432 Class 4 Slides

github.com/THOMASELOVE/2020-432

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Today's Agenda

1. Continuing our discussion of two-way ANOVA and ANCOVA with binary factors
2. Building a two-factor ANOVA model with multi-categorical factors
    - again, focus on interpreting the interaction
    - add covariates, as desired

Setup

```
library(here); library(magrittr); library(janitor)
library(broom); library(simputation); library(patchwork)
library(naniar); library(visdat)
library(tidyverse)

theme_set(theme_bw())

smart1 <- readRDS(here("data/smart1.Rds"))
smart1_sh <- readRDS(here("data/smart1_sh.Rds"))
```

`smart1_sh` Variables, by Type

Variable	Type	Description
`landline`	Binary (1/0)	survey conducted by landline? (vs. cell)
`healthplan`	Binary (1/0)	subject has health insurance?
`age_imp`	Quantitative	age (imputed from groups - see Notes)
`fruit_day`	Quantitative	mean servings of fruit / day
`drinks_wk`	Quantitative	mean alcoholic drinks / week
`bmi`	Quantitative	body-mass index (in kg/m^2)
`physhealth`	Count (0-30)	of last 30 days, # in poor physical health
`dm_status`	Categorical	diabetes status (now 2 levels)
`activity`	Categorical	physical activity level (4 levels)
`smoker`	Categorical	tobacco use status (now 3 levels)
`genhealth`	Categorical	self-reported overall health (5 levels)

Modeling with ANOVA for Binary Factors

Models we have fit (so far)

```
a1 <- smart1_sh %$% lm(bmi ~ dm_status)

a2 <- smart1_sh %$% lm(bmi ~ dm_status * healthplan)

a2_noint <- smart1_sh %$% lm(bmi ~ dm_status + healthplan)
```

Is the interaction term important here?

1. Does the interaction plot display important non-parallelism?
2. Does the interaction term account for a substantial fraction of the variation in our outcome?
3. Does the interaction term's estimate/standard error/uncertainty interval meet usual standards for statistical significance?

If **all** of these things are true, then it's easy to conclude that the interaction is important, and we cannot interpret the main effects of `dm_status` and `healthplan` without thinking first about the interaction of those two factors.

- So let's walk through the decision. I've repeated the interaction plot on the next slide.

Interaction Plot

We'll plot the means of the `bmi` in the four combinations:

- two levels of `dm_status` combined with
- two levels of `healthplan`

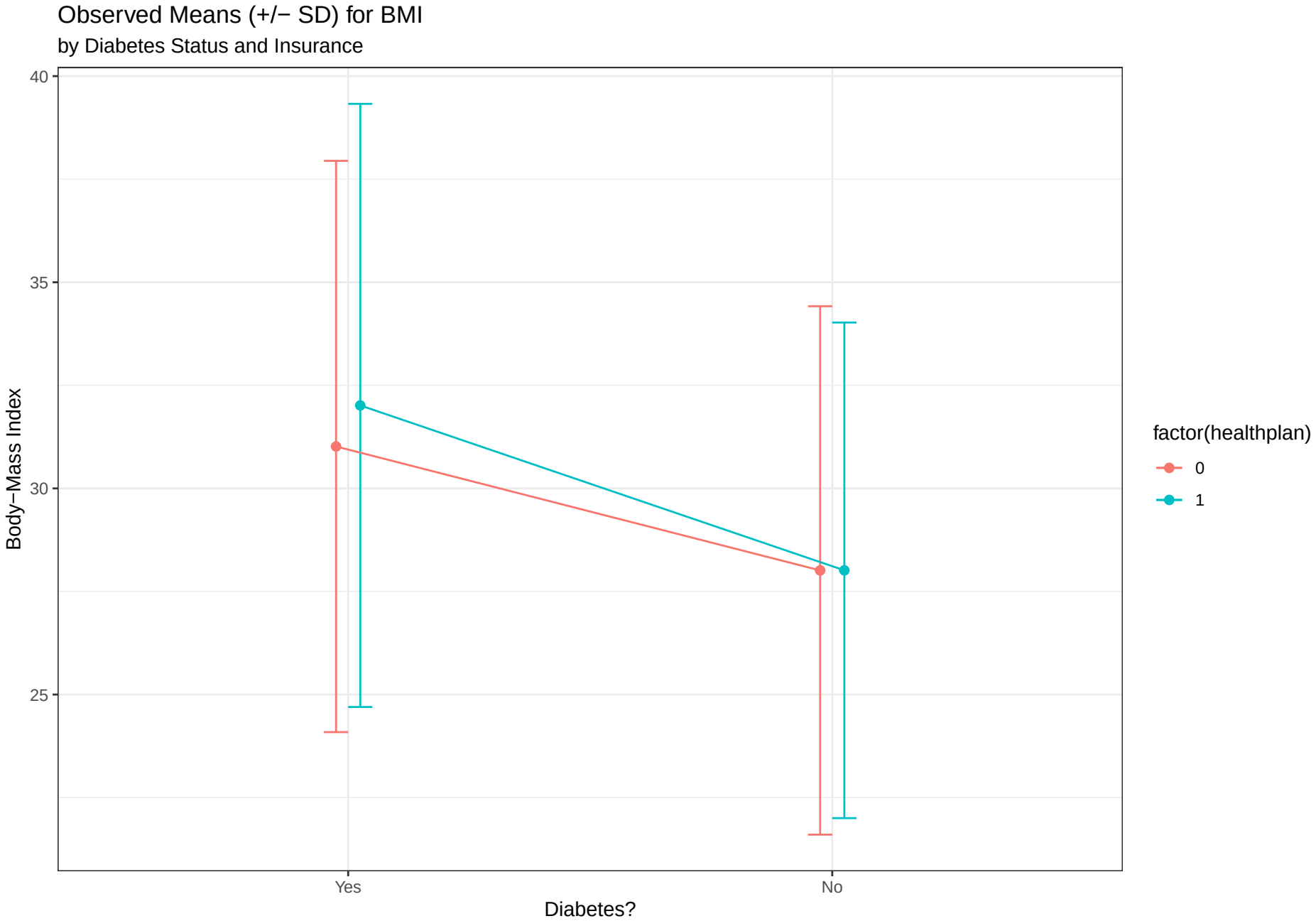
```
summaries1 <- smart1_sh %>%
  group_by(dm_status, healthplan) %>%
  summarize(n = n(), mean = mean(bmi), stdev = sd(bmi))

summaries1 %>% knitr::kable(digits = 2)
```

dm_status	healthplan	n	mean	stdev
Yes	0	35	31.02	6.93
Yes	1	1067	32.01	7.31
No	0	364	28.01	6.41
No	1	5946	28.01	6.01

Interaction Plot for Two-Way ANOVA (code)

```
pd <- position_dodge(0.1)
ggplot(summaries1, aes(x = dm_status, y = mean,
                       col = factor(healthplan))) +
  geom_errorbar(aes(ymin = mean - stdev,
                    ymax = mean + stdev),
                width = 0.1, position = pd) +
  geom_point(size = 2, position = pd) +
  geom_line(aes(group = healthplan), position = pd) +
  labs(y = "Body-Mass Index",
       x = "Diabetes?",
       title = "Observed Means (+/- SD) for BMI",
       subtitle = "by Diabetes Status and Insurance")
```

Interaction Plot for Two-Way ANOVA



Evaluation in our Two-Way ANOVA of Interaction

1. Does the interaction plot display important non-parallelism?
   - No, I don't think so.
2. Does the interaction term account for a substantial fraction of the variation in our outcome?

```
anova(a2) %>% knitr::kable(digits = 0)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dm_status	1	14775	14775	380	0
healthplan	1	3	3	0	1
dm_status:healthplan	1	30	30	1	0
Residuals	7408	288338	39	NA	NA

- SS(total) = 288,338 + 30 + 3 + 14,775 = 303,146.
- SS(interaction) = 30
- η^2(interaction) = $\frac{30}{303146}$ = .000099, or about 0.01% of `bmi` variation.

Is the interaction term important here?

1. Does the interaction plot display important non-parallelism?
   - No.
2. Does the interaction term account for a substantial fraction of the variation in our outcome?
   - It accounts for just under 0.01% of variation, so no.
3. Does the interaction term's estimate/standard error/uncertainty interval meet usual standards for statistical significance?

```
tidy(a2, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	31.017	1.055	29.282	32.752
dm_statusNo	-3.006	1.104	-4.823	-1.190
healthplan	0.996	1.072	-0.767	2.759
dm_statusNo:healthplan	-0.994	1.123	-2.842	0.855

Is the interaction term important here?

1. Does the interaction plot display important non-parallelism?
   - No.
2. Does the interaction term account for a substantial fraction of the variation in our outcome?
   - No.
3. Does the interaction term's estimate/standard error/uncertainty interval meet usual standards for statistical significance?
   - No.

It's clearly easier to ignore the interaction term (and fit the no-interaction model) if none of these three things are true.

Interpreting the "No Interaction" Model

```
tidy(a2_noint, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	31.893	0.364	31.295	32.491
dm_statusNo	-3.966	0.204	-4.301	-3.631
healthplan	0.091	0.321	-0.437	0.620

- If Harry and Sally have the same `healthplan` status, but only Harry has diabetes, then Harry's BMI is estimated to be 3.97 kg/m^2 higher than Sally's. (90% uncertainty interval: 3.63, 4.30).
- If Harry and Sally have the same `dm_status` but Harry has a health plan and Sally doesn't, our model will estimate Harry's BMI as 0.09 kg/m^2 higher than Sally's (90% interval: -0.44, 0.62).

Adding a covariate

We saw that the no-interaction model might well be sufficient for BMI as a function of `dm_status` and `healthplan`. Would this still be true if we first adjusted for the impact of a continuous covariate, like `physhealth`, that is meaningfully correlated with BMI?

```
a3 <- smart1_sh %$%
  lm(bmi ~ physhealth + dm_status * healthplan)

anova(a3) %>% knitr::kable(digits = 1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
physhealth	1	4986.2	4986.2	129.2	0.0
dm_status	1	12185.9	12185.9	315.7	0.0
healthplan	1	0.3	0.3	0.0	0.9
dm_status:healthplan	1	22.1	22.1	0.6	0.4
Residuals	7407	285952.2	38.6	NA	NA

Model without the Covariate

Compare that ANOVA table to this one for our interaction model without the covariate. What changes?

```
anova(a2) %>% knitr::kable(digits = 1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dm_status	1	14774.8	14774.8	379.6	0.0
healthplan	1	3.1	3.1	0.1	0.8
dm_status:healthplan	1	30.4	30.4	0.8	0.4
Residuals	7408	288338.2	38.9	NA	NA

a3 covariate model without interaction term

```
a3_noint <- smart1_sh %$%
  lm(bmi ~ physhealth + dm_status + healthplan)

anova(a3_noint) %>% knitr::kable(digits = 1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
physhealth	1	4986.2	4986.2	129.2	0.0
dm_status	1	12185.9	12185.9	315.7	0.0
healthplan	1	0.3	0.3	0.0	0.9
Residuals	7408	285974.3	38.6	NA	NA

Interpreting "No Interaction" Model + Covariate

```
tidy(a3_noint, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(digits = 2)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	31.39	0.37	30.79	32.00
physhealth	0.06	0.01	0.05	0.07
dm_statusNo	-3.67	0.21	-4.01	-3.33
healthplan	0.03	0.32	-0.50	0.56

- If Harry and Sally have the same `healthplan` status and the same `physhealth`, but only Harry has diabetes, then Harry's BMI is estimated to be 3.67 kg/m^2 higher than Sally's. (90% uncertainty interval: 3.33, 4.01).
- See next slide, too.

Interpreting "No Interaction" Model + Covariate

```
tidy(a3_noint, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(digits = 2)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	31.39	0.37	30.79	32.00
physhealth	0.06	0.01	0.05	0.07
dm_statusNo	-3.67	0.21	-4.01	-3.33
healthplan	0.03	0.32	-0.50	0.56

- If Harry and Sally have the same `dm_status` and the same `physhealth`, but Harry has a health plan and Sally doesn't, our model will estimate Harry's BMI as 0.03 kg/m^2 higher than Sally's (90% uncertainty interval: -0.50, 0.56).
- Why aren't I talking here about the covariate's effect?

Does the model fit the data well?

We have the usual strategies applicable in any linear model:

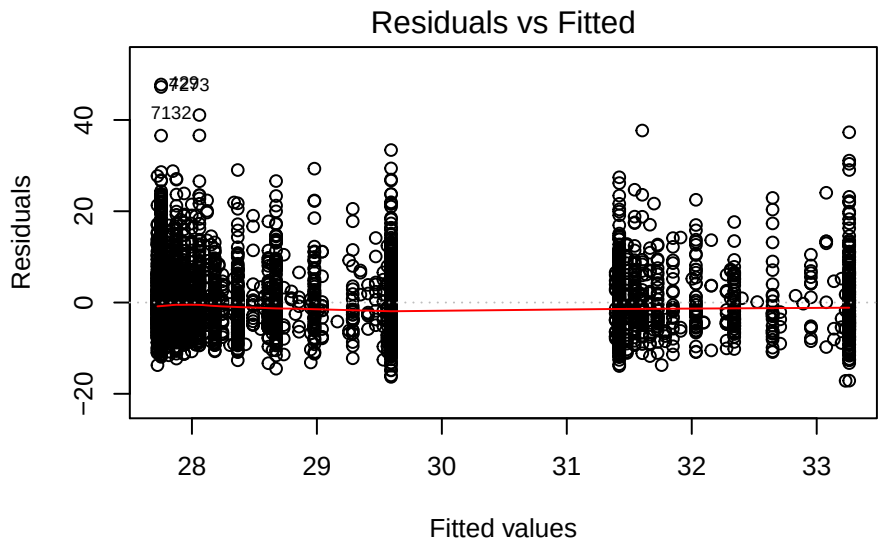
- evaluate the R^2 and other summary statistics, especially in comparison to alternative specifications of models for the same outcome.
- evaluate the fit of the model to regression assumptions, mostly through diagnostics based on residuals
- cross-validate our model selection process, perhaps by partitioning the sample into a training sample (where candidate models are developed) and a holdout / test sample (where we choose between the candidates)

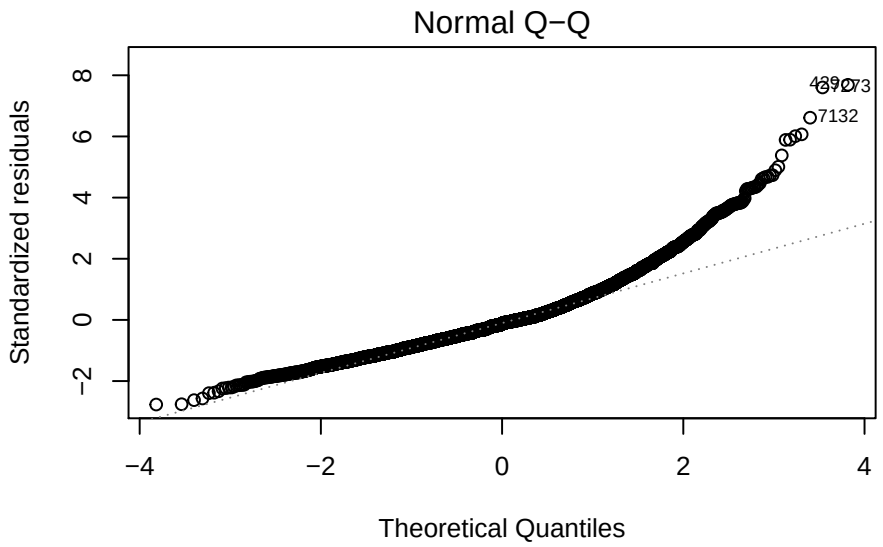
Summary Statistics (Whole Sample)

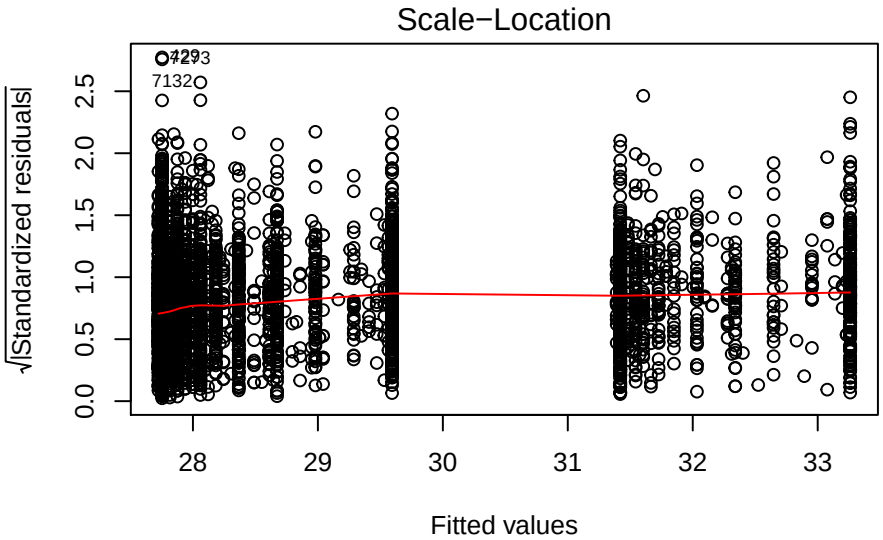
```
bind_rows(glance(a1), glance(a2_noint), glance(a3_noint)) %>%
  mutate(model =
           c("dm_status", "+ healthplan", "+ physhealth")) %>%
  select(model, r.squared, sigma, AIC, BIC, adj.r.squared) %>%
  knitr::kable(digits = 3)
```

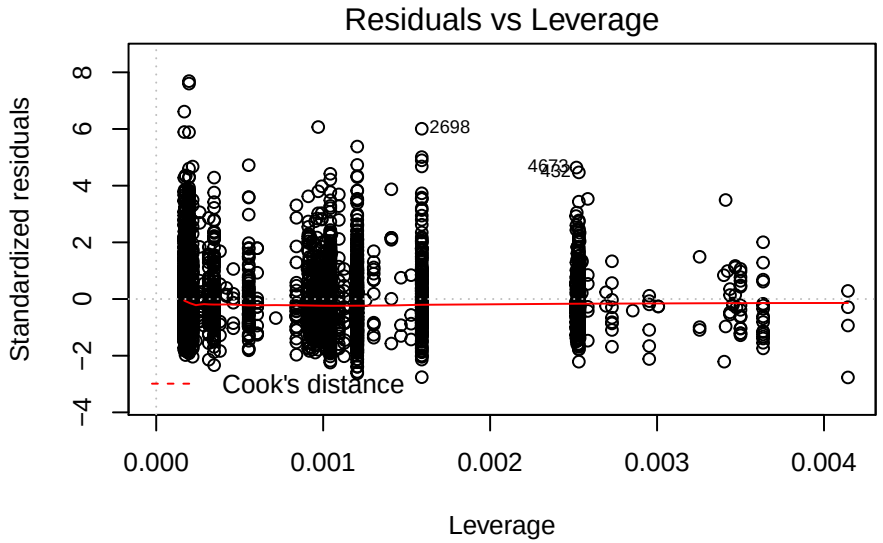
model	r.squared	sigma	AIC	BIC	adj.r.squared
dm_status	0.049	6.238	48176.79	48197.52	0.049
+ healthplan	0.049	6.239	48178.71	48206.35	0.048
+ physhealth	0.057	6.213	48118.91	48153.46	0.056

plot(a3_noint)









ANOVA and ANCOVA with Multi-Categorical Predictors in Linear Models

New Questions

1. How does a subject's self-reported general health and their tobacco status combine when predicting their body mass index?
2. Does adjusting for the number of alcoholic drinks consumed per week affect our assessment?

Addressing Question 1: Simple Summary

1. How does a subject's genhealth and smoker status combine when predicting their body mass index?

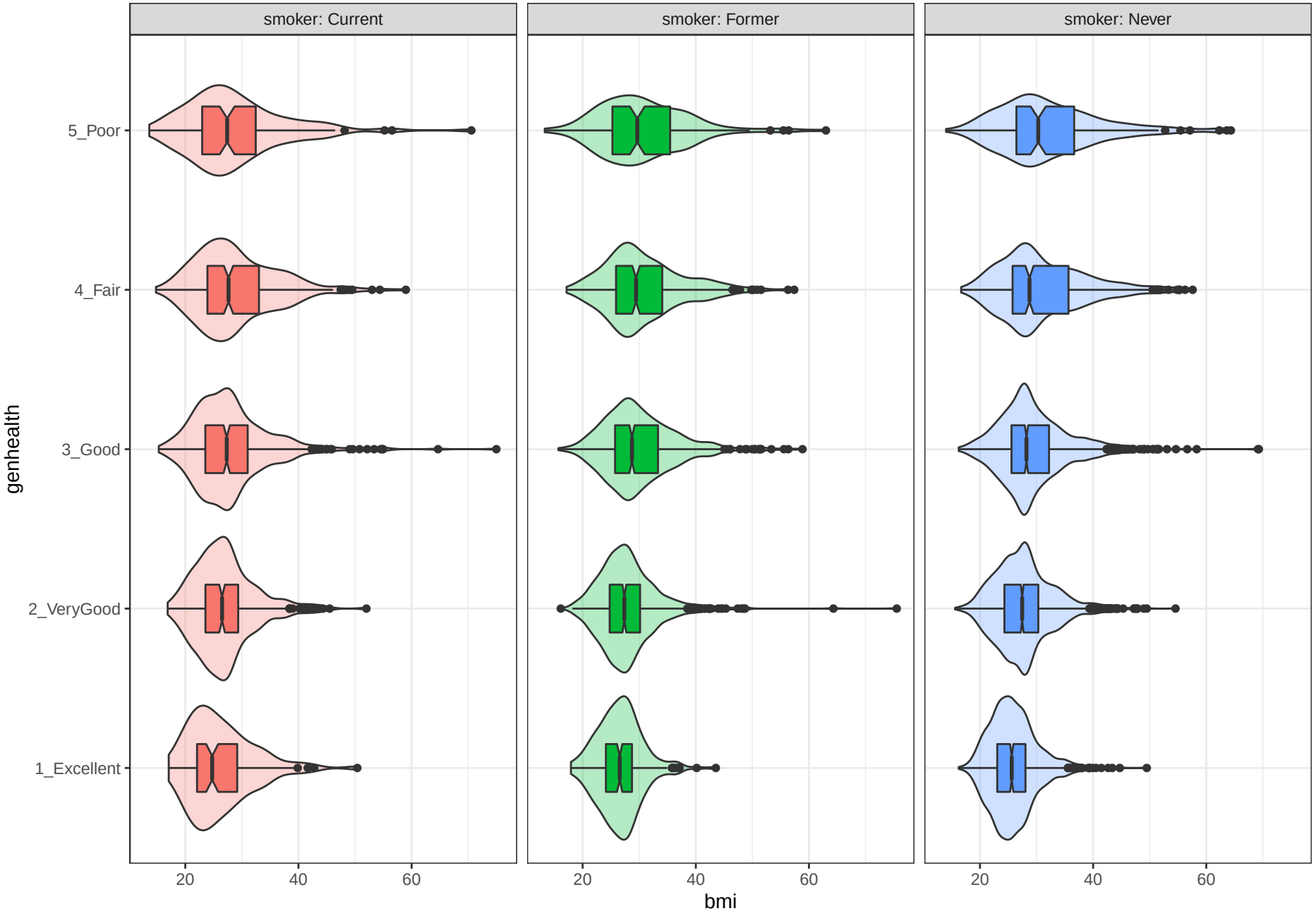
```
smart1_sh %$%
  mosaic::favstats(bmi ~ smoker + genhealth) %>%
  rename(smoke.health = smoker.genhealth) %>%
  knitr::kable(digits = 1)
```

smoke.health	min	Q1	median	Q3	max	mean	sd	
Current.1_Excellent	17.1	22.1	24.8	29.2	50.4	26.2	5.9	1
Former.1_Excellent	17.9	24.1	26.5	28.7	43.5	26.6	4.0	2
Never.1_Excellent	16.2	23.1	25.6	28.0	49.5	26.0	4.3	7
Current.2_VeryGood	16.9	23.6	26.5	29.4	52.0	27.0	5.4	3
Former.2_VeryGood	16.1	24.8	27.4	30.1	75.5	28.0	5.5	6
Never.2_VeryGood	15.6	24.3	27.5	30.3	54.6	27.8	5.3	14
Current.3_Good	15.3	23.5	27.3	31.0	75.0	28.1	7.1	4
Former.3_Good	15.7	25.7	28.7	33.3	58.9	30.0	6.4	6
Never.3_Good	16.2	25.6	28.2	32.2	69.3	29.4	6.4	12

Visualize Three Variables (Code)

```
ggplot(smart1_sh, aes(x = genhealth, y = bmi,
                      fill = smoker)) +
  geom_violin(alpha = 0.3) +
  geom_boxplot(width = 0.3, notch = TRUE) +
  facet_wrap(~ smoker, labeller = label_both) +
  coord_flip() +
  guides(fill = FALSE)
```

Visualize Three Variables



Interaction Plot

We'll plot the means of the `bmi` in the fifteen combinations:

- three levels of `smoker` combined with
- five levels of `genhealth`

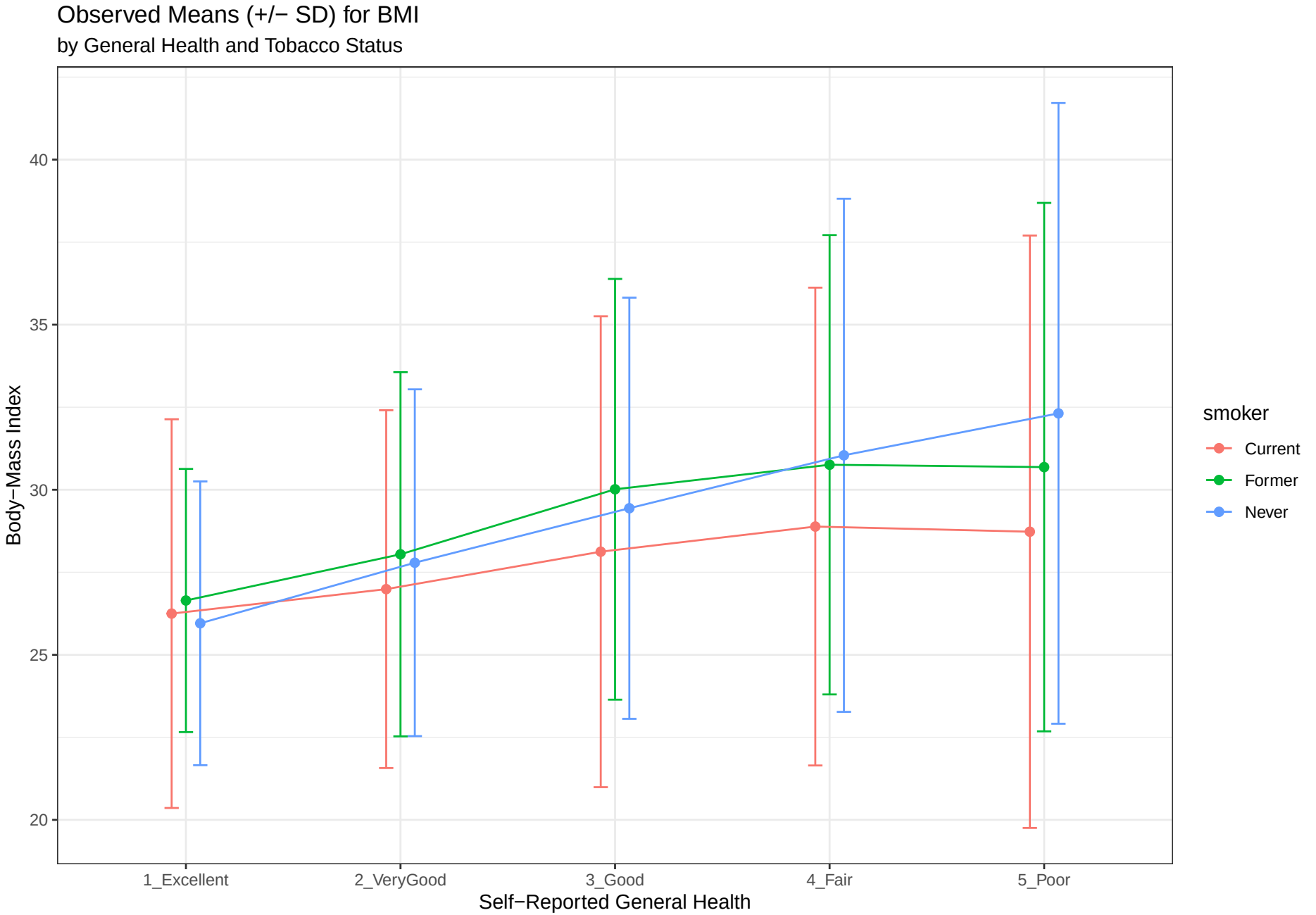
```
summaries4 <- smart1_sh %>%
  group_by(genhealth, smoker) %>%
  summarize(n = n(), mean = mean(bmi), stdev = sd(bmi))

summaries4 %>% knitr::kable(digits = 2)
```

genhealth	smoker	n	mean	stdev
1_Excellent	Current	111	26.25	5.89
1_Excellent	Former	232	26.64	3.99
1_Excellent	Never	714	25.95	4.30
2_VeryGood	Current	332	26.99	5.42
2_VeryGood	Former	635	28.04	5.52
2_VeryGood	Never	1453	27.79	5.25

Interaction Plot for Two-Way ANOVA (code)

```
pd <- position_dodge(0.2)
ggplot(summaries4, aes(x = genhealth, y = mean,
                       col = smoker)) +
  geom_errorbar(aes(ymin = mean - stdev,
                    ymax = mean + stdev),
                width = 0.2, position = pd) +
  geom_point(size = 2, position = pd) +
  geom_line(aes(group = smoker), position = pd) +
  labs(y = "Body-Mass Index",
       x = "Self-Reported General Health",
       title = "Observed Means (+/- SD) for BMI",
       subtitle = "by General Health and Tobacco Status")
```

Interaction Plot for Two-Way ANOVA



Two-Way Analysis of Variance

```
a4 <- smart1_sh %$% lm(bmi ~ genhealth * smoker)

anova(a4) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	14911.707	3727.927	96.724	0.000
smoker	2	2198.101	1099.050	28.516	0.000
genhealth:smoker	8	943.286	117.911	3.059	0.002
Residuals	7397	285093.553	38.542	NA	NA

Model a4 tidied coefficients

```
tidy(a4, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error, conf.low, conf.high, p.val
  knitr::kable(digits = 2)
```

term	estimate	std.error	conf.low	conf.
(Intercept)	26.25	0.59	25.28	2
genhealth2_VeryGood	0.74	0.68	-0.38	
genhealth3_Good	1.88	0.66	0.79	
genhealth4_Fair	2.64	0.69	1.50	
genhealth5_Poor	2.48	0.80	1.16	
smokerFormer	0.40	0.72	-0.78	
smokerNever	-0.29	0.63	-1.34	
genhealth2_VeryGood:smokerFormer	0.66	0.83	-0.71	
genhealth3_Good:smokerFormer	1.49	0.81	0.16	
genhealth4_Fair:smokerFormer	1.48	0.86	0.06	
genhealth5_Poor:smokerFormer	1.56	1.03	-0.14	
genhealth2_VeryGood:smokerNever	1.09	0.74	-0.12	

The Equations

The model with the interaction term is

```
BMI = 26.25 + 0.74 (genhealth = Very Good)
            + 1.88 (genhealth = Good)
            + ...
            + 2.48 (genhealth = Poor)
            + 0.40 (smoker = Former)
            - 0.29 (smoker = Never)
            + 0.66 (genhealth = Very Good)(smoker = Former)
            + ...
            + 1.09 (genhealth = Very Good)(smoker = Never)
            + ...
            + 3.88 (genhealth = Poor)(smoker = Never)
```

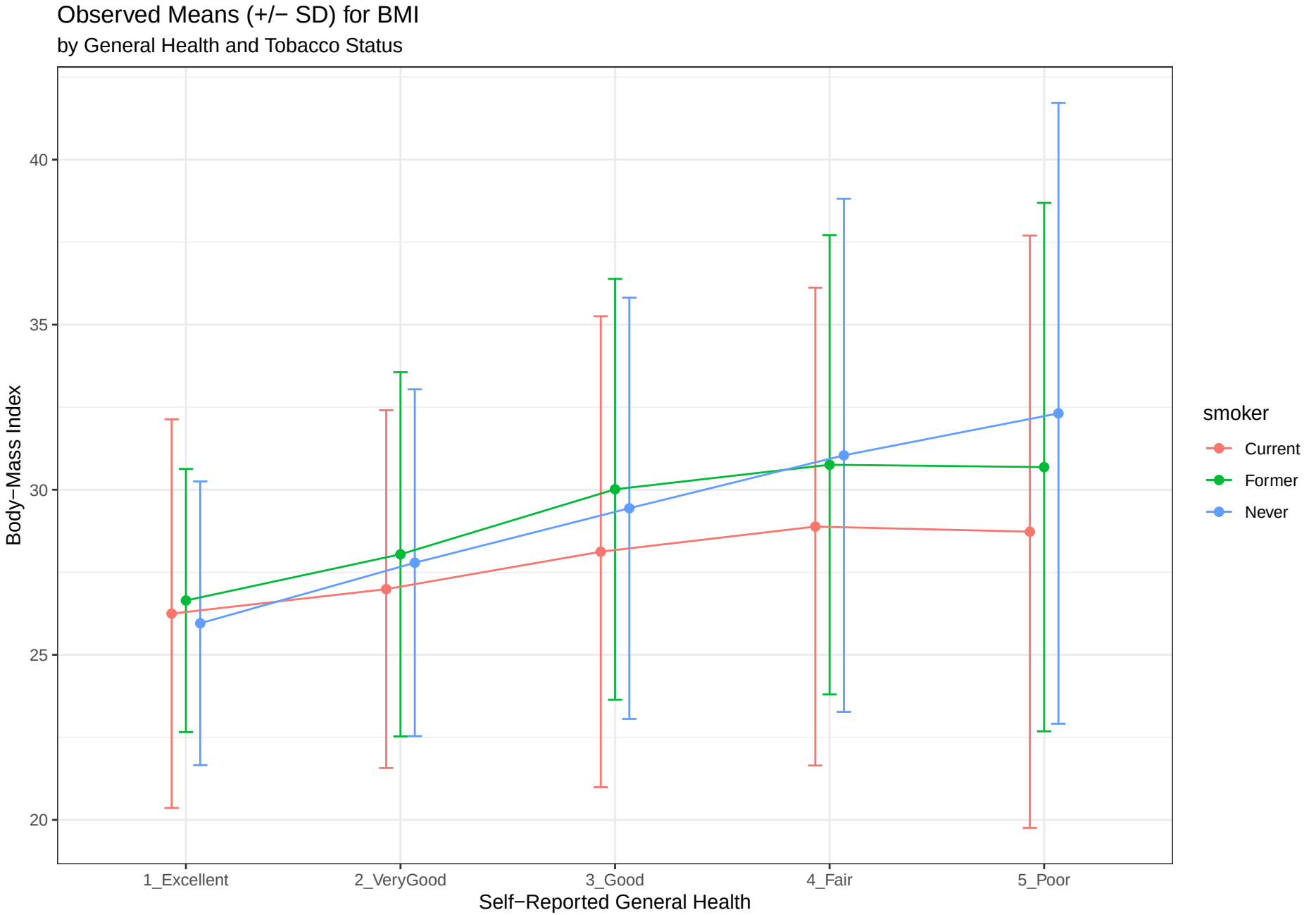
- Predict Harry, who's in Excellent health but a Current smoker
- Predict Sally, who's in Very Good Health and a Former smoker

Is the interaction term important here?

1. Does the interaction plot display important non-parallelism?
2. Does the interaction term account for a substantial fraction of the variation in our outcome?
3. Does the interaction term's estimate/standard error/uncertainty interval meet usual standards for statistical significance?

- See the next 3 slides for the answers. . .

Interaction Plot, again. . .



Fraction of Variation accounted for by Interaction

```
anova(a4) %>% knitr::kable(digits = 0)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	14912	3728	97	0
smoker	2	2198	1099	29	0
genhealth:smoker	8	943	118	3	0
Residuals	7397	285094	39	NA	NA

- SS(total) = 14,912 + 2,198 + 943 + 285,094 = 303,147.
- SS(interaction) = 943
- η^2(interaction) = $\frac{943}{303147}$ = .0031, or about 0.31% of `bmi` variation.

Are the interaction terms statistically significant?

```
a4 <- smart1_sh %$% lm(bmi ~ genhealth * smoker)
a4_noint <- smart1_sh %$% lm(bmi ~ genhealth + smoker)

anova(a4_noint, a4)
```

```
Analysis of Variance Table

Model 1: bmi ~ genhealth + smoker
Model 2: bmi ~ genhealth * smoker
  Res.Df    RSS Df Sum of Sq      F  Pr(>F)
1   7405 286037
2   7397 285094  8    943.29 3.0593 0.00193 **
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So which model should we use? (Interaction or No Interaction)

Equation for the Interaction Model (a4)

```
bmi = 26.248
  + 0.741 (genhealth = Very Good)
  + 1.875 (genhealth = Good)
  + 2.637 (genhealth = Fair)
  + 2.481 (genhealth = Poor)
  + 0.397 (smoker = Former)
  - 0.293 (smoker = Never)
  + 0.658 (Very Good)(Former)
  + 1.493 (Good)(Former)
  + 1.475 (Fair)(Former)
  + 1.560 (Poor)(Former)
  + 1.093 (Very Good)(Never)
  + 1.610 (Good)(Never)
  + 2.452 (Fair)(Never)
  + 3.878 (Poor)(Never)
```

Comparing Harry and Sally (interaction model)

Scenario	Subject	genhealth	smoker
1	Harry	Very Good	Current
1	Sally	Very Good	Never

- Harry's predicted BMI is 26.248 + 0.741 = 26.989
- Sally's predicted BMI is 26.248 + 0.741 - 0.293 + 0.658 = 27.354
- If genhealth Very Good, effect of Never vs. Current is 0.365

Scenario	Subject	genhealth	smoker
2	Harry	Poor	Current
2	Sally	Poor	Never

- Harry's predicted BMI is 26.248 + 2.481 = 28.729
- Sally's predicted BMI is 26.248 + 2.481 - 0.293 + 3.878 = 32.314
- If genhealth Poor, effect of Never vs. Current is 3.585

Comparing Harry and Sally (interaction model)

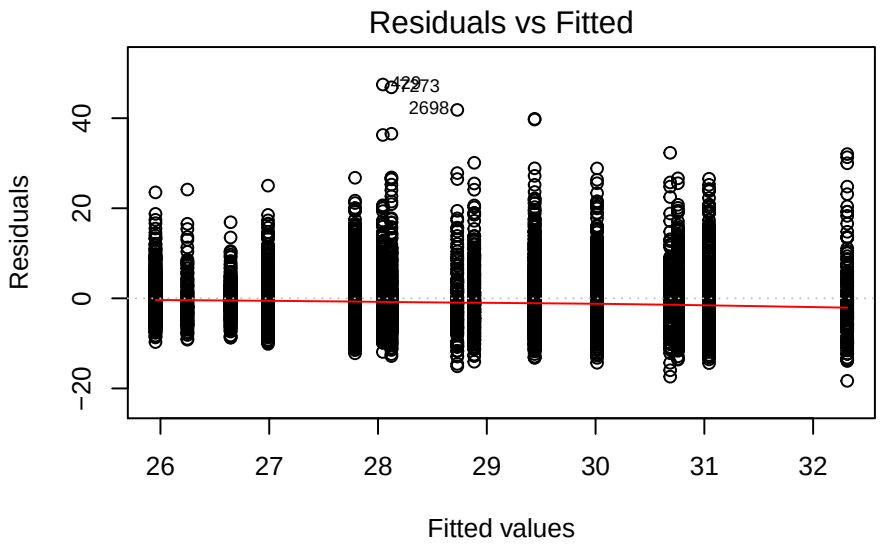
Scenario	Subject	genhealth	smoker
3	Harry	Very Good	Current
3	Sally	Poor	Current

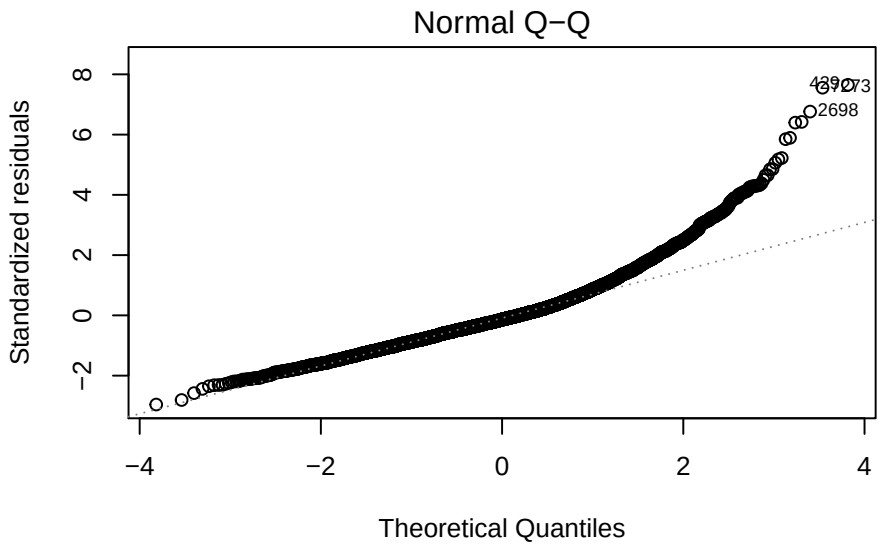
- Harry's predicted BMI is 26.248 + 0.741 = 26.989
- Sally's predicted BMI is 26.248 + 2.481 = 28.729
- If Current smoker, effect of Poor vs. Very Good is 1.740

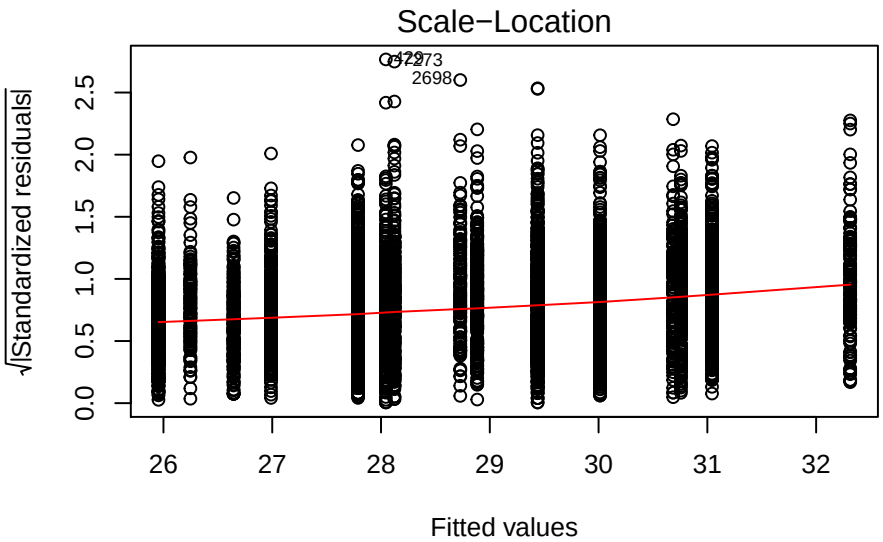
Scenario	Subject	genhealth	smoker
4	Harry	Very Good	Never
4	Sally	Poor	Never

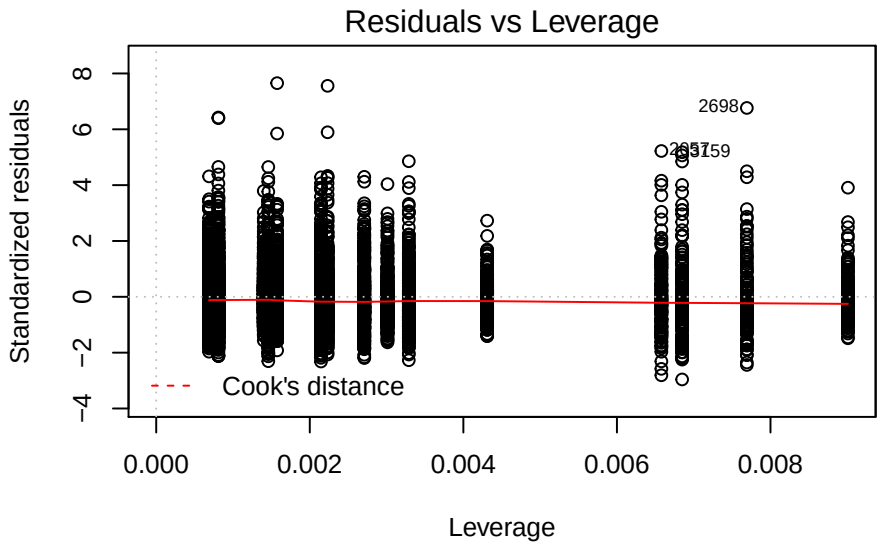
- Harry's predicted BMI is 26.248 + 0.741 - 0.293 + 1.093 = 27.789
- Sally's predicted BMI is 26.248 + 2.481 - 0.293 + 3.878 = 32.314
- If Never smoker, effect of Poor vs. Very Good is 4.525

Residual Plots for model a4







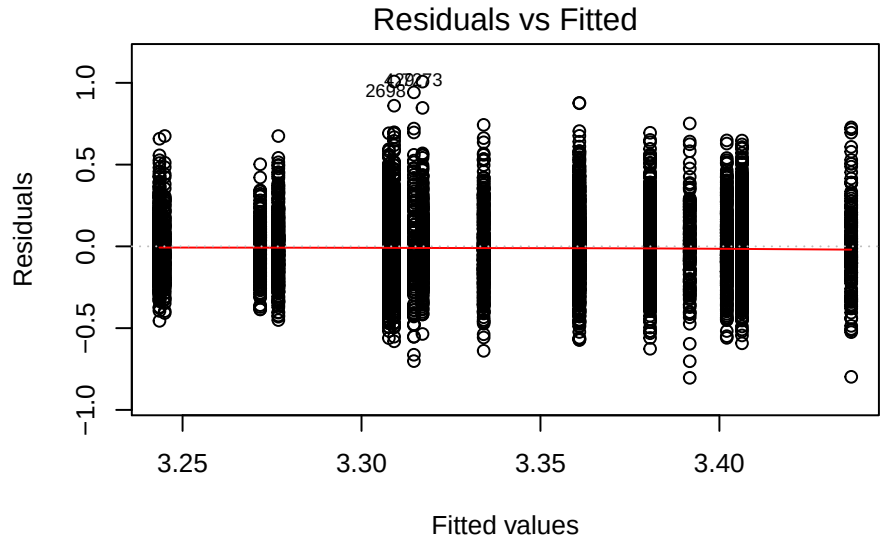


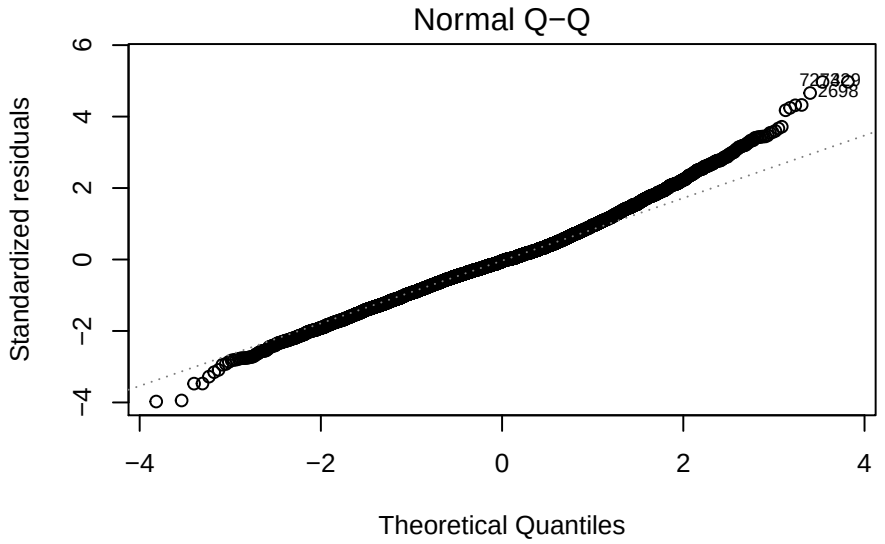
Would using `log(BMI)` make the difference?

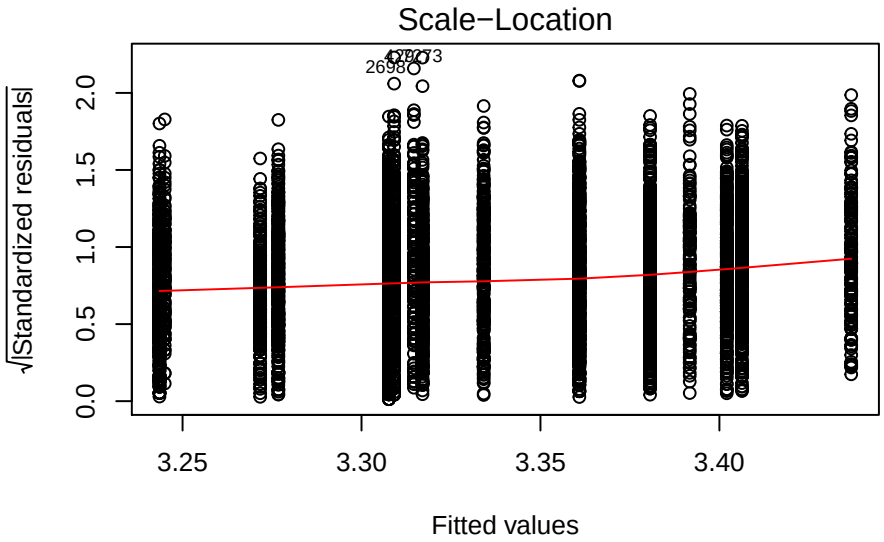
```
a4_log <- smart1_sh %$% lm(log(bmi) ~ genhealth * smoker)

anova(a4_log) %>% knitr::kable(digits = 3)
```

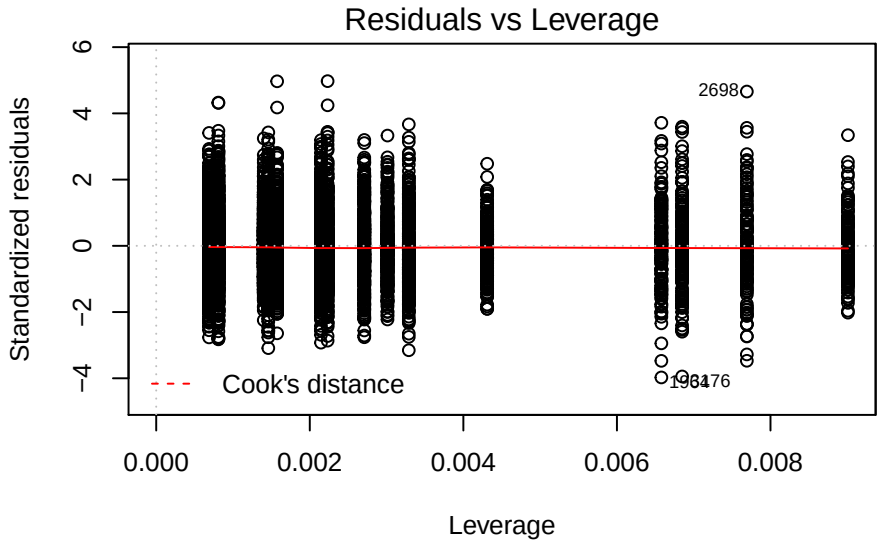
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	14.651	3.663	88.951	0.000
smoker	2	3.149	1.575	38.242	0.000
genhealth:smoker	8	0.933	0.117	2.833	0.004
Residuals	7397	304.582	0.041	NA	NA

Residual Plots for model a4_log









What if we add a covariate?

```
smart1_sh <- smart1_sh %>%
  mutate(drinks_c = drinks_wk - mean(drinks_wk))

a5_log <- smart1_sh %$%
  lm(log(bmi) ~ drinks_c + genhealth * smoker)

anova(a5_log) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
drinks_c	1	1.239	1.239	30.148	0.000
genhealth	4	14.229	3.557	86.545	0.000
smoker	2	2.895	1.448	35.220	0.000
genhealth:smoker	8	0.958	0.120	2.914	0.003
Residuals	7396	303.994	0.041	NA	NA

1. Can we make predictions?
2. Why center the drinks_wk?

Equation for model a5_log

```
log(BMI) = = 3.248
  - 0.0014 drinks_c
  + 0.033 (genhealth = Very Good)
  + 0.063 (genhealth = Good)
  + 0.087 (genhealth = Fair)
  + 0.067 (genhealth = Poor)
  + 0.025 (smoker = Former)
  - 0.005 (smoker = Never)
  + 0.013 (Very Good)(Former)
  + 0.045 (Good)(Former)
  + 0.041 (Fair)(Former)
  + 0.052 (Poor)(Former)
  + 0.031 (Very Good)(Never)
  + 0.053 (Good)(Never)
  + 0.074 (Fair)(Never)
  + 0.125 (Poor)(Never)
```

Comparing Models

- Does the addition of the covariate add statistically detectable predictive value?

```
anova(a4_log, a5_log)
```

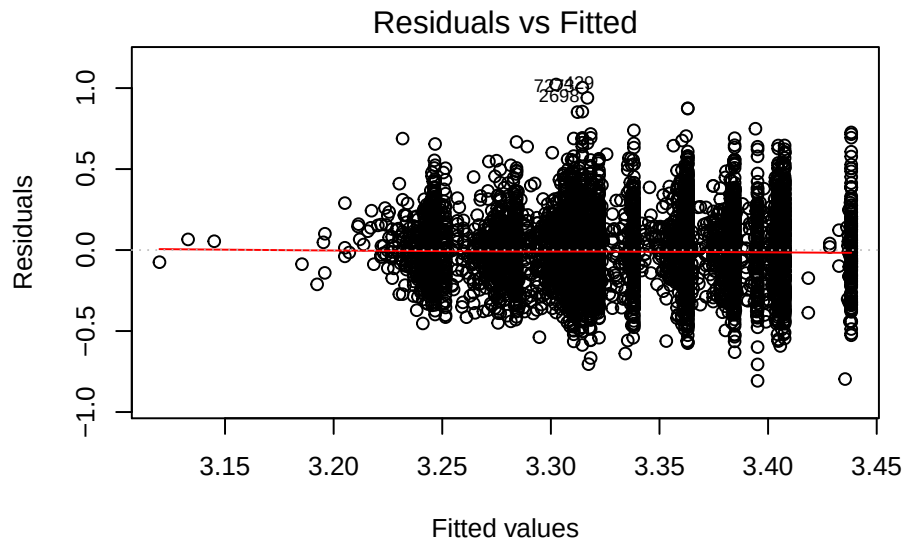
```
Analysis of Variance Table

Model 1: log(bmi) ~ genhealth * smoker
Model 2: log(bmi) ~ drinks_c + genhealth * smoker
  Res.Df    RSS Df Sum of Sq     F    Pr(>F)
1   7397 304.58
2   7396 303.99  1   0.58817 14.31 0.0001563 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

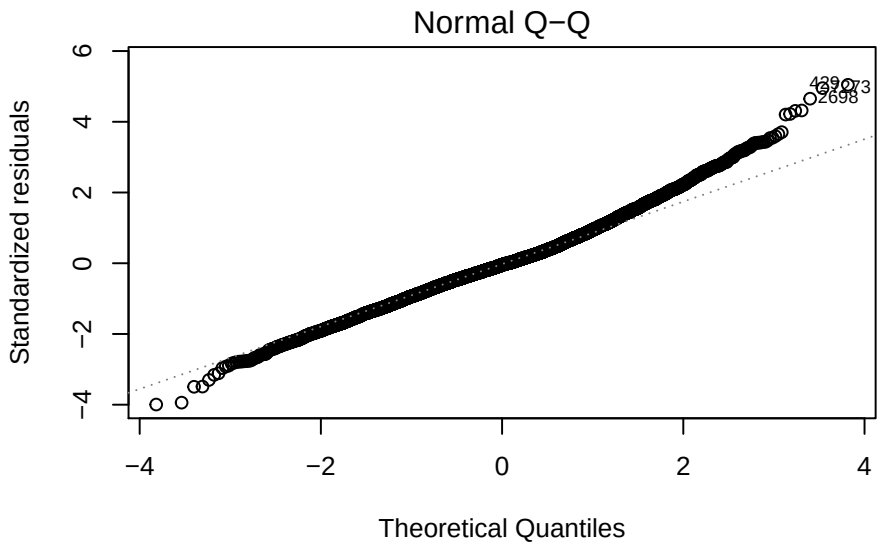
Comparing Models

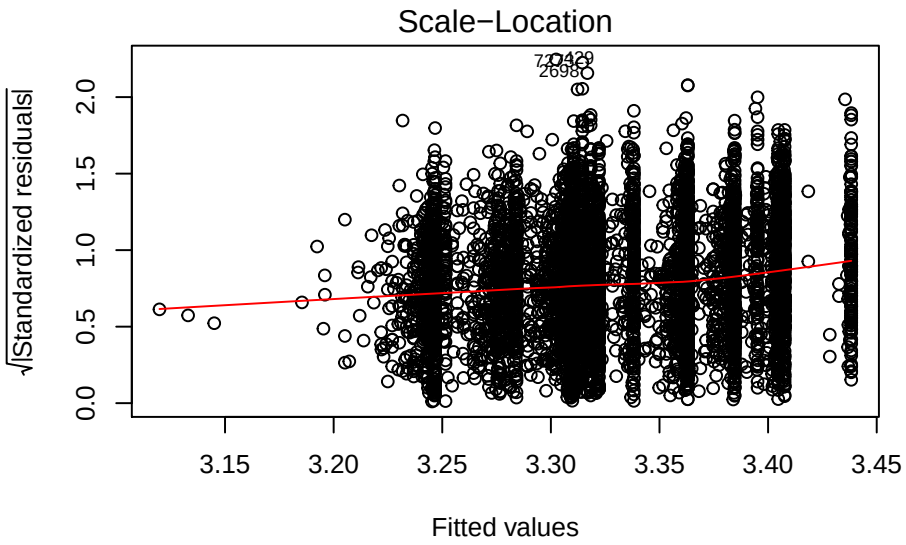
```
bind_rows(glance(a4_log), glance(a5_log)) %>%
  mutate(model = c("ANOVA", "+ drinks_c")) %>%
  select(model, r2 = r.squared, sigma, AIC, BIC,
         adjr2 = adj.r.squared) %>%
  knitr::kable(digits = c(0, 3, 3, 0, 0, 3))
```

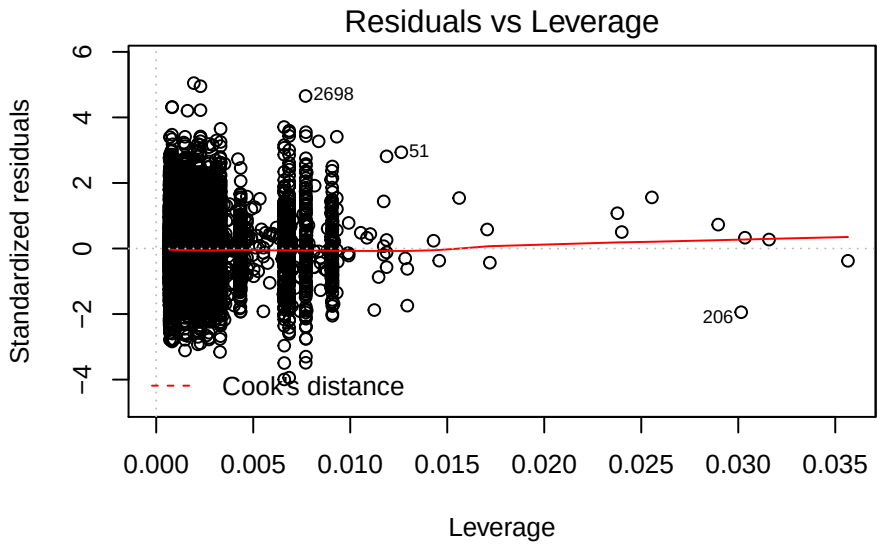
model	r2	sigma	AIC	BIC	adjr2
ANOVA	0.058	0.203	-2592	-2482	0.056
+ drinks_c	0.060	0.203	-2604	-2487	0.058

Residual Plots for model a5_log









Next up

What if we have a binary outcome?