432 Class 4 Slides

github.com/THOMASELOVE/2019-432

2019-01-31

SMART BRFSS 2017 data: A New Pull

```r
library(skimr); library(broom); library(janitor)
library(simputation); library(tidyverse)

smart_oh_2017 <- readRDS("data/smart_2017_oh.rds")

smart2_raw <- smart_oh_2017 %>%
    mutate(personcode = as.character(1:nrow(smart_oh_2017))) %
    select(personcode, genhealth, alcdays, female,
           bmi, height_m, weight_kg, exerany,
           seatbelt = seatbelt_always, mmsaname)
```

Missingness?

```r
colSums(is.na(smart2_raw))
```

```
personcode  genhealth    alcdays     female        bmi
         0         11         46          0        323
  height_m  weight_kg    exerany   seatbelt   mmsaname
        84        296         13         26          0
```

Simple Imputation and Re-calculating of BMI

```
set.seed(20190131)

smart2 <- smart2_raw %>%
    impute_cart(seatbelt ~ mmsaname) %>%
    impute_pmm(exerany ~ mmsaname) %>%
    impute_pmm(height_m ~ exerany + female) %>%
    impute_pmm(weight_kg ~ exerany + female) %>%
    impute_cart(genhealth ~ mmsaname + weight_kg) %>%
    impute_pmm(alcdays ~ mmsaname + female) %>%
    mutate(bmi = weight_kg / (height_m^2))
```

```
colSums(is.na(smart2))
```

```
personcode  genhealth    alcdays     female        bmi 
         0          0          0          0          0 
  height_m  weight_kg    exerany   seatbelt   mmsaname 
         0          0          0          0          0 
```

Saving as an R data set

```
saveRDS(smart2, "data/smart2.rds")
```

Now, we could have started with . . .

```
smart2 <- readRDS("data/smart2.rds")
```

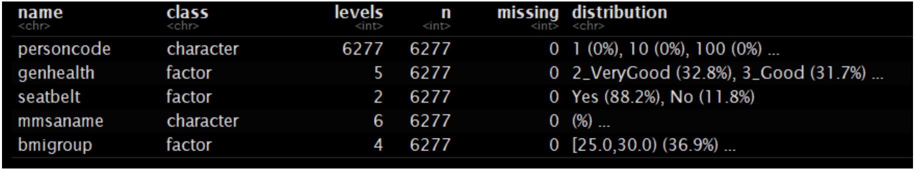
and ignored everything except for the package loading.

Using mosaic::inspect

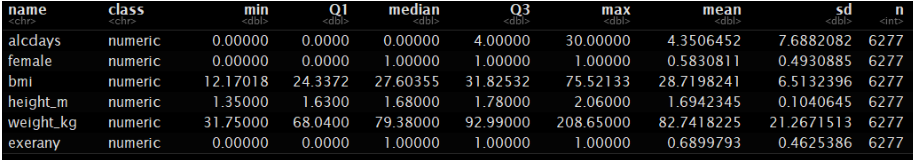
```r
mosaic::inspect(smart2)
```

```

categorical variables:
        name     class levels    n missing
1 personcode character   6277 6277       0
2  genhealth    factor      5 6277       0
3   seatbelt    factor      2 6277       0
4   mmsaname character      6 6277       0
                                   distribution
1 1 (0%), 10 (0%), 100 (0%) ...
2 2_VeryGood (32.8%), 3_Good (31.7%) ...
3 Yes (88.2%), No (11.8%)
4  (%) ...

quantitative variables:
       name   class      min      Q1   median       Q3
```

mosaic::inspect(smart2)



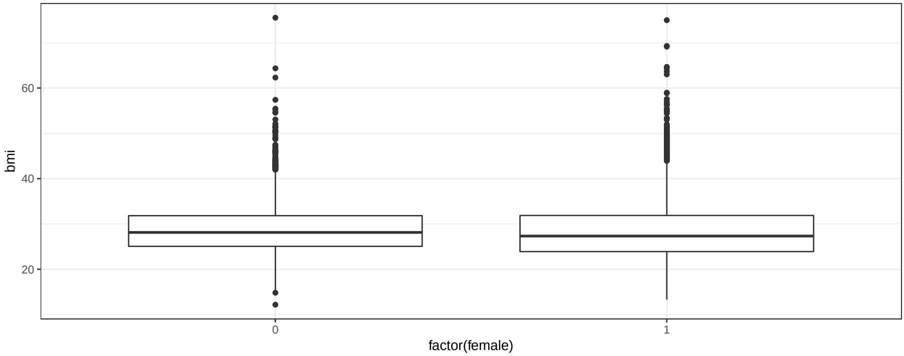
name	class	levels	n	missing	distribution
<chr>	<chr>	<int>	<int>	<int>	<chr>
personcode	character	6277	6277	0	1 (0%), 10 (0%), 100 (0%) ...
genhealth	factor	5	6277	0	2_VeryGood (32.8%), 3_Good (31.7%) ...
seatbelt	factor	2	6277	0	Yes (88.2%), No (11.8%)
mmsaname	character	6	6277	0	(%) ...
bmigroup	factor	4	6277	0	[25.0,30.0) (36.9%) ...



name	class	min	Q1	median	Q3	max	mean	sd	n
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<int>
alcdays	numeric	0.00000	0.0000	0.00000	4.00000	30.00000	4.3506452	7.6882082	6277
female	numeric	0.00000	0.0000	1.00000	1.00000	1.00000	0.5830811	0.4930885	6277
bmi	numeric	12.17018	24.3372	27.60355	31.82532	75.52133	28.7198241	6.5132396	6277
height_m	numeric	1.35000	1.6300	1.68000	1.78000	2.06000	1.6942345	0.1040645	6277
weight_kg	numeric	31.75000	68.0400	79.38000	92.99000	208.65000	82.7418225	21.2671513	6277
exerany	numeric	0.00000	0.0000	1.00000	1.00000	1.00000	0.6899793	0.4625386	6277

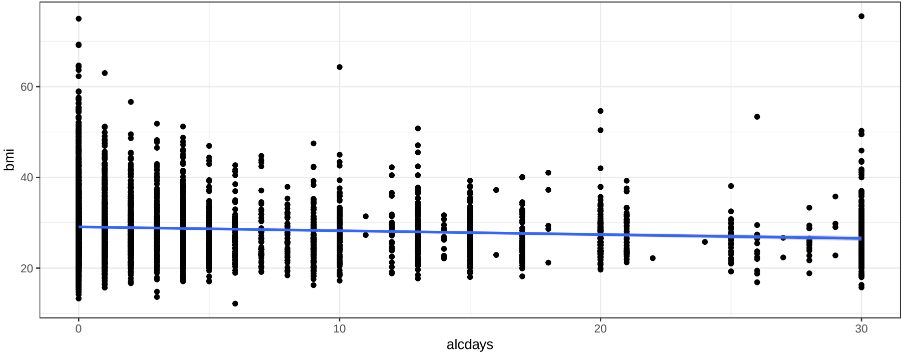
Using `female` to model `bmi`

```
ggplot(smart2, aes(x = factor(female), y = bmi)) +
  geom_boxplot() + theme_bw()
```



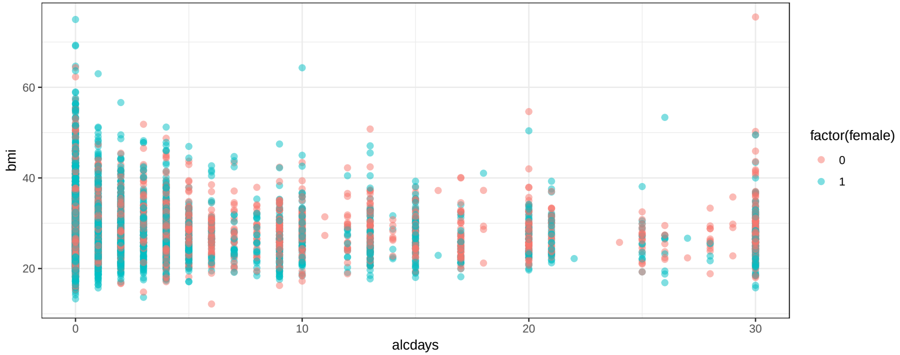
Using alcdays to model bmi

```
ggplot(smart2, aes(x = alcdays, y = bmi)) +
    geom_point() + geom_smooth(method = "lm") + theme_bw()
```



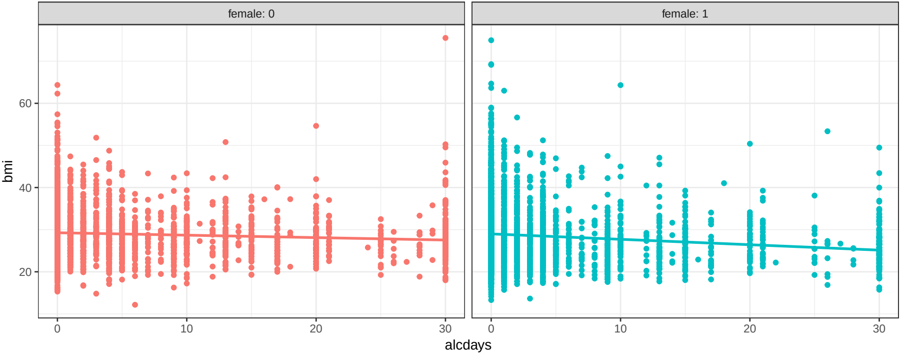
Using alcdays to model bmi, stratified by female

```
ggplot(smart2, aes(x = alcdays, y = bmi,
                   color = factor(female))) +
  geom_point(alpha = 0.5, size = 2) + theme_bw()
```



alcdays, female and interaction to model bmi

```
ggplot(smart2, aes(x = alcdays, y = bmi,
                   color = factor(female))) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE) +
    guides(col = FALSE) + theme_bw() +
    facet_wrap(~ female, labeller = label_both)
```



Building Two Models

We'll predict bmi using female and alcdays...

- and their interaction

```
model_2i <- lm(bmi ~ female * alcdays, data = smart2)
```

- without their interaction

```
model_2no <- lm(bmi ~ female + alcdays, data = smart2)
```

ANOVA comparison for Nested Models

```
anova(model_2i, model_2no)
```

```
Analysis of Variance Table

Model 1: bmi ~ female * alcdays
Model 2: bmi ~ female + alcdays
  Res.Df    RSS Df Sum of Sq      F   Pr(>F)
1   6273 262619
2   6274 263070 -1   -451.24 10.778 0.001032 **
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comparing Nested Models via glance

```
glance(model_2i) %>% round(., 2) %>% print.data.frame
```

```
  r.squared adj.r.squared sigma statistic p.value df
1      0.01          0.01  6.47     28.85       0  4
     logLik      AIC      BIC deviance df.residual
1 -20625.25 41260.49 41294.21 262618.9        6273
```

```
glance(model_2no) %>% round(., 2) %>% print.data.frame
```

```
  r.squared adj.r.squared sigma statistic p.value df
1      0.01          0.01  6.48     37.83       0  3
     logLik      AIC      BIC deviance df.residual
1 -20630.63 41269.27 41296.25 263070.1        6274
```

Predictions with `model_2i`

```r
tidy(model_2i) %>% print.data.frame
```

```
             term    estimate  std.error  statistic
1     (Intercept) 29.27018647 0.15145149 193.264430
2          female -0.27412942 0.19301062  -1.420282
3         alcdays -0.05764733 0.01461732  -3.943768
4 female:alcdays -0.07076169 0.02155357  -3.283062
       p.value
1 0.000000e+00
2 1.555754e-01
3 8.108538e-05
4 1.032485e-03
```

Interpreting the Interaction Model

With interaction, the model is

`bmi` = 29.26 - 0.27 `female` - 0.06 `alcdays` - 0.07 `female` x `alcdays`

1. What is the predicted `bmi` for a male who used alcohol on 10 of the last 30 days?
2. What is the predicted `bmi` for a female who used alcohol on 10 of the last 30 days?

Interpreting the Interaction Model

With interaction, the model is

`bmi` = 29.26 - 0.27 `female` - 0.06 `alcdays` - 0.07 `female` x `alcdays`

So, for males, the model is:

`bmi` = 29.26 - 0.06 `alcdays`

And, for females, the model is:

`bmi` = (29.26 - 0.27) + (-0.06 - 0.07) `alcdays`, or 28.99 - 0.13 `alcdays`

Both the slope and the intercept of the `bmi` - `alcdays` model depend on `female`.

Predictions with the Main Effects Model

```r
tidy(model_2no)
```

```
# A tibble: 3 x 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)  29.5       0.141     209.   0.
2 female       -0.589     0.168      -3.51 4.44e- 4
3 alcdays      -0.0902    0.0108     -8.39 5.96e-17
```

`bmi` = 29.46 - 0.59 `female` - 0.09 `alcdays`

1. What is the predicted `bmi` for a male who used alcohol on 10 of the last 30 days?
2. What is the predicted `bmi` for a female who used alcohol on 10 of the last 30 days?

Interpreting the Main Effects Model

Without the interaction, the model is

`bmi` = 29.46 - 0.59 `female` - 0.09 `alcdays`

So, for males, the model is:

`bmi` = 29.46 - 0.59 `female` - 0.09 `alcdays`

And, for females, the model is:

`bmi` = (29.46 - 0.59) - 0.09 `alcdays`, or 28.87 - 0.09 `alcdays`

Only the intercept of the `bmi` - `alcdays` model depends on `female`.

- The change in `bmi` per additional day of alcohol use does not depend on sex.

What if we had a multi-categorical factor?

Suppose we want to study the impact of both `exerany` and `genhealth` on BMI.

```r
smart2 %>% count(genhealth)
```

```
# A tibble: 5 x 2
  genhealth       n
  <fct>       <int>
1 1_Excellent   872
2 2_VeryGood   2057
3 3_Good       1987
4 4_Fair        991
5 5_Poor        370
```

Does it seem like we need to collapse any levels here?

Collapsing?

```
smart2 %>% count(genhealth, exerany)
```

```
# A tibble: 10 x 3
   genhealth   exerany     n
   <fct>         <dbl> <int>
 1 1_Excellent       0   124
 2 1_Excellent       1   748
 3 2_VeryGood        0   474
 4 2_VeryGood        1  1583
 5 3_Good            0   651
 6 3_Good            1  1336
 7 4_Fair            0   464
 8 4_Fair            1   527
 9 5_Poor            0   233
10 5_Poor            1   137
```

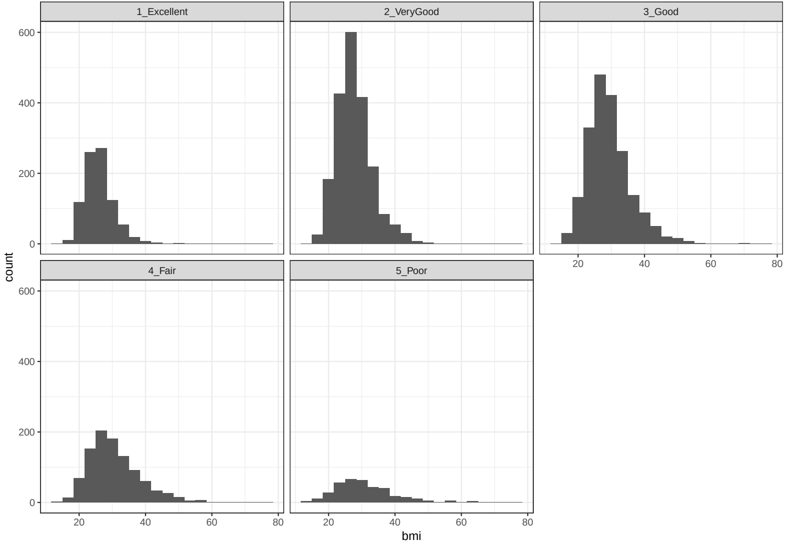
Now does it seem like we need to collapse any levels here?

Cross-Tabulation?

```r
smart2 %>% tabyl(genhealth, exerany)
```

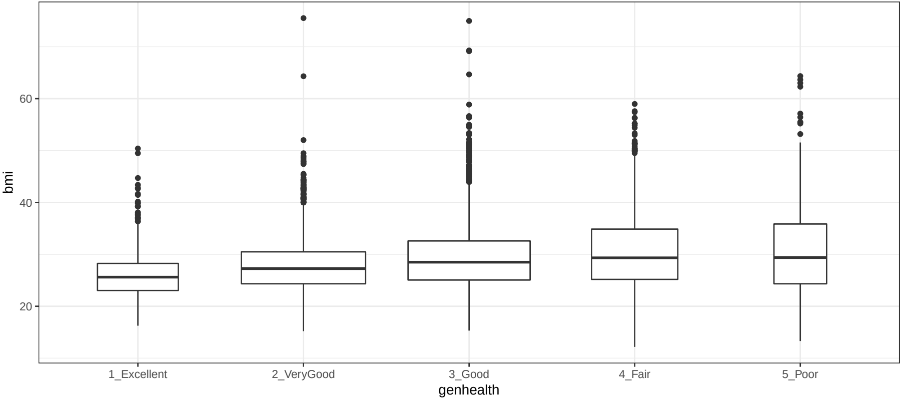
```
   genhealth   0    1
 1_Excellent 124  748
  2_VeryGood 474 1583
      3_Good 651 1336
      4_Fair 464  527
      5_Poor 233  137
```

Distribution of bmi by genhealth?



Boxplots with variable widths?

```
ggplot(smart2, aes(x = genhealth, y = bmi)) +
    geom_boxplot(varwidth = TRUE) + theme_bw()
```

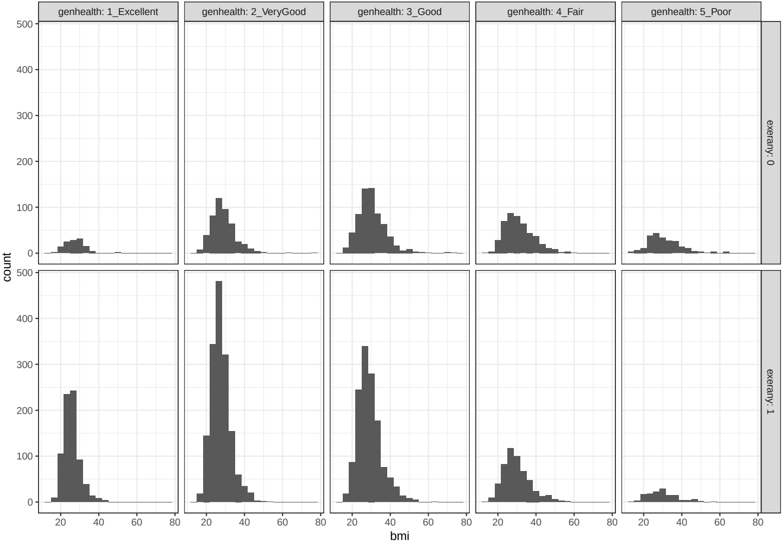


Summary Statistics?

```
mosaic::favstats(bmi ~ genhealth, data = smart2)
```

```
    genhealth      min       Q1   median       Q3      max
1 1_Excellent 16.25310 23.03495 25.60879 28.25260 50.40000
2  2_VeryGood 15.19440 24.32872 27.25224 30.48356 75.52133
3      3_Good 15.30622 25.05365 28.49379 32.58449 74.97521
4      4_Fair 12.17018 25.17792 29.32571 34.86687 58.97888
5      5_Poor 13.29938 24.32673 29.38125 35.84917 64.34948
      mean       sd    n missing
1 26.04942 4.496603  872       0
2 27.83312 5.442950 2057       0
3 29.50860 6.659790 1987       0
4 30.57877 7.581389  991       0
5 30.72796 8.826062  370       0
```

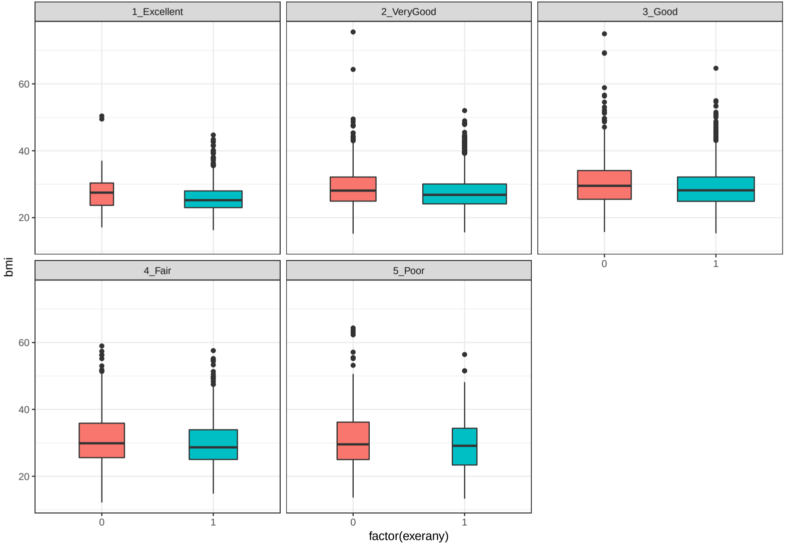
bmi by genhealth and exerany?



Code for Previous Slide

```r
ggplot(smart2, aes(x = bmi)) +
    geom_histogram(bins = 20) +
    theme_bw() +
    facet_grid(exerany ~ genhealth, labeller = "label_both")
```

Boxplots instead?



Code for previous plot

```
ggplot(smart2, aes(x = factor(exerany), y = bmi)) +
    geom_boxplot(aes(fill = factor(exerany)),
                 varwidth = TRUE) +
    theme_bw() + guides(fill = FALSE) +
    facet_wrap(~ genhealth)
```

Can we use favstats for two factors at once?

```
mosaic::favstats(bmi ~ genhealth + exerany,
                 data = smart2)[c("genhealth.exerany",
                          "mean", "sd", "n", "missing")]
```

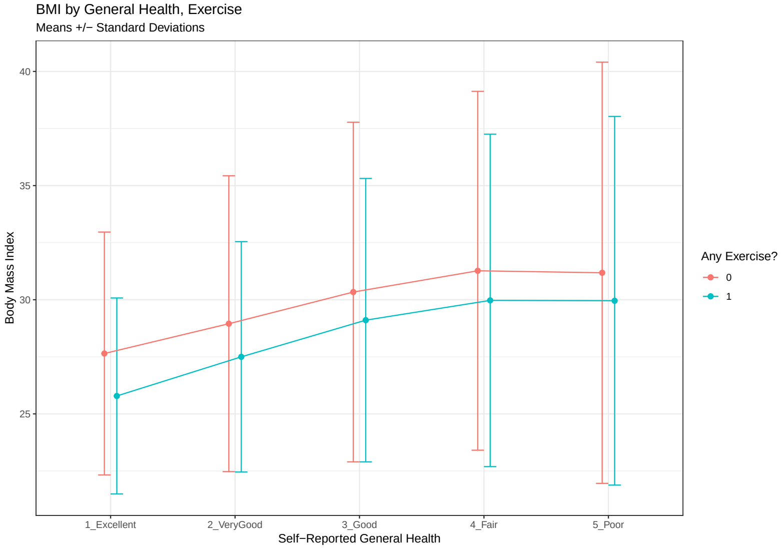
```
   genhealth.exerany     mean       sd    n missing
1      1_Excellent.0 27.64487 5.320510  124       0
2       2_VeryGood.0 28.94985 6.479965  474       0
3           3_Good.0 30.33703 7.438949  651       0
4           4_Fair.0 31.26841 7.859391  464       0
5           5_Poor.0 31.18231 9.226123  233       0
6      1_Excellent.1 25.78493 4.292097  748       0
7       2_VeryGood.1 27.49874 5.046002 1583       0
8           3_Good.1 29.10493 6.208035 1336       0
9           4_Fair.1 29.97157 7.281440  527       0
10          5_Poor.1 29.95524 8.074475  137       0
```

Table of Means and Standard Deviations

```
smart2 %>% group_by(genhealth, exerany) %>%
    summarize(mean.bmi = mean(bmi), sd.bmi = sd(bmi))
```

```
# A tibble: 10 x 4
# Groups:   genhealth [?]
   genhealth   exerany mean.bmi sd.bmi
   <fct>         <dbl>    <dbl>  <dbl>
 1 1_Excellent       0     27.6   5.32
 2 1_Excellent       1     25.8   4.29
 3 2_VeryGood        0     28.9   6.48
 4 2_VeryGood        1     27.5   5.05
 5 3_Good            0     30.3   7.44
 6 3_Good            1     29.1   6.21
 7 4_Fair            0     31.3   7.86
 8 4_Fair            1     30.0   7.28
 9 5_Poor            0     31.2   9.23
10 5_Poor            1     30.0   8.07
```

Check interaction first with means plot?



Means Plot code

```
pd <- position_dodge(0.2)
smart_sum <- smart2 %>%
    group_by(genhealth, exerany) %>%
    summarize(mean.bmi = mean(bmi), sd.bmi = sd(bmi))
ggplot(smart_sum, aes(x = genhealth, y = mean.bmi,
                       col = factor(exerany))) +
    geom_errorbar(aes(ymin = mean.bmi - sd.bmi,
                      ymax = mean.bmi + sd.bmi),
                  width = 0.2, position = pd) +
    geom_point(size = 2, position = pd) +
    geom_line(aes(group = factor(exerany)), position = pd) +
    scale_color_discrete(name = "Any Exercise?") +
    theme_bw() +
    labs(y = "Body Mass Index",
         x = "Self-Reported General Health",
         title = "BMI by General Health, Exercise",
         subtitle = "Means +/- Standard Deviations")
```

ANOVA with and without interaction term

```r
model_3no <- lm(bmi ~ genhealth + exerany, data = smart2)
model_3i <- lm(bmi ~ genhealth * exerany, data = smart2)

anova(model_3i)
```

```
Analysis of Variance Table

Response: bmi
                    Df Sum Sq Mean Sq F value    Pr(>F)    
genhealth            4  13988  3497.1 87.6981 < 2.2e-16 ***
exerany              1   2306  2306.2 57.8321 3.274e-14 ***
genhealth:exerany    4     39     9.8  0.2462    0.9121    
Residuals         6267 249908    39.9                      
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Does the interaction have a meaningful impact?

- Means plot is essentially parellel: no clear interaction.
- SS(interaction) $= 39$, SS(Total) $= 266241$, so $\eta^2 = .00015$ or 0.015%
- *p* value for interaction term is 0.91

What does this imply about which model might be more helpful?

Making Predictions with `model_3no`

- Anna exercises and is in very good health.
- Brad doesn't exercise and is in poor health.

```
round(coef(model_3no),2)
```

```
      (Intercept) genhealth2_VeryGood     genhealth3_Good 
            27.22                1.66                3.21 
  genhealth4_Fair     genhealth5_Poor             exerany 
             4.09                4.01               -1.36 
```

Making Predictions with model_3i

- Anna exercises and is in very good health.
- Brad doesn't exercise and is in poor health.

```
round(coef(model_3i),2)
```

```
                (Intercept)         genhealth2_VeryGood
                      27.64                        1.30
            genhealth3_Good             genhealth4_Fair
                       2.69                        3.62
            genhealth5_Poor                     exerany
                       3.54                       -1.86
genhealth2_VeryGood:exerany     genhealth3_Good:exerany
                       0.41                        0.63
    genhealth4_Fair:exerany     genhealth5_Poor:exerany
                       0.56                        0.63
```

Predictions

```
newpeople <- tibble(
    name = c("Anna", "Brad"),
    genhealth = c("2_VeryGood", "5_Poor"),
    exerany = c(1, 0))

predict(model_3no, newdata = newpeople)
```

```
       1        2 
27.51911 31.23254 
```

```
predict(model_3i, newdata = newpeople)
```

```
       1        2 
27.49874 31.18231 
```

What if we add in alcdays?

```
model4 <- lm(bmi ~ alcdays + genhealth * exerany,
             data = smart2)

anova(model4)
```

```
Analysis of Variance Table

Response: bmi
                    Df Sum Sq Mean Sq F value    Pr(>F)    
alcdays              1   2654  2654.4 66.8526 3.511e-16 ***
genhealth            4  12655  3163.7 79.6799 < 2.2e-16 ***
exerany              1   2109  2109.4 53.1260 3.514e-13 ***
genhealth:exerany    4     33     8.2  0.2067    0.9348    
Residuals         6266 248791    39.7                      
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Coming Up

Building Linear Regression Models

- Using Stepwise Regression to Select Variables (review)
- Using Best Subsets approaches to Select Variables (new)
    - Mallows' C_p, Adjusted R^2, Corrected AIC, BIC
- Box-Cox plots to motivate outcome transformation (review)
- Spearman ρ^2 Plot to help motivate non-linearity via transformations and interaction terms in Linear Regression (new)
- Cross-Validation of Linear Regression Models (old and new)

to be followed by . . .

- Logistic Regression Models for Binary Outcomes