Regression: Interactions and dummy variables

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This material is part of the **statsTeachR** *project*

Outline

- Dummy variables for categorical covariates
- Modeling interactions
- Model selection

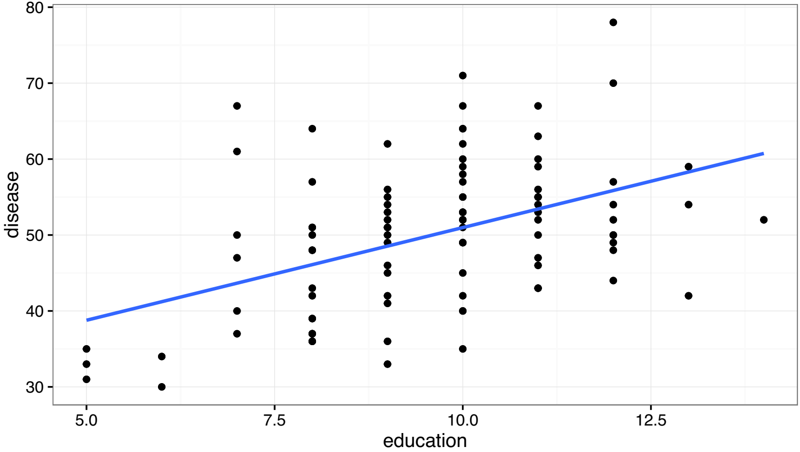
dummy variables

Categorical predictors

- Assume X is a categorical / nominal / factor variable with k levels
- Can't use a single predictor with levels $1, 2, \ldots, K$ – this has the wrong interpretation
- Need to create *indicator* or *dummy* variables

Categorical predictor example: lung data

```
qplot(education, disease, data=dat) + geom_point() +
  geom_smooth(method="lm", se=FALSE)
```



Indicator variables

- Let x be a categorical variable with k levels (e.g. with $k = 3$ "red", "green", "blue").
- Choose one group as the baseline (e.g. "red")
- Create $\underline{(k-1)}$ binary terms to include in the model:

$$x_{1,i} = \begin{cases} 0, & \text{otherwise} \\ 1, & x = \text{green} \end{cases}$$

$$x_{2,i} = \begin{cases} 1, & x = \text{blue} \\ 0, & \text{o.w.} \end{cases}$$

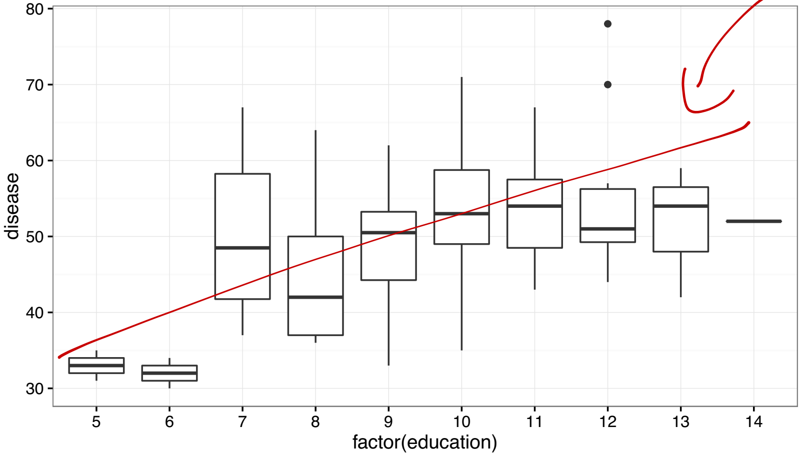
$$Y \sim X \implies Y \sim X_1 + X_2$$

Categorical predictor example: lung data

$Y \sim X$

```
qplot(factor(education), disease, geom="boxplot", data=dat)
```

continuous model



Standard model interpretation

$y \sim \text{factor}(x)$

Using the model $y_i = \beta_0 + \beta_1 x_{1,i} + \ldots + \beta_{k-1} x_{k-1,i} + \epsilon_i$, interpret

$\beta_0 =$ predicted value of outcome given x is reference level

$\beta_1 =$ difference between predicted y for green and red

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

$\hat{y} \mid (X = \text{blue}) = \beta_0 + \beta_2$

$\hat{y} \mid (X = \text{red}) = \beta_0$

$\hat{y} \mid (X = \text{green} = \beta_0 + \beta_1$

Equivalent model

$y \sim factor(x) - 1$

Define the model $y_i = \beta_1 x_{i1} + \ldots + \beta_k x_{i,k} + \epsilon_i$ where there are indicators for each possible group

$\beta_1 =$ predicted value of y when x is red

"expected"

$y_i \mid (x = \text{"red"}) = \beta_1 + \epsilon_i$

$\hat{y}_i \mid (x = \text{"red"}) = \beta_1$

$\beta_2 =$

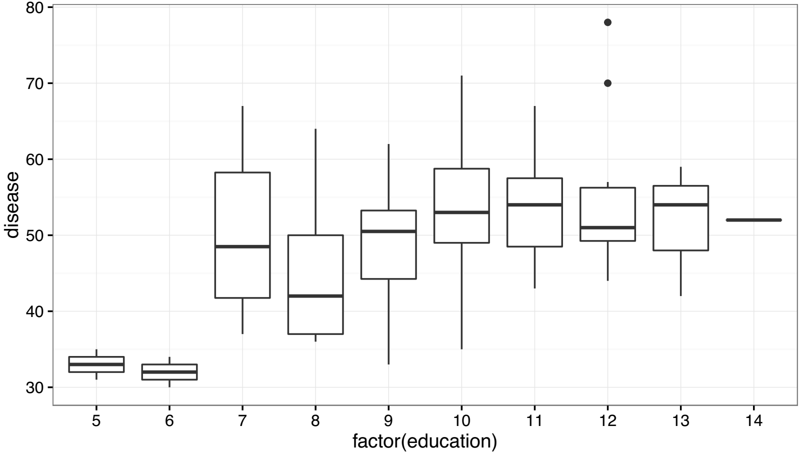
$X_1 \Rightarrow$ dummy var for red

$X_2 \Rightarrow$ dummy var for green

$X_3 \Rightarrow$ —— " —— blue

Categorical predictor example: lung data

```
qplot(factor(education), disease, geom="boxplot", data=dat)
```



Categorical predictor example: lung data

$$dis_i = \beta_0 + \beta_1 educ_{6,i} + \beta_2 educ_{7,i} + \cdots + \beta_9 educ_{14,i}$$

+1

```
mlr7 <- lm(disease ~ factor(education), data=dat)
summary(mlr7)$coef

##                      Estimate Std. Error    t value
## (Intercept)          33.00000   4.912705  6.7172765
## factor(education)6   -1.00000   7.767669 -0.1287387
## factor(education)7   17.33333   6.016811  2.8808175
## factor(education)8   11.17647   5.328577  2.0974588
## factor(education)9   15.50000   5.353496  2.8953040
## factor(education)10  20.38462   5.188395  3.9288865
## factor(education)11  20.53333   5.381599  3.8154707
## factor(education)12  22.20000   5.601346  3.9633332
## factor(education)13  18.66667   6.947614  2.6867735
## factor(education)14  19.00000   9.825411  1.9337614
##                          Pr(>|t|)
## (Intercept)          1.689481e-09
## factor(education)6   8.978549e-01
## factor(education)7   4.969406e-03
## factor(education)8   3.878868e-02
```

5 is reference level

Categorical predictor releveling

$$dis_i = \beta_0 + \beta_1 educ_{5,i} + \beta_2 educ_{6,i} + \beta_1 educ_{7,i} + \beta_2 educ_{9,i} + \cdots + \beta_{14} educ_{14,i}$$

```
dat$educ_new <- relevel(factor(dat$education), ref="8")
mlr8 <- lm(disease ~ educ_new, data=dat)
summary(mlr8)$coef
```

$\hat{y} \mid educ=8$

```
##               Estimate Std. Error    t value     Pr(>|t|)
## (Intercept)  44.176471   2.063749 21.4059318 7.303151e-37
## educ_new5   -11.176471   5.328577 -2.0974588 3.878868e-02
## educ_new6   -12.176471   6.360902 -1.9142680 5.879890e-02
## educ_new7     6.156863   4.040594  1.5237520 1.311162e-01
## educ_new9     4.323529   2.963834  1.4587624 1.481508e-01
## educ_new10    9.208145   2.654021  3.4695065 8.059293e-04
## educ_new11    9.356863   3.014298  3.1041594 2.558604e-03
## educ_new12   11.023529   3.391086  3.2507375 1.625933e-03
## educ_new13    7.490196   5.328577  1.4056653 1.633049e-01
## educ_new14    7.823529   8.755746  0.8935309 3.739828e-01
```

Categorical predictor: no baseline group

$$dis_i = \beta_1 educ_{5,i} + \beta_2 educ_{6,i} + \cdots + \beta_{14} educ_{14,i}$$

```
mlr9 <- lm(disease ~ factor(education) - 1, data=dat)
summary(mlr9)$coef

##                     Estimate Std. Error   t value
## factor(education)5  33.00000   4.912705  6.717277
## factor(education)6  32.00000   6.016811  5.318432
## factor(education)7  50.33333   3.473807 14.489386
## factor(education)8  44.17647   2.063749 21.405932
## factor(education)9  48.50000   2.127264 22.799241
## factor(education)10 53.38462   1.668763 31.990531
## factor(education)11 53.53333   2.197029 24.366243
## factor(education)12 55.20000   2.690800 20.514349
## factor(education)13 51.66667   4.912705 10.516948
## factor(education)14 52.00000   8.509055  6.111137
##                         Pr(>|t|)
## factor(education)5  1.689481e-09
## factor(education)6  7.715960e-07
## factor(education)7  3.845787e-25
## factor(education)8  7.303151e-37
```

estimates of g "directly"

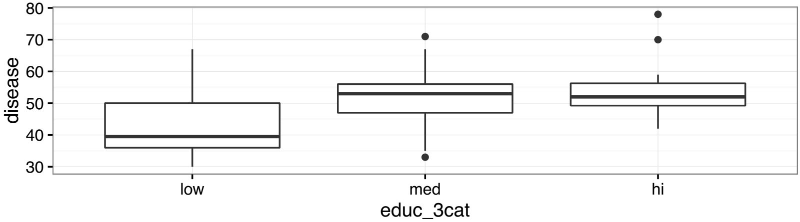
Creating categories using cut()

$$dis_i = \beta_1 educ_{low,i} + \beta_2 educ_{med,i} + \cdots + \beta_{14} educ_{hi,i}$$

```
dat$educ_3cat <- cut(dat$education, breaks=3,
                     labels=c("low", "med", "hi"))
mlr10 <- lm(disease ~ educ_3cat - 1, data=dat)
coef(mlr10)

## educ_3catlow educ_3catmed  educ_3cathi
##     43.42857     52.05263     54.21429

qplot(educ_3cat, disease, geom="boxplot", data=dat)
```



interaction

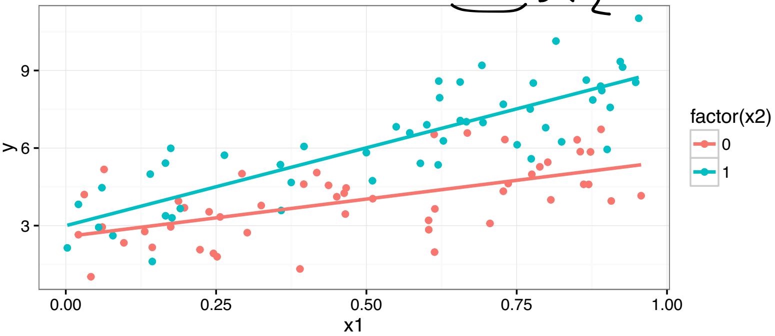
What is interaction?

effect modification

$y \sim x_1$

Definition of interaction

Interaction occurs when the relationship between two variables depends on the value of a third variable. x_2



Interaction vs. confounding

Definition of interaction

Interaction occurs when the relationship between two variables depends on the value of a third variable. E.g. you could hypothesize that the true relationship between physical activity level and cancer risk may be different for men and women.

Definition of confounding

β_1

Confounding occurs when the measurable association between two variables is distorted by the presence of another variable. Confounding can lead to biased estimates of a true relationship between variables.

- It is important to include confounding variables (if possible!) when they may be biasing your results.
- Unmodeled interactions do not lead to “biased” estimates in the same way that confounding does, but it can lead to a richer and more detailed description of the data at hand.

Some real world examples?

How to include interaction in a MLR

no int.

Model A: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \epsilon_i$
Model B: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \underline{\beta_3 x_{i1} \cdot x_{i2}} + \epsilon_i$

interaction term

Key points

- "easily" conceptualized with 1 continuous, 1 categorical variable
- models possible with other variable combinations, but interpretation/visualization harder
- two variable interactions are considered "first-order" interactions
- still a **linear** model, but no longer a strictly **additive** model

How to interpret an interaction model

For now, assume x_1 is continuous, x_2 is 0/1 binary.

Model A: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \epsilon_i$

Model B: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i1} \cdot x_{i2} + \epsilon_i$

$$\hookrightarrow \hat{y} \mid (x_2 = 0) = \beta_0 + \beta_1 x_1$$

$$\hat{y} \mid (x_2 = 1) = \underbrace{(\beta_0 + \beta_2)}_{\text{new intercept}} + \underbrace{(\beta_1 + \beta_3)}_{\text{new slope}} x_1$$

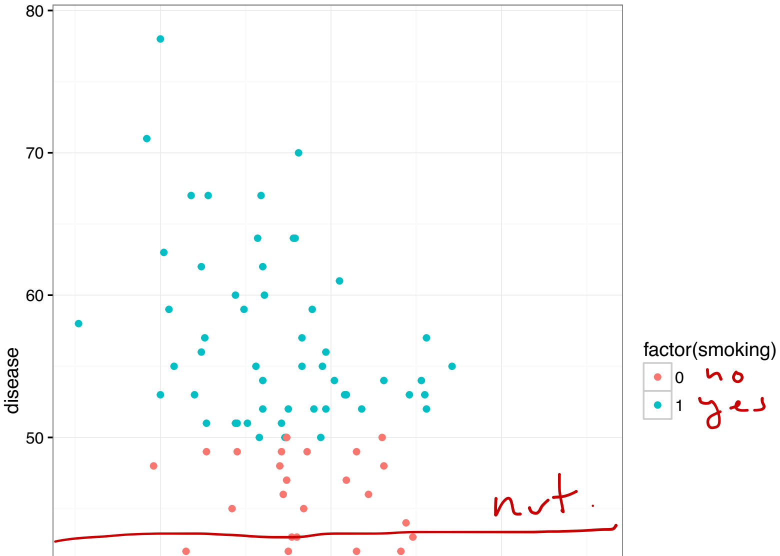
How to interpret an interaction model

For now, assume x_1 is continuous, x_2 is 0/1 binary.
Model A: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \epsilon_i$
Model B: $y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i1} \cdot x_{i2} + \epsilon_i$

β_3 is the change in the slope of the line that describes the relationship of $y \sim x_1$ comparing the groups defined by $x_2 = 0$ and $x_2 = 1$.
$\beta_1 + \beta_3$ is the expected change in y for a one-unit increase in x_1 in the group $x_2 = 1$.
$\beta_0 + \beta_2$ is the expected value of y in the group $x_2 = 1$ when $x_1 = 0$.

Example interaction model with lung data

```
ggplot(dat, aes(nutrition, disease, color=factor(smoking))) +
    geom_point()
```



Example interaction model with lung data

$$dis_i = \beta_0 + \beta_1 nutrition_i + \beta_2 smoking_i + \beta_3 nutrition \cdot smoking_i + \epsilon_i$$

```
mi1 <- lm(disease ~ nutrition + smoking, data=dat)
mi2 <- lm(disease ~ nutrition*smoking, data=dat)
c(summary(mi1)$adj.r.squared, summary(mi2)$adj.r.squared)
round(summary(mi2)$coef,2)

## [1] 0.6190283 0.6483849
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          39.60       1.65   24.05     0.00
## nutrition             0.03       0.02    1.49     0.14
## smoking              20.69       2.15    9.61     0.00
## nutrition:smoking    -0.08       0.03   -3.00     0.00
```

$\hat{y}$ for non-smoker w/ 0 nutrition

expected ↑ in $\hat{y}$ for a 1-unit ↑ in nut, for non-smokers

Example interaction model with lung data

$$dis_i = \beta_0 + \beta_1 nutrition_i + \beta_2 smoking_i + \beta_3 nutrition \cdot smoking_i + \epsilon_i$$

```
mi1 <- lm(disease ~ nutrition + smoking, data=dat)
mi2 <- lm(disease ~ nutrition*smoking, data=dat)
c(summary(mi1)$adj.r.squared, summary(mi2)$adj.r.squared)
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## [1] 0.6190283 0.6483849
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## (Intercept)          39.60       1.65   24.05     0.00
## nutrition             0.03       0.02    1.49     0.14
## smoking              20.69       2.15    9.61     0.00
## nutrition:smoking    -0.08       0.03   -3.00     0.00
```

change in slope between
nutrition/disease, comparing
smokers to non-smokers

Example interaction model with lung data

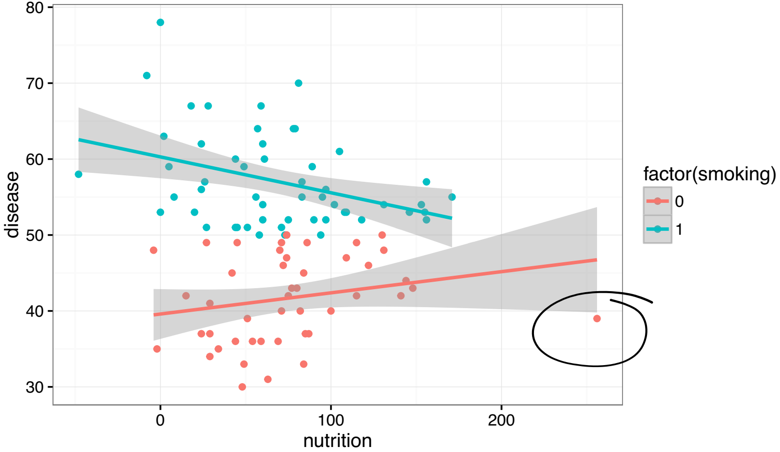
$$dis_i = \beta_0 + \beta_1 nutrition_i + \beta_2 smoking_i + \beta_3 nutrition \cdot smoking_i + \epsilon_i$$

```
mi1 <- lm(disease ~ nutrition + smoking, data=dat)
mi2 <- lm(disease ~ nutrition*smoking, data=dat)
c(summary(mi1)$adj.r.squared, summary(mi2)$adj.r.squared)
round(summary(mi2)$coef,2)

## [1] 0.6190283 0.6483849
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          39.60       1.65   24.05     0.00
## nutrition             0.03       0.02    1.49     0.14
## smoking              20.69       2.15    9.61     0.00
## nutrition:smoking    -0.08       0.03   -3.00     0.00
```

Among non-smokers there is little evidence to support an association between nutrition and disease status. For every 10 units increase in nutrition score, the expected disease score increases by 0.3 points. For non-smokers The models find evidence that this relationship is significantly different for smokers, estimating that for every 10 unit increase in nutrition, disease score would decrease by 0.5 points.

Example interaction model with FEV data

```
ggplot(dat, aes(nutrition, disease, color=factor(smoking))) +
    geom_point() + geom_smooth(method="lm")
```



Example interaction model with lung data

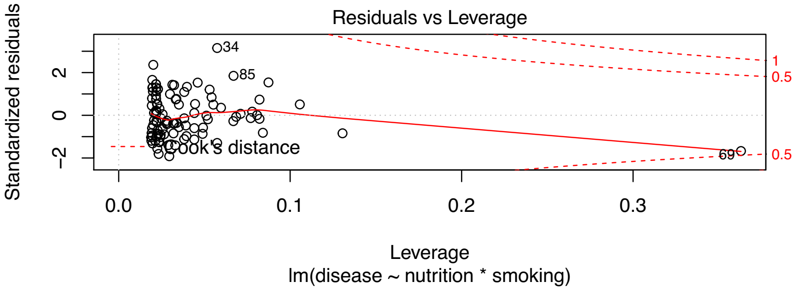
```
dat$smoking_relevel <- factor(dat$smoking, levels=c(1,0))
mi3 <- lm(disease ~ nutrition*smoking_relevel, data=dat)
round(summary(mi3)$coef, 2)

##                              Estimate Std. Error t value
## (Intercept)                     60.29       1.39   43.46
## nutrition                       -0.05       0.02   -2.84
## smoking_relevel0               -20.69       2.15   -9.61
## nutrition:smoking_relevel0       0.08       0.03    3.00
##                              Pr(>|t|)
## (Intercept)                      0.00
## nutrition                        0.01
## smoking_relevel0                 0.00
## nutrition:smoking_relevel0       0.00
```

Indeed, we see that there is a 'significant' negative slope for smokers.

Checking influential points

We note that these results are sensitive to the inclusion of an influential outlying observation which had a much higher value of nutrition than any other observation.

```r
plot(mi2, which=5)
```




```r
dat[69,]
```

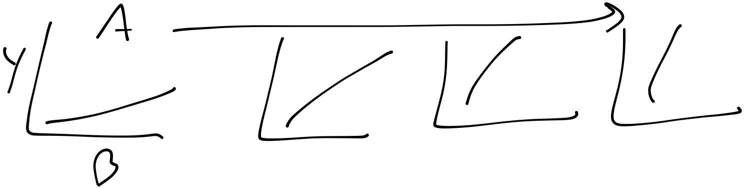
```
##    disease education crowding airqual nutrition smoking
## 69      39         8       20      54       256       0
```

Results sensitivity to outlier

```
round(summary(mi2)$coef, 2)

##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          39.60       1.65   24.05     0.00
## nutrition             0.03       0.02    1.49     0.14
## smoking              20.69       2.15    9.61     0.00
## nutrition:smoking    -0.08       0.03   -3.00     0.00

mi2a <- lm(disease ~ nutrition*smoking, data=dat, subset=-69)
round(summary(mi2a)$coef, 2)

##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          38.13       1.85   20.66     0.00
## nutrition             0.05       0.02    2.21     0.03
## smoking              22.15       2.30    9.63     0.00
## nutrition:smoking    -0.10       0.03   -3.47     0.00
```

Interaction modeling summary

- Interactions can give you a more detailed story about your data.
- They are 'easier' to interpret/visualize with a binary and continuous variable interaction.
- They are also valid for continuous x continuous variables: as the value of variable A increases, the association between B and Y changes.
- Interaction is sometimes referred to as 'effect modification'.



model selection

Model selection

Why are you building a model in the first place?

Model selection: considerations

Things to keep in mind...

- **Why am I building a model?** Some common answers
  - Estimate an association
  - Test a particular hypothesis
  - Predict new values
- What predictors will I allow?
- What predictors are needed?

Different answers to these questions will yield different final models.

Model selection: realities

All models are wrong. Some are more useful than others.
- George Box

- In practice, issues with sample size, collinearity, and available predictors are real problems.
- There is not a single best algorithm for model selection! It pretty much always requires thougfhul reasoning and knowledge about the data at hand.
- When in doubt (unless you are specifically "data mining"), err on the side creating a process that does not require choices being made (by you or the computer) about which covariates to include.

Basic ideas for model selection

For association studies, when your sample size is large

- Include key covariates of interest.
- Include covariates needed because they might be confounders.
- Include covariates that your colleagues/reviewers/collaborators will demand be included for face validity.
- Do NOT go on a fishing expedition for significant results!
- Do NOT use "stepwise selection" methods!
- Subject the selected model to model checking/diagnostics, possibly adjust model structure (i.e. include non-linear relationships with covariates) as needed.

Basic ideas for model selection

For association studies, when your sample size is small

- Same as above, but may need to be more frugal with how many predictors/parameters you include.
- Rule of thumb for multiple linear regression is to have at least 15 observations for each regression coefficient you include in your model.