

## 432 Week 3 Slides

[github.com/THOMASELOVE/2020-432](https://github.com/THOMASELOVE/2020-432)

2020-01-28 & 01-30

# This Week's Agenda

- ➊ Predicting a binary outcome using linear probability models.
- ➋ Predicting a binary outcome with logistic regression

# Setup

```
library(here); library(magrittr); library(janitor)
library(broom); library(simputation); library(patchwork)
library(naniar); library(visdat); library(caret)
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 <sup>2</sup> )
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)

# Today's Questions

Can we predict  $\text{Prob}(\text{BMI} < 30)$  for a subject in the `smart1_sh` data:

- using the mean number of servings of fruit per day that they consume?
- using their diabetes status?
- using their self-reported general health status?
- using some combination of these predictors?

## Let's predict the probability that BMI < 30

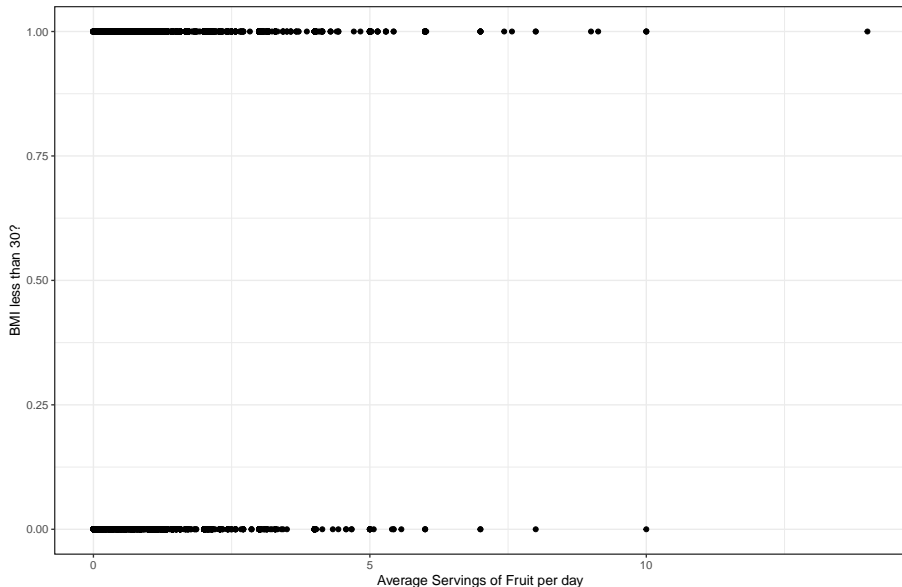
```
smart1_sh <- smart1_sh %>%  
  mutate(bmilt30 = as.numeric(bmi < 30),  
         dm_status = fct_relevel(dm_status, "No"))  
  
smart1_sh %>% tabyl(bmilt30) %>% adorn_pct_formatting()
```

bmilt30	n	percent
0	2343	31.6%
1	5069	68.4%

# Association of BMI < 30 and Fruit Consumption

Fruit Servings per day vs. Obesity Status

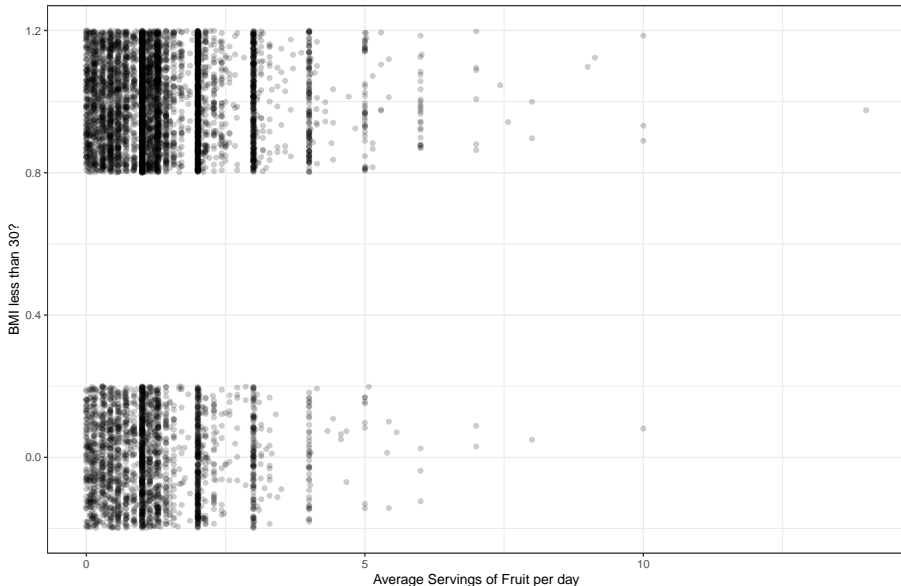
7412 subjects in SMART Ohio for 2017



# Add some vertical jitter and shading to the plot

Fruit Servings per day vs. Obesity Status

7412 subjects in SMART Ohio for 2017





# Linear Probability Model to predict BMI < 30?

```
m1 <- smart1_sh %$% lm(bmilt30 ~ fruit_day)

tidy(m1, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.645	0.009	0.628	0.662
fruit_day	0.029	0.005	0.019	0.039

## Linear Probability Model to predict BMI < 30?

```
tidy(m1, conf.int = TRUE, conf.level = 0.95) %>%  
  select(term, estimate, std.error, conf.low, conf.high) %>%  
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.645	0.009	0.628	0.662
fruit_day	0.029	0.005	0.019	0.039

- What's the predicted probability of BMI < 30 if a subject eats 5 servings of fruit per day?

$$Pr(BMI < 30) = 0.645 + 0.029(5) = 0.645 + 0.145 = 0.790$$

- What's the predicted probability of BMI < 30 if a subject eats no fruit?

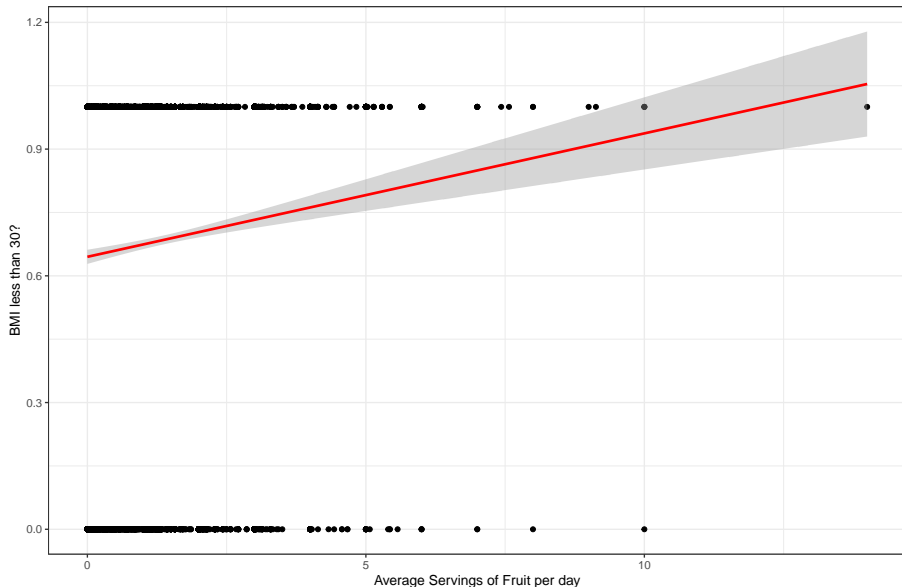
## Linear Probability Model $m_1$ in a plot (code)

```
ggplot(smart1_sh, aes(x = fruit_day, y = bmilt30)) +  
  geom_point() +  
  geom_smooth(method = "lm", col = "red") +  
  labs(title = "Predicting BMI < 30 using Fruit Servings per c",  
        subtitle = "7412 subjects in SMART Ohio for 2017",  
        y = "BMI less than 30?",  
        x = "Average Servings of Fruit per day")
```

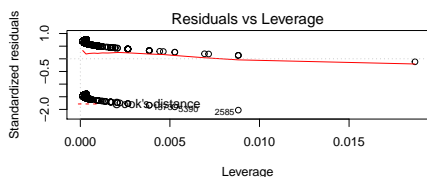
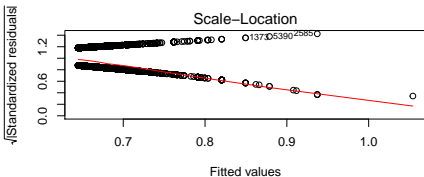
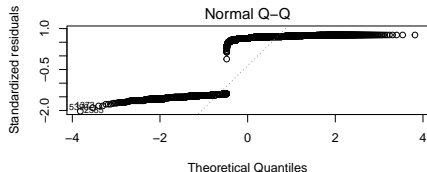
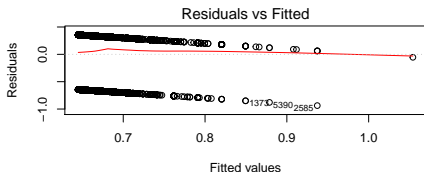
# Linear Probability Model $m_1$ predicting BMI < 30

Predicting BMI < 30 using Fruit Servings per day

7412 subjects in SMART Ohio for 2017



# Residual Plots for the Linear Probability Model (m1)



# Models to predict a Binary Outcome

Our outcome takes on two values (zero or one) and we then model the probability of a “one” response given a linear function of predictors.

Idea 1: Use a *linear probability model*

- Main problem: predicted probabilities that are less than 0 and/or greater than 1
- Also, how can we assume Normally distributed residuals when outcomes are 1 or 0?

Idea 2: Build a *non-linear* regression approach

- Most common approach: logistic regression, part of the class of *generalized* linear models

# The Logit Link and Logistic Function

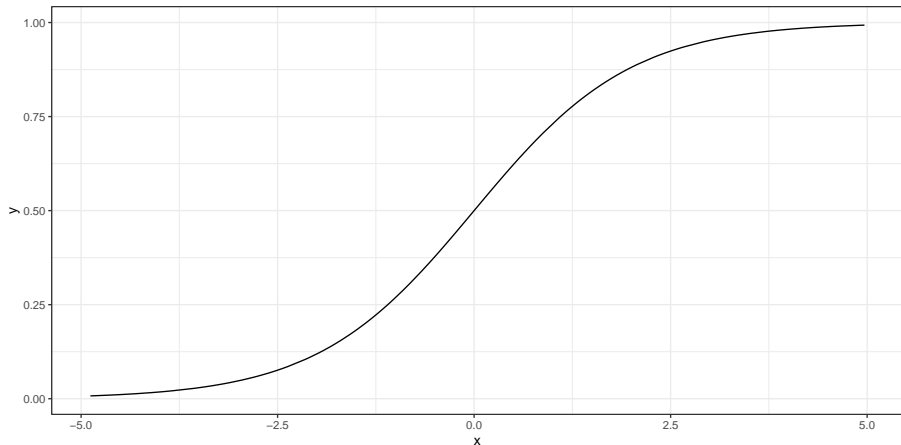
The particular link function we use in logistic regression is called the **logit link**.

$$\text{logit}(\pi) = \log\left(\frac{\pi}{1 - \pi}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_k X_k$$

The inverse of the logit function is called the **logistic function**. If  $\text{logit}(\pi) = \eta$ , then  $\pi = \frac{\exp(\eta)}{1 + \exp(\eta)}$ .

- The logistic function  $\frac{e^x}{1 + e^x}$  takes any value  $x$  in the real numbers and returns a value between 0 and 1.

# The Logistic Function $y = \frac{e^x}{1+e^x}$





# The logit or log odds

We usually focus on the **logit** in statistical work, which is the inverse of the logistic function.

- If we have a probability  $\pi < 0.5$ , then  $\text{logit}(\pi) < 0$ .
- If our probability  $\pi > 0.5$ , then  $\text{logit}(\pi) > 0$ .
- Finally, if  $\pi = 0.5$ , then  $\text{logit}(\pi) = 0$ .

## Why is this helpful?

- $\log(\text{odds}(Y = 1))$  or  $\text{logit}(Y = 1)$  covers all real numbers.
- $\text{Prob}(Y = 1)$  is restricted to  $[0, 1]$ .

## Returning to the prediction of $\text{Prob}(\text{BMI} < 30)$

We'll use the `glm` function in R, specifying a logistic regression model.

- Instead of predicting  $\text{Pr}(\text{BMI} < 30)$ , we're predicting  $\log(\text{odds}(\text{BMI} < 30))$  or  $\text{logit}(\text{BMI} < 30)$ .

```
m2 <- smart1_sh %$%  
  glm(bmilt30 ~ fruit_day, family = binomial)  
  
tidy(m2, conf.int = TRUE, conf.level = 0.95) %>%  
  select(term, estimate, std.error, conf.low, conf.high) %>%  
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.583	0.040	0.505	0.662
fruit_day	0.145	0.025	0.097	0.194

## Our model $m_2$

$$\text{logit}(\text{BMI} < 30) = \log(\text{odds}(\text{BMI} < 30)) = 0.583 + 0.145 \text{ fruit\_day}$$

- If Jaime consumes 5 servings of fruit per day, what is the prediction?

$$\log(\text{odds}(\text{BMI} < 30)) = 0.583 + 0.145 (5) = 0.583 + 0.725 = 1.308$$

- Exponentiate to get the odds, on our way to estimating the probability.

$$\text{odds}(\text{BMI} < 30) = \exp(1.308) = 3.699$$

- so, we can estimate his Probability of  $\text{BMI} < 30$  as...

$$\Pr(\text{BMI} < 30) = \frac{3.699}{(3.699 + 1)} = 0.787.$$

## Another Prediction

What is the predicted probability of  $BMI < 30$  if a subject (Cersei) eats no fruit?

$$\log(odds(BMI < 30)) = 0.583 + 0.145(0) = 0.583$$

$$odds(BMI < 30) = \exp(0.583) = 1.791$$

$$Pr(BMI < 30) = \frac{1.791}{(1.791 + 1)} = 0.642$$

Can we get R to do this work for us?

# Predictions from a Logistic Regression Model

```
new2 <- tibble( fruit_day = c(0, 5) )
```

```
predict(m2, newdata = new2, type = "link") # predicted logit
```

1	2
0.5834646	1.3082673

```
exp(predict(m2, newdata = new2, type = "link")) # odds
```

1	2
1.792237	3.699758

```
predict(m2, newdata = new2, type = "response") # probability
```

1	2
0.6418642	0.7872231

## Will augment do this, as well?

```
new2 <- tibble( fruit_day = c(0, 5) )
```

```
augment(m2, newdata = new2, type.predict = "link")
```

```
# A tibble: 2 x 3  
  fruit_day .fitted .se.fit  
    <dbl>    <dbl>    <dbl>  
1         0    0.583  0.0403  
2         5    1.31   0.0964
```

```
augment(m2, newdata = new2, type.predict = "response")
```

```
# A tibble: 2 x 3  
  fruit_day .fitted .se.fit  
    <dbl>    <dbl>    <dbl>  
1         0    0.642  0.00925  
2         5    0.787  0.0161
```

# Plotting the Logistic Regression Model

Use the `augment` function to get the fitted probabilities into the original data, then plot.

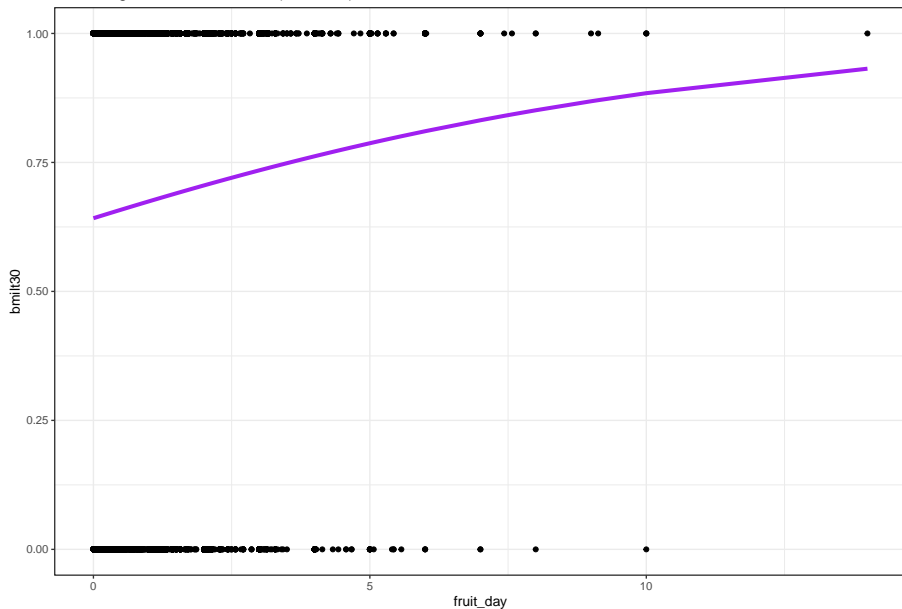
```
m2_aug <- augment(m2, type.predict = "response")

ggplot(m2_aug, aes(x = fruit_day, y = bmilt30)) +
  geom_point() +
  geom_line(aes(x = fruit_day, y = .fitted),
            col = "purple", size = 1.5) +
  labs(title = "Fitted Logistic Model m2 for Pr(BMI < 30)")
```

- Results on next slide

# Plotting Model $m_2$

Fitted Logistic Model  $m_2$  for  $\Pr(\text{BMI} < 30)$





## Evaluating the Model, again

m2

```
Call: glm(formula = bmilt30 ~ fruit_day, family = binomial)
```

Coefficients:

(Intercept)	fruit_day
0.5835	0.1450

```
Degrees of Freedom: 7411 Total (i.e. Null); 7410 Residual
```

```
Null Deviance: 9249
```

```
Residual Deviance: 9213 AIC: 9217
```

$$\text{logit}(BMI < 30) = \log(\text{odds}(BMI < 30)) = 0.583 + 0.145\text{fruit}$$

How can we interpret the coefficients of the model?

## Could we try exponentiating the coefficients?

```
coef(m2)
```

(Intercept)	fruit_day
0.5834646	0.1449605

```
exp(coef(m2))
```

(Intercept)	fruit_day
1.792237	1.155994

Suppose Charlie ate one more piece of fruit per day than Harry.

- The **odds** of Charlie having BMI  $< 30$  are 1.156 times as large as they are for Harry.
- Odds Ratio comparing two subjects whose `fruit_day` differ by 1 serving is 1.156.

## More details on m2 coefficients

```
tidy(m2, exponentiate = TRUE, conf.int = TRUE) %>%  
  select(term, estimate, std.error, conf.low, conf.high) %>%  
  knitr::kable(digits = 3)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	1.792	0.040	1.656	1.939
fruit_day	1.156	0.025	1.101	1.214

- What would it mean if the Odds Ratio for fruit\_day was 1?
- If Charlie eats more servings of fruit than Harry, what would an odds ratio for fruit\_day that was greater than 1 mean?
- How about an odds ratio that was less than 1?
- What is the smallest possible Odds Ratio?

## m2: some additional output

```
m2
```

```
Call: glm(formula = bmilt30 ~ fruit_day, family = binomial)
```

```
Coefficients:
```

(Intercept)	fruit_day
0.5835	0.1450

```
Degrees of Freedom: 7411 Total (i.e. Null); 7410 Residual
```

```
Null Deviance: 9249
```

```
Residual Deviance: 9213 AIC: 9217
```

- Think of the Deviance as a measure of “lack of fit”.
- Deviance accounted for by m2 is
  - $9249 - 9213 = 36$  points on  $7411 - 7410 = 1$  df
- Can do a likelihood ratio test via `anova`.

# anova(m2) for our logistic regression model

Analysis of Deviance

```
anova(m2, test = "LRT")
```

Analysis of Deviance Table

Model: binomial, link: logit

Response: bmilt30

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			7411	9248.7	
fruit_day	1	35.737	7410	9213.0	2.259e-09 ***
---					

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## m2: output from glance

```
glance(m2) %>% select(1:2, 6:7, 3)
```

```
# A tibble: 1 x 5  
  null.deviance df.null deviance df.residual logLik  
      <dbl>    <int>    <dbl>        <int>  <dbl>  
1      9249.    7411    9213.         7410 -4606.
```

$\text{logLik} = \text{log-likelihood} = - \text{deviance} / 2$

```
glance(m2) %>% select(4:5)
```

```
# A tibble: 1 x 2  
  AIC    BIC  
  <dbl> <dbl>  
1 9217. 9231.
```

- AIC and BIC still useful for comparing models using the same outcome.

## Can we predict BMI < 30 using dm\_status?

```
smart1_sh <- smart1_sh %>%  
  mutate(bmilt30 = as.numeric(bmi < 30),  
         dm_status = fct_relevel(dm_status, "No"))  
  
smart1_sh %>% tabyl(bmilt30) %>% adorn_pct_formatting()
```

bmilt30	n	percent
0	2343	31.6%
1	5069	68.4%

## Two-Factor Linear Probability model for bmilt30

```
m3 <- smart1_sh %$%  
  lm(bmilt30 ~ dm_status * genhealth)  
  
anova(m3) %>% knitr::kable(digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dm_status	1	56.215	56.215	276.320	0.000
genhealth	4	38.003	9.501	46.700	0.000
dm_status:genhealth	4	2.273	0.568	2.793	0.025
Residuals	7402	1505.867	0.203	NA	NA



## Equation for model m3

```
tidy(m3) %>%  
  select(term, estimate) %>% knitr::kable(digits = 3)
```

term	estimate
(Intercept)	0.847
dm_statusYes	-0.120
genhealth2_VeryGood	-0.090
genhealth3_Good	-0.193
genhealth4_Fair	-0.213
genhealth5_Poor	-0.189
dm_statusYes:genhealth2_VeryGood	-0.101
dm_statusYes:genhealth3_Good	-0.041
dm_statusYes:genhealth4_Fair	-0.047
dm_statusYes:genhealth5_Poor	-0.198

- Prediction for a subject without diabetes who is in Excellent Health?

## Get predictions for all subjects in our data

```
m3_aug <- augment(m3)
```

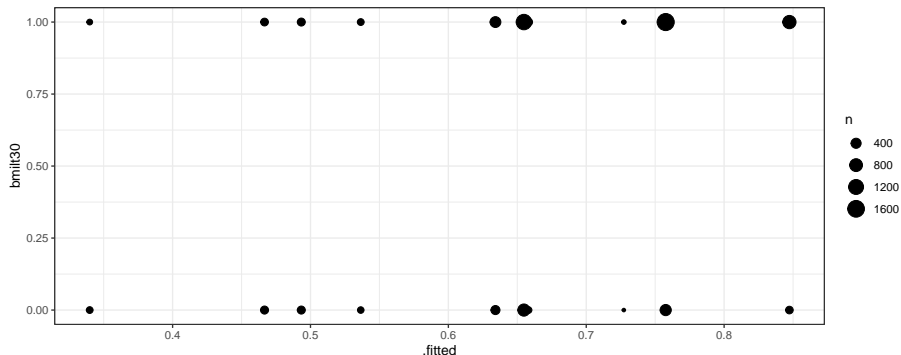
```
m3_aug %>% count(.fitted, dm_status, genhealth)
```

```
# A tibble: 10 x 4
```

	.fitted	dm_status	genhealth	n
	<dbl>	<fct>	<fct>	<int>
1	0.340	Yes	5_Poor	153
2	0.467	Yes	4_Fair	360
3	0.493	Yes	3_Good	375
4	0.536	Yes	2_VeryGood	192
5	0.634	No	4_Fair	779
6	0.655	No	3_Good	1993
7	0.658	No	5_Poor	275
8	0.727	Yes	1_Excellent	22
9	0.758	No	2_VeryGood	2228
10	0.847	No	1_Excellent	1035

# Plot observed vs. predicted values

```
ggplot(m3_aug, aes(x = .fitted, y = bmilt30)) +  
  geom_count()
```



# Making Classification Decisions (0.5 as cutoff)

- Our outcome is `bmilt30`, where `bmilt30 = 1` if BMI < 30, and otherwise `bmilt30 = 0`.
- We establish a classification rule based on our model's predicted probabilities of BMI < 30.
  - If `.fitted` is below 0.5, we classify that as a prediction that `bmilt30 = 0`.
  - If `.fitted` is 0.5 or larger, we classify that as a prediction that `bmilt30 = 1`.
- 0.5 is a natural cut point here but not the only possible one.

```
m3_aug %>% table(.fitted >= 0.5, bmilt30)
```

	bmilt30	
	0	1
FALSE	483	405
TRUE	1860	4664

# Standard Epidemiological Format

```
confuse3_small <- m3_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)
```

```
confuse3_small
```

```
      bmilt30_act
```

```
bmilt30_pre TRUE FALSE
```

```
  TRUE  4664  1860
```

```
 FALSE   405   483
```

# (Mis-)Classification Table / Confusion Matrix

```
confuse3_small
```

```
          bmlt30_act
bmlt30_pre TRUE FALSE
      TRUE  4664   1860
      FALSE   405    483
```

- Total Observations:  $483 + 1860 + 405 + 4664 = 7412$
- Correct Predictions:  $483 + 4664 = 5147$ , or 69.4% **accuracy**
- Incorrect Predictions:  $405 + 1860 = 2265$  (30.6%)
- Actual TRUE:  $4664 + 405 = 5069$ , or 68.4% **prevalence**
- Predicted TRUE:  $4664 + 1860 = 6524$ , or 88.0% **detection prevalence**

## Other Summaries from a Confusion Matrix

```
confuse3_small
```

```
          bmilt30_act
bmilt30_pre TRUE FALSE
      TRUE  4664   1860
      FALSE  405    483
```

- **Sensitivity** =  $4664 / (4664 + 405) = 92.01\%$  (also called Recall)
  - if the subject actually has BMI < 30 our model predicts that 92.01% of the time.
- **Specificity** =  $483 / (1860 + 403) = 20.61\%$ 
  - if the subject actually has BMI  $\geq 30$  our model predicts that 20.61% of the time.
- **Positive Predictive Value** or *Precision* =  $4664 / (4664 + 1860) = 71.49\%$ 
  - our predictions of BMI < 30 were correct 71.49% of the time.
- **Negative Predictive Value** =  $483 / (483 + 405) = 54.39\%$ 
  - our predictions that BMI  $\geq 30$  were correct 54.39% of the time.

# Big Summary of Confusion Matrix (from caret)

```
m3_aug %$% confusionMatrix(  
  data = factor(.fitted >= 0.5),  
  reference = factor(bmilt30 == 1),  
  positive = "TRUE")
```

Results on next two slides...



## Confusion Matrix statistics for m3

Reference

Prediction FALSE TRUE

FALSE 483 405

TRUE 1860 4664

Accuracy : 0.6944

95% CI : (0.6838, 0.7049)

No Information Rate : 0.6839

P-Value [Acc > NIR] : 0.02617

Kappa : 0.1516

McNemar's Test P-Value : < 2e-16

- Kappa is a correlation statistic ranging from -1 to +1. It measures the inter-rater reliability of our predictions and the true classifications, in this context. Complete agreement would be +1, and complete disagreement would be -1.

## Confusion Matrix statistics for m3

```
'Positive' Class : TRUE  
  Sensitivity : 0.9201  
  Specificity : 0.2061  
  Pos Pred Value : 0.7149  
  Neg Pred Value : 0.5439  
  Prevalence : 0.6839  
  Detection Rate : 0.6292  
  Detection Prevalence : 0.8802  
  Balanced Accuracy : 0.5631
```

# Tidying a Confusion Matrix

```
confuse3 <- m3_aug %$% confusionMatrix(  
  data = factor(.fitted >= 0.5),  
  reference = factor(bmilt30 == 1),  
  positive = "TRUE")  
  
tidy(confuse3) %>% knitr::kable(digits = 3)
```

Results next slide.

term	class	estimate	conf.low	conf.high	p.value
accuracy	NA	0.694	0.684	0.705	0.026
kappa	NA	0.152	NA	NA	0.000
sensitivity	TRUE	0.920	NA	NA	NA
specificity	TRUE	0.206	NA	NA	NA
pos_pred_value	TRUE	0.715	NA	NA	NA
neg_pred_value	TRUE	0.544	NA	NA	NA
precision	TRUE	0.715	NA	NA	NA
recall	TRUE	0.920	NA	NA	NA
f1	TRUE	0.805	NA	NA	NA
prevalence	TRUE	0.684	NA	NA	NA
detection_rate	TRUE	0.629	NA	NA	NA
detection_prevalence	TRUE	0.880	NA	NA	NA
balanced_accuracy	TRUE	0.563	NA	NA	NA

# How do we fit a simple logistic regression model?

```
m4 <- smart1_sh %$%  
  glm(bmilt30 ~ dm_status, family = binomial(link = logit))
```

# How do we interpret the coefficients?

```
tidy(m4) %>% select(term, estimate) %>%  
  knitr::kable(digits = 3)
```

term	estimate
(Intercept)	0.946
dm_statusYes	-1.044

Equation:  $\text{logit}(\text{BMI} < 30) = 0.946 - 1.044 (\text{dm\_status} = \text{Yes})$

How can we interpret this result?

# Interpreting our Logistic Regression Equation

$$\text{logit}(\text{BMI} < 30) = 0.946 - 1.044 (\text{dm\_status} = \text{Yes})$$

- Harry has diabetes.
  - His predicted  $\text{logit}(\text{BMI} < 30)$  is  $0.946 - 1.044 (1) = -0.098$
- Sally does not have diabetes.
  - Her predicted  $\text{logit}(\text{BMI} < 30)$  is  $0.946 - 1.044 (0) = 0.946$

Now,  $\text{logit}(\text{BMI} < 30) = \log(\text{odds}(\text{BMI} < 30))$ , so exponentiate to get the odds...

- Harry has predicted  $\text{odds}(\text{BMI} < 30) = \exp(-0.098) = 0.9066$
- Sally has predicted  $\text{odds}(\text{BMI} < 30) = \exp(0.946) = 2.575$

Can we convert these odds into something more intuitive?

# Converting Odds to Probabilities

- Harry has predicted  $\text{odds}(\text{BMI} < 30) = \exp(-0.098) = 0.9066$
- Sally has predicted  $\text{odds}(\text{BMI} < 30) = \exp(0.946) = 2.575$

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

and

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

- So Harry's predicted  $\text{Pr}(\text{BMI} < 30) = 0.9066 / 1.9066 = 0.48$
- Sally's predicted  $\text{Pr}(\text{BMI} < 30) = 2.575 / 3.575 = 0.72$
- odds range from 0 to  $\infty$ , and  $\log(\text{odds})$  range from  $-\infty$  to  $\infty$ .
- odds  $> 1$  if probability  $> 0.5$ . If odds = 1, then probability = 0.5.



## What about the odds ratio?

$\text{logit}(\text{BMI} < 30) = 0.946 - 1.044 (\text{dm\_status} = \text{Yes})$

- Harry, with diabetes, has  $\text{odds}(\text{BMI} < 30) = 0.9066$
- Sally, without diabetes, has  $\text{odds}(\text{BMI} < 30) = 2.575$

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

$$\frac{0.9066}{2.575} = 0.352$$

- Our model estimates that a subject with diabetes has 35.2% of the odds of a subject without diabetes of having  $\text{BMI} < 30$ .

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

- Yes,  $\exp(-1.044) = 0.352$ .

## Tidy with exponentiation

```
tidy(m4, exponentiate = TRUE,  
     conf.int = TRUE, conf.level = 0.9) %>%  
select(term, estimate, conf.low, conf.high) %>%  
knitr::kable(digits = 3)
```

term	estimate	conf.low	conf.high
(Intercept)	2.575	2.459	2.697
dm_statusYes	0.352	0.316	0.393

- The odds ratio for BMI < 30 among subjects with diabetes as compared to those without diabetes is 0.352
- The odds of BMI < 30 are 35.2% 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 (0.316, 0.393).

# 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  $\text{BMI} < 30$ , then the odds would also be the same, and so the odds ratio would be 1.
- If the probabilities of  $\text{BMI} < 30$  were the same and thus the odds were the same, then the log odds ratio would be  $\log(1) = 0$ .

$\text{logit}(\text{BMI} < 30) = 0.946 - 1.044 (\text{dm\_status} = \text{Yes})$

- 1 If the log odds of a coefficient (like  $\text{diabetes} = \text{Yes}$ ) are negative, then what does that imply?
- 2 What if we flipped the order of the levels for diabetes so our model was about  $\text{diabetes} = \text{No}$ ?

New model:  $\text{logit}(\text{BMI} < 30) = -0.098 + 1.044 (\text{dm\_status} = \text{No})$

## Two-Factor Logistic Regression (model m5)

First, let's try a model without interaction.

```
m5_without <- smart1_sh %$%  
  glm(bmilt30 ~ dm_status + genhealth,  
      family = binomial()) # logit is default link  
  
tidy(m5_without) %>% select(term, estimate) %>%  
  knitr::kable(digits = 3)
```

term	estimate
(Intercept)	1.716
dm_statusYes	-0.813
genhealth2_VeryGood	-0.595
genhealth3_Good	-1.051
genhealth4_Fair	-1.124
genhealth5_Poor	-1.244

## Our model `m5_without`

```
logit(BMI < 30) = log(odds(BMI < 30))  
= 1.72 - 0.81 (dm_status = Yes)  
      - 0.60 (genhealth = Very Good)  
      - 1.05 (genhealth = Good)  
      - 1.12 (genhealth = Fair)  
      - 1.24 (genhealth = Poor)
```

- 1 How do we interpret the meaning of the -0.81 coefficient for `dm_status = Yes` in this model?
- 2 How do we interpret the meaning of the -1.05 coefficient for `genhealth = Good`?

## Our model `m5_without`

```
logit(BMI < 30) =  
  = 1.72 - 0.81 (dm = Yes) - 0.60 (Very Good) - 1.05 (Good)  
    - 1.12 (Fair) - 1.24 (Poor)
```

- 1 How do we interpret the meaning of the -0.81 coefficient for `dm_status = Yes` in this model?

If Harry and Sally have the **same `genhealth` status**, but Harry has diabetes and Sally does not, the model predicts that Harry's  $\log(\text{odds}(\text{BMI} < 30))$  will be 0.81 lower than Sally's.

- Harry:  $\text{logit}(\text{BMI} < 30) = (1.72 - 0.81) - 0.60 \text{ (Very Good)} - 1.05 \text{ (Good)} - 1.12 \text{ (Fair)} - 1.24 \text{ (Poor)}$
- Sally:  $\text{logit}(\text{BMI} < 30) = 1.72 - 0.60 \text{ (VG)} - 1.05 \text{ (G)} - 1.12 \text{ (F)} - 1.24 \text{ (P)}$

Suppose that, for example, Harry and Sally each had Excellent `genhealth`...

## Question 1 (continued)

$$\begin{aligned}\text{logit}(\text{BMI} < 30) &= \\ &= 1.72 - 0.81 \text{ (dm = Yes)} - 0.60 \text{ (Very Good)} - 1.05 \text{ (Good)} \\ &\quad - 1.12 \text{ (Fair)} - 1.24 \text{ (Poor)}\end{aligned}$$

- ❶ How do we interpret the meaning of the -0.81 coefficient for `dm_status = Yes` in this model?

Subject	Harry	Sally
genhealth	Excellent	Excellent
dm_status	Yes	No
$\log(\text{odds}(\text{BMI} < 30))$	$1.72 - 0.81 = 0.91$	1.72
$\text{odds}(\text{BMI} < 30)$	$\exp(0.91) = 2.484$	$\exp(1.72) = 5.585$
$\text{Pr}(\text{BMI} < 30)$	$2.484 / 3.484 = 0.71$	$5.585 / 6.585 = 0.85$

## Our model `m5_without`

$$\begin{aligned}\text{logit}(\text{BMI} < 30) &= \\ &= 1.72 - 0.81 \text{ (dm = Yes)} - 0.60 \text{ (Very Good)} - 1.05 \text{ (Good)} \\ &\quad - 1.12 \text{ (Fair)} - 1.24 \text{ (Poor)}\end{aligned}$$

- 2 How do we interpret the meaning of the -1.05 coefficient for `genhealth = Good`?

If Harry and Sally have the **same** `dm_status`, but Harry has Good `genhealth` and Sally has Excellent `genhealth`, the model predicts that Harry's  $\text{log}(\text{odds}(\text{BMI} < 30))$  will be 1.05 lower than Sally's.

- Harry:  $\text{logit}(\text{BMI} < 30) = 1.72 - 0.81 \text{ (dm = Yes)} - 1.05$
- Sally:  $\text{logit}(\text{BMI} < 30) = 1.72 - 0.81 \text{ (dm = Yes)}$

Why are we comparing Harry at Good to Sally at Excellent here?



## Question 2 (continued)

$$\begin{aligned}\text{logit}(\text{BMI} < 30) &= \\ &= 1.72 - 0.81 \text{ (dm = Yes)} - 0.60 \text{ (Very Good)} - 1.05 \text{ (Good)} \\ &\quad - 1.12 \text{ (Fair)} - 1.24 \text{ (Poor)}\end{aligned}$$

- 2 How do we interpret the meaning of the -1.05 coefficient for `genhealth = Good`?

Subject	Harry	Sally
<code>genhealth</code>	Good	Excellent
<code>dm_status</code>	No	No
<code>log(odds(BMI &lt; 30))</code>	$1.72 - 1.05 = 0.67$	1.72
<code>odds(BMI &lt; 30)</code>	$\exp(0.67) = 1.954$	$\exp(1.72) = 5.585$
<code>Pr(BMI &lt; 30)</code>	$1.954 / 2.954 = 0.66$	$5.585 / 6.585 = 0.85$

- What is the odds ratio for  $\text{BMI} < 30$  comparing Harry to Sally?  
 $1.954 / 5.585 = 0.350$
- Now, what if Harry and Sally each had diabetes?

## Question 2 (continued)

$$\begin{aligned}\text{logit}(\text{BMI} < 30) &= \\ &= 1.72 - 0.81 \text{ (dm = Yes)} - 0.60 \text{ (Very Good)} - 1.05 \text{ (Good)} \\ &\quad - 1.12 \text{ (Fair)} - 1.24 \text{ (Poor)}\end{aligned}$$

- 2 How do we interpret the meaning of the -1.05 coefficient for `genhealth = Good`?

Subject	Harry	Sally
<code>genhealth</code>	Good	Excellent
<code>dm_status</code>	Yes	Yes
<code>log(odds(BMI &lt; 30))</code>	$1.72 - 1.05 - 0.81 = -0.14$	$1.72 - 0.81 = 0.91$
<code>odds(BMI &lt; 30)</code>	$\exp(-0.14) = 0.869$	$\exp(0.91) = 2.484$
<code>Pr(BMI &lt; 30)</code>	$0.869/1.869 = 0.46$	$2.484/3.484 = 0.71$

Now what is the odds ratio for `BMI < 30` comparing Harry to Sally?

$$0.869/2.484 = 0.350$$

## Tidying our m5\_without model

```
tidy(m5_without, exponentiate = TRUE,  
     conf.int = TRUE, conf.level = 0.90) %>%  
  select(term, estimate, conf.low, conf.high) %>%  
  knitr::kable(digits = 3)
```

term	estimate	conf.low	conf.high
(Intercept)	5.565	4.848	6.416
dm_statusYes	0.444	0.396	0.498
genhealth2_VeryGood	0.551	0.469	0.646
genhealth3_Good	0.350	0.298	0.409
genhealth4_Fair	0.325	0.272	0.387
genhealth5_Poor	0.288	0.232	0.358

How do we interpret the odds ratios here?

# How well does our model predict the outcome?

We can build a table of predicted outcomes.

```
augment(m5_without, type.predict = "response") %>%  
  count(.fitted, dm_status, genhealth)
```

# A tibble: 10 x 4

	.fitted	dm_status	genhealth	n
	<dbl>	<fct>	<fct>	<int>
1	0.416	Yes	5_Poor	153
2	0.445	Yes	4_Fair	360
3	0.463	Yes	3_Good	375
4	0.577	Yes	2_VeryGood	192
5	0.616	No	5_Poor	275
6	0.644	No	4_Fair	779
7	0.660	No	3_Good	1993
8	0.712	Yes	1_Excellent	22
9	0.754	No	2_VeryGood	2228
10	0.848	No	1_Excellent	1035

# Making Classification Decisions (0.5 as cutoff)

- Our outcome is `bmi<30`, where `bmi<30 = 1` if  $\text{BMI} < 30$ , and otherwise `bmi<30 = 0`.
- We establish a classification rule based on our model's predicted probabilities of  $\text{BMI} < 30$ .
  - If `.fitted` is below 0.5, we classify that as a prediction that `bmi<30 = 0`.
  - If `.fitted` is 0.5 or larger, we classify that as a prediction that `bmi<30 = 1`.
- 0.5 is a natural cut point here but not the only possible one.

## (Mis-)Classification Table / Confusion Matrix

```
m5_without_aug <- augment(m5_without, data = smart1_sh,
                           type.predict = "response")

confuse5_without <- m5_without_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)

confuse5_without
```

	bmilt30_act	
bmilt30_pre	TRUE	FALSE
TRUE	4664	1860
FALSE	405	483

- Same results as linear probability model m3!

## m5\_with: Adding an interaction term?

```
m5_with <- smart1_sh %$%  
  glm(bmilt30 ~ dm_status * genhealth, family = binomial())  
  
tidy(m5_with) %>%  
  select(term, estimate, std.error, p.value) %>%  
  knitr::kable(digits = 3)
```

Results on next slide...

## Coefficients of model m5\_with

```
m5_with <- smart1_sh %$%  
  glm(bmilt30 ~ dm_status * genhealth, family = binomial())
```

term	estimate	std.error	p.value
(Intercept)	1.714	0.086	0.000
dm_statusYes	-0.733	0.486	0.132
genhealth2_VeryGood	-0.574	0.100	0.000
genhealth3_Good	-1.074	0.098	0.000
genhealth4_Fair	-1.164	0.114	0.000
genhealth5_Poor	-1.059	0.154	0.000
dm_statusYes:genhealth2_VeryGood	-0.261	0.510	0.609
dm_statusYes:genhealth3_Good	0.066	0.500	0.894
dm_statusYes:genhealth4_Fair	0.050	0.503	0.922
dm_statusYes:genhealth5_Poor	-0.586	0.531	0.270



# Interpreting m5\_with Coefficients

Equation for  $\log(\text{odds}(\text{BMI} < 30)) =$

$1.71 - 0.73 \text{ (dm = Yes)}$   
 $- 0.57 \text{ (Very Good)} - 1.07 \text{ (Good)} - 1.16 \text{ (Fair)} - 1.06 \text{ (Poor)}$   
 $- 0.26 \text{ (dm = Yes)(Very Good)} + 0.07 \text{ (dm = Yes)(Good)}$   
 $+ 0.05 \text{ (dm = Yes)(Fair)} - 0.59 \text{ (dm = Yes)(Poor)}$

How do we understand the -0.59 coefficient here?

Suppose Cersei has Excellent and Jaime has Poor genhealth. What are their model equations for  $\log(\text{odds}(\text{BMI} < 30))$ ?

- Cersei:  $1.71 - 0.73 \text{ dm\_status}$
- Jaime:  $(1.71 - 1.06) + ((-0.73) + (-0.59)) \text{ dm\_status}$ ,
- so Jaime:  $0.65 - 1.32 \text{ dm\_status}$ .

## Making Predictions with m5\_with

Equation for  $\log(\text{odds}(\text{BMI} < 30)) =$

$1.71 - 0.73 \text{ (dm = Yes)}$

$- 0.57 \text{ (Very Good)} - 1.07 \text{ (Good)} - 1.16 \text{ (Fair)} - 1.06 \text{ (Poor)}$

$- 0.26 \text{ (dm = Yes)(Very Good)} + 0.07 \text{ (dm = Yes)(Good)}$

$+ 0.05 \text{ (dm = Yes)(Fair)} - 0.59 \text{ (dm = Yes)(Poor)}$

Subject	dm_status	genhealth	$\log(\text{odds}(\text{BMI} < 30))$
Harry	No	Excellent	1.71
Sally	No	Poor	$1.71 - 1.06 = 0.65$
Cersei	Yes	Excellent	$1.71 - 0.73 = 0.98$
Jaime	Yes	Poor	$1.71 - 0.73 - 1.06 - 0.59 = -0.67$

# Getting R to make the predictions

(Reducing rounding errors)

```
new_m5 <- tibble(  
  subject = c("Harry", "Sally", "Cersei", "Jaime"),  
  dm_status = c("No", "No", "Yes", "Yes"),  
  genhealth = c("1_Excellent", "5_Poor",  
                "1_Excellent", "5_Poor"))  
  
predict(m5_with, newdata = new_m5, type = "link")
```

1	2	3	4
1.7139120	0.6552022	0.9808293	-0.6638768

## Making Predictions with m5\_with (again)

1.71 - 0.73 (dm = Yes)

- 0.57 (Very Good) - 1.07 (Good) - 1.16 (Fair) - 1.06 (Poor)

- 0.26 (dm = Yes)(Very Good) + 0.07 (dm = Yes)(Good)

+ 0.05 (dm = Yes)(Fair) - 0.59 (dm = Yes)(Poor)

Subject	dm	genhealth	odds(BMI < 30)
Harry	No	Excellent	$\exp(1.71) = 5.53$
Sally	No	Poor	$\exp(0.65) = 1.92$
Cersei	Yes	Excellent	$\exp(0.98) = 2.66$
Jaime	Yes	Poor	$\exp(-0.67) = 0.51$

# Getting R to make the predictions

(Reducing rounding errors)

```
predict(m5_with, newdata = new_m5, type = "link") # logit
```

1	2	3	4
1.7139120	0.6552022	0.9808293	-0.6638768

```
exp(predict(m5_with, newdata = new_m5, type = "link")) # odds
```

1	2	3	4
5.5506329	1.9255319	2.6666667	0.5148515

## Making Predictions with m5\_with (one more time)

1.71 - 0.73 (dm = Yes)  
- 0.57 (Very Good) - 1.07 (Good) - 1.16 (Fair) - 1.06 (Poor)  
- 0.26 (dm = Yes)(Very Good) + 0.07 (dm = Yes)(Good)  
+ 0.05 (dm = Yes)(Fair) - 0.59 (dm = Yes)(Poor)

How do we understand the -0.59 coefficient here?

Subject	dm	genhealth	Pr(BMI < 30)
Harry	No	Excellent	5.53/6.53 = 0.85
Sally	No	Poor	1.92/2.92 = 0.66
Cersei	Yes	Excellent	2.66/3.66 = 0.73
Jaime	Yes	Poor	0.51/1.51 = 0.34

# Getting R to make the predictions

```
predict(m5_with, newdata = new_m5,  
        type = "response") # probs
```

1	2	3	4
0.8473430	0.6581818	0.7272727	0.3398693

## Model m5\_with Results (from R's predict)

Subject	dm	genhealth	logit	odds	Pr(BMI < 30)
Harry	No	Excellent	1.714	5.551	0.847
Sally	No	Poor	0.655	1.926	0.658
Cersei	Yes	Excellent	0.981	2.667	0.727
Jaime	Yes	Poor	-0.664	0.515	0.340

### Calculating Odds Ratios

- Comparing DM to No DM (if GenHealth = Excellent) =  $2.667/5.551 = 0.480$
- Comparing Poor to Excellent (if no DM) =  $1.926 / 5.551 = 0.347$
- Comparing DM to No DM (if GenHealth = Poor) =  $0.515/1.926 = 0.267$
- Comparing Poor to Excellent (if DM) =  $0.515 / 2.667 = 0.193$



## Exponentiating the m5\_with Coefficients

```
tidy(m5_with, exponentiate = TRUE, conf.int = TRUE,  
     conf.level = 0.90) %>%  
  select(term, estimate, conf.low, conf.high) %>%  
  knitr::kable(digits = 3)
```

Results on the next slide...

## Exponentiating the m5\_with Coefficients

term	estimate	conf.low	conf.high
(Intercept)	5.551	4.826	6.414
dm_statusYes	0.480	0.224	1.132
genhealth2_VeryGood	0.563	0.477	0.662
genhealth3_Good	0.342	0.290	0.401
genhealth4_Fair	0.312	0.259	0.376
genhealth5_Poor	0.347	0.270	0.447
dm_statusYes:genhealth2_VeryGood	0.771	0.316	1.726
dm_statusYes:genhealth3_Good	1.068	0.445	2.349
dm_statusYes:genhealth4_Fair	1.051	0.435	2.326
dm_statusYes:genhealth5_Poor	0.557	0.221	1.292

- 1 Interpret the dm\_statusYes coefficient (0.480).
- 2 Interpret the genhealth5\_Poor coefficient (0.347).

## Model m5\_with Predictions, Again

- 1 Interpret the dm\_statusYes coefficient (0.480).
- 2 Interpret the genhealth5\_Poor coefficient (0.347).

Subject	dm	genhealth	odds(BMI < 30)
Harry	No	Excellent	5.551
Sally	No	Poor	1.926
Cersei	Yes	Excellent	2.667
Jaime	Yes	Poor	0.515

### Odds Ratios we calculated earlier...

- 1 Comparing DM to No DM (if GenHealth = Excellent) =  $2.667/5.551 = 0.480$
- 2 Comparing Poor to Excellent (if no DM) =  $1.926 / 5.551 = 0.347$

## Exponentiating the m5\_with Coefficients

term	estimate	conf.low	conf.high
(Intercept)	5.551	4.826	6.414
dm_statusYes	0.480	0.224	1.132
genhealth2_VeryGood	0.563	0.477	0.662
genhealth3_Good	0.342	0.290	0.401
genhealth4_Fair	0.312	0.259	0.376
genhealth5_Poor	0.347	0.270	0.447
dm_statusYes:genhealth2_VeryGood	0.771	0.316	1.726
dm_statusYes:genhealth3_Good	1.068	0.445	2.349
dm_statusYes:genhealth4_Fair	1.051	0.435	2.326
dm_statusYes:genhealth5_Poor	0.557	0.221	1.292

- ③ How do we interpret the interaction coefficients, like 0.557 for (DM = Yes)(GenHealth = Poor)?

# Interpreting m5\_with Interaction Odds Ratios

- ③ How do we interpret the interaction coefficients, like 0.557 for (DM = Yes)(GenHealth = Poor)?

Odds Ratios we calculated earlier...

- Comparing DM to No DM (if GenHealth = Poor)  $\approx 0.267$
- Comparing DM to No DM (if GenHealth = Excellent)  $\approx 0.480$
- Comparing Poor to Excellent (if DM)  $\approx 0.193$
- Comparing Poor to Excellent (if no DM)  $\approx 0.347$

Within rounding error,

$$\frac{0.267}{0.480} \approx \frac{0.193}{0.347} \approx 0.557$$

## Using glance on these models

```
bind_rows(glance(m5_with), glance(m5_without)) %>%  
  mutate(model = c("With Interaction", "No Interaction"),  
         deviance_diff = null.deviance - deviance,  
         df_diff = df.null - df.residual) %>%  
  select(model, AIC, BIC, deviance_diff, df_diff) %>%  
  knitr::kable(digits = 1)
```

model	AIC	BIC	deviance_diff	df_diff
With Interaction	8821.6	8890.7	447.1	9
No Interaction	8823.5	8864.9	437.2	5

## Confusion Matrix for m5\_with

```
m5_with_aug <- augment(m5_with, data = smart1_sh,
                        type.predict = "response")

confuse5_with <- m5_with_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)

confuse5_with
```

	bmilt30_act	
bmilt30_pre	TRUE	FALSE
TRUE	4664	1860
FALSE	405	483

- Still  $4664 + 483 = 5147$  accurate predictions (69.4%)

# Logistic Regression Comparisons via anova

Based on Likelihood Ratio Test

```
anova(m5_without, m5_with, test = "LRT")
```

Analysis of Deviance Table

Model 1: bmilt30 ~ dm\_status + genhealth

Model 2: bmilt30 ~ dm\_status \* genhealth

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
1	7406	8811.5			
2	7402	8801.6	4	9.8769	0.04255 *

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Other options include Rao's efficient score test (`test = "Rao"`) and Pearson's chi-square test (`test = "Chisq"`)



# Logistic Regression Comparisons via anova

Another potentially attractive option compares the models based on Mallows'  $C_p$  statistic, which is closely related to the AIC, in general, and identical to what glance provides for AIC in this case.

```
anova(m5_without, m5_with, test = "Cp")
```

## Analysis of Deviance Table

Model 1: bmilt30 ~ dm\_status + genhealth

Model 2: bmilt30 ~ dm\_status \* genhealth

	Resid. Df	Resid. Dev	Df	Deviance	Cp
1	7406	8811.5			8823.5
2	7402	8801.6	4	9.8769	8821.6

## m6: Logistic Regression (Interaction & Covariate)

```
m6 <- smart1_sh %$%  
  glm(bmilt30 ~ fruit_day + dm_status * genhealth,  
      family = binomial)  
  
tidy(m6) %>%  
  select(term, estimate, std.error, p.value) %>%  
  knitr::kable(digits = 3)
```

Results on next slide...

## m6 model coefficients

term	estimate	std.error	p.value
(Intercept)	1.548	0.094	0.000
fruit_day	0.114	0.025	0.000
dm_statusYes	-0.741	0.487	0.128
genhealth2_VeryGood	-0.563	0.100	0.000
genhealth3_Good	-1.052	0.099	0.000
genhealth4_Fair	-1.129	0.114	0.000
genhealth5_Poor	-1.016	0.154	0.000
dm_statusYes:genhealth2_VeryGood	-0.258	0.511	0.614
dm_statusYes:genhealth3_Good	0.071	0.500	0.887
dm_statusYes:genhealth4_Fair	0.051	0.504	0.920
dm_statusYes:genhealth5_Poor	-0.601	0.532	0.259

# The m6 model

```
log(odds(BMI < 30)) =  
  1.548 +  
  + 0.114 fruit_day  
  - 0.741 dm_status = Yes  
  - 0.563 genhealth = Very Good  
  - 1.052 genhealth = Good  
  - 1.129 genhealth = Fair  
  - 1.016 genhealth = Poor  
  - 0.258 (dm_status = Yes)(genhealth = Very Good)  
  + 0.071 (dm_status = Yes)(genhealth = Good)  
  + 0.051 (dm_status = Yes)(genhealth = Fair)  
  - 0.601 (dm_status = Yes)(genhealth = Poor)
```

Does the impact of fruit\_day change depending on dm\_status and genhealth?

## Confusion Matrix for m6

```
m6_aug <- augment(m6, data = smart1_sh,
                  type.predict = "response")

confuse6 <- m6_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)

confuse6
```

	bmilt30_act	
bmilt30_pre	TRUE	FALSE
TRUE	4731	1925
FALSE	338	418

- $4731 + 418 = 5149$  accurate predictions (69.5%)
- Sensitivity 93.3%, and Specificity 17.8%

# The m7 model with factor-covariate interactions

```
m7 <- smart1_sh %$%  
  glm(bmilt30 ~  
    fruit_day*dm_status +  
    fruit_day*genhealth +  
    dm_status*genhealth,  
    family = binomial)  
  
tidy(m7) %>%  
  select(term, estimate, std.error, p.value) %>%  
  knitr::kable(digits = 3)
```

## The m7 model

term	estimate	std.error	p.value
(Intercept)	1.463	0.149	0.000
fruit_day	0.175	0.088	0.048
dm_statusYes	-0.788	0.498	0.113
genhealth2_VeryGood	-0.481	0.168	0.004
genhealth3_Good	-0.957	0.166	0.000
genhealth4_Fair	-1.039	0.180	0.000
genhealth5_Poor	-0.798	0.224	0.000
fruit_day:dm_statusYes	0.029	0.065	0.656
fruit_day:genhealth2_VeryGood	-0.059	0.099	0.555
fruit_day:genhealth3_Good	-0.069	0.099	0.486
fruit_day:genhealth4_Fair	-0.066	0.107	0.542
fruit_day:genhealth5_Poor	-0.184	0.132	0.163
dm_statusYes:genhealth2_VeryGood	-0.251	0.512	0.624
dm_statusYes:genhealth3_Good	0.081	0.502	0.872
dm_statusYes:genhealth4_Fair	0.063	0.506	0.901
dm_statusYes:genhealth5_Poor	-0.567	0.534	0.288

## Confusion Matrix for m7

```
m7_aug <- augment(m7, data = smart1_sh,
                  type.predict = "response")

confuse7 <- m7_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)

confuse7
```

	bmilt30_act	
bmilt30_pre	TRUE	FALSE
TRUE	4724	1915
FALSE	345	428

- $4724 + 428 = 5152$  accurate predictions (69.5%)
- Sensitivity 93.1%, and Specificity 18.3%



## Could we do a three-way interaction?

```
m8 <- smart1_sh %$%  
  glm(bmilt30 ~ fruit_day*dm_status*genhealth,  
      family = binomial)
```

term	estimate
(Intercept)	1.504
fruit_day	0.145
dm_statusYes	-2.526
genhealth2_VeryGood	-0.527
dm_statusYes:genhealth5_Poor	0.734
fruit_day:dm_statusYes:genhealth2_VeryGood	-1.599
fruit_day:dm_statusYes:genhealth3_Good	-1.676
fruit_day:dm_statusYes:genhealth4_Fair	-1.609
fruit_day:dm_statusYes:genhealth5_Poor	-1.225

These are just 9 of the 20 coefficients fit in total.

## Confusion Matrix for m8

```
m8_aug <- augment(m8, data = smart1_sh,
                  type.predict = "response")

confuse8 <- m8_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)

confuse8
```

	bmilt30_act	
bmilt30_pre	TRUE	FALSE
TRUE	4729	1919
FALSE	340	424

- $4729 + 424 = 5153$  accurate predictions (69.5%)
- Sensitivity 93.2%, and Specificity 18.1%

# Comparison of Models with Deviance Tests

```
anova(m5_without, m5_with, m6, m7, m8, test = "LRT")
```

## Analysis of Deviance Table

Model 1: bmilt30 ~ dm\_status + genhealth

Model 2: bmilt30 ~ dm\_status \* genhealth

Model 3: bmilt30 ~ fruit\_day + dm\_status \* genhealth

Model 4: bmilt30 ~ fruit\_day \* dm\_status + fruit\_day \* genhealth  
genhealth

Model 5: bmilt30 ~ fruit\_day \* dm\_status \* genhealth

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
1	7406	8811.5			
2	7402	8801.6	4	9.8769	0.04255 *
3	7401	8780.3	1	21.3157	3.895e-06 ***
4	7396	8778.2	5	2.0927	0.83617
5	7392	8770.2	4	7.9755	0.09248 .

---

Signif. codes:

# Comparison of Models with AIC/BIC

```
bind_rows(glance(m5_without), glance(m5_with), glance(m6),  
          glance(m7), glance(m8)) %>%  
  mutate(model = c("m5_without", "m5_with",  
                   "m6", "m7", "m8")) %>%  
  select(model, AIC, BIC)
```

```
# A tibble: 5 x 3  
  model      AIC    BIC  
  <chr>    <dbl> <dbl>  
1 m5_without 8823. 8865.  
2 m5_with    8822. 8891.  
3 m6         8802. 8878.  
4 m7         8810. 8921.  
5 m8         8810. 8948.
```

# Comparison of Models by Confusion Matrix

Model	Correct Preds.	Accuracy	Sensitivity	Specificity
m5_without	5,147	69.44%	92.0%	20.6%
m5_with	5,147	69.44%	92.0%	20.6%
m6	5 149	69.47%	93.3%	17.8%
m7	5,152	69.51%	93.1%	18.3%
m8	5,153	69.52%	93.2%	18.1%

# What's Coming Up?

Building on what we know about Linear & Logistic Regression

- Model Selection and Cross-Validation Strategies
- Incorporating the Survey Weights into our Analyses
- Checking Assumptions (in Logistic Regression)
- ROC Curve Analysis (in Logistic Regression)
- Multiple Imputation (rather than Simple Imputation) to deal with missing data

At which point, we'll move on to ...

- Other methods for predicting 1/0 and quantitative outcomes (via the `rms` package)
- Using regression-style approaches to predict other kinds of outcomes (counts, multiple categories, times to event with censoring)