  - Sometimes, it will conclude that something does NOT need to be transformed
  - A little counter-intuitive from what we saw in plots

Step 4: Approach 3: Spline functions

- Spline function is to fit a series of smooth curves that joined at specific points (called knots)





Step 4: Approach 3: Spline functions

- Need to specify knots for spline functions
  - More knots are flexible, but requires more parameters to estimate
  - In most applications three to five knots are sufficient

- Within our class, fractional polynomials will be sufficient (more in Longitudinal Data Analysis)

- If you think this is cool, I highly suggest you look into Functional Data Analysis (FDA) or Functional Regression
  - Jeffrey Morris is a big name in that field

- In R there are a few options to incorporate splines
  - `pspline( )`: More information
  - `smoothHR()`: More information

Step 4 Conclusion: main effects model

- We concluded that we will use:
  - Income levels (categorical) that Gapminder created
  - Quartiles for basic sanitation

Note

This is also a good step to decide if you would like to score a categorical variable (Lesson 5)

- Question: Do you see any visual issues with my regression table?

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
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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

Learning Objectives

1. Understand the overall steps for purposeful selection as a model building strategy

2. Apply purposeful selection to a dataset using R

3. Use different approaches to assess the linear scale of continuous variables in linear regression

Step 5: Check for interactions

- Create a list of interaction terms from variables in the "main effects model" that has clinical plausibility

- Add the interaction variables, one at a time, to the main effects model, and assess the significance using a F-test
  - May keep interaction terms with p-value < 0.10 (or 0.05)

- Keep the main effects untouched, only simplify the interaction terms

- Use methods from Step 2 (comparing model with no interactions to a larger model with 1 interaction) to determine which interactions to keep

- The model by the end of Step 5 is called the **preliminary final model**

Step 5: Check for interactions

- We test with $\alpha = 0.10$
- Follow the F-test procedure in Lesson 10 (MLR: Using the F-test)
  - This means we need to follow the 7 steps of the general F-test in previous slide (taken from Lesson 10)
- Use the hypothesis tests for the specific variable combo:

Binary & continuous variable (Lesson 11, LOB 2)

Testing a single coefficient for the interaction term using F-test comparing full model to reduced model

Multi-level & continuous variables (Lesson 11, LOB 3)

Testing group of coefficients for the interaction terms using F-test comparing full to reduced model

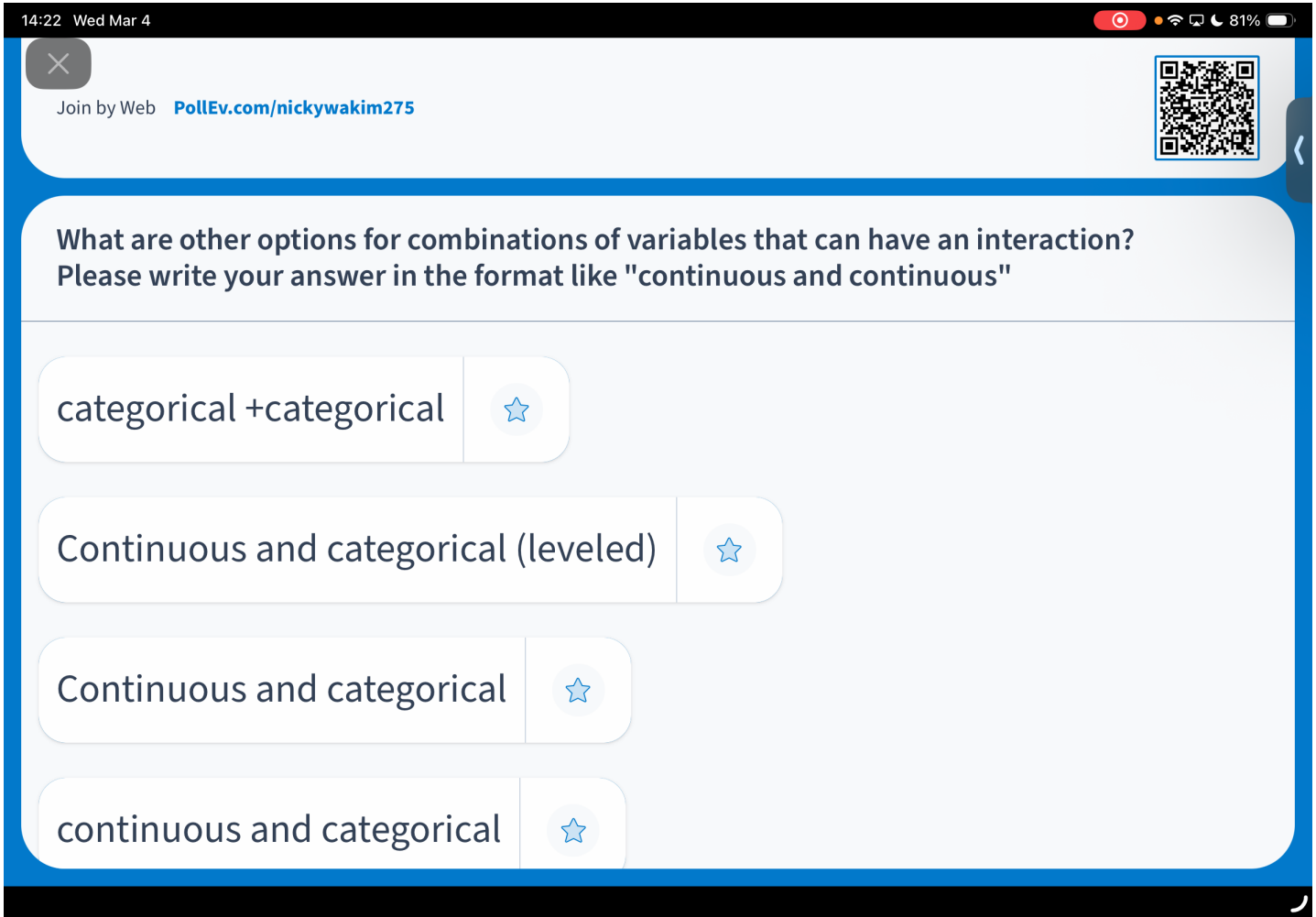
Binary & multi-level variable (Lesson 12, LOB 4)

Testing group of coefficients for the interaction terms using F-test comparing full to reduced model

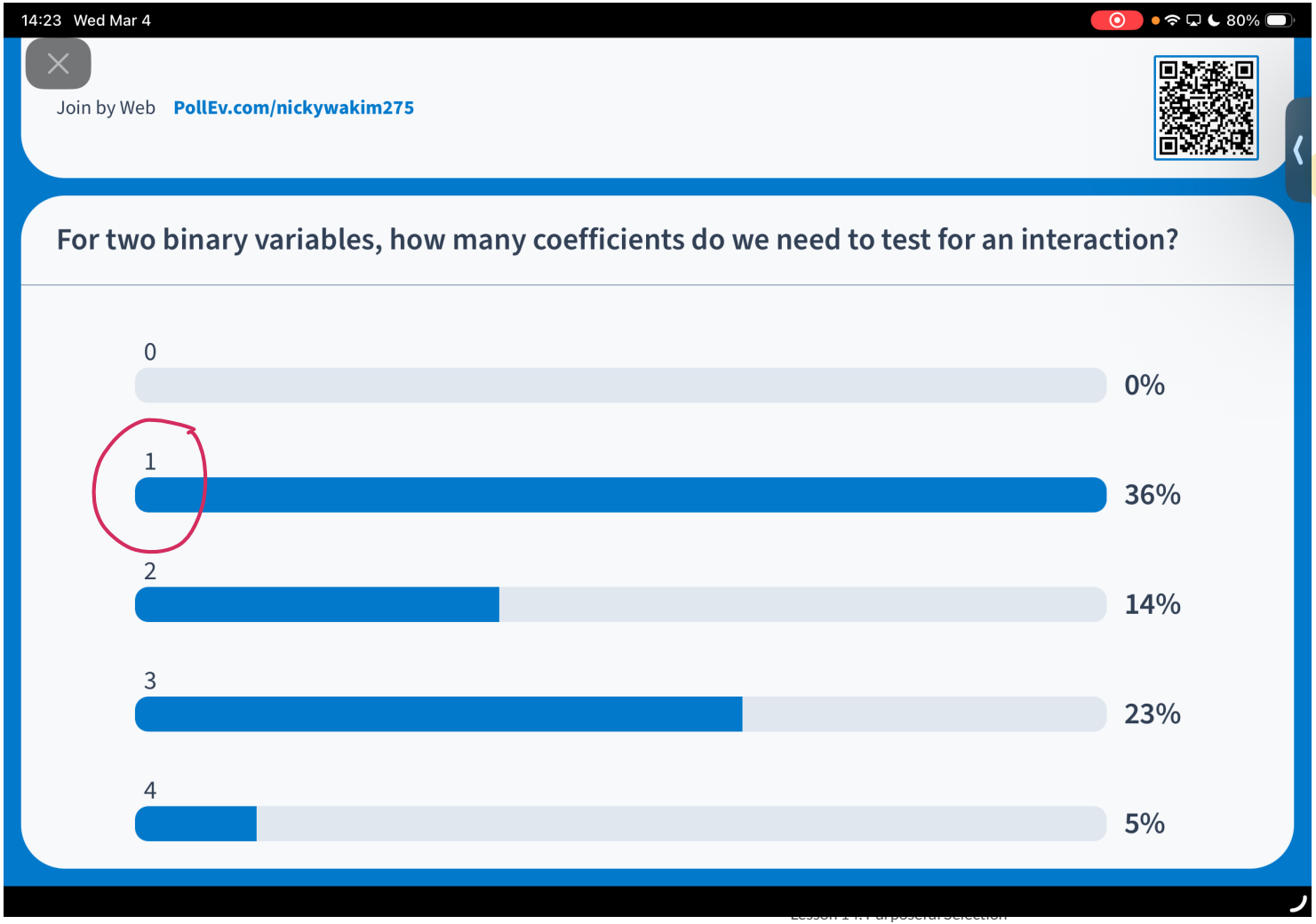
Two continuous variables (Lesson 12, LOB 5)

Testing a single coefficient for the interaction term using F-test comparing full to reduced model

Poll Everywhere Questions 5-7



Poll Everywhere Questions 5-7



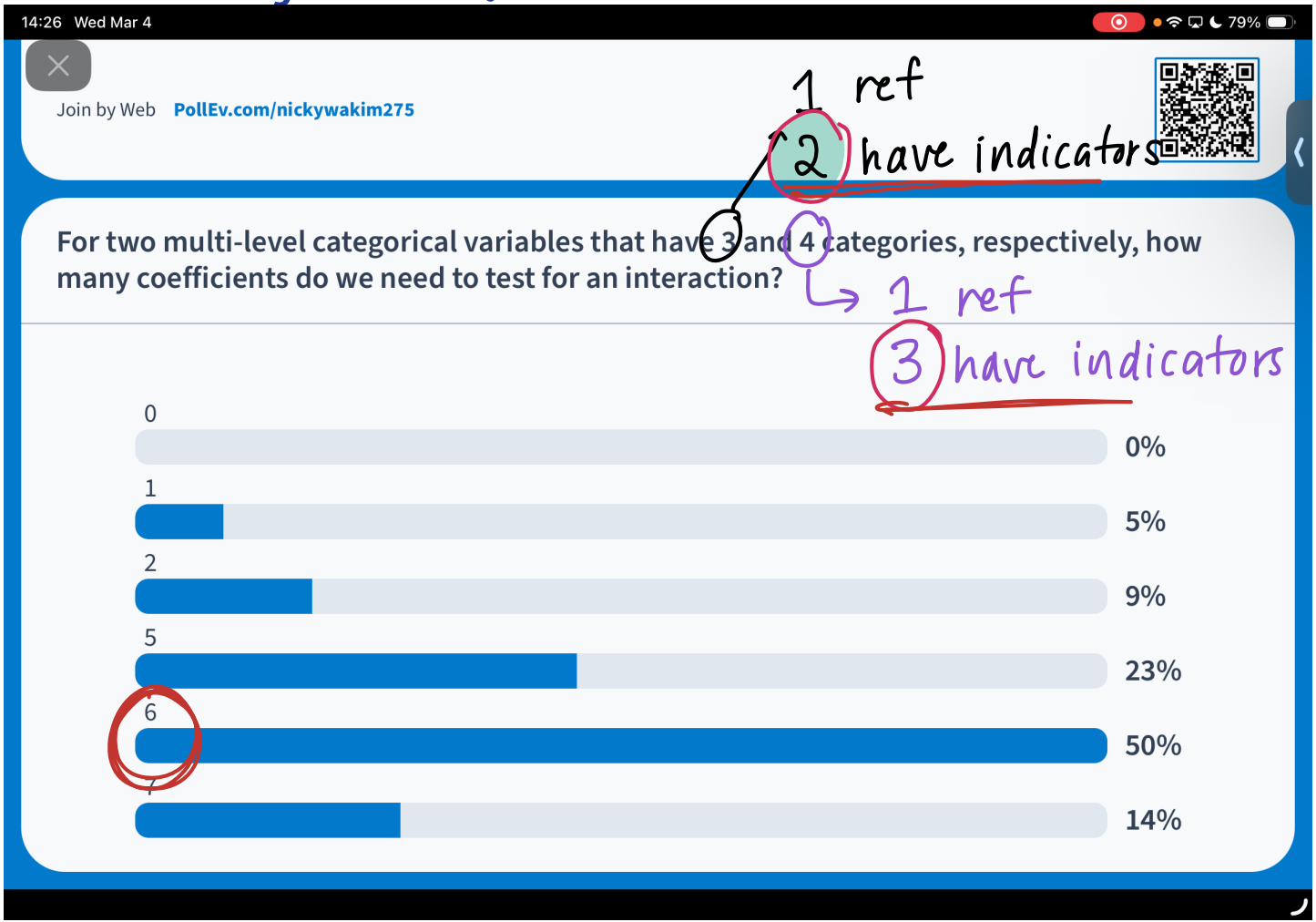
X_1 & X_2

$I(X_1 = yes)$ $I(X_2 = blue)$

$I(X_1 = no)$ $I(X_2 = red)$

$$Y = \beta_0 + \beta_1 I(X_1 = yes) + \beta_2 I(X_2 = red) + \beta_3 I(X_1 = yes) \cdot I(X_2 = red) + \varepsilon$$

Poll Everywhere Questions 5-7



1 ref
2 have indicators

↳ 1 ref
3 have indicators

2 × 3 combos of indicators

$I(X_1 = 2) \cdot I(X_2 = 2)$

$I(X_1 = 3) \cdot I(X_2 = 2)$

Step 5: Check for interactions

- Use `add1()` function to compare a full model (interactions with CP) and reduced model (main effects model)

```
add1(main_eff_model, scope = ~ cell_phones_100 * . , test = "F")
```

```
Single term additions

Model:
life_exp ~ cell_phones_100 + BS_q + freedom_status + income_level_4 +
    vax_rate + happiness_score
                          Df Sum of Sq    RSS    AIC F value Pr(>F)
<none>                                1513.0 304.13
cell_phones_100:BS_q       3    23.295 1489.7 308.50  0.4691 0.7046
cell_phones_100:freedom_status   2    69.314 1443.7 303.21  2.1845 0.1184
cell_phones_100:income_level_4   3    82.787 1430.2 304.22  1.7365 0.1652
cell_phones_100:vax_rate   1    41.315 1471.7 303.22  2.5827 0.1115
cell_phones_100:happiness_score  1     0.949 1512.1 306.06  0.0577 0.8106
```

< 0.1

- No significant interactions with cell phones per 100 people (p-value > 0.1), so we would not include any interactions with that variable
- **Think about it:** does that track with what we saw in our interactions lecture?

Step 5: Example test in `add1()` for `income_level_4`

Null H_0

$\beta_8 = \beta_9 = \beta_{10} = 0$

$\beta_{10} = \beta_{11} = \beta_{12} = 0$

Alternative H_1

$\beta_{10} \neq 0$ and/or $\beta_{11} \neq 0$ and/or $\beta_{12} \neq 0$

Null / Smaller / Reduced model main eff mode

$$\begin{aligned} LE = &\beta_0 + \beta_1 \text{CP} + \beta_2 I(\text{FS} = \text{PF}) + \\ &\beta_3 I(\text{FS} = \text{F}) + \beta_4 \text{BS} + \beta_5 \text{VR} + \\ &\beta_6 \text{HS} + \beta_7 I(\text{IL} = \text{lower middle}) + \\ &\beta_8 I(\text{IL} = \text{upper middle}) + \\ &\beta_9 I(\text{IL} = \text{upper}) + \epsilon \end{aligned}$$

no int

Alternative / Larger / Full model

$$\begin{aligned} LE = &\beta_0 + \beta_1 \text{CP} + \beta_2 I(\text{FS} = \text{PF}) + \beta_3 I(\text{FS} = \text{F}) + \\ &\beta_4 \text{BS} + \beta_5 \text{VR} + \beta_6 \text{HS} + \beta_7 I(\text{IL} = \text{lower middle}) + \\ &\beta_8 I(\text{IL} = \text{upper middle}) + \beta_9 I(\text{IL} = \text{upper}) + \\ &\beta_{10} \text{CP} \cdot I(\text{IL} = \text{lower middle}) + \\ &\beta_{11} \text{CP} \cdot I(\text{IL} = \text{upper middle}) + \\ &\beta_{12} \text{CP} \cdot I(\text{IL} = \text{upper}) + \epsilon \end{aligned}$$

- From the output of `add1()`, we can see that the p-value for dropping `income_level_4` is 0.165, which is > 0.1, so we do not reject the null, aka no interaction

Step 6: Assess model fit

- Assess the adequacy of the model (diagnostics) and check its fit

- Methods for diagnostics will be discussed next class
  - Combination of diagnostics and model fit statistics!
  - Looked at model fit statistics in last lesson
  - Look at diagnostics in Lesson 15: MLR Diagnostics

- If the model is adequate and fits well, then it is the **Final model**

Step 6: Assess model fit

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

Step 6: Assess model fit: Model fit statistics

- Way I did it in the lab instructions (and last class)

```
sum_fm = summary(final_model)
model_fit_stats = data.frame(Model = "Final model",
                             Adjusted_R_sq = sum_fm$adj.r.squared,
                             AIC = AIC(final_model), BIC = BIC(final_model))

model_fit_stats %>% gt() %>%
  tab_options(table.font.size = 35) %>% fmt_number(decimals = 3)
```

Model	Adjusted_R_sq	AIC	BIC
Final model	0.644	604.108	638.609

- Another (maybe faster?) way to do it (`glance()` in `broom` package)

```
glance(final_model) %>% mutate(Model = "Final model") %>%
  select(Model, adj.r.squared, AIC, BIC) %>% gt() %>%
  tab_options(table.font.size = 35) %>% fmt_number(decimals = 3)
```

Model	adj.r.squared	AIC	BIC
Final model	0.644	604.108	638.609

Step 6: Assess model fit: Comparing model fits

- Remember the preliminary main effects model (at end of Step 3): same as final model but basic sanitation was not categorized
- We can compare model fit statistics of the preliminary main effects model and the final model

```
fm_glance = glance(final_model) %>% mutate(Model = "Final model") %>%
  select(Model, `Adj R-squared` = adj.r.squared, AIC, BIC)
pmem_glance = glance(prelim_me_model) %>%
  mutate(Model = "Preliminary main effects model") %>%
  select(Model, `Adj R-squared` = adj.r.squared, AIC, BIC)
rbind(fm_glance, pmem_glance) %>% gt() %>%
  tab_options(table.font.size = 35) %>% fmt_number(decimals = 3)
```

Model	Adj R-squared	AIC	BIC
Final model	0.644	604.108	638.609
Preliminary main effects model	0.627	608.269	640.116

- Remember, adjusted R^2, AIC, and BIC penalize models for more coefficients
- Final model has better model fit statistics (higher adjusted R^2, lower AIC and BIC)