432 Class 06 Slides

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2021-02-18

Today's Agenda

- Predicting a Binary outcome
    - using a linear probability model
    - using logistic regression and `glm`

Setup

```
library(here); library(magrittr)
library(janitor); library(knitr)
library(patchwork); library(broom)
library(simputation); library(naniar)
library(rsample); library(yardstick)
library(tidyverse)

theme_set(theme_bw())
```

Regression on a Binary Outcome

Linear Probability Model (a linear model)

```
lm(event ~ predictor1 + predictor2 + ..., data = tibblename)
```

- Pr(event) is linear in the predictors

Logistic Regression Model (generalized linear model)

```
glm(event ~ pred1 + pred2 + ..., data = tibblename,
            family = binomial(link = "logit"))
```

- Logistic Regression forces a prediction in (0, 1)
- log(odds(event)) is linear in the predictors

The logistic regression model

$$logit(event) = log \left(\frac{Pr(event)}{1 - Pr(event)} \right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + ... + \beta_k X_k$$

$$odds(event) = \frac{Pr(event)}{1 - Pr(event)}$$

$$Pr(event) = \frac{odds(event)}{odds(event) + 1}$$

$$Pr(event) = \frac{exp(logit(event))}{1 + exp(logit(event))}$$

BRFSS and SMART (Creating smart3)

```
smart3 <- read_csv(here("data/smart_ohio.csv")) %>%
    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)
```

`smart3` 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

```
smart3 <- smart3 %>% 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"))
```

"Simple" Imputation Strategy, with Shadow

```
smart3_sh <- smart3 %>% bind_shadow()

set.seed(2021432)
smart3_sh <- smart3_sh %>%
    data.frame() %>%
        impute_rhd(dm_status + smoker ~ 1) %>%
        impute_rhd(healthplan + activity ~ 1) %>%
        impute_rlm(age_imp + fruit_day + drinks_wk + bmi ~
                       mmsa + landline + healthplan) %>%
        impute_knn(physhealth ~ bmi) %>%
        impute_cart(genhealth ~ activity + physhealth +
                        mmsa + healthplan) %>%
    tibble()
```

Saving the `smart3` and `smart3_sh` tibbles to `.Rds`

```
saveRDS(smart3, "data/smart3.Rds")
saveRDS(smart3_sh, "data/smart3_sh.Rds")
```

Create binary outcome variable

```
smart3_sh <- readRDS("data/smart3_sh.Rds") %>%
  mutate(bmilt30 = as.numeric(bmi < 30),
         dm_status = fct_relevel(dm_status, "No"))

smart3_sh %>%
  group_by(bmilt30) %>%
  summarize(n = n(), mean(bmi), min(bmi), max(bmi)) %>%
  kable(digits = 2)
```

bmilt30	n	mean(bmi)	min(bmi)	max(bmi)
0	2343	35.84	30.0	75.52
1	5069	25.26	13.3	29.99

Predicting BMI < 30 using diabetes status (a factor)

```
mod_DM <- smart3_sh %$%
  glm(bmilt30 ~ dm_status,
      family = binomial(link = logit))

tidy(mod_DM) %>% select(term, estimate) %>%
  kable(digits = 3)
```

term	estimate
(Intercept)	0.947
dm_statusYes	-1.053

Equation: `logit(BMI < 30) = 0.947 - 1.053 (dm_statusYes)`

How can we interpret this result?

Interpreting the `mod_DM` Equation

```
logit(BMI < 30) = 0.947 - 1.053 (dm_status = Yes)
```

- Harry has diabetes.
    - His predicted `logit(BMI < 30)` is 0.947 - 1.053 (1) = -0.106
- Sally does not have diabetes.
    - Her predicted `logit(BMI < 30)` is 0.947 - 1.053 (0) = 0.947

Now, `logit(BMI < 30)` = `log(odds(BMI < 30))`, so exponentiate to get the odds…

- Harry has predicted `odds(BMI < 30)` = exp(-0.106) = 0.899
- Sally has predicted `odds(BMI < 30)` = exp(0.947) = 2.578

Can we convert these odds into something more intuitive?

Converting Odds to Probabilities

- Harry has predicted `odds(BMI < 30)` = exp(-0.106) = 0.899
- Sally has predicted `odds(BMI < 30)` = exp(0.947) = 2.578

$$odds(BMI < 30) = \frac{Pr(BMI < 30)}{1 - Pr(BMI < 30)}$$

and

$$Pr(BMI < 30) = \frac{odds(BMI < 30)}{odds(BMI < 30) + 1}$$

- So Harry's predicted `Pr(BMI < 30)` = 0.899 / 1.899 = 0.47
- Sally's predicted `Pr(BMI < 30)` = 2.578 / 3.578 = 0.72
- odds range from 0 to ∞, and log(odds) range from $-\infty$ to ∞.
- odds > 1 if probability > 0.5. If odds $= 1$, then probability $= 0.5$.

What about the odds ratio?

```
logit(BMI < 30) = 0.947 - 1.053 (dm_status = Yes)
```

- Harry, with diabetes, has odds(BMI $<$ 30) $=$ 0.899
- Sally, without diabetes, has odds(BMI $<$ 30) $=$ 2.578

Odds Ratio for BMI $<$ 30 associated with having diabetes (vs. not) $=$

$$\frac{0.899}{2.578} = 0.349$$

- Our model estimates that a subject with diabetes has 34.9% of the odds of a subject without diabetes of having BMI $<$ 30.

Can we calculate the odds ratio from the equation's coefficients?

- Yes, `exp(-1.053)` $=$ 0.349.

Tidy with exponentiation

```
tidy(mod_DM, exponentiate = TRUE,
     conf.int = TRUE, conf.level = 0.9) %>%
  select(term, estimate, conf.low, conf.high) %>%
  kable(digits = 3)
```

term	estimate	conf.low	conf.high
(Intercept)	2.578	2.462	2.700
dm_statusYes	0.349	0.313	0.389

- The odds ratio for BMI $<$ 30 among subjects with diabetes as compared to those without diabetes is 0.349
- The odds of BMI $<$ 30 are 34.9% as large for subjects with diabetes as they are for subjects without diabetes, according to this model.
- A 90% uncertainty interval for the odds ratio estimate includes (0.313, 0.389).

Interpreting these summaries

Connecting the Odds Ratio and Log Odds Ratio to probability statements...

- If the probabilities were the same (for diabetes and non-diabetes subjects) of having BMI < 30, then the odds would also be the same, and so the odds ratio would be 1.
- If the probabilities of BMI < 30 were the same and thus the odds were the same, then the log odds ratio would be `log(1)` $= 0$.

```
logit(BMI < 30) = 0.947 - 1.053 (dm_status = Yes)
```

1. If the log odds of a coefficient (like `diabetes = Yes`) are negative, then what does that imply?

2. What if we flipped the order of the levels for diabetes so our model was about `diabetes = No`?

Flipping the model changes slope and intercept!

```
mod_DM_no <- smart3_sh %$%
  glm(bmilt30 ~ (dm_status == "No"),
      family = binomial(link = logit))

tidy(mod_DM_no) %>% select(term, estimate) %>%
  kable(digits = 3)
```

term	estimate
(Intercept)	-0.106
dm_status == "No"TRUE	1.053

Old: `logit(BMI < 30) = 0.947 - 1.053 (dm_status = Yes)` New: `logit(BMI < 30) = -0.106 + 1.053 (dm_status = No)`

Predictions from the two models?

DMYes: `logit(BMI < 30) = 0.947 - 1.053 (dm_status = Yes)`
DMNo: `logit(BMI < 30) = -0.106 + 1.053 (dm_status = No)`

Harry lives with diabetes. Sally does not.

Using the DMYes model:

- logit(Harry's BMI $<$ 30) $=$ 0.947 - 1.053 $=$ -0.106
- logit(Sally's BMI $<$ 30) $=$ 0.947

Using the DMNo model:

- logit(Harry's BMI $<$ 30) $=$ -0.106
- logit(Sally's BMI $<$ 30) $=$ -0.106 $+$ 1.053 $=$ 0.947

Two Predictor Model

We'll fit the model with and without an interaction term...

```
mod_FDmain <- glm(bmilt30 ~ fruit_day + dm_status,
              data = smart3_sh, family = binomial)
mod_FDint <- glm(bmilt30 ~ fruit_day * dm_status,
               data = smart3_sh, family = binomial)
```

1. How will we interpret the model coefficients?
2. Can we compare the models based on in-sample performance?
3. (later) How can we assess predictive quality (with a holdout sample)?

Coefficients in the Model without Interaction

```
tidy(mod_FDint, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  kable(dig = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.762	0.045	0.673	0.851
fruit_day	0.142	0.028	0.087	0.198
dm_statusYes	-1.053	0.104	-1.258	-0.850
fruit_day:dm_statusYes	0.001	0.062	-0.119	0.125

ID	fruit	dm	logit($BMI < 30$)	odds($BMI < 30$)	Pr($BMI < 30$)
Art	1	Yes	-0.147	0.863	0.463
Bob	0	Yes	-0.289	0.749	0.428
Cal	1	No	0.904	2.469	0.712
Don	0	No	0.762	2.143	0.682

Exponentiating `fruit_day` coefficient to get OR

```
tidy(mod_FDmain, exponentiate = TRUE) %>%
  select(term, estimate) %>% kable(dig = 2)
```

term	estimate
(Intercept)	2.14
fruit_day	1.15
dm_statusYes	0.35

ID	fruit	dm	logit(BMI $<$ 30)	odds(BMI $<$ 30)	Pr(BMI $<$ 30)
Art	1	Yes	-0.147	0.863	0.463
Bob	0	Yes	-0.289	0.749	0.428

- Art's odds $= 0.863$. Bob's odds $= 0.749$
- Art/Bob odds ratio $= 0.863/0.749 = 1.15$

Exponentiating `dm_status` coefficient to get OR

```
tidy(mod_FDmain, exponentiate = TRUE) %>%
  select(term, estimate) %>% kable(dig = 2)
```

term	estimate
(Intercept)	2.14
fruit_day	1.15
dm_statusYes	0.35

ID	fruit	dm	logit(BMI $<$ 30)	odds(BMI $<$ 30)	Pr(BMI $<$ 30)
Bob	0	Yes	-0.289	0.749	0.428
Don	0	No	0.762	2.143	0.682

- Bob's odds $= 0.749$, Don's odds (2.143)
- Bob/Don odds ratio $= 0.749/2.143 = 0.35$

Same result when `fruit_day` = 1?

```
tidy(mod_FDmain, exponentiate = TRUE) %>%
  select(term, estimate) %>% kable(dig = 2)
```

term	estimate
(Intercept)	2.14
fruit_day	1.15
dm_statusYes	0.35

ID	fruit	dm	logit(BMI $<$ 30)	odds(BMI $<$ 30)	Pr(BMI $<$ 30)
Art	1	Yes	-0.147	0.863	0.463
Cal	1	No	0.904	2.469	0.712

- Art's odds = 0.863, Cal's odds (2.469)
- Art/Cal odds ratio = 0.863/2.469 = 0.35 as well.

Coefficients in the Model WITH Interaction

```
tidy(mod_FDint, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  kable(dig = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.762	0.045	0.673	0.851
fruit_day	0.142	0.028	0.087	0.198
dm_statusYes	-1.053	0.104	-1.258	-0.850
fruit_day:dm_statusYes	0.001	0.062	-0.119	0.125

- Again, these estimates are on the logit scale
- Does the interaction look like it has a large effect?

Resulting Predictions from `mod_FDint`

ID	fruit	dm	logit(BMI $<$ 30)	odds(BMI $<$ 30)	Pr(BMI $<$ 30)
Art	1	Yes	-0.148	0.862	0.463
Bob	0	Yes	-0.291	0.748	0.428
Cal	1	No	0.904	2.469	0.712
Don	0	No	0.762	2.143	0.682

Predicted logits (also rounded to 3 decimal places) from `mod_FDmain` were:

- Art: -0.147, Bob: -0.289, Cal: 0.904, Don: 0.762

That's a small enough difference to leave the (rounded) probability estimates unchanged.

Split the Sample and Compare Models?

Let's split our sample

```
set.seed(432)

sm3_split <- initial_split(smart3_sh, prop = 0.7,
                           strata = bmilt30)

sm3_train <- training(sm3_split)
sm3_test <- testing(sm3_split)
```

- What does `strata = bmilt30` do?

Impact of using `strata = bmilt30` in split

```
sm3_train %>% tabyl(bmilt30)
```

```
 bmilt30    n  percent
       0 1641 0.316185
       1 3549 0.683815
```

```
sm3_test %>% tabyl(bmilt30)
```

```
 bmilt30    n   percent
       0  702 0.3159316
       1 1520 0.6840684
```

Now, we'll build and compare three models...

```
mod_2 <- glm(bmilt30 ~ fruit_day + dm_status,
             data = sm3_train, family = binomial)

mod_4 <- glm(bmilt30 ~ fruit_day + dm_status +
               genhealth + age_imp,
             data = sm3_train, family = binomial)

mod_6 <- glm(bmilt30 ~ fruit_day + dm_status +
               genhealth + age_imp + smoker + physhealth,
    data = sm3_train, family = binomial)
```

Tidied Coefficients for Model 2

```
tidy(mod_2, conf.int = TRUE) %>%
  select(term, est = estimate, se = std.error,
         conf.low, conf.high) %>%
  kable(dig = 3)
```

term	est	se	conf.low	conf.high
(Intercept)	0.732	0.051	0.633	0.832
fruit_day	0.164	0.030	0.105	0.224
dm_statusYes	-1.045	0.080	-1.202	-0.888

Tidied Coefficients for Model 6

term	est	se	conf.low	conf.high
(Intercept)	1.020	0.140	0.747	1.297
fruit_day	0.129	0.030	0.070	0.189
dm_statusYes	-0.903	0.086	-1.072	-0.734
genhealth2_VeryGood	-0.620	0.117	-0.853	-0.394
genhealth3_Good	-1.072	0.116	-1.303	-0.848
genhealth4_Fair	-1.217	0.129	-1.473	-0.967
genhealth5_Poor	-1.338	0.158	-1.650	-1.029
age_imp	0.010	0.002	0.007	0.014

Tidied Coefficients for Model 6

term	est	se	conf.low	conf.high
(Intercept)	1.284	0.153	0.987	1.587
fruit_day	0.138	0.031	0.079	0.200
dm_statusYes	-0.890	0.087	-1.060	-0.720
genhealth2_VeryGood	-0.628	0.117	-0.861	-0.401
genhealth3_Good	-1.077	0.117	-1.310	-0.850
genhealth4_Fair	-1.171	0.138	-1.444	-0.902
genhealth5_Poor	-1.187	0.183	-1.547	-0.829
age_imp	0.013	0.002	0.009	0.016
smokerFormer	-0.547	0.096	-0.737	-0.358
smokerNever	-0.390	0.089	-0.565	-0.217
physhealth	-0.011	0.004	-0.019	-0.003

Summary Statistics for In-Sample Fit

```
bind_rows(glance(mod_2), glance(mod_4), glance(mod_6)) %>%
  mutate(preds = c("2", "4", "6")) %>%
  select(preds, nobs, deviance, df.residual, AIC, BIC) %>%
  kable(digits = 1)
```

preds	nobs	deviance	df.residual	AIC	BIC
2	5190	6276.3	5187	6282.3	6301.9
4	5190	6109.7	5182	6125.7	6178.1
6	5190	6070.3	5179	6092.3	6164.4

Likelihood Ratio Test comparing Models 2 and 4

```
anova(mod_2, mod_4, test = "LRT")
```

```
Analysis of Deviance Table

Model 1: bmilt30 ~ fruit_day + dm_status
Model 2: bmilt30 ~ fruit_day + dm_status + genhealth + age_imp
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1      5187     6276.3
2      5182     6109.7  5   166.63 < 2.2e-16 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Could also consider

- Rao's efficient score test (`test = "Rao"`)
- Pearson's chi-square test (`test = "Chisq"`).

Likelihood Ratio Test comparing Models 4 and 6

```
anova(mod_4, mod_6, test = "LRT")
```

```
Analysis of Deviance Table

Model 1: bmilt30 ~ fruit_day + dm_status + genhealth + age_imp
Model 2: bmilt30 ~ fruit_day + dm_status + genhealth + age_imp
    physhealth
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1      5182     6109.7
2      5179     6070.3  3   39.321 1.484e-08 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mallows' Cp statistic?

```
anova(mod_2, mod_4, mod_6, test = "Cp")
```

```
Analysis of Deviance Table

Model 1: bmilt30 ~ fruit_day + dm_status
Model 2: bmilt30 ~ fruit_day + dm_status + genhealth + age_imp
Model 3: bmilt30 ~ fruit_day + dm_status + genhealth + age_imp
    physhealth
  Resid. Df Resid. Dev Df Deviance     Cp
1      5187     6276.3                6282.3
2      5182     6109.7  5  166.628 6125.7
3      5179     6070.3  3   39.321 6092.3
```

- Same as what glance provided for AIC in this case.

Build mod_2 Confusion Matrix with 0.5 cutoff

```
mod2_aug <- augment(mod_2, data = sm3_train,
                    type.predict = "response")

confuse2 <- mod2_aug %>%
  mutate(bmilt30_act = factor(bmilt30 == "1"),
         bmilt30_pre = factor(.fitted >= 0.5),
         bmilt30_act = fct_relevel(bmilt30_act, "TRUE"),
         bmilt30_pre = fct_relevel(bmilt30_pre, "TRUE")) %$%
  table(bmilt30_pre, bmilt30_act)
```

- We'll review the confusion matrix on the next slide...

Confusion Matrix for `mod_2` with 0.5 cutoff

```
confuse2
```

```
           bmilt30_act
bmilt30_pre TRUE FALSE
      TRUE  3291  1333
      FALSE  258   308
```

- Total # of Predictions = 3291 + 1333 + 258 + 308 = 5190
- 3291 + 308 = 3599 accurate predictions (69.3% accuracy)
- *Sensitivity* = 3291 / (3291 + 258) = 0.927
  - if subject actually has BMI < 30 `mod_2` with this 0.5 cutoff decision rule correctly predicts BMI < 30 92.7% of the time.
- *Specificity* = 308 / (308 + 1333) = 0.188
  - if subject actually doesn't have BMI < 30 `mod_2` with this 0.5 cutoff decision rule correctly predicts BMI >= 30 18.8% of the time.

Get confusion matrix more easily?

```
mod2_aug <- mod2_aug %>%
  mutate(obs = factor(bmilt30),
         pred = factor(ifelse(.fitted >= 0.5, 1, 0)))

conf_mat(data = mod2_aug, truth = obs, estimate = pred)
```

```
          Truth
Prediction    0    1
         0  308  258
         1 1333 3291
```

Accuracy and Kappa Results for `mod_2`

```
metrics(data = mod2_aug, truth = obs, estimate = pred)
```

```
# A tibble: 2 x 3
  .metric  .estimator .estimate
  <chr>    <chr>          <dbl>
1 accuracy binary         0.693
2 kap      binary         0.140
```

- Kappa = a correlation statistic from -1 to +1, with complete agreement +1 and complete disagreement -1.
- Kappa measures the inter-rater reliability of our predicted and true classifications.

Confusion Matrix for `mod_4` with 0.5 cutoff

```
mod4_aug <- augment(mod_4, data = sm3_train,
                    type.predict = "response") %>%
  mutate(obs = factor(bmilt30),
         pred = factor(ifelse(.fitted >= 0.5, 1, 0)))

conf_mat(data = mod4_aug, truth = obs, estimate = pred)
```

```
          Truth
Prediction    0    1
         0  309  224
         1 1332 3325
```

- 3325 + 309 = 3634 accurate predictions (70.0% accuracy)
- *Sensitivity* = 3325 / (3325 + 224) = 0.937
- *Specificity* = 309 / (309 + 1332) = 0.188

Confusion Matrix for `mod_6` with 0.5 cutoff

```
conf_mat(data = mod6_aug, truth = obs, estimate = pred)
```

```
          Truth
Prediction    0    1
         0  312  218
         1 1329 3331
```

- $3331 + 312 = 3643$ accurate predictions (70.2% accuracy)
- *Sensitivity* $= 3331 \ / \ (3331 + 218) = 0.939$
- *Specificity* $= 312 \ / \ (312 + 1329) = 0.190$

metrics for models 2, 4 and 6

```
bind_cols(
metrics(data = mod2_aug, truth = obs, estimate = pred) %>%
  select(.metric, mod2 = .estimate),
metrics(data = mod4_aug, truth = obs, estimate = pred) %>%
  select(mod4 = .estimate),
metrics(data = mod6_aug, truth = obs, estimate = pred) %>%
  select(mod6 = .estimate),
)
```

```
# A tibble: 2 x 4
  .metric   mod2  mod4  mod6
  <chr>    <dbl> <dbl> <dbl>
1 accuracy 0.693 0.700 0.702
2 kap      0.140 0.153 0.157
```

Holdout Sample?

```
mod2_aug_test <- augment(mod_2,
                         newdata = sm3_test,
                         type.predict = "response") %>%
  mutate(obs = factor(bmilt30),
         pred = factor(ifelse(.fitted >= 0.5, 1, 0)))
```

- do the same thing for models 4 and 6...

metrics for test sample: models 2, 4 and 6

```
bind_cols(
metrics(data = mod2_aug_test,
        truth = obs, estimate = pred) %>%
  select(.metric, mod2 = .estimate),
metrics(data = mod4_aug_test,
        truth = obs, estimate = pred) %>%
  select(mod4 = .estimate),
metrics(data = mod6_aug_test,
        truth = obs, estimate = pred) %>%
  select(mod6 = .estimate)
)
```

```
# A tibble: 2 x 4
  .metric    mod2  mod4  mod6
  <chr>     <dbl> <dbl> <dbl>
1 accuracy  0.686 0.694 0.694
2 kap       0.118 0.136 0.136
```

What's next?

- ROC curve analysis
- Using `lrm` and `ols` from the `rms` package to fit and evaluate logistic and linear regressions, respectively