432 Class 02 Slides

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2021-02-04

Today's Agenda

- Linear Regression with Categorical Predictors
- Building Two-Way ANOVA models with interaction
- Building Analysis of Covariance Models

We'll use some BRFSS/SMART data about Ohio residents to address the following questions.

1. What is the association of diabetes diagnosis and smoking status on BMI?
2. Does adjusting for subject's age affect our assessments?
3. How does the subject's level of physical activity fit into this?

Chapter 2 of the Course Notes builds the BRFSS/SMART data.

Setup

```
knitr::opts_chunk$set(comment = NA)
options(width = 60)       ## for the slides

library(here)             ## project management
library(knitr)            ## mostly for kable
library(mosaic)           ## mostly for favstats
library(patchwork)        ## combine plots
library(janitor)          ## mostly for tabyl
library(naniar)           ## missing data tools
library(simputation)      ## for single imputation
library(broom)            ## for tidying model output
library(tidyverse)        ## as always (dplyr, ggplot2, etc.)

theme_set(theme_bw())     ## my personal preference
```

- I used `message = FALSE` in the code chunk setup.

Codebook of variables we'll select from `smart_ohio`

```
smart_ohio <- read_csv(here("data/smart_ohio.csv"))

dim(smart_ohio)
```

```
[1] 7412   99
```

We'll sample 432 observations from `smart_ohio` on these six variables. . .

Variable	Type	Description
`SEQNO`	ID code	we'll represent as a character
`bmi`	Quantity	body-mass index (in kg/m^2)
`smoker`	4 levels	smoking status (we'll collapse to 3 levels)
`dm_status`	4 levels	diabetes status (we'll collapse to 2)
`activity`	4 levels	physical activity level (we'll re-level)
`age_imp`	Quantity	age (imputed from groups, see Chapter 2)

Create our working data set (day2)

```
set.seed(43202)                                          ## note 1

day2 <- smart_ohio %>%                                   ## note 2
    select(SEQNO, bmi, smoker, dm_status,
           activity, age_imp) %>%                        ## note 3
    slice_sample(n = 432) %>%                            ## note 4
    type.convert() %>%                                   ## note 5
    mutate(SEQNO = as.character(SEQNO))                  ## note 6
```

1. set seed for random sampling
2. modify `smart_ohio` data and place in new `day2` tibble
3. select our six variables
4. take a random sample of 432 rows from the data
5. convert all character variables into factors
6. set ID code as a character variable

The day2 tibble, printed

```
day2
```

```
# A tibble: 432 x 6
   SEQNO       bmi smoker dm_status    activity         age_imp
   <chr>     <dbl> <fct>  <fct>        <fct>              <int>
 1 2017000~   NA   Never  No-Diabetes  Inactive              71
 2 2017000~   27.3 Never  No-Diabetes  <NA>                  69
 3 2017001~   19.2 Former No-Diabetes  Inactive              NA
 4 2017000~   20.5 Never  No-Diabetes  Highly_Active         22
 5 2017000~   25.1 Never  No-Diabetes  Insufficientl~        61
 6 2017000~   24.8 Never  Pregnancy-I~ Inactive              40
 7 2017001~   31.2 Former No-Diabetes  Highly_Active         57
 8 2017000~   29.4 Never  No-Diabetes  Active                27
 9 2017000~   26.7 Former No-Diabetes  Highly_Active         71
10 2017000~   27.4 Former No-Diabetes  Inactive              91
# ... with 422 more rows
```

Initial Data Checking (Quantities)

```
favstats(~ bmi, data = day2) %>% kable(dig = 1)
```

min	Q1	median	Q3	max	mean	sd	n	missing
16.9	23.9	27.4	31.2	56.6	28.4	6.3	400	32

```
favstats(~ age_imp, data = day2) %>% kable(dig = 1)
```

min	Q1	median	Q3	max	mean	sd	n	missing
18	43	58.5	70	96	56.9	19	424	8

1. Do the observed ranges of values look plausible in context?
2. Are there missing values we need to deal with?

Checking the Categorical Data (activity)

```
day2 %>% count(activity)
```

```
# A tibble: 5 x 2
  activity                 n
* <fct>                <int>
1 Active                  60
2 Highly_Active          114
3 Inactive               124
4 Insufficiently_Active   87
5 <NA>                    47
```

- What does <NA> mean? What should we do with this variable?

Checking the Categorical Data (activity)

```
day2 %>% count(activity)
```

```
# A tibble: 5 x 2
  activity                 n
* <fct>                <int>
1 Active                  60
2 Highly_Active          114
3 Inactive               124
4 Insufficiently_Active   87
5 <NA>                    47
```

- What does <NA> mean? What should we do with this variable?
- Shortly, we'll **reorder** these levels in a more sensible way (suggestions?) and then we'll have to deal with the missing values, somehow.

Checking the Categorical Data (smoker)

```
day2 %>% count(smoker)
```

```
# A tibble: 5 x 2
  smoker                n
* <fct>             <int>
1 Current_daily        58
2 Current_not_daily    19
3 Former              124
4 Never               216
5 <NA>                 15
```

- OK. Some missing values to deal with. What else might we do here?

Checking the Categorical Data (smoker)

```
day2 %>% count(smoker)
```

```
# A tibble: 5 x 2
  smoker                n
* <fct>             <int>
1 Current_daily        58
2 Current_not_daily    19
3 Former              124
4 Never               216
5 <NA>                 15
```

- OK. Some missing values to deal with. What else might we do here?
- Shortly, we'll **collapse** this from 4 to 3 levels (how?)

Checking the Categorical Data (smoker)

```
day2 %>% count(smoker)
```

```
# A tibble: 5 x 2
  smoker                n
* <fct>             <int>
1 Current_daily        58
2 Current_not_daily    19
3 Former              124
4 Never               216
5 <NA>                 15
```

- OK. Some missing values to deal with. What else might we do here?
- Shortly, we'll **collapse** this from 4 to 3 levels (how?)
- I think we'll go with Current, Former and Never

Checking the Categorical Data (dm_status)

```
day2 %>% count(dm_status)
```

```
# A tibble: 5 x 2
  dm_status              n
* <fct>              <int>
1 Diabetes              67
2 No-Diabetes          351
3 Pre-Diabetes           9
4 Pregnancy-Induced      4
5 <NA>                   1
```

- Next Steps?

Checking the Categorical Data (dm_status)

```
day2 %>% count(dm_status)
```

```
# A tibble: 5 x 2
  dm_status              n
* <fct>              <int>
1 Diabetes              67
2 No-Diabetes          351
3 Pre-Diabetes           9
4 Pregnancy-Induced      4
5 <NA>                   1
```

- Next Steps?
- Shortly, we'll collapse this to two levels (how might we do that?) and then we'll deal with the missing information.

Re-ordering and collapsing in day2

```
day2 <- day2 %>%
    mutate(activity =
                fct_relevel(activity, "Highly_Active",
                            "Active", "Insufficiently_Active",
                            "Inactive")) %>%
    mutate(smoker =
                fct_collapse(smoker,
                     Current = c("Current_not_daily",
                                 "Current_daily"))) %>%
    mutate(dm_status =
                fct_collapse(dm_status,
                             No = c("No-Diabetes",
                                    "Pre-Diabetes",
                                    "Pregnancy-Induced"),
                             Yes = "Diabetes"))
```

Sanity Checks

```
day2 %>% tabyl(activity) %>% adorn_pct_formatting()
```

activity	n	percent	valid_percent
Highly_Active	114	26.4%	29.6%
Active	60	13.9%	15.6%
Insufficiently_Active	87	20.1%	22.6%
Inactive	124	28.7%	32.2%
<NA>	47	10.9%	-

- Still need to deal with the missing values, but now the order makes sense.

Sanity Checks

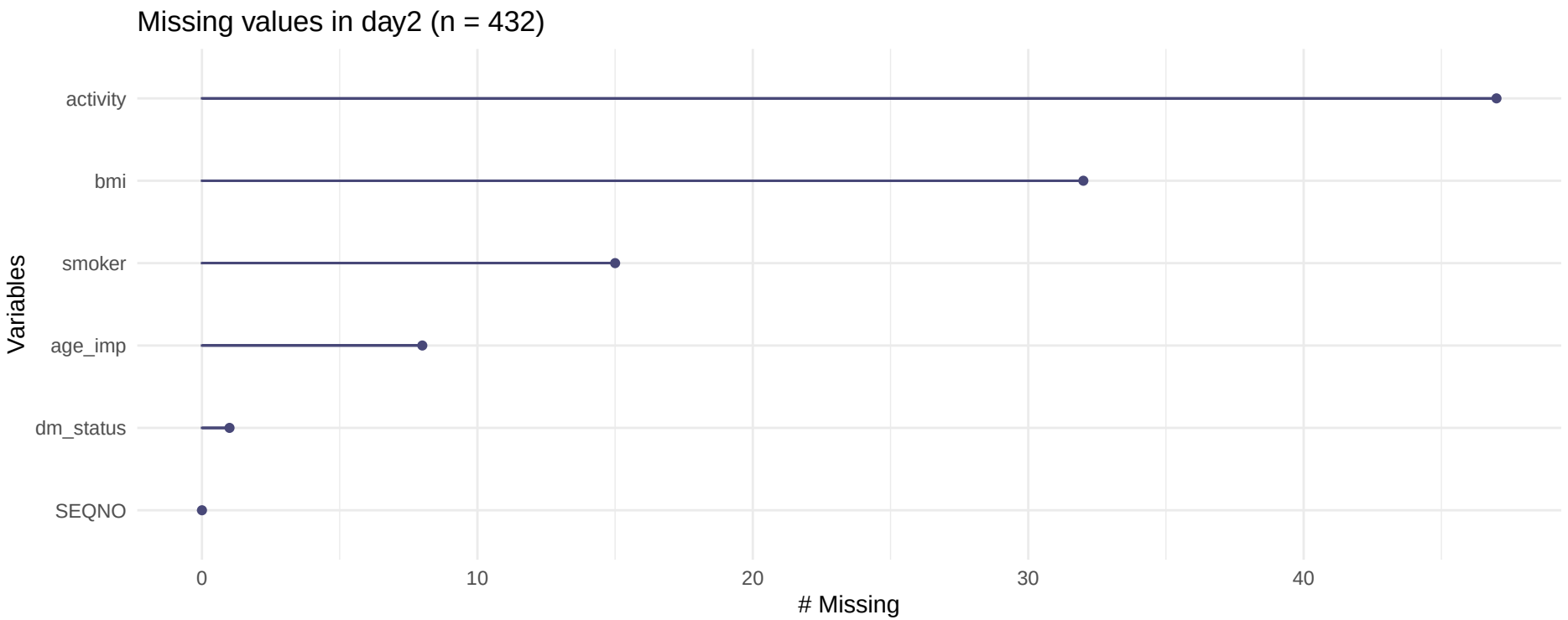
```
day2 %>% tabyl(dm_status, smoker)
```

dm_status	Current	Former	Never	NA_
Yes	10	23	33	1
No	67	100	183	14
<NA>	0	1	0	0

- OK, now we have two `dm_status` levels and three `smoker` levels, although we don't have a lot of currently smoking people with diabetes.
- Once we deal with the missing values, we should be all set.

How many missing values in each variable?

```
gg_miss_var(day2) +
    labs(title = "Missing values in day2 (n = 432)")
```



- Get a count of missing values by variable with `miss_var_summary(day2)`, also from the `naniar` package.

How many missing values per row (subject)?

```
miss_case_table(day2)  ## from naniar package
```

```
# A tibble: 5 x 3
  n_miss_in_case n_cases pct_cases
*          <int>   <int>     <dbl>
1              0     362    83.8
2              1      48    11.1
3              2      14     3.24
4              3       5     1.16
5              4       3     0.694
```

- How many observations would we lose in a complete case analysis?
- Can we make the necessary assumption for a complete case analysis?

What do we lose in a complete case analysis?

```
day2_cc <- day2 %>%
    filter(complete.cases(.))

dim(day2_cc)
```

```
[1] 362   6
```

This seems clean in some ways (and is the default approach in software), but actually it hides a very important assumption, that the data are **missing completely at random**.

```
prop_miss_case(day2); prop_miss_case(day2_cc)
```

```
[1] 0.162037
```

```
[1] 0
```

Missing Data Mechanisms (Notes, Chapter 3)

- Missing Completely at Random (MCAR)
  - The probability of missing data is the same for every subject, so that throwing out cases with missing data does not bias inferences.
- Missing at Random (MAR)
  - Here, the probability that a variable is missing depends only on available information in your data (the other variables we have). If this is so, then **imputation** is the most appropriate option.
- Missing Not at Random (MNAR)
  - Whether data are missing is dependent on either unobserved predictors, or on the actual true (but unavailable) value of the observation itself or both. Even imputation cannot solve the problem.

What should we assume in our `day2` scenario?

Formulating a single imputation plan

```
miss_var_summary(day2) %>% kable()
```

variable	n_miss	pct_miss
activity	47	10.8796296
bmi	32	7.4074074
smoker	15	3.4722222
age_imp	8	1.8518519
dm_status	1	0.2314815
SEQNO	0	0.0000000

Today, use a *naive* approach to generating a single imputation.

- Impute `dm_status` with a random draw from its distribution.
- Use CART to impute `smoker` and `activity` from `dm_status`.
- Impute quantities with robust linear models on factors.

Single imputation in day2 to yield day2_im

```
set.seed(432021)
day2_im <- day2 %>%
    data.frame() %>%
    impute_rhd(., dm_status ~ 1) %>%
    impute_cart(., smoker + activity ~ dm_status) %>%
    impute_rlm(., age_imp + bmi ~
                   dm_status + smoker + activity) %>%
    tibble()
```

- impute_rhd (random hot deck) for dm_status
- impute_cart (classification and regression trees) for other factors
- impute_rlm (robust linear model) for age_imp and bmi

```
prop_miss_case(day2_im)
```

```
[1] 0
```

Draw the outcome?

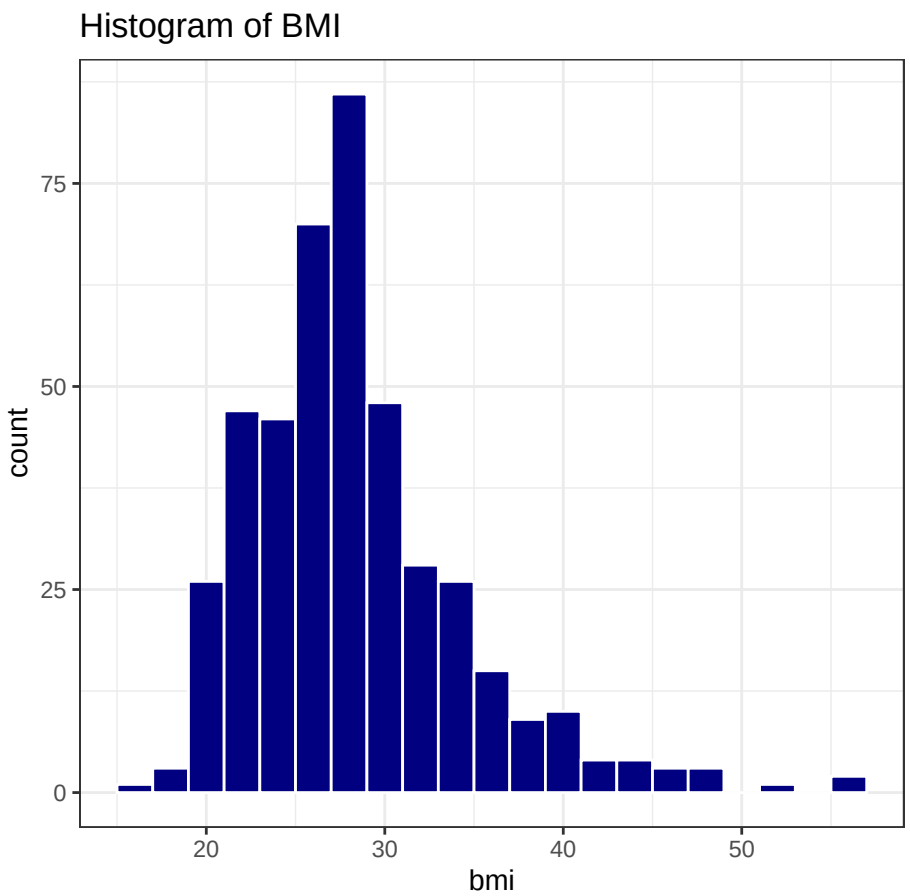
- We're interested in diabetes and smoking's association with BMI
  - What do the BMI data look like? (plots shown on next slide)

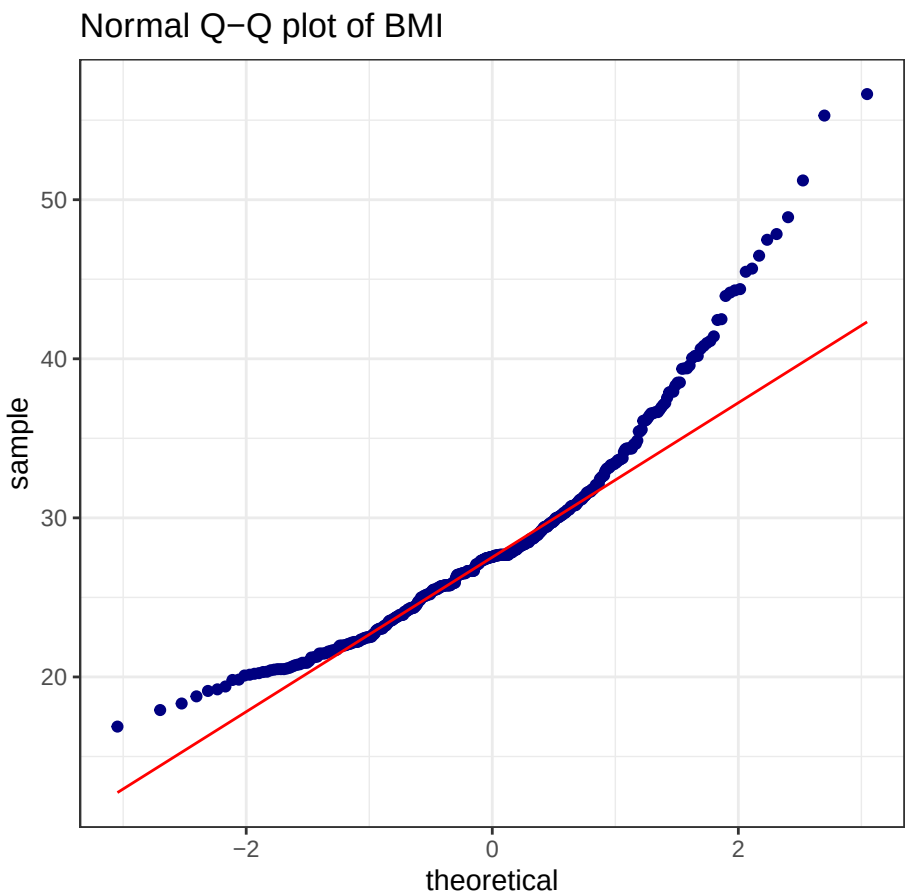
```
p1 <- ggplot(day2_im, aes(x = bmi)) +
    geom_histogram(fill = "navy", col = "white",
                   binwidth = 2) +
    labs(title = "Histogram of BMI")

p2 <- ggplot(day2_im, aes(sample = bmi)) +
    geom_qq(col = "navy") + geom_qq_line(col = "red") +
    labs(title = "Normal Q-Q plot of BMI")

p1 + p2
```

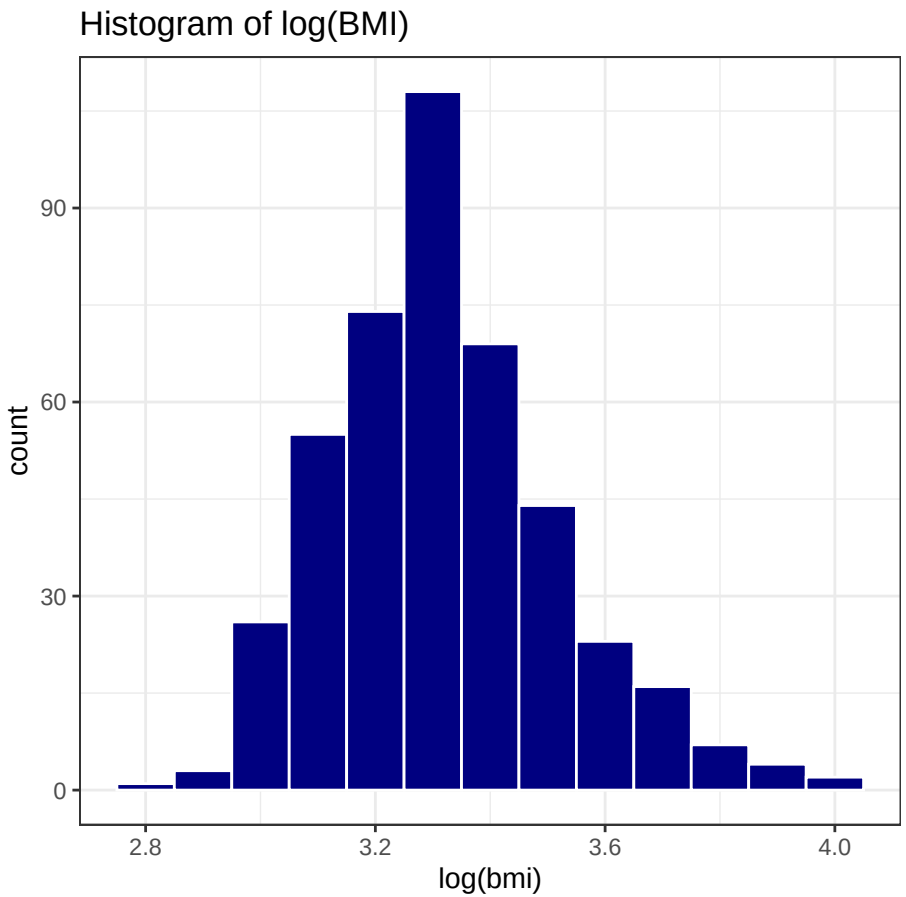
BMI data in `day2_im`

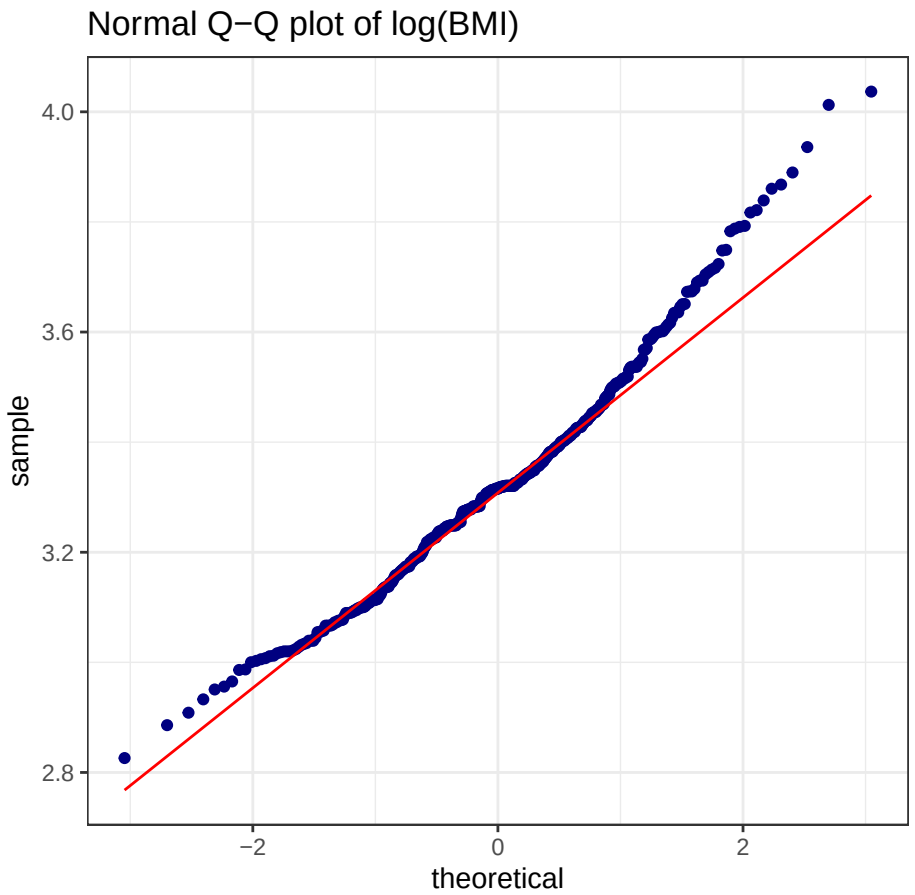




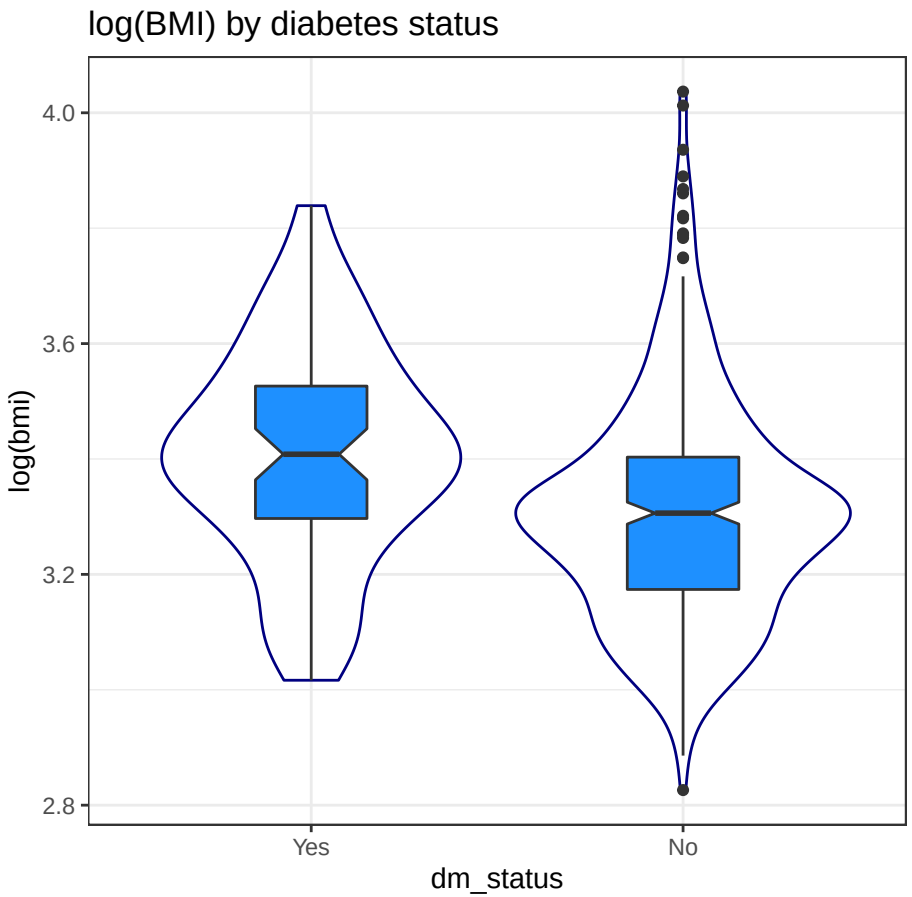
- These data are a little right-skewed. Transform?

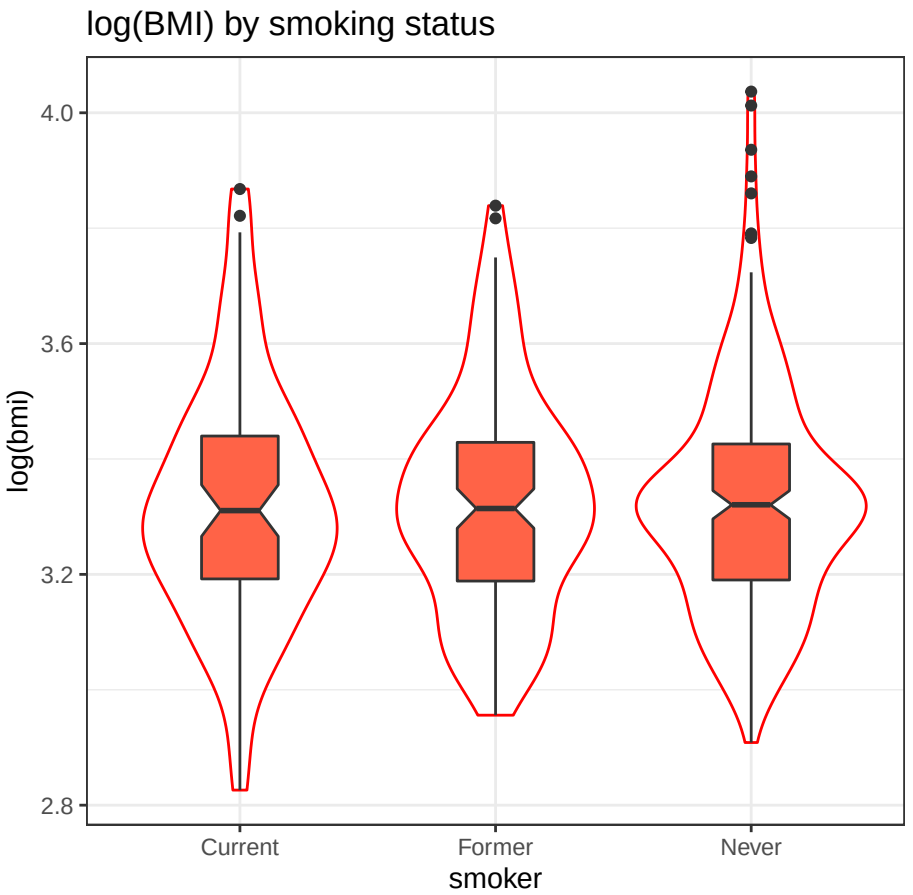
Consider a logarithmic transformation of BMI?





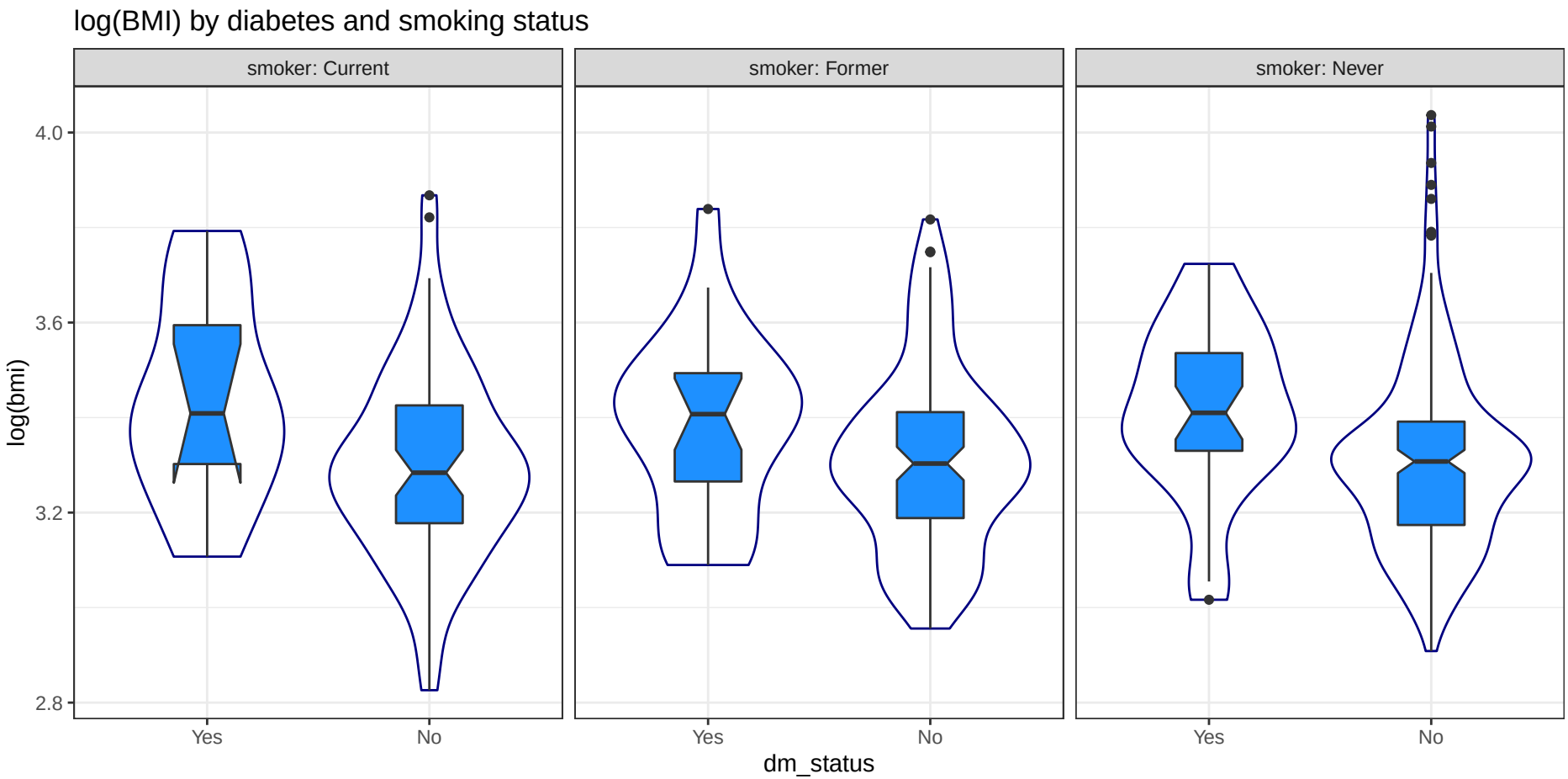
Compare log(BMI) by diabetes and by smoking





log(BMI) by diabetes and smoking together

```
notch went outside hinges. Try setting notch=FALSE.
```



Finding the Means of Each Group

We'll plot the mean of `log(bmi)` in six combinations:

- two levels of `dm_status` combined with
- three levels of `smoker`

```
summaries_1 <- day2_im %>%
    group_by(dm_status, smoker) %>%
    summarise(n = n(), mean = mean(log(bmi)),
              stdev = sd(log(bmi)))
```

```
`summarise()` has grouped output by 'dm_status'. You can overr
```

We can suppress this message with `message = FALSE` in the code chunk label.

Here are the means of log(BMI) in each group

```
summaries_1 %>% kable(digits = 2)
```

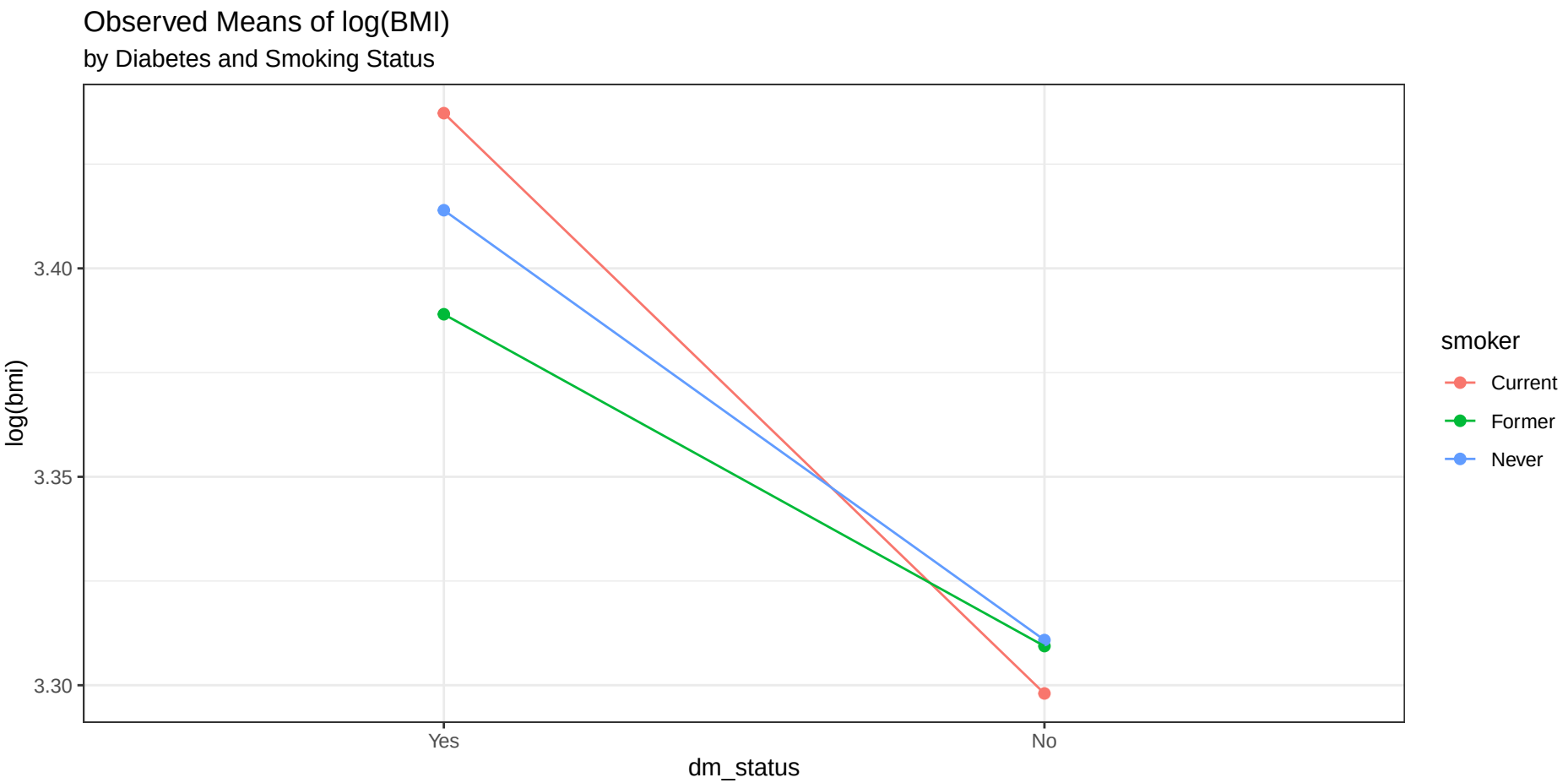
dm_status	smoker	n	mean	stdev
Yes	Current	10	3.44	0.22
Yes	Former	23	3.39	0.19
Yes	Never	34	3.41	0.18
No	Current	67	3.30	0.20
No	Former	101	3.31	0.19
No	Never	197	3.31	0.20

- Can we plot this information?

Plotting the Means (code)

```
ggplot(summaries_1, aes(x = dm_status, y = mean,
                        col = smoker)) +
    geom_point(size = 2) +
    geom_line(aes(group = smoker)) +
    labs(y = "log(bmi)",
         title = "Observed Means of log(BMI)",
         subtitle = "by Diabetes and Smoking Status")
```

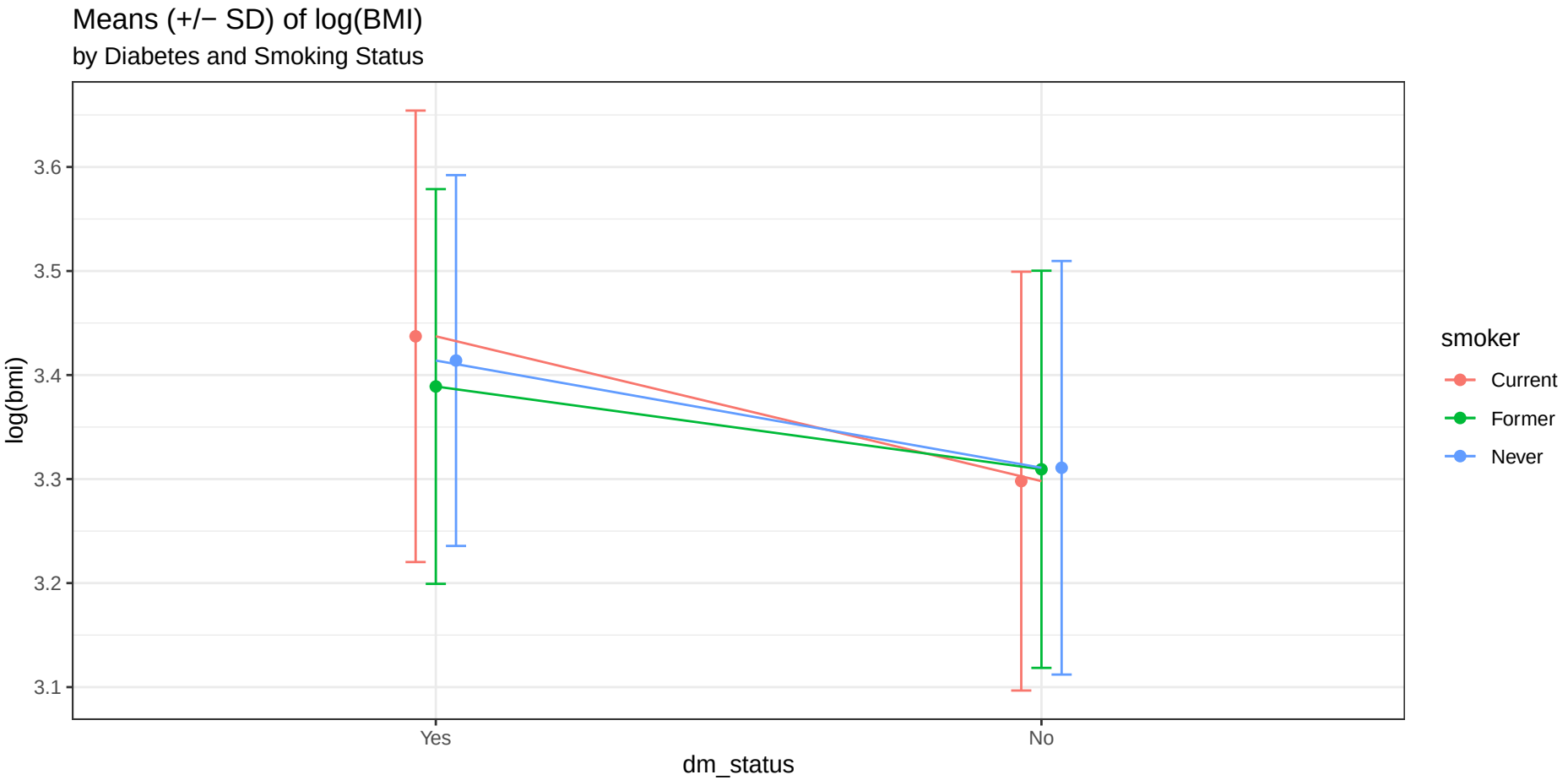
Plotting the Means (results)



Adding in standard deviations (code)

```
pd <- position_dodge(0.1)
ggplot(summaries_1, aes(x = dm_status, y = mean,
                        col = smoker)) +
    geom_errorbar(aes(ymin = mean - stdev,
                      ymax = mean + stdev),
                      width = 0.1, position = pd) +
    geom_point(size = 2, position = pd) +
    geom_line(aes(group = smoker)) +
    labs(y = "log(bmi)",
         title = "Means (+/- SD) of log(BMI)",
         subtitle = "by Diabetes and Smoking Status")
```

Adding in standard deviations (code)



Review: One-Factor Analysis of Variance

```
m1 <- lm(log(bmi) ~ dm_status, data = day2_im)

anova(m1)
```

```
Analysis of Variance Table

Response: log(bmi)
            Df  Sum Sq Mean Sq F value    Pr(>F)
dm_status    1  0.5748 0.57482  15.113 0.0001172 ***
Residuals  430 16.3546 0.03803
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tidied `m1` output

```
tidy(m1, conf.int = TRUE, conf.level = 0.90) %>%
    select(term, estimate,
           low90 = conf.low, high90 = conf.high,
           se = std.error, t = statistic, p = p.value) %>%
    kable(digits = c(0,2,2,2,2,2,5))
```

term	estimate	low90	high90	se	t	p
(Intercept)	3.41	3.37	3.45	0.02	143.07	0.00000
dm_statusNo	-0.10	-0.14	-0.06	0.03	-3.89	0.00012

Revising the order?

```
day2_im <- day2_im %>%
    mutate(dm_status = fct_relevel(dm_status, "No", "Yes"))

m1 <- lm(log(bmi) ~ dm_status, data = day2_im)

tidy(m1, conf.int = TRUE, conf.level = 0.90) %>%
    select(term, estimate,
           low90 = conf.low, high90 = conf.high,
           se = std.error, t = statistic, p = p.value) %>%
    kable(digits = c(0,2,2,2,2,2,5))
```

term	estimate	low90	high90	se	t	p
(Intercept)	3.31	3.29	3.32	0.01	324.07	0.00000
dm_statusYes	0.10	0.06	0.14	0.03	3.89	0.00012

Glancing at m1

```
glance(m1) %>%
    select(r.squared, adj.r.squared, sigma, AIC, BIC) %>%
    kable(digits = c(3, 3, 2, 1, 1))
```

r.squared	adj.r.squared	sigma	AIC	BIC
0.034	0.032	0.2	-182.4	-170.2

Developing a Two-Factor Model

We want to describe the mean of log(BMI) as a function of **both**

- the two-level factor `dm_status`, and
- the three-level factor `smoker`

One decision is whether we'll consider an **interaction** term between these two factors.

- A model with the interaction will fit the data a bit better, by some measures.
- A model with the interaction is most appropriate if we believe the `dm_status` relationship with log(BMI) changes depending on the level of `smoker`.
  - or at least if we are unwilling to assume the `smoker` effect is the same regardless of `dm_status`

What is an interaction term (a product term)?

When we build our two-way model with interaction, we'll include a product term

```
m2 <- lm(log(bmi) ~ dm_status*smoker, data = day2_im)
```

as compared to a model without interaction, which we'd fit with:

```
m2_no <- lm(log(bmi) ~ dm_status + smoker, data = day2_im)
```

Our main tool in thinking about these will be a means plot.

Two-Way ANOVA with Interaction

```
m2 <- lm(log(bmi) ~ dm_status*smoker, data = day2_im)

anova(m2)
```

```
Analysis of Variance Table

Response: log(bmi)
                   Df  Sum Sq Mean Sq F value    Pr(>F)
dm_status           1  0.5748 0.57482 14.9970 0.0001246 ***
smoker              2  0.0051 0.00253  0.0659 0.9362544
dm_status:smoker    2  0.0214 0.01070  0.2791 0.7566000
Residuals         426 16.3282 0.03833
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tidied m2 coefficients

```
tidy(m2, conf.int = TRUE, conf.level = 0.90) %>%
    select(term, estimate,
           low90 = conf.low, high90 = conf.high,
           se = std.error, p = p.value) %>%
    kable(digits = c(0,3,2,2,2,3))
```

term	estimate	low90	high90	se	p
(Intercept)	3.298	3.26	3.34	0.02	0.000
dm_statusYes	0.139	0.03	0.25	0.07	0.037
smokerFormer	0.011	-0.04	0.06	0.03	0.713
smokerNever	0.013	-0.03	0.06	0.03	0.644
dm_statusYes:smokerFormer	-0.060	-0.19	0.07	0.08	0.459
dm_statusYes:smokerNever	-0.036	-0.16	0.09	0.08	0.634

Interpreting `m2` (the interaction model)

`m2` estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?

Interpreting `m2` (the interaction model)

`m2` estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
- log(BMI) = 3.298, so estimated BMI = exp(3.298) = 27.06

Interpreting `m2` (the interaction model)

`m2` estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
- log(BMI) = 3.298, so estimated BMI = exp(3.298) = 27.06
- Estimated mean for a never smoker with no diabetes diagnosis?

Interpreting `m2` (the interaction model)

`m2` estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
- log(BMI) = 3.298, so estimated BMI = exp(3.298) = 27.06
- Estimated mean for a never smoker with no diabetes diagnosis?
- log(BMI) = 3.298 + 0.013 = 3.311, so BMI = exp(3.311) = 27.41

Interpreting m2 (the interaction model)

m2 estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
- log(BMI) = 3.298, so estimated BMI = exp(3.298) = 27.06
- Estimated mean for a never smoker with no diabetes diagnosis?
- log(BMI) = 3.298 + 0.013 = 3.311, so BMI = exp(3.311) = 27.41
- Estimated mean for a never smoker with a diabetes diagnosis?

Interpreting m2 (the interaction model)

m2 estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.298 + 0.139 (dm_status = Yes)
         + 0.011 (smoker = Former) + 0.013 (smoker = Never)
         - 0.060 (dm = Yes)(smoker = Former)
         - 0.036 (dm = Yes)(smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
- log(BMI) = 3.298, so estimated BMI = exp(3.298) = 27.06
- Estimated mean for a never smoker with no diabetes diagnosis?
- log(BMI) = 3.298 + 0.013 = 3.311, so BMI = exp(3.311) = 27.41
- Estimated mean for a never smoker with a diabetes diagnosis?
- log(BMI) = 3.298 + 0.139 + 0.013 - 0.036 = 3.414; BMI = 30.39

What if we assume there's no interaction?

```
m2_no <- lm(log(bmi) ~ dm_status + smoker, data = day2_im)

anova(m2_no)
```

```
Analysis of Variance Table

Response: log(bmi)
            Df  Sum Sq Mean Sq F value    Pr(>F)
dm_status    1  0.5748 0.57482 15.0477 0.0001213 ***
smoker       2  0.0051 0.00253  0.0661 0.9360460
Residuals  428 16.3496 0.03820
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tidied m2_no coefficients

```
tidy(m2_no, conf.int = TRUE, conf.level = 0.90) %>%
    select(term, estimate,
           low90 = conf.low, high90 = conf.high,
           se = std.error, p = p.value) %>%
    kable(digits = c(0,3,2,2,2,3))
```

term	estimate	low90	high90	se	p
(Intercept)	3.303	3.27	3.34	0.02	0.000
dm_statusYes	0.101	0.06	0.14	0.03	0.000
smokerFormer	0.002	-0.04	0.05	0.03	0.932
smokerNever	0.008	-0.03	0.05	0.03	0.751

Interpreting `m2_no` (no interaction model)

`m2` estimates derived from the indicator (1/0) variables

```
log(BMI) = 3.303 + 0.101 (dm_status = Yes)
                 + 0.002 (smoker = Former)
                 + 0.008 (smoker = Never)
```

- Estimated mean for a current smoker with no diabetes diagnosis?
  - log(BMI) = 3.303, so estimated BMI = exp(3.303) = 27.19
- Estimated mean for a never smoker with no diabetes diagnosis?
  - log(BMI) = 3.303 + 0.008 = 3.311, so BMI = exp(3.311) = 27.41
- Estimated mean for a never smoker with a diabetes diagnosis?
  - log(BMI) = 3.303 + 0.008 + 0.101 = 3.412 so BMI = 30.33

What did we see in the data?

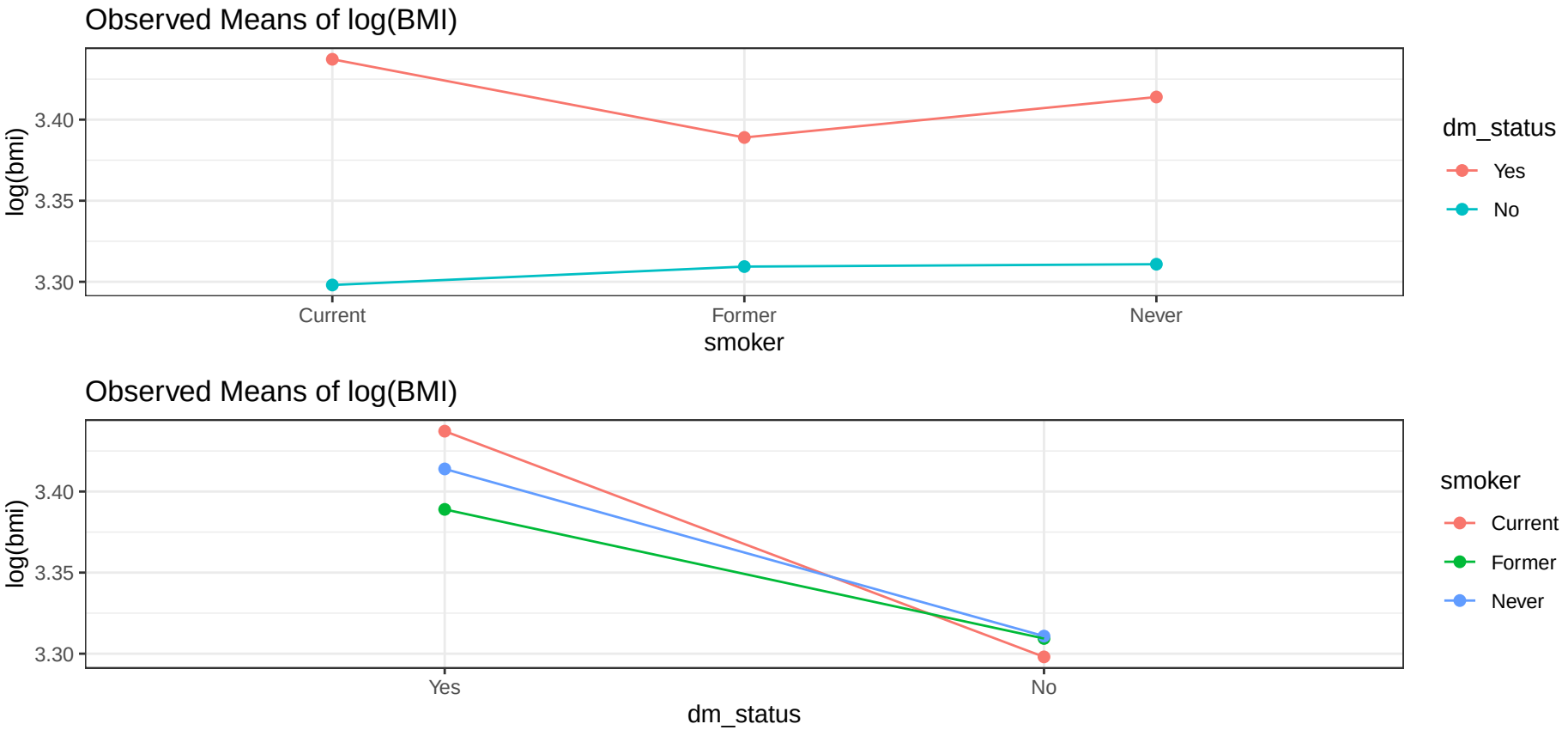
Estimates of mean(log(BMI)) from the two models, vs. the actual data.

dm_status	smoker	n	actual	m2 est.	m2_no est.
No	Current	67	3.298	3.298	3.303
No	Never	197	3.311	3.311	3.311
Yes	Never	34	3.414	3.414	3.412
No	Former	101	3.309	3.309	3.305
Yes	Current	10	3.437	3.437	3.404
Yes	Former	23	3.389	3.389	3.406

- The two-way ANOVA model with interaction simply reproduces the observed means.
- Not clear we want to assume the interaction effect is actually zero.

Interaction Plot shows non-parallel lines?

Two versions of the Means Plot



How about % of variation explained measures?

```
tidy(anova(m2)) %>% select(term, df, sumsq) %>%
    kable(dig = c(0, 0, 4))
```

term	df	sumsq
dm_status	1	0.5748
smoker	2	0.0051
dm_status:smoker	2	0.0214
Residuals	426	16.3282

- R^2 associated with the interaction term?
  - SS(interaction) is 0.0214
  - SS(m2) = 0.5748 + 0.0051 + 0.0214 = 0.6013
  - Interaction accounts for 3.6% of the variation explained by m2
  - Interaction accounts for 0.0214 / (0.6013 + 16.3282) = 0.0013, or about 0.13% of the variation in log(BMI)

Comparison of Fit across the models?

```
comp_table <- bind_rows( glance(m2), glance(m2_no) ) %>%
    mutate(mod = c("m2", "m2_no"))

comp_table %>%
    select(mod, r.squared, adj.r.squared, sigma, AIC, BIC) %>%
    kable(dig = c(0, 3, 3, 3, 1, 1))
```

mod	r.squared	adj.r.squared	sigma	AIC	BIC
m2	0.036	0.024	0.196	-175.1	-146.6
m2_no	0.034	0.027	0.195	-178.5	-158.2

- Is there much to choose from in comparing the in-sample performance?

How else can we assess the fit of these models?

We're not keen on making model decisions based on significance tests. Model selection doesn't actually work well, in practice.

```
anova(m2, m2_no)
```

```
Analysis of Variance Table

Model 1: log(bmi) ~ dm_status * smoker
Model 2: log(bmi) ~ dm_status + smoker
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1    426 16.328
2    428 16.350 -2 -0.021396 0.2791 0.7566
```

- We'd rather think about how the two models reflect the data we have *and* predict on new data.

OK, what if we add age as a covariate?

ANCOVA model `m3` takes our model `m2` (with interaction) and adds in `age_imp` (centered by subtracting off its mean) as a predictor.

```
day2_im <- day2_im %>%
    mutate(age_c = scale(age_imp,
                         center = T, scale = F))

day2_im %>% select(age_imp, age_c) %>% summary()
```

```
    age_imp          age_c.V1       
 Min.   :18.00   Min.   :-38.94239  
 1st Qu.:44.00   1st Qu.:-12.94239  
 Median :59.00   Median :  2.05761  
 Mean   :56.94   Mean   :  0.00000  
 3rd Qu.:70.00   3rd Qu.: 13.05761  
 Max.   :96.00   Max.   : 39.05761  
```

OK, what if we add age as a covariate?

Here's an analysis of **covariance** model `m3` with a factor-factor interaction, plus a centered quantitative covariate.

```
m3 <- lm(log(bmi) ~ dm_status * smoker + age_c,
         data = day2_im)
```

Does this change the nature of the relationship we see between `dm_status`, `smoker` and `bmi`?

Model m3 coefficients

```
tidy(m3, conf.int = TRUE, conf.level = 0.90) %>%
    select(term, estimate, low90 = conf.low,
           high90 = conf.high) %>% kable(dig = 3)
```

term	estimate	low90	high90
(Intercept)	3.288	3.249	3.328
dm_statusYes	0.148	0.039	0.257
smokerFormer	0.026	-0.025	0.077
smokerNever	0.019	-0.026	0.064
age_c	-0.001	-0.002	-0.001
dm_statusYes:smokerFormer	-0.056	-0.188	0.075
dm_statusYes:smokerNever	-0.025	-0.149	0.099

ANOVA results for m2 and m3

```
tidy(anova(m3)) %>% select(term, df, sumsq) %>% kable(dig = 3)
```

term	df	sumsq
dm_status	1	0.575
smoker	2	0.005
age_c	1	0.307
dm_status:smoker	2	0.021
Residuals	425	16.021

```
tidy(anova(m2)) %>% select(term, df, sumsq) %>% kable(dig = 3)
```

term	df	sumsq
dm_status	1	0.575
smoker	2	0.005
dm_status:smoker	2	0.021
Residuals	426	16.328

Does age_imp improve quality of fit?

```
comp_table <- bind_rows( glance(m2), glance(m3) ) %>%
    mutate(mod = c("m2", "m3"))

comp_table %>%
    select(mod, r.squared, adj.r.squared, sigma, AIC, BIC) %>%
    kable(dig = c(0, 3, 3, 3, 1, 1))
```

mod	r.squared	adj.r.squared	sigma	AIC	BIC
m2	0.036	0.024	0.196	-175.1	-146.6
m3	0.054	0.040	0.194	-181.3	-148.7

How about if we add a third factor (activity)?

```
m4 <- lm(log(bmi) ~ dm_status * smoker + age_c + activity,
         data = day2_im)
tidy(anova(m4)) %>% select(term, df, sumsq) %>%
    kable(dig = 3)
```

term	df	sumsq
dm_status	1	0.575
smoker	2	0.005
age_c	1	0.307
activity	3	0.269
dm_status:smoker	2	0.036
Residuals	422	15.737

Does activity improve quality of fit?

```
comp_table <- bind_rows( glance(m1), glance(m2), glance(m3),
                         glance(m4)) %>%
    mutate(mod = c("m1", "m2", "m3", "m4"))

comp_table %>%
    select(mod, r.squared, adj.r.squared, sigma, AIC, BIC) %>%
    kable(dig = c(0, 3, 3, 3, 1, 1))
```

mod	r.squared	adj.r.squared	sigma	AIC	BIC
m1	0.034	0.032	0.195	-182.4	-170.2
m2	0.036	0.024	0.196	-175.1	-146.6
m3	0.054	0.040	0.194	-181.3	-148.7
m4	0.070	0.051	0.193	-183.0	-138.3

What's next?

- Is it feasible to look at the assumptions of these models?
- Could we consider additional interaction terms?
  - factor-factor interactions?
  - factor-covariate interactions?
- Interaction is just one type of non-linearity. Can we include other types?
- Should we think more about back-transformation in this setting?
- Could we split the sample and consider how well we'd predict in new data?
- Is `lm` the best way to fit regression models to a quantitative outcome like log(`bmi`)?

Can we build up our framework for developing regression models?