Logistic Regression

This whole semester has been linear regression (on steroids)

- We've had continuous IVs (regression)
- We've had categorical IVs (factorial ANOVA)
- We've had a mixture of continuous/categorical IVs (more regression)
- But we've never had a DV variable that is categorical... in comes Logistic Regression

When we have a continuous DV, we can...

- Calculate the R^2 and determine if our IVs & DV are correlated (large value implying = large effect)
- Calculate a p-value to determine if R^2 (or our model) is statistically significant
- Use the line/slope of a linear regression to make a calculated prediction of *y* given *x*
- Compare models
- Add in predictors & look at interactions

Logistic Regression

What is the goal of prediction when you have a categorial (dichotomous) outcome?

We are trying to see if something is ***TRUE*** or ***FALSE***

Learning Goals

1. WTF is logistic regression. When to use it?
2. WTF is the generalized linear model. When to use it?
3. WTF is maximum likelihood estimation
4. HTF do I do this in R

Learning goals today are *not*:

- know every little thing about odds/probabilities/weird things I'm going to introduce
- know every element of the output
- memorize anything

Logistic Regression

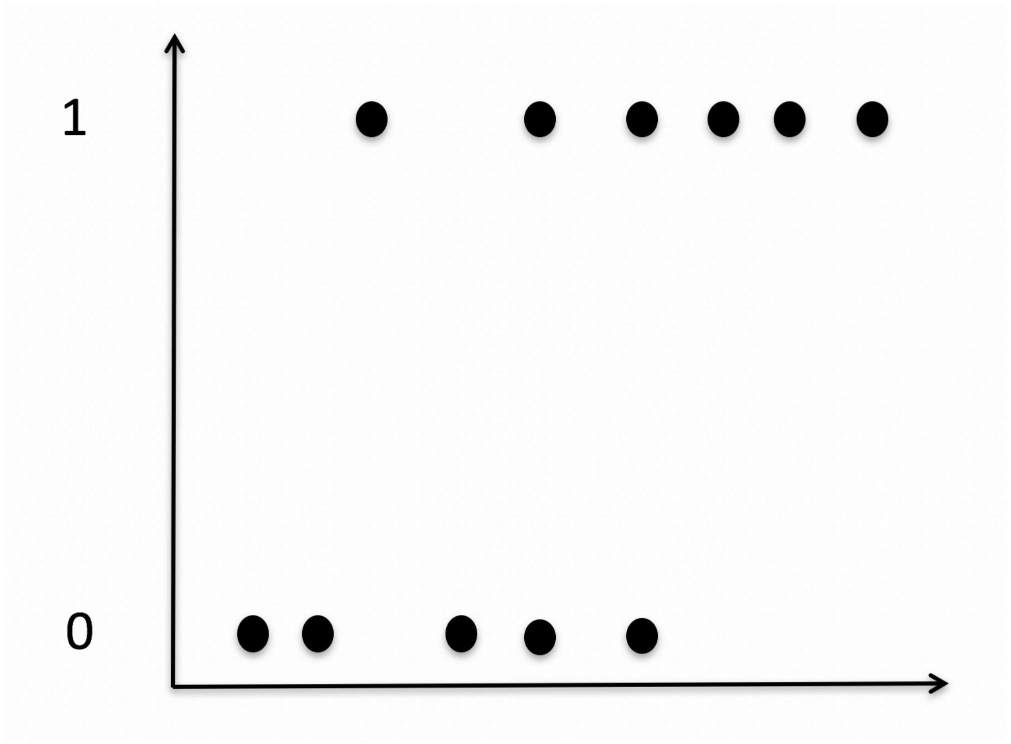
Used when your DV is binary (0,1)

- Clinical diagnosis
- Disease prevalence
- Experiences (Yes/No)
- Correct/Incorrect

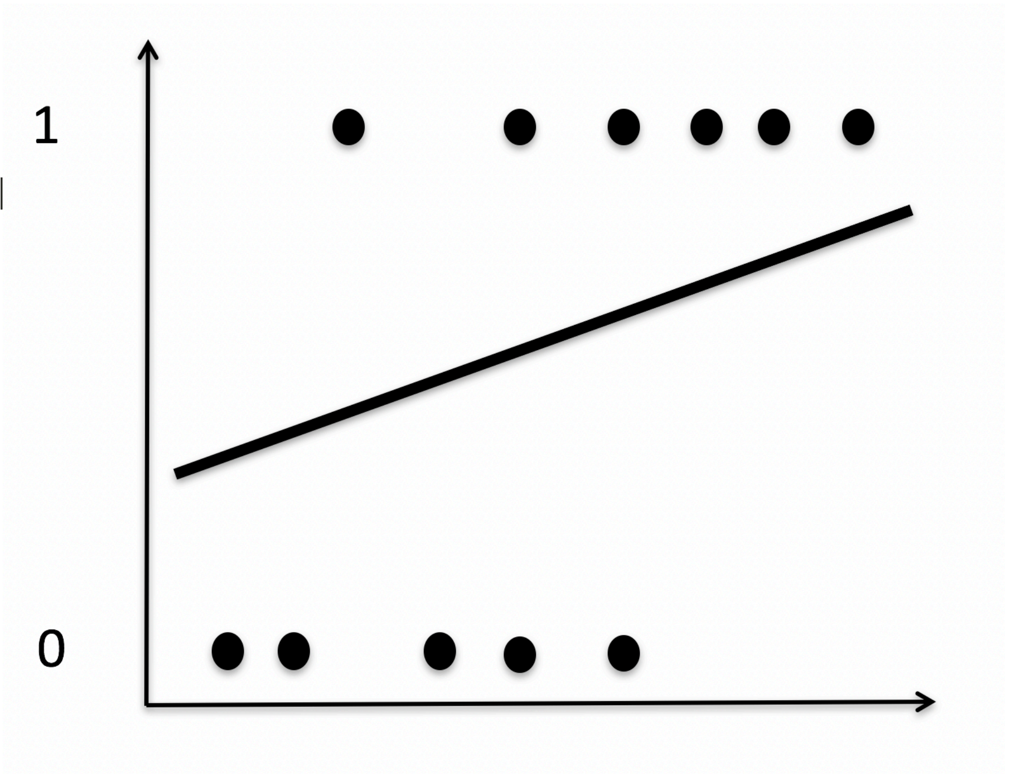
The mean of the distribution is the same as the proportion of 1's in the distribution.

- Out of 100 people, 27 have PTSD (1) and 73 do not have PTSD (0)
- The mean of the distribution is .27
- Probability of getting a 1 is .27

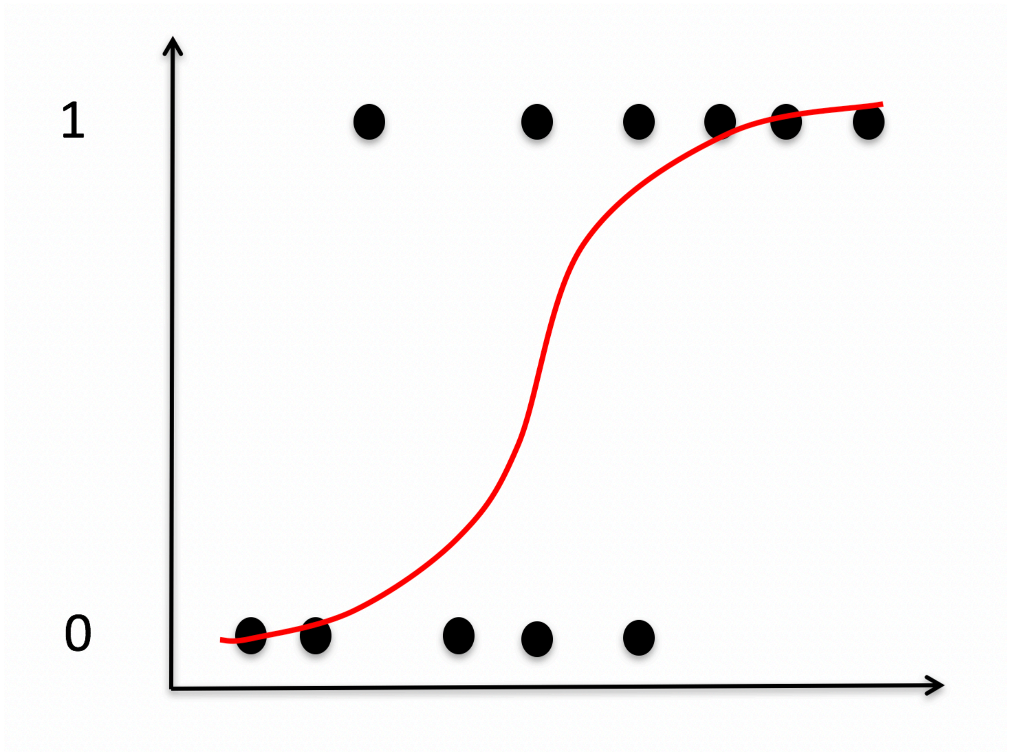
If we plotted these points, they are either 1's or 0's



OLS regressio line. It doesn't make sense! Predicted values can go above 1 or below 0...yikes



Instead, we fit this non-linear function. None of our data fall on the line!



Where is the line??

Logistic Regression, rather than a straight, fitted line like linear regression, logistic regression fits an S-shaped logistic function.

This curved line can tell us the **probability that something will be "1" given *X***

Model Complexity

...and just like linear regression, we can make simple models (a relationship between *x* and *y*, with *y* being a binary variable) or more complicated models (with covariates).

Unlike linear regression, it isn't as easy to just compare a more complex model to a simple model

Assumption violations

When our outcome is binary, we violate OLS regression assumptions

Violates:

- Correctly specified form (not linear)
- Homoscedasticity (as probability approaches 1 or 0, variance approaches 0)
- Normality of the errors (lol not close)

Need to think in terms of probabilities

- If we use OLS, we violate assumptions and have predicted values that go outside 0 & 1
- How does the predicted probability of getting a 0 or a 1 relate to our predictors?

$$\hat{p}_i \leftrightsquigarrow b_0 + b_1 X_1 + b_2 X_2 \ldots b_3 X_p$$

Generalized linear models

- Extends the general linear model framework
- Used to describe different Data Generating Processes (DGPs) other than Gaussian normal
- Need to use if we cannot use the Gaussian normal e.g. the range of Y is restricted (e.g. binary, count) and/or the variance of Y depends on the mean, etc...
- In other words, **what is your DGP?**

Generalized linear models

- Gaussian model

$$y_i \sim N(\mu_i, \sigma)$$

$$\mu_i = \alpha + \beta x_i$$

- The parameters of the normal distribution are the mean μ and the standard deviation σ (or the variance σ^2)

- Binomial outcome

$$y_i \sim Binomial(n, p_i)$$

$$f(p_i) = \alpha + \beta x_i$$

- **n** stands for the number of times the experiment runs.
- ***p*** represents the probability of one specific outcome.

GLM components

It is not common to have an average outcome μ (other than in a normal distribution)

It is not common to have parameters range from negative to positive infinity.

We need something that translates our model into the parameters that describe the distribution.

Logistic regression

$$y_i \sim Binomial(n, p_i)$$

$$f(p_i) = \alpha + \beta x_i$$

Our number of trials is N, so we are predicting the probability of y. Probabilities are bounded between zero and one.

Because our variables are not in probability units we need to "link" them via a function. The linear right side of the equation is not in the same units as the non-linear left side.

Two most popular are logit and log.

Link function for logistic

- We need to map (0,1) to $(-\infty, \infty)$
- Logistic regression uses the logistic function to link the predicted probabilities to the predictors
- Think of it as a transformation of $\hat{Y}$s

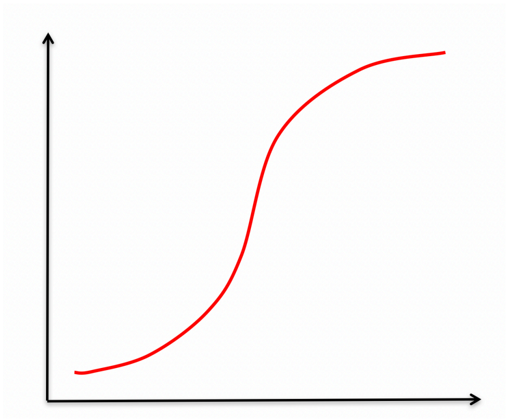
Sigmoid function

$$f(x) = \frac{1}{1 + e^{-X}}$$

... where e is Euler's number

```r
exp(1)
```

```
## [1] 2.718282
```



The y-axis is the "rolling mean" of the DV (or the proportion of 1's). This logistic curve relates X (the IV) to our $P(\bar{Y})$

Sigmoid function (cont.)

For the Sigmoid function, as x approaches ∞, it reaches a natural limit at 1.

As x approaches $-\infty$, it reaches a natural limit of 0

This all keeps the limits within the 0, 1 range.

$$f(x) = \frac{1}{1 + e^{-X}}$$

$$\hat{p} = \frac{1}{1 + e^{-b_0 + b_1 X}}$$

- The form of the logistic function is still nonlinear (because probabilities can only range from 0 to 1)
- Since it's nonlinear, b can't be interpreted as easily as we've been doing with OLS regression.
- So in order to interpret our model parameter, we need to convert to **odds**

Odds

- Odds are defined as the probability of being a case divided by the probability of being a noncase
- Not bound between 0 and 1
- Range from 0 to infinity
- Less than one is less than 50% probability

$$odds = \frac{\hat{p}}{1 - \hat{p}}$$

$$probability = \frac{o\hat{d}ds}{1 + o\hat{d}ds}$$

Odds versus Probability

Put simply:

- Odds are the ratio of something happening over something not happening.
- Probability is the ratio of something happening over everything that could happen.

The odds being so asymmetrical (unlike probability) make it difficult to compare the odds of being 0 versus the odds of being 1. So we use something called log odds.

Log Odds

Taking the log of the odds solves this problem by making everything symmetrical!

Odds are 1 to 6:

- log(1/6) = log(0.17) = -1.79

Odds are 6 to 1:

- log(6/1) = log(6) = 1.79

Linear Probability Model

$$f(x) = \frac{1}{1 + e^{-X}}$$

$$\hat{p} = \frac{1}{1 + e^{-b_0 + b_1 X}}$$

$$odds = \frac{\hat{p}}{1 - \hat{p}} = e^{b_0 + b_1 X}$$

$$logit = Log(odds) = ln(\frac{\hat{p}}{1 - \hat{p}}) = b_0 + b_1 X$$

Logit

$$logit = Log(odds) = ln(\frac{\hat{p}}{1-\hat{p}}) = b_0 + b_1X$$

- DV is a logit, the natural log of odds
- Predicted scores are not dichotomous
- Instead of predicting probabilities directly, we are instead predicting the log of the odds.
- The regression we are used to is not predicting $\hat{Y}$, because we're predicting (or relating our IV) *logits*

Now what?

- In order to get the probability of a value of X being 1 or 0 based on some model parameters (b_0, b_1 etc.), we rearrange our equation so that we actually get the predicted logit (log of odds) given our model parameters.
- How the hell do you interpret a logit? Not easily...
- Convert back into odds
- Convert your odds back into probabilities

Uhhhhhh

Does this seem convoluted?

We are predicting logits, which happen to be the log of odds. It's bananas.

How do we get these numbers in the first place? Can we use OLS?

Estimation with Maximum Likelihood

- OLS minimizes the errors (SS_{res}), which maximizes (SS_{reg})
- In logistic regression we are not so lucky
- Need to rely on iterative procedure, Maximum Likelihood (ML) Estimation:
    - Pick parameters of your model (b_0, b_1 etc.), and calculate the *likelihood* of the data, given those parameters. We do this iteratively until we find the best parameters -- the ones that *maximize* the *likelihood* of your data.

Estimation with Maximium Likelihood

Do any of you hike? Know how to read a topographic map?

ML Estimation is sort of like going hiking with your data to find the highest point. And most of the time you can!

But if if you take a wrong turn, you might get screwed. It's the risk we take when using ML Estimation!

Estimation with Maximum Likelihood

We are using the distribution of the data to find the location that maximizes the likelihood of observing the variable that we measured.

We are essentially trying to find the optimal value for the mean (or standard deviation) for a distribution given our observed data.

We are talking here about the mean of the distribution, not the mean of the data. (However, in a normal distribution, these are the same thing.)

Estimation with Maximum Likelihood

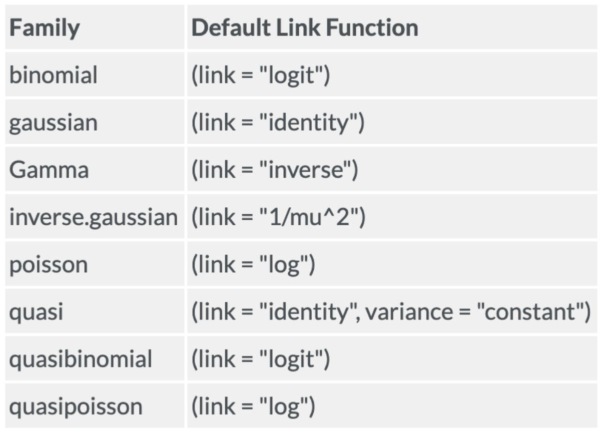
- So we get model parameters, estimated via MLE (instead of OLS)
- Same but different:
  - Asymptotic standard errors (an approximation to the standard error)
  - Interpret test statistics as z's, not t's
  - No t-tests; instead a Wald test = χ^2 test with 1 df = $(\frac{coef}{se})^2$

- We try to predict binary outcomes. Our DV is dichotomous.
- We can use categorical or continuous predictors (IVs) to do so
- We can write the equation in roughly the same way
- We cannot use OLS because it will give us impossible values and just logically it doesn't work. We use ML Estimation to determine our logistic regression coefficients instead. This gives us a S-shaped curve
- We can ask if our coefficients are significantly different from 0
- We convert to odds and/or probabilities

GLM in R

```
glm(formula,
    family = gaussian(link="
    data,
    weights,
    subset,
    na.action,
    start = NULL,
    etastart,
    mustart,
    offset,
    control = glm.control(..
    model = TRUE,
    method = ”glm.fit”,
    x = FALSE,
    y = TRUE,
    contrasts = NULL, ...)
```

The `family` argument specifies the distribution. In R, families have default links.



Family	Default Link Function
binomial	(link = "logit")
gaussian	(link = "identity")
Gamma	(link = "inverse")
inverse.gaussian	(link = "1/mu^2")
poisson	(link = "log")
quasi	(link = "identity", variance = "constant")
quasibinomial	(link = "logit")
quasipoisson	(link = "log")

GLM in R

```
glm(y ~ X1+ X2 + X3 ,
    family = binomial,
    data = dataset)
```

Specify the model like you would with `lm`

GLM in R

```
glm(y ~ X1+ X2 + X3 ,
    family = binomial,
    data = dataset)
```

Specify the distribution you're working with. When binary outcomes, we'll use the binomial.

GLM in R

```
glm(y ~ X1+ X2 + X3 ,
    family = binomial,
    data = dataset)
```

Specify your dataset.

How to interpret

- b_1 is the predicted change in the logit for a 1-unit change in X, holding the other predictors constant
- For a 1-unit change in X, holding other predictors constant, the odds that Y = 1 changes by e^{b_1}
  - e.g,. b_1 = .4, $e^{.4}$ = 1.49
- For fitted values, need to use entire equation $\hat{Y} = e^{b_0+b_1X_1}$
- Turn to probabilities by: $\frac{\text{odds}}{(1+\text{odds})}$

Example

```r
# 1 = not premature
mortality
```

```
## # A tibble: 300 × 4
##    Intelligence_Self Intelligence_Mate premature.d NOT.premature
##                <dbl>             <dbl> <fct>               <dbl>
##  1                22                19 normal                  1
##  2                22                18 normal                  1
##  3                21                21 normal                  1
##  4                22                17 normal                  1
##  5                19                18 normal                  1
##  6                19                20 premature               0
##  7                16                18 normal                  1
##  8                15                11 premature               0
##  9                16                21 normal                  1
## 10                19                22 normal                  1
## # ℹ 290 more rows
```

```r
death.1 <- lm(NOT.premature ~ Intelligence_Self , data = mort
summary(death.1)
```

```
##
## Call:
## lm(formula = NOT.premature ~ Intelligence_Self, data = mortality)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.9030  0.1084  0.1538  0.1907  0.3355
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.641769   0.098636   6.506 3.25e-10 ***
## Intelligence_Self 0.011357   0.005807   1.956   0.0514 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3745 on 298 degrees of freedom
## Multiple R-squared:  0.01267,    Adjusted R-squared:  0.009362
## F-statistic: 3.826 on 1 and 298 DF,  p-value: 0.05141
```

```
death.2 <- glm(NOT.premature ~ Intelligence_Self , data = mor
summary(death.2)
```

```
##
## Call:
## glm(formula = NOT.premature ~ Intelligence_Self, data = mortality)
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.641769   0.098636   6.506 3.25e-10 ***
## Intelligence_Self 0.011357   0.005807   1.956   0.0514 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1402466)
##
##     Null deviance: 42.330  on 299  degrees of freedom
## Residual deviance: 41.793  on 298  degrees of freedom
## AIC: 266.05
##
## Number of Fisher Scoring iterations: 2
```

```r
death.3 <- glm(NOT.premature ~ Intelligence_Self,
               family = binomial, data = mortality)
summary(death.3)
```

```
##
## Call:
## glm(formula = NOT.premature ~ Intelligence_Self, family = binomial,
##     data = mortality)
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.28695    0.67490   0.425   0.6707
## Intelligence_Self  0.08012    0.04143   1.934   0.0532 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 273.53  on 299  degrees of freedom
## Residual deviance: 269.75  on 298  degrees of freedom
## AIC: 273.75
##
## Number of Fisher Scoring iterations: 4
```

Interpretation

For each 1-unit change in X, holding other predictors constant, the odds of the outcome occurring (that Y = 1) changes by e^{b_1}

```r
exp(1)^.08012
```

```
## [1] 1.083417
```

For every 1-unit increase in Intelligence, the odds of not having a premature death increase by ~8%

1.083-1 = .08

What if you want the probability of being a premature death for a given level of Intelligence? (Now that we've run our model and have parameters...)

For fitted values, need to use entire equation $\hat{Y} = e^{b_0 + b_1 X_1}$

```r
# get fitted value with a given value of X (here 20)
exp(1)^(0.28695 + (.08012*20))
```

```
## [1] 6.615067
```

```r
# now get odds
6.615067 / (1+6.615067)
```

```
## [1] 0.8686814
```

Probit

We can have different link functions. When your response variable (DV) is truly binary -- the data generating process generates legit binary data -- logit is your pick.

What if your response variable is binary, but the underlying construct you are trying to measure is likely Gaussian? Ex: depressed vs. not depressed. But the underlying latent construct is continuous. More appropriate then is the **probit** link function.

Stack exchange thread if you're going down this route

Probit

```
death.4 <- glm(NOT.premature ~ Intelligence_Self,
         family = binomial(link = "probit"), data = mortality)
summary(death.4)
```

```
##
## Call:
## glm(formula = NOT.premature ~ Intelligence_Self, family = binomial(lin
##     data = mortality)
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.21961    0.38376   0.572   0.5671
## Intelligence_Self  0.04513    0.02319   1.946   0.0516 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 273.53  on 299  degrees of freedom
## Residual deviance: 269.72  on 298  degrees of freedom
## AIC: 273.72
##
```