432 Class 3 Slides

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Today's Agenda

- Creating the `smart1` and `smart1_sh` data sets
  - Working with factors
  - Working with simple imputation (`naniar` tools)
  - Creating a "shadow" to track what is imputed
- A few words on PPDAC and the combination of knowledge
- What is the effect of a diabetes diagnosis on BMI?
  - One-way analysis of variance (linear model)
- Does whether you have health insurance matter?
  - Two-way analysis of variance (linear model)
  - Thinking meaningfully about interaction
- Adjusting for a covariate: poor physical health days
  - Analysis of Covariance

Setup

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

theme_set(theme_bw())

smart0 <- read_csv(here("data/smart_ohio.csv"))
```

BRFSS and SMART (Creating `smart1`)

```
smart1 <- smart0 %>%
    mutate(SEQNO = as.character(SEQNO)) %>%
    select(SEQNO, mmsa, mmsa_wt, landline,
           age_imp, healthplan, dm_status,
           fruit_day, drinks_wk, activity,
           smoker, physhealth, bmi, genhealth)
```

`smart1` 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 (4 levels, *we'll collapse to 2*)
`activity`	Categorical	physical activity level (4 levels, *we'll re-level*)
`smoker`	Categorical	smoking status (4 levels, *we'll collapse to 3*)
`genhealth`	Categorical	self-reported overall health (5 levels)

Collapsing Two Factors, Re-leveling another

```
smart1 <- smart1 %>% type.convert() %>%
    mutate(SEQNO = as.character(SEQNO)) %>%
    mutate(dm_status =
           fct_collapse(factor(dm_status),
                        Yes = "Diabetes",
                        No = c("No-Diabetes",
                               "Pre-Diabetes",
                               "Pregnancy-Induced"))) %>%
    mutate(smoker =
           fct_collapse(factor(smoker),
                        Current = c("Current_not_daily",
                                    "Current_daily"))) %>%
    mutate(activity =
             fct_relevel(factor(activity),
                         "Highly_Active", "Active",
                         "Insufficiently_Active",
                         "Inactive"))
```

The `naniar` and `visdat` packages

add functions to:

- display missing data, in many useful ways, often with `ggplot` approaches that you can modify as desired
- replace existing values with NA
- visualize imputed values
- numerically summarize imputed values
- model missingness

See Getting Started with `naniar` vignette linked at our Class 3 README.

How many missing values in `smart1`?

```
miss_var_table(smart1)
```

```
# A tibble: 11 x 3
   n_miss_in_var n_vars pct_vars
           <int>  <int>    <dbl>
 1             0      4    28.6
 2            14      1     7.14
 3            15      1     7.14
 4            20      1     7.14
 5            68      1     7.14
 6           138      1     7.14
 7           242      1     7.14
 8           392      1     7.14
 9           493      1     7.14
10           557      1     7.14
11           723      1     7.14
```

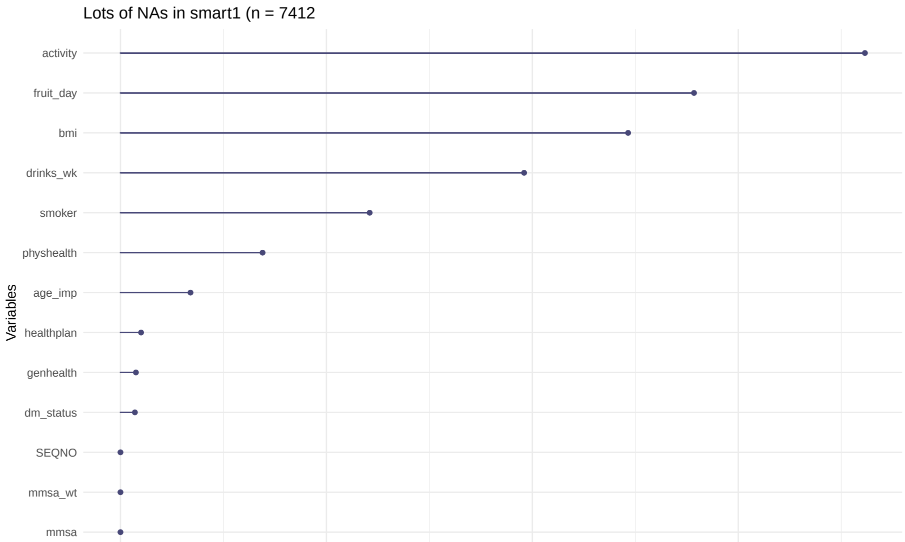
How many missing values in `smart1`?

```
miss_var_summary(smart1)
```

```
# A tibble: 14 x 3
   variable   n_miss pct_miss
   <chr>       <int>    <dbl>
 1 activity      723    9.75
 2 fruit_day     557    7.51
 3 bmi           493    6.65
 4 drinks_wk     392    5.29
 5 smoker        242    3.26
 6 physhealth    138    1.86
 7 age_imp        68    0.917
 8 healthplan     20    0.270
 9 genhealth      15    0.202
10 dm_status      14    0.189
11 SEQNO           0    0
12 mmsa            0    0
13 mmsa_wt         0    0
```

Visualizing Missingness in Variables

```r
gg_miss_var(smart1) +
  labs(title = "Lots of NAs in smart1 (n = 7412")
```



prop_miss_case and pct_miss_case

```
prop_miss_case(smart1)
```

```
[1] 0.1891527
```

```
smart1 %>% select(genhealth) %>% pct_miss_case(.)
```

```
[1] 0.2023745
```

Obtain the proportion or percentage of missing values in the data frame, or any piece of it.

prop_miss_var or pct_miss_var

```r
prop_miss_var(smart1)
```

```
[1] 0.7142857
```

```r
pct_miss_var(smart1)
```

```
[1] 71.42857
```

This is the proportion (or percentage) of variables in the data frame with missing values.

miss_case_table

```
miss_case_table(smart1)
```

```
# A tibble: 7 x 3
  n_miss_in_case n_cases pct_cases
           <int>   <int>     <dbl>
1              0    6010    81.1
2              1     830    11.2
3              2     223     3.01
4              3     119     1.61
5              4     133     1.79
6              5      85     1.15
7              6      12     0.162
```

miss_case_summary

```
miss_case_summary(smart1)
```

```
# A tibble: 7,412 x 3
    case n_miss pct_miss
   <int>  <int>    <dbl>
 1   336      6     42.9
 2   786      6     42.9
 3  1102      6     42.9
 4  1389      6     42.9
 5  2788      6     42.9
 6  3094      6     42.9
 7  3373      6     42.9
 8  5524      6     42.9
 9  5733      6     42.9
10  6422      6     42.9
# ... with 7,402 more rows
```

Creating a "Shadow" to track what is imputed

```
smart1_sh <- smart1 %>% bind_shadow()
```

`smart1_sh` creates new variables, ending in `_NA`

```r
names(smart1_sh)
```

```
 [1] "SEQNO"          "mmsa"           "mmsa_wt"
 [4] "landline"       "age_imp"        "healthplan"
 [7] "dm_status"      "fruit_day"      "drinks_wk"
[10] "activity"       "smoker"         "physhealth"
[13] "bmi"            "genhealth"      "SEQNO_NA"
[16] "mmsa_NA"        "mmsa_wt_NA"     "landline_NA"
[19] "age_imp_NA"     "healthplan_NA" "dm_status_NA"
[22] "fruit_day_NA"   "drinks_wk_NA"   "activity_NA"
[25] "smoker_NA"      "physhealth_NA" "bmi_NA"
[28] "genhealth_NA"
```

What are the new variables tracking?

```
smart1_sh %>% count(smoker, smoker_NA)
```

```
Warning: Factor `smoker` contains implicit NA, consider
using `forcats::fct_explicit_na`
```

```
# A tibble: 4 x 3
  smoker  smoker_NA     n
  <fct>   <fct>     <int>
1 Current !NA        1290
2 Former  !NA        1999
3 Never   !NA        3881
4 <NA>    NA          242
```

The `fct_explicit_na` warning: A pain point

My general preference is to not use `fct_explicit_na` in general, and I typically suppress this warning from printing by labeling the code chunk with `{r, warning = FALSE}`

What do new variables track? (with `warning = FALSE`)

```
smart1_sh %>% count(genhealth, genhealth_NA)
```

```
# A tibble: 6 x 3
  genhealth   genhealth_NA     n
  <fct>       <fct>        <int>
1 1_Excellent !NA           1057
2 2_VeryGood  !NA           2406
3 3_Good      !NA           2367
4 4_Fair      !NA           1139
5 5_Poor      !NA            428
6 <NA>        NA              15
```

“Simple” Imputation of Missing Factor Values

Let’s impute some of the factors by random draws from their distributions. . .

```
set.seed(2020432)
smart1_sh <- smart1_sh %>%
    data.frame() %>%
      impute_rhd(.,
                 dm_status + smoker + activity ~ 1) %>%
  tbl_df()
```

Did this work? (Code Chunk has `warning = FALSE`)

```
smart1 %>% count(dm_status)
```

```
# A tibble: 3 x 2
  dm_status     n
  <fct>     <int>
1 Yes        1098
2 No         6300
3 <NA>         14
```

```
smart1_sh %>% count(dm_status)
```

```
# A tibble: 2 x 2
  dm_status     n
  <fct>     <int>
1 Yes        1102
2 No         6310
```

What happens if you impute a 1/0 variable this way?

```
set.seed(2020432)
smart1_sh <- smart1_sh %>%
    data.frame() %>%
      impute_rhd(.,
                 healthplan ~ 1) %>%
  tbl_df()
```

Look at whether this worked...

```
smart1 %>% tabyl(healthplan)
```

```
 healthplan    n     percent valid_percent
          0  398 0.053696708    0.05384199
          1 6994 0.943604965    0.94615801
         NA   20 0.002698327            NA
```

```
smart1_sh %>% tabyl(healthplan)
```

```
 healthplan    n    percent
          0  399 0.05383162
          1 7013 0.94616838
```

Looks OK

```
smart1_sh %$% n_distinct(healthplan)
```

```
[1] 2
```

Another Sanity Check

```
smart1 %>%
  select(healthplan, dm_status, smoker, activity) %>%
  summarize_each(list(n_miss))
```

```
# A tibble: 1 x 4
  healthplan dm_status smoker activity
       <int>     <int>  <int>    <int>
1         20        14    242      723
```

```
smart1_sh %>%
  select(healthplan, dm_status, smoker, activity) %>%
  summarize_each(list(n_miss))
```

```
# A tibble: 1 x 4
  healthplan dm_status smoker activity
       <int>     <int>  <int>    <int>
1          0         0      0        0
```

"Simple" Imputation with Robust Linear Models

```
set.seed(2020432)
smart1_sh <- smart1_sh %>%
    data.frame() %>%
      impute_rlm(.,
                 age_imp + fruit_day +
                   drinks_wk + bmi ~
                   mmsa + landline + healthplan) %>%
    tbl_df()
```

“Simple” Imputation with Other Methods

```
set.seed(2020432)
smart1_sh <- smart1_sh %>%
    data.frame() %>%
      impute_knn(., physhealth ~ bmi) %>%
      impute_cart(.,
                  genhealth ~ activity +
                    physhealth +
                    mmsa + healthplan) %>%
    tbl_df()
```

Sanity Check 2

Before imputation. . .

```
pct_miss_var(smart1)
```

```
[1] 71.42857
```

After imputation . . .

```
pct_miss_var(smart1_sh)
```

```
[1] 0
```

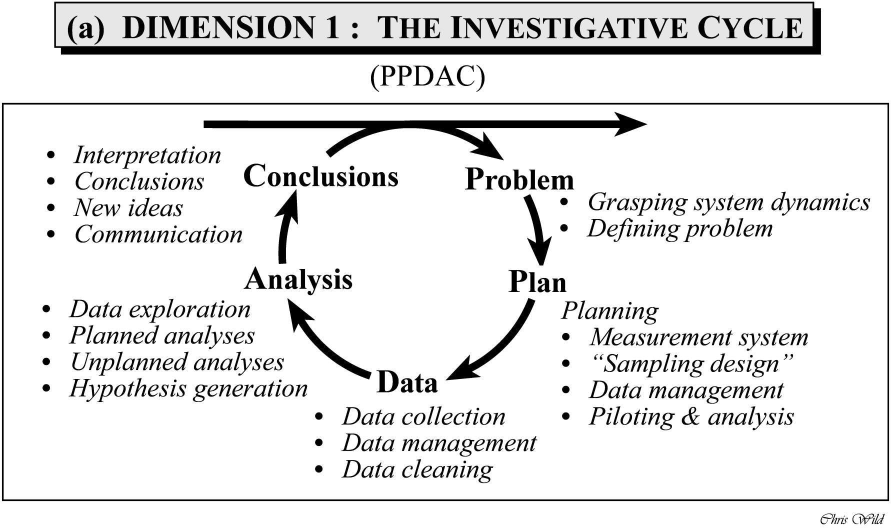
Resulting smart1 and smart1_sh tibbles saved to .Rds

```
saveRDS(smart1, "data/smart1.Rds")
saveRDS(smart1_sh, "data/smart1_sh.Rds")
```

The Art of Statistics: How to Learn From Data

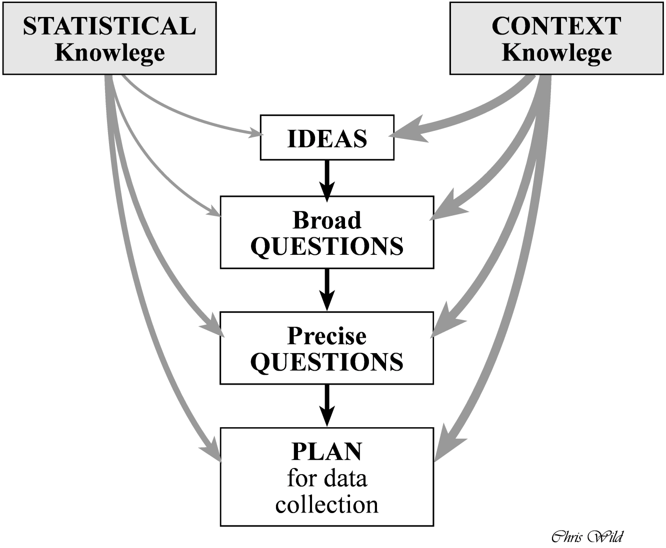
Introduction: Why We Need Statistics / Turning the World into Data

- Turning experiences into data is not straightforward, and data is inevitably limited in its capacity to describe the world.
- Statistical science has a long and successful history, but is now changing in the light of increased availability of data.
- The PPDAC cycle provides a convenient framework...
  - Problem - Plan - Data - Analysis - Conclusion and communication.



- Chris Wild, https://www.stat.auckland.ac.nz/~wild/StatThink/

From inkling to plan



Using the Analysis of Variance (ANOVA) and the Analysis of Covariance (ANCOVA) to model Categorical Predictors in Linear Models

Answering Questions

1. What is the effect of having a diagnosis of diabetes on body mass index (BMI)?
2. Does whether you have health insurance affect how we think about the BMI-diabetes association?
3. Does adjusting for physical health (as measured by the number of poor physical health days in the past 30) affect our Question 2 assessment?

Answering Questions

1. What is the effect of having a diagnosis of diabetes on body mass index?

```
smart1_sh %$% mosaic::favstats(bmi ~ dm_status)
```

```
Registered S3 method overwritten by 'mosaic':
  method                           from
  fortify.SpatialPolygonsDataFrame ggplot2

  dm_status   min       Q1 median      Q3   max     mean
1       Yes 16.07 27.37061 30.295 35.7875 70.56 31.98108
2        No 13.30 24.11000 27.320 30.6100 75.52 28.01261
        sd    n missing
1 7.301795 1102       0
2 6.033544 6310       0
```

How can we repair this?

- `r, message = FALSE` in chunk name
- show only a single decimal place?

Answering Questions

1. What is the effect of having a diagnosis of diabetes on body mass index?

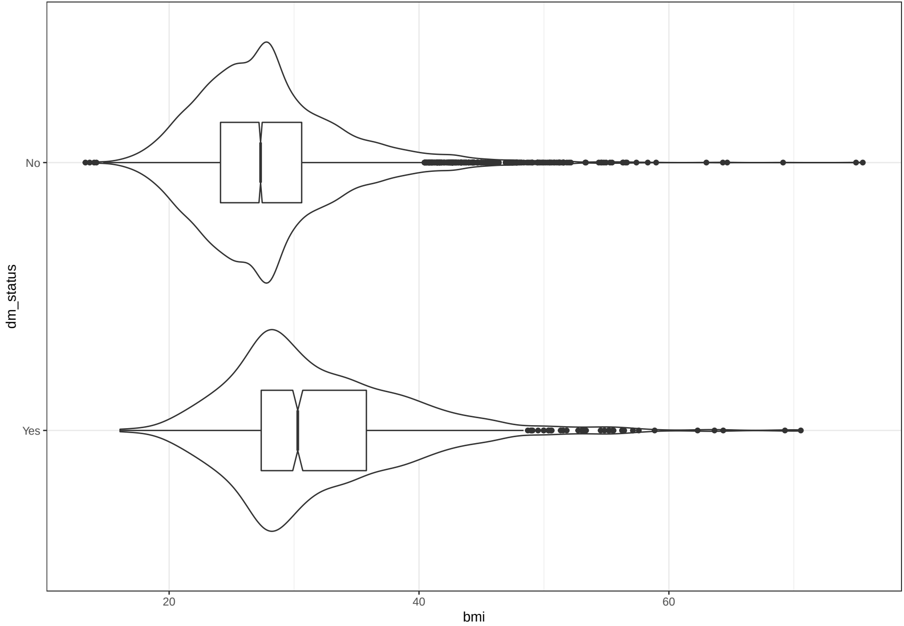
```
smart1_sh %$% mosaic::favstats(bmi ~ dm_status) %>%
  rename(dm = dm_status) %>%
  knitr::kable(digits = 1)
```

dm	min	Q1	median	Q3	max	mean	sd	n	missing
Yes	16.1	27.4	30.3	35.8	70.6	32	7.3	1102	0
No	13.3	24.1	27.3	30.6	75.5	28	6.0	6310	0

Plot the data!

```
ggplot(smart1_sh, aes(x = dm_status, y = bmi)) +
  geom_violin() + geom_boxplot(width = 0.3, notch = TRUE) +
  coord_flip()
```

Visualizing the Data in Boxplots (with Violins)



Analysis of Variance

1. What is the effect of having a diagnosis of diabetes on body mass index?

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

```
Analysis of Variance Table

Response: bmi
            Df Sum Sq Mean Sq F value    Pr(>F)
dm_status    1  14775 14774.8  379.65 < 2.2e-16 ***
Residuals 7410 288372    38.9
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Estimate effect of `dm_status` on `bmi`...

```
tidy(a1, 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)	31.981	0.188	31.672	32.290
dm_statusNo	-3.968	0.204	-4.304	-3.633

Is this easy to interpret?

Re-level the dm_status variable...

```
smart1_sh <- smart1_sh %>%
  mutate(dm_status = fct_relevel(dm_status, "No", "Yes"))

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

anova(a1)
```

```
Analysis of Variance Table

Response: bmi
            Df Sum Sq Mean Sq F value    Pr(>F)
dm_status    1  14775 14774.8  379.65 < 2.2e-16 ***
Residuals 7410 288372    38.9
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Estimate effect of re-leveled dm_status on bmi...

```
tidy(a1, 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)	28.013	0.079	27.883	28.142
dm_statusYes	3.968	0.204	3.633	4.304

Answering Questions

2. Does whether you have health insurance affect this association?

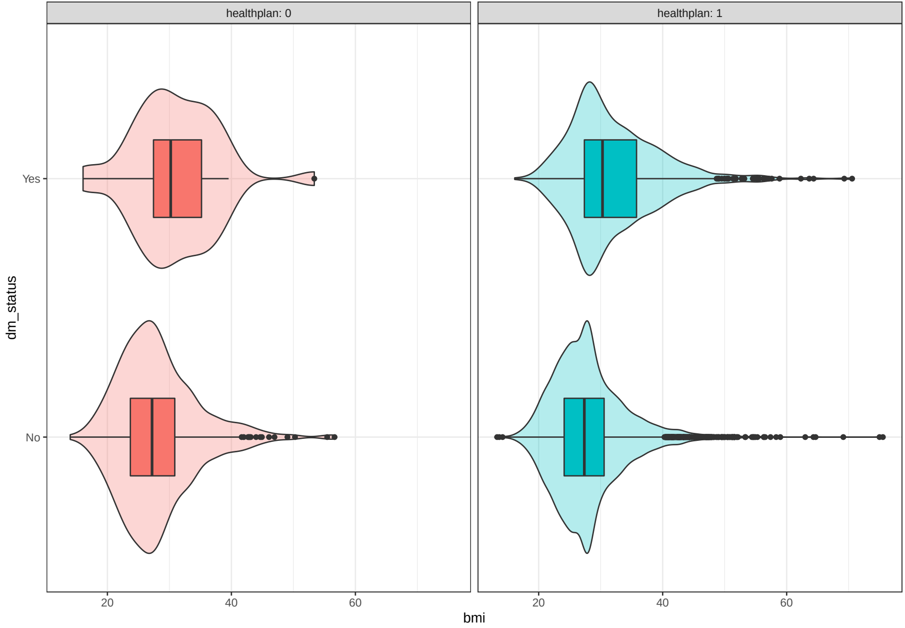
```
smart1_sh %$%
  mosaic::favstats(bmi ~ dm_status + healthplan) %>%
  rename(dm_hp = dm_status.healthplan) %>%
  knitr::kable(digits = 1)
```

dm_hp	min	Q1	median	Q3	max	mean	sd	n	missing
No.0	14.0	23.7	27.2	30.9	56.6	28	6.4	364	0
Yes.0	16.1	27.4	30.2	35.2	53.4	31	6.9	35	0
No.1	13.3	24.1	27.4	30.6	75.5	28	6.0	5946	0
Yes.1	16.1	27.4	30.3	35.8	70.6	32	7.3	1067	0

Visualize Three Variables (Code)

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

Visualize Three Variables



Direct Approach: An 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

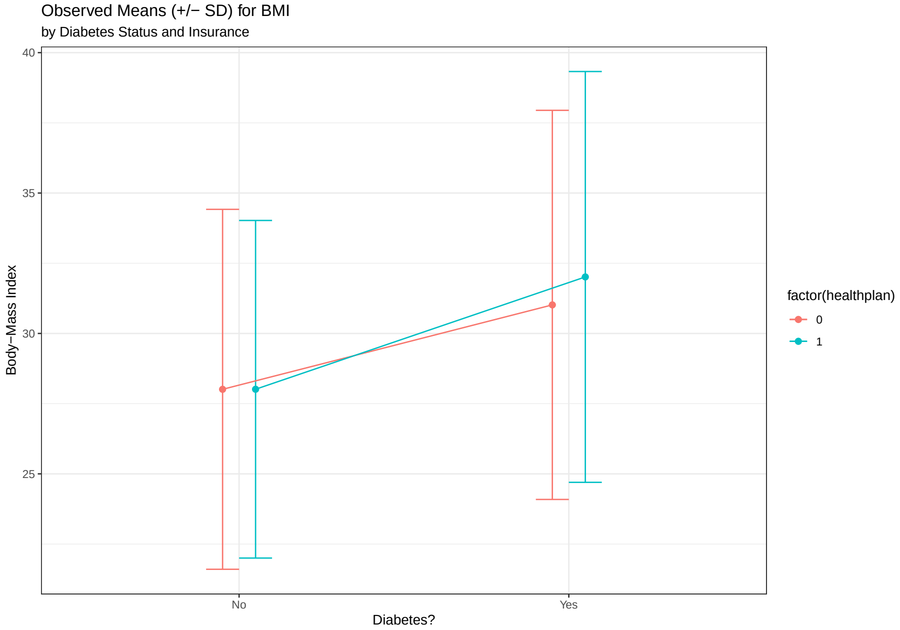
```
summaries1 <- smart1_sh %>%
  group_by(dm_status, healthplan) %>%
  summarize(n = n(), mean = mean(bmi), stdev = sd(bmi))

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

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

Interaction Plot for Two-Way ANOVA (code)

```
pd <- position_dodge(0.2)
ggplot(summaries1, aes(x = dm_status, y = mean,
                       col = factor(healthplan))) +
  geom_errorbar(aes(ymin = mean - stdev,
                    ymax = mean + stdev),
                width = 0.2, 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



Two-Way (Two Factor) Analysis of Variance

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

anova(a2) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dm_status	1	14774.816	14774.816	379.595	0.000
healthplan	1	3.148	3.148	0.081	0.776
dm_status:healthplan	1	30.444	30.444	0.782	0.377
Residuals	7408	288338.239	38.923	NA	NA

Why am I using * rather than + to connect `dm_status` and `healthplan`?

Two-Way (Two Factor) Analysis of Variance

Model without an interaction term:

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

anova(a2_noint) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dm_status	1	14774.816	14774.816	379.606	0.000
healthplan	1	3.148	3.148	0.081	0.776
Residuals	7409	288368.683	38.921	NA	NA

Model including an interaction term:

```
a2_switch <- smart1_sh %$% lm(bmi ~ healthplan * dm_status)

anova(a2_switch) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
healthplan	1	45.436	45.436	1.167	0.280
dm_status	1	14732.528	14732.528	378.509	0.000
healthplan:dm_status	1	30.444	30.444	0.782	0.377
Residuals	7408	288338.239	38.923	NA	NA

I switched the order of the two factors here. Does order matter?

Model a2 tidied coefficients

```
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)	28.011	0.327	27.473	28.549
dm_statusYes	3.006	1.104	1.190	4.823
healthplan	0.002	0.337	-0.552	0.556
dm_statusYes:healthplan	0.994	1.123	-0.855	2.842

Model `a2_switch` coefficients

```r
tidy(a2_switch, 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)	28.011	0.327	27.473	28.549
healthplan	0.002	0.337	-0.552	0.556
dm_statusYes	3.006	1.104	1.190	4.823
healthplan:dm_statusYes	0.994	1.123	-0.855	2.842

We can use this model to make predictions for each of four types of people:

- Those with diabetes, but not a health plan
- Those with diabetes and a health plan
- Those without diabetes, but who have a health plan
- Those without diabetes, and also without a health plan

The Resulting Equations

The model with the interaction term is

```
BMI = 28.011 + 3.006 (dm_status = Yes)
             + 0.002 (healthplan = 1)
             + 0.994 (dm_status = Yes)(healthplan = 1)
```

dm_status	healthplan	Predicted BMI
Yes	1 (Yes)	$28.011 + 3.006 + 0.002 + 0.994 = 32.013$
Yes	0 (No)	$28.011 + 3.006 = 31.017$
No	1 (Yes)	$28.011 + 0.002 = 28.013$
No	0 (No)	28.011

These are the original means (except for rounding error) of the four groups.

Interpreting the Model with Interaction

```
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)	28.011	0.327	27.473	28.549
dm_statusYes	3.006	1.104	1.190	4.823
healthplan	0.002	0.337	-0.552	0.556
dm_statusYes:healthplan	0.994	1.123	-0.855	2.842

- Our interpretation here would involve specifying that the interaction between `dm_status` and `healthplan` is important, and focusing on what that means, perhaps by specifying what happens to the four types of people we could see (Yes/Yes, Yes/No, No/Yes and No/No) in terms of our two factors.
- Do we need the interaction term here, or could we simplify the model?

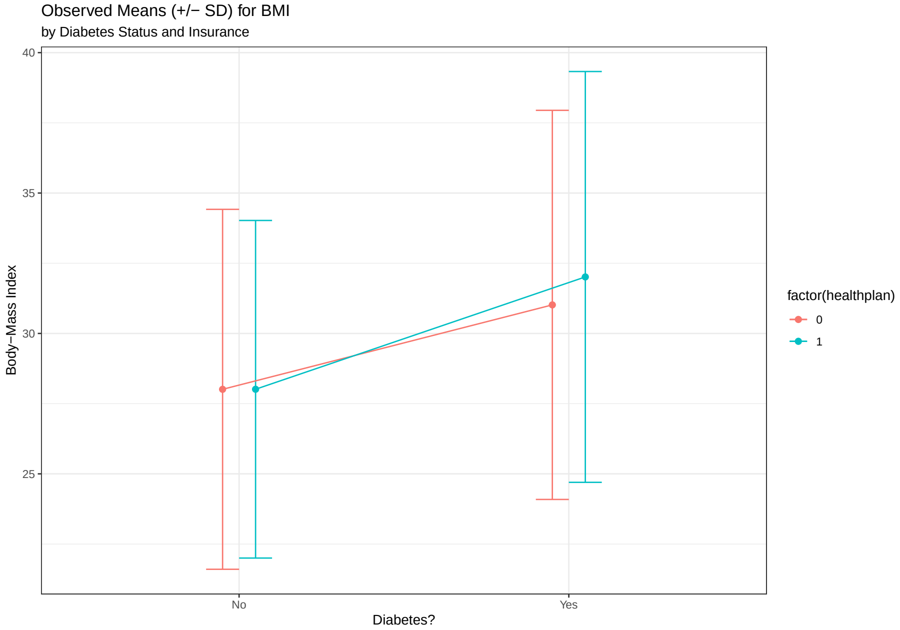
Is the interaction term important here?

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 (Substantial Non-Parallelism?)



Evaluation in our Two-Way ANOVA of Interaction

1. Does the interaction plot display important non-parallelism?
   - 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) $= 288338 + 30 + 3 + 14775 = 3.03146 \times 10^5$
- 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?
   - I've repeated it on the next slide.
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)	28.011	0.327	27.473	28.549
dm_statusYes	3.006	1.104	1.190	4.823
healthplan	0.002	0.337	-0.552	0.556
dm_statusYes:healthplan	0.994	1.123	-0.855	2.842

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)	27.926	0.313	27.412	28.441
dm_statusYes	3.966	0.204	3.631	4.301
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)	27.72	0.31	27.21	28.24
physhealth	0.06	0.01	0.05	0.07
dm_statusYes	3.67	0.21	3.33	4.01
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)	27.72	0.31	27.21	28.24
physhealth	0.06	0.01	0.05	0.07
dm_statusYes	3.67	0.21	3.33	4.01
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)

What's next?

1. Building a two-factor ANOVA model with multi-categorical factors
    - again, focus on interpreting the interaction
    - add covariates, as desired
2. Building similar models for a binary outcome using linear probability models and then generalized linear models (specifically logistic regression).