Microeconometrics (Causal Inference)
Week 3 - Discrete Choice

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What are we doing today?

- This week we will review methods for limited dependent variables
  - We will also discuss how to interpret the results

- Some of this will be review, but there will be some new stuff, too
  - For example, we will discuss poisson regression, which you might not have seen before

What are we doing today?

- Much of the mathematical notation and theory comes from *Econometrics* by Bruce Hansen
  - I already discussed the older version of the textbook that is available for free online

- A small note:
  - You can use OLS for binary outcomes! This is actually pretty common in economics.
  - I'll discuss this more in a bit.
  - Other disciplines (e.g. public health) really like some of the new methods we will discuss today, so they are worth knowing.

Binary choice

- Let's start with the simplest possibility: binary choice
- You can think of this as a No/Yes or False/True question, but we will generally refer to it as 0/1 choice
  - In programming, always remember that $FALSE = 0$ and $TRUE = 1$
- Focusing on the binary choice case will allow us to build intuition for the more general case of discrete choice
  - We will also be able to use the same data as we move to the more general case

- We will be thinking about this $Y \in \{0, 1\}$
  - In other words, Y is a dichotomous (dummy) variable that can only be equal to 0 or 1

- We are going to discuss methods to output *conditional probabilities*:

$$\mathbb{P}[Y = 1|X] \tag{1}$$

- Consider the following model:

$$Y = \beta X + \epsilon, \tag{2}$$

  where X can have any number of columns (variables), k.

- We already know that ϵ does not need to be normally distributed

- In fact, if $Y \in \{0, 1\}$, then ϵ *will never be normally distributed*
  - Why?

- ϵ has a two-point conditional distribution:

$$\epsilon = \begin{cases} 1 - P(X), & \text{with probability } P(X) \\ P(X), & \text{with probability } 1 - P(X) \end{cases} \tag{3}$$

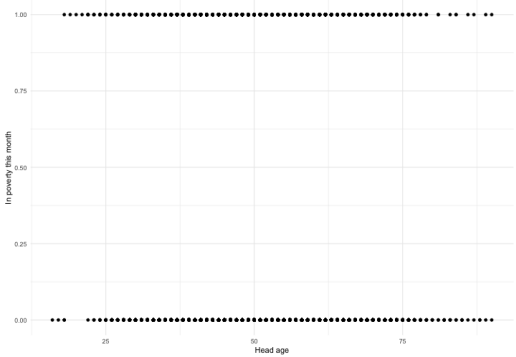
- ϵ is *heteroskedastic*:

$$\text{Var}(\epsilon|X) = P(X)(1 - P(X)) \tag{4}$$

- In fact, the variance of any dummy variable is $P(1 - P)$, where P is the probability of the dummy variable being equal to 1

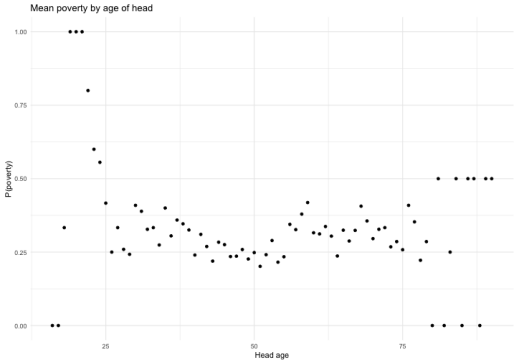
Scatterplots are pretty worthless!

```r
# for reading in Stata data.
# Install this using your console
library(haven)
# read in data for the week:
df <- read_dta("data.dta")

# scatter of in_poverty on h_age:
ggplot(data = df) +
  geom_point(aes(x = h_age, y = in_poverty)) +
  labs(x = "Head age", y = "In poverty this month") +
  theme_minimal()
```



Let's plot out the conditional probabilities (means)

```r
# means by age
povmeans <- df %>%
            group_by(h_age) %>%
            summarize(mean = mean(in_poverty)) %>%
            ungroup

# scatter of in_poverty on h_age:
ggplot(data = povmeans) +
  geom_point(aes(x = h_age, y = mean)) +
  labs(x = "Head age", y = "P(poverty)") +
  theme_minimal()
```



- We can estimate this using OLS:

$$Y = \beta X + \epsilon \tag{5}$$

```
summary(feols(in_poverty ~ h_male + h_age, data = df, vcov = "HC1"))
```

```
## OLS estimation, Dep. Var.: in_poverty
## Observations: 4,609
## Standard-errors: Heteroskedasticity-robust
##              Estimate Std. Error   t value  Pr(>|t|)
## (Intercept)  0.352347   0.037235  9.462735 < 2.2e-16 ***
## h_male      -0.060625   0.025993 -2.332375  0.019724 *
## h_age       -0.000050   0.000553 -0.089808  0.928443
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## RMSE: 0.455294   Adj. R2: 8.54e-4
```

Linear probability model (LPM)

```
summary(feols(in_poverty ~ h_male + h_age, data = df, vcov = "HC1"))
```

```
## OLS estimation, Dep. Var.: in_poverty
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## RMSE: 0.455294   Adj. R2: 8.54e-4
```

- The interpretation of these coefficients is pretty straightforward:
  - It is the change in the probability of being in poverty for a one-unit change in the variable of interest
  - Male-headed households are 6.1 *percentage points* less likely to be poor than female-headed households, controlling for age.
  - Each addidition year of age *increases* the probability of being in poverty by 0.005 *percentage points*, controlling for gender of the head.

- Sometimes people motivate other estimation methods based on heteroskedasticity
  - But we can easily correct for this using robust standard errors (HC1 in feols)

- There are two other problems with LPM, though:
  - The predicted values can be outside of the 0-1 range
    - Is this a problem? Maybe. Maybe not. It depends on what you're doing.
  - Constant effects throughout the probability distribution
    - Is this realistic? If we think someone has a 95 percent probability of being poor, do we think the percentage point change would be the same for changing a variable relative to someone with a 5 percent probability of being poor?

- We can think of this as a *latent variable* model:

$$Y^* = \beta X + \epsilon \tag{6}$$

$$\epsilon \sim G(\epsilon) \tag{7}$$

$$Y = \mathbb{1}(Y^* > 0) = \begin{cases} 1, & \text{if } Y^* > 0 \\ 0, & \text{otherwise} \end{cases} \tag{8}$$

  where Y^* is the latent variable, $G(\cdot)$ is the distribution of ϵ, and $\mathbb{1}(\cdot)$ is the indicator function.

- One way to think about this is that y^* is utility, but we only observe whether the choice increases utility ($y = 1$) or doesn't ($y = 0$).

Let's give this a bit more structure

- Note that $Y = 1$ iff $Y^* > 0$, which is the same as saying $\beta X + \epsilon > 0$
- The response probability is then given by the CDF of ϵ evaluated at $-\beta X$:

$$\mathbb{P}[Y = 1|X] = \mathbb{P}[\epsilon > -\beta X] = 1 - G(-\beta X) = G(\beta X) \tag{9}$$

- Note that CDFs (cumulative distribution functions) give us probabilities of being *less than or equal to* a given value
  - The last equality holds because $G(\cdot)$ will always be *symmetric around 0* here
  - That value here is βX

- The function $G(\cdot)$ is called the *link function* and plays an important role here
- Two common link functions are the *logit* and *probit* link functions:
  - They are defined as follows:
  - Logit: $G(\epsilon) = \frac{e^{\epsilon}}{1+e^{\epsilon}} = \frac{1}{1+e^{-\epsilon}}$
  - Probit: $G(\epsilon) = \Phi(\epsilon)$, where $\Phi(\cdot)$ is the CDF of the standard normal distribution
- We will discuss these in more detail in a bit

- Likelihood: the joint probability of the data evaluated with the sample, as a function of the parameters
  - What?

- Let's start with probit, which uses a normal distribution. Here is the conditional density of Y given X under this assumption:

$$f(Y|X) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}(Y - \beta X)^2\right) \tag{10}$$

$$f(Y|X) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}(y - \beta X)^2\right) \tag{11}$$

- In this case, what is the probability we *observe our sample given the values of* β *and* σ?

$$\begin{aligned} f(y_1, \ldots, y_n | x_1, \ldots, x_n) &= \prod_{i=1}^{n} f(y_i|x_i) && (12)\\ &= \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}(y_i - \beta x_i)^2\right) && (13)\\ &= \frac{1}{(2\pi\sigma^2)^{n/2}} \exp\left(-\frac{1}{2\sigma^2} \prod_{i=1}^{n} (y_i - \beta x_i)^2\right) && (14)\\ &= L_n(\beta, \sigma^2) && (15) \end{aligned}$$

$$f(y_1, \ldots, y_n | x_1, \ldots, x_n) = L_n(\beta, \sigma^2) \tag{16}$$

- This is the *likelihood function*
  - Note that it is a function of the parameters, β and σ^2
- The properties of logs make this easier to work with:

$$\ell_n(\beta, \sigma^2) = \log(L_n(\beta, \sigma^2)) = -\frac{n}{2}\log(2\pi\sigma^2) - \frac{1}{2\sigma^2}\sum_{i=1}^{n}(y_i - \beta x_i)^2 \tag{17}$$

- This is the *log likelihood function*
  - It is of course also a function of the parameters, β and σ^2

$$\ell_n(\beta, \sigma^2) = \log(L_n(\beta, \sigma^2)) = -\frac{n}{2}\log(2\pi\sigma^2) - \frac{1}{2\sigma^2}\sum_{i=1}^{n}(y_i - \beta x_i)^2 \tag{18}$$

- We have our log likelihood function, which is a function of the parameters, β and σ^2
- What we want to do is find the values of β and σ^2 that *maximize* this function
  - In other words, the values that make our sample the most likely to have been observed, or the biggest probability of observing our sample
- This is called *maximum likelihood estimation*

$$\left(\hat{\beta}, \hat{\sigma}^2\right) = \underset{\beta \in \mathbb{R}^k, \sigma^2 > 0}{\operatorname{argmax}} \ \ell_n(\beta, \sigma^2) \tag{19}$$

where k is the number of variables (coefficients), including the intercept.

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- Let's say we flip a coin. If it's a fair coin, what is the probability of obtaining heads?

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- Three times in a row?

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- What is the probability of obtaining heads twice in a row?
  - 0.5 * 0.5 = 0.25
- Three times in a row?
  - 0.5 * 0.5 * 0.5 = 0.125

- Say we flip the coin a bunch of times
  - For argument's sake, let's say we flip it 100 times and obtain 60 heads
- If we know nothing about whether the coin is actually fair, what is the *most likely distribution* that would give us 60 heads and 40 tails?

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  - It's a distribution in which the probability of heads is 0.6!

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  - For argument's sake, let's say we flip it 100 times and obtain 60 heads
- If we know nothing about whether the coin is actually fair, what is the *most likely distribution* that would give us 60 heads and 40 tails?
  - It's a distribution in which the probability of heads is 0.6!
- This is like maximum likelihood estimation. We are trying to find the parameters that makes our sample the most likely to have been observed.
  - In this case, the parameter would be the true mean of the distribution of the coin (where heads $= 1$ and tails $= 0$).
  - We could then of course test whether this is significantly different from 0.5, which might be our null hypothesis.

$$\left(\hat{\beta}, \hat{\sigma}^2\right) = \underset{\beta \in \mathbb{R}^k, \sigma^2 > 0}{\text{argmax}} \; \ell_n(\beta, \sigma^2) \tag{20}$$

- MLE is generally always estimated using numerical optimization
  - We will not discuss the details of this here
  - The basic reason is that most likelihood functions are not easy to maximize analytically (i.e. they have no closed-form solution)

- In the case of the normal regression model, however, there is a closed-form solution
  - And this is the same closed-form solution as OLS!

- Let's return to our binary choice model.
  - Regardless of how you estimate it, the probability mass function for Y is:

$$\pi(y) = p^y(1-p)^{1-y}, \tag{21}$$

where p is the probability of $Y = 1$, or the mean. Remember that $Y \in \{0, 1\}$; i.e., it can only equal 0 or 1.

- Let's bring our link function back into it. The *conditional* probability is:

$$\pi(Y|X) = G(\beta X)^Y(1 - G(\beta X))^{1-Y} = G(\beta X)^Y(G - \beta X)^{1-Y} = G(\beta Z), \tag{22}$$

where $Z = \begin{cases} X, & \text{if } Y = 1 \\ -X, & \text{if } Y = 0 \end{cases}$

$$\pi(Y|X) = G(\beta Z), \tag{23}$$

- Taking logs (because they're easy to work with), we get the log likelihood function:

$$\ell_n(\beta) = \sum_{i=1}^{n} \log G(\beta Z) \tag{24}$$

- This is the same as the log likelihood function for probit, except that the link function is different.

- Again, we want to find the values of β (and σ, which will show up in the link function) that maximize this function.

$$\left(\hat{\beta}, \hat{\sigma}^2\right) = \underset{\beta \in \mathbb{R}^k, \sigma^2 > 0}{\text{argmax}} \; \ell_n(\beta, \sigma^2) \tag{25}$$

- Something interesting is that in practice, we don't numerically optimize...
  - Instead, we *minimize* the *negative* of the log likelihood function!

$$\left(\hat{\beta}, \hat{\sigma}^2\right) = \underset{\beta \in \mathbb{R}^k, \sigma^2 > 0}{\text{argmin}} \; -\ell_n(\beta, \sigma^2) \tag{26}$$

An example in R - Household variables and poverty using glm()

```r
summary(glm(in_poverty ~ h_male, data = df, family = binomial(link = "logit")))
```

```
##
## Call:
## glm(formula = in_poverty ~ h_male, family = binomial(link = "logit"),
##     data = df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9280  -0.8263  -0.8263   1.5752   1.5752
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.6196     0.1101  -5.631  1.8e-08 ***
## h_male       -0.2796     0.1151  -2.428   0.0152 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 5583.2  on 4608  degrees of freedom
## Residual deviance: 5577.5  on 4607  degrees of freedom
## AIC: 5581.5
##
## Number of Fisher Scoring iterations: 4
```

Interpreting logit output

```
##               Estimate Std. Error   z value     Pr(>|z|)
## (Intercept) -0.6196447  0.1100514 -5.630505 1.796828e-08
## h_male      -0.2795628  0.1151389 -2.428047 1.518036e-02
```

- How do we interpret these coefficients?
  - The coefficients are "log odds"

- For male household heads, the log odds of being in poverty is 0.280 *lower* than that for female household heads
  - What?

- What are log odds?
  - Let's start with odds:

$$\text{odds} = \frac{p}{1-p}, \tag{27}$$

where p is the probability of $y = 1$ (being poor in this case).

- Log odds?

$$\log \text{odds} = \log\left(\frac{p}{1-p}\right) \tag{28}$$

- Logit regression is basically estimating:

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X_1 + \ldots + \beta_k X_k \tag{29}$$

The intercept is the log odds of being in poverty for female households

```
##               Estimate Std. Error   z value     Pr(>|z|)
## (Intercept) -0.6196447  0.1100514 -5.630505 1.796828e-08
## h_male      -0.2795628  0.1151389 -2.428047 1.518036e-02
```

$$\log\left(\frac{p}{1-p}\right) = -0.6196447 \tag{30}$$

$$\left(\frac{p}{1-p}\right) = exp(-0.6196447) \tag{31}$$

$$\left(\frac{p}{1-p}\right) \approx 0.538 \tag{32}$$

$$p = 0.538 - 0.538p \tag{33}$$

$$1.538p = 0.538 \tag{34}$$

$$p \approx 0.350 \tag{35}$$

What is the actual mean for female headed households? 0.35

$$\log\left(\frac{p_m}{1-p_m}\right) - \log\left(\frac{p_f}{1-p_f}\right) = -0.2795628 \tag{36}$$

$$\log\left(\frac{\frac{p_m}{1-p_m}}{\frac{p_f}{1-p_f}}\right) = -0.2795628 \tag{37}$$

$$\left(\frac{\frac{p_m}{1-p_m}}{\frac{p_f}{1-p_f}}\right) = exp(-0.2795628) \tag{38}$$

$$\left(\frac{\frac{p_m}{1-p_m}}{\frac{p_f}{1-p_f}}\right) = 0.7561142 \tag{39}$$

- In the last line, this is referred to as an *odds ratio*.
  - It's less than one, which means male-headed households are *less likely* to be in poverty.
  - Their *odds* of being in poverty are around 24% lower.

The coefficient?

- Mean for female-headed households: 0.35
  - odds ($\frac{p_f}{1-p_f}$): 0.538
- Mean for male-headed households: 0.289
  - odds ($\frac{p_m}{1-p_m}$): 0.407
- Odds ratio: 0.756
- Exponentiating shows us the odds ratio!

- We can also calculate marginal effects
  - These are the change in the probability of being in poverty for a one-unit change in the variable of interest
  - An important note is that this *depends on where you are located in the distribution*

- We just calculated the means, so with only the binary independent variable, we know that the marginal effect is:
  - -0.0606

- We will use the "mfx" package for this, so please install it in the console.

Marginal effects

```
logitmfx(in_poverty ~ h_male, data = df)
```

```
## Call:
## logitmfx(formula = in_poverty ~ h_male, data = df)
##
## Marginal Effects:
##            dF/dx Std. Err.       z   P>|z|
## h_male -0.060649  0.025981 -2.3343 0.01958 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## dF/dx is for discrete change for the following variables:
##
## [1] "h_male"
# for binary outcomes, it shows the change from 0 to 1!
```

logit with more coefficients

```
logitmfx(in_poverty ~ h_male + h_age, data = df)
```

```
## Call:
## logitmfx(formula = in_poverty ~ h_male + h_age, data = df)
##
## Marginal Effects:
##              dF/dx   Std. Err.       z   P>|z|
## h_male -6.0623e-02  2.5982e-02 -2.3333 0.01963 *
## h_age  -4.9739e-05  5.3672e-04 -0.0927 0.92616
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## dF/dx is for discrete change for the following variables:
##
## [1] "h_male"
```

```
# for binary outcomes, it shows the change from 0 to 1!
# for continuous variables, it's the derivative (i.e. instantaneous change)!
# By default, it calculates these by holding variables AT THEIR MEANS
```

Probit

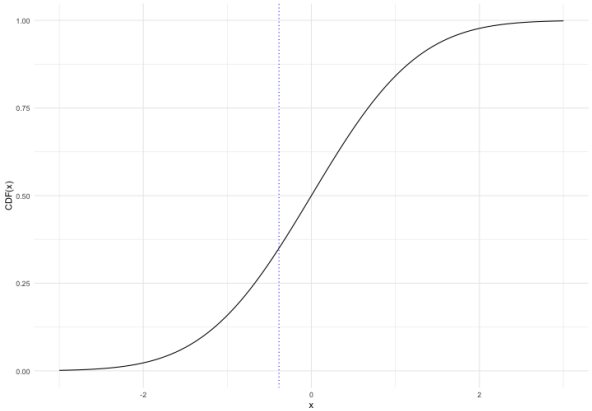
```
summary(glm(in_poverty ~ h_male, data = df, family = binomial(link = "probit")))$coefficients
```

```
##               Estimate Std. Error   z value     Pr(>|z|)
## (Intercept) -0.3856924 0.06759123 -5.706248 1.154935e-08
## h_male      -0.1699918 0.07058912 -2.408188 1.603194e-02
```

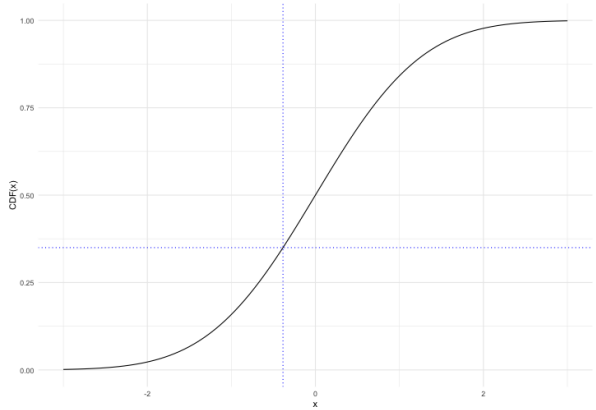
- What about probit coefficients?
  - These relate to the *CDF of the standard normal distribution*

- The intercept is the mean for female-headed households

- The intercept is -0.3856924
  - The mean poverty for female-headed households is 0.35
- Here's the CDF for the standard normal distribution with the intercept:



- The intercept is -0.3856924
  - The mean poverty for female-headed households is 0.35
- Here's the CDF for the standard normal distribution with BOTH:

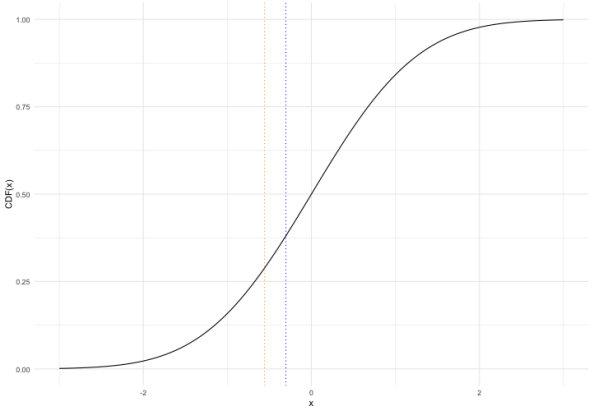


Now let's look at the coefficient on h_male

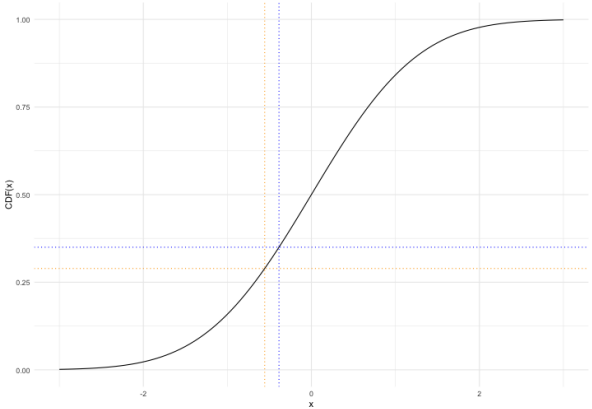
```
summary(glm(in_poverty ~ h_male, data = df, family = binomial(link = "probit")))$coefficients
```

```
##               Estimate Std. Error   z value     Pr(>|z|)
## (Intercept) -0.3856924 0.06759123 -5.706248 1.154935e-08
## h_male      -0.1699918 0.07058912 -2.408188 1.603194e-02
```

- The intercept is -0.3038412 and the coefficient is -0.1699918
- Here's the CDF for the standard normal distribution with BOTH:



- The intercept is -0.3856924 and the coefficient is -0.1699918
- What's the change in PROBABILITY? mean(male) − mean(female) or -0.0606



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##
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```

Probit and marginal effects

```r
# change in z-scores
summary(glm(in_poverty ~ h_male + h_age, data = df, family = binomial(link = "probit")))$coefficients
```

```
##                 Estimate  Std. Error     z value     Pr(>|z|)
## (Intercept) -0.3783277748 0.103202161 -3.66589005 0.0002464798
## h_male      -0.1699296493 0.070592873 -2.40717853 0.0160763088
## h_age       -0.0001469862 0.001557869 -0.09435083 0.9248304734
```

```r
# change in probability, holding other variables at their means
probitmfx(in_poverty ~ h_male + h_age, data = df)
```

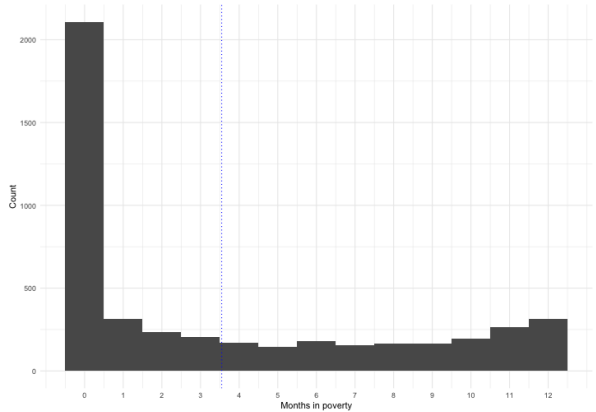
```
## Call:
## probitmfx(formula = in_poverty ~ h_male + h_age, data = df)
##
## Marginal Effects:
##              dF/dx   Std. Err.       z   P>|z|
## h_male -6.0626e-02  2.5982e-02 -2.3334 0.01963 *
## h_age  -5.0621e-05  5.3651e-04 -0.0944 0.92483
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## dF/dx is for discrete change for the following variables:
##
## [1] "h_male"
```

What if the outcome has more than two categories?

- Many outcomes are not 0/1.
- We can think of outcomes with discrete categories, but more than two:
  - Religion
  - Political party
  - Opinion on a likert scale (e.g. strongly agree, agree, neutral, disagree, strongly disagree)
  - Months in poverty
- There's a key difference between the first two and the last two:
  - The first two are *unordered*
  - The last two are *ordered*

Months in poverty - distribution

```
ggplot() +
    geom_histogram(data = df, aes(x = months_in_poverty), binwidth = 1) +
    theme_minimal() +
    labs(x = "Months in poverty", y = "Count") +
    scale_x_continuous(breaks = seq(0, 12, 1)) +
    geom_vline(xintercept = mean(df$months_in_poverty), linetype = "dotted", color = "blue")
```



Ordered logistic regression with the polr function

```r
# note that the outcome must be a FACTOR variable for polr
summary(polr(as_factor(months_in_poverty) ~ h_male + h_age, data = df, Hess = TRUE))
```

```
## Call:
## polr(formula = as_factor(months_in_poverty) ~ h_male + h_age,
##     data = df, Hess = TRUE)
##
## Coefficients:
##             Value Std. Error  t value
## h_male -0.3826883    0.10035 -3.81337
## h_age   0.0001876    0.00216  0.08681
##
## Intercepts:
##       Value   Std. Error t value
## 0|1   -0.5168  0.1457    -3.5478
## 1|2   -0.2434  0.1455    -1.6730
## 2|3   -0.0376  0.1455    -0.2585
## 3|4    0.1472  0.1455     1.0119
## 4|5    0.3078  0.1455     2.1149
## 5|6    0.4514  0.1456     3.1004
## 6|7    0.6416  0.1458     4.4014
## 7|8    0.8171  0.1460     5.5975
## 8|9    1.0249  0.1463     7.0044
## 9|10   1.2665  0.1469     8.6198
## 10|11  1.6049  0.1482    10.8280
## 11|12  2.2775  0.1529    14.8999
##
## Residual Deviance: 18592.59
## AIC: 18620.59
```

- When we have ordered discrete variable, we can use an ordered logit or probit model
  - These are also called *ordinal* logit/probit models
- The idea is that we have a latent variable, Y^*, that is continuous
  - We observe Y as a discrete variable, but it is *ordered*
  - We can think of Y as being *binned* into categories

$$Y = \begin{cases} 1, & \text{if } Y^* \in (-\infty, \theta_1] \\ 2, & \text{if } Y^* \in (\theta_1, \theta_2] \\ \vdots & \vdots \\ J, & \text{if } Y^* \in (\theta_{J-1}, \infty) \end{cases} \tag{40}$$

The interpretation?

```
## Call:
## polr(formula = as_factor(months_in_poverty) ~ h_male + h_age,
##     data = df, Hess = TRUE)
##
## Coefficients:
##             Value Std. Error  t value
## h_male -0.3826883    0.10035 -3.81337
## h_age   0.0001876    0.00216  0.08681
##
## Intercepts:
##       Value   Std. Error t value
## 0|1   -0.5168  0.1457    -3.5478
## 1|2   -0.2434  0.1455    -1.6730
## 2|3   -0.0376  0.1455    -0.2585
## 3|4    0.1472  0.1455     1.0119
## 4|5    0.3078  0.1455     2.1149
## 5|6    0.4514  0.1456     3.1004
## 6|7    0.6416  0.1458     4.4014
## 7|8    0.8171  0.1460     5.5975
## 8|9    1.0249  0.1463     7.0044
## 9|10   1.2665  0.1469     8.6198
## 10|11  1.6049  0.1482    10.8280
## 11|12  2.2775  0.1529    14.8999
##
## Residual Deviance: 18592.59
## AIC: 18620.59
```

- The interpretation is similar to logit: a change in the log-odds of being in a higher level of months in poverty!

- There is no r-squared in MLE
  - It is not a true r-squared *because there is no sense of "mean" with discrete data, especially unordered data*
- We can use the log likelihood function to compare models
  - The log likelihood function is a function of the parameters, β and σ^2
  - The higher the log likelihood, the better the fit
- We can also use the *Akaike Information Criterion* (AIC) and *Bayesian Information Criterion* (BIC)
  - These are functions of the log likelihood function and the number of parameters
  - The lower the AIC/BIC, the better the fit
- These are best thought of as useful for comparing across models
  - Difficult to interpret them on their own

AIC

- AIC is defined as follows:
  - k is the number of parameters in the model
  - L is the log likelihood function
  - AIC: $2k - 2\log(L)$

```
# save our model
results <- glm(in_poverty ~ h_male + h_age, data = df, family = binomial(link = "probit"))

# log likelihood
logLik(results)
```

```
## 'log Lik.' -2788.727 (df=3)
```

```
# aic from temp
results$aic
```

```
## [1] 5583.453
```

```
# Calculate AIC by hand:
2*3 - 2*(-2788.727)
```

```
## [1] 5583.454
```

- BIC is defined as follows:
  - k is the number of parameters in the model
  - L is the log likelihood function
  - n is the number of observations
  - BIC: $k \log(n) - 2 \log(L)$

```
# save our model
results <- glm(in_poverty ~ h_male + h_age, data = df, family = binomial(link = "probit"))

# log likelihood
logLik(results)
```

```
## 'log Lik.' -2788.727 (df=3)
```

```
nrow(df)
```

```
## [1] 4609
```

```
# Calculate BIC by hand:
3*log(4609) - 2*(-2788.727)
```

```
## [1] 5602.761
```

Pseudo r-squared

- We can also calculate a pseudo r-squared
  - This is a measure of the change in the log likelihood function relative to the null model (no coefficients except intercepts)

```
# null model
logLik(glm(in_poverty ~ 1, data = df, family = binomial(link = "probit")))
```

```
## 'log Lik.' -2791.606 (df=1)
```

```
# our model
logLik(glm(in_poverty ~ h_male + h_age, data = df, family = binomial(link = "probit")))
```

```
## 'log Lik.' -2788.727 (df=3)
```

```
# pseudo r-squared: 1 - (log likelihood of model / log likelihood of null model)
1 - (-2788.727/-2791.606)
```

```
## [1] 0.001031306
```

```
# Same thing: (null - model) / null
(-2791.606 - -2788.727)/-2791.606
```

```
## [1] 0.001031306
```

- Ordered logit/probit is used when the outcome is *ordered*
- But what if it's not, like trying to predict what the species of a flower is?
  - Let's use a built-in dataset in R called "iris" to look at this:

```
data(iris)
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

Multinomial probit/logit

```
data(iris)
table(iris$Species)
```

```
##
##     setosa versicolor  virginica
##         50         50         50
```

```
colnames(iris)
```

```
## [1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"
```

- Let's use sepal/pedal length/width to predict the species

Multinomial probit/logit

```
data(iris)
library(nnet)
multinomresults <- multinom(Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width, data = iris)
```

```
summary(multinomresults)$coefficients
```

```
##            (Intercept) Sepal.Length Sepal.Width Petal.Length Petal.Width
## versicolor    18.69037    -5.458424   -8.707401     14.24477   -3.097684
## virginica    -23.83628    -7.923634  -15.370769     23.65978   15.135301
```

- Note how setosa isn't there... it's the omitted category - We can interpret the coefficients as the log odds of being in a particular category relative to setosa (the omitted category)

- GLM is a very general framework
  - We can use it for other distributions, too

- Let's look at a poisson distribution
  - The poisson distribution is often used for count data
  - It has assumptions (mean = variance), but violation isn't a big deal!

- The poisson distribution is defined as follows:

$$f(y;\lambda) = \frac{\lambda^y e^{-\lambda}}{y!} \tag{41}$$

- Note the e: this is going to lead to a nice log interpretation
- y is the number of occurrences of the variable (in our example, it will be number of months in poverty)
- As mentioned, one implication of this distribution is:

$$E(y) = Var(y) = \lambda \tag{42}$$

i.e. the mean of y equals its variance. But we can work around this if it's false (which it probably is).

Possion, months in poverty (with feols - feglm)

```
# could save results. Not going to here... just display them
summary(feglm(months_in_poverty ~ h_male + h_age, data = df, family = "poisson"))
```

```
## GLM estimation, family = poisson, Dep. Var.: months_in_poverty
## Observations: 4,609
## Standard-errors: IID
##              Estimate Std. Error   t value  Pr(>|t|)
## (Intercept)  1.456020   0.039857  36.53087 < 2.2e-16 ***
## h_male      -0.277845   0.025915 -10.72158 < 2.2e-16 ***
## h_age        0.001255   0.000625   2.00869   0.04457 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Log-Likelihood: -17,506.6   Adj. Pseudo R2: 0.00303
##            BIC:  35,038.6     Squared Cor.: 0.004978
```

```
# notice the difference in standard errors if we use HC1 (which we want to here because of overdispersion)
summary(feglm(months_in_poverty ~ h_male + h_age, data = df, family = "poisson", vcov = "HC1"))
```

```
## GLM estimation, family = poisson, Dep. Var.: months_in_poverty
## Observations: 4,609
## Standard-errors: Heteroskedasticity-robust
##              Estimate Std. Error   t value   Pr(>|t|)
## (Intercept)  1.456020   0.092210 15.790222  < 2.2e-16 ***
## h_male      -0.277845   0.057268 -4.851679 1.2242e-06 ***
## h_age        0.001255   0.001487  0.844145 3.9859e-01
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Log-Likelihood: -17,506.6   Adj. Pseudo R2: 0.00303
##            BIC:  35,038.6     Squared Cor.: 0.004978
```

Interpreting poisson coefficients

```
summary(feglm(months_in_poverty ~ h_male, data = df, family = "poisson", vcov = "HC1"))$coefficients
```

```
## (Intercept)      h_male
##   1.5189645  -0.2772304
```

- How do we interpret poisson coefficients?
  - They are the *log* of the *rate* of the outcome
  - i.e. the log of the number of months in poverty

- The log count for male-headed households is around -0.28 *lower* than for female-headed households

The intercept is log count for female households

```
summary(feglm(months_in_poverty ~ h_male, data = df, family = "poisson", vcov = "HC1"))$coefficients
```

```
## (Intercept)      h_male
##   1.5189645  -0.2772304
```

```
# intercept is log count, so exponentiate for levels
exp(1.5189645)
```

```
## [1] 4.567493
```

```
# what is the mean for female-headed households?
mean(df$months_in_poverty[df$h_male==0])
```

```
## [1] 4.567493
```

```
# intercept plus coefficient for male-headed households
exp(1.5189645 - 0.2772304)
```

```
## [1] 3.461611
```

```
# mean for male-headed households?
mean(df$months_in_poverty[df$h_male==1])
```

```
## [1] 3.461611
```

- The poisson distribution has a mean = variance assumption
  - This is often violated
  - We can use quasi-poisson instead
- The quasi-poisson is the same as poisson, but the variance is estimated from the data
  - With feglm, it estimates the variance as a *linear function of the mean*
- Small note: if you use glm, you can use the "quasipoisson" family
  - This is more similar to poisson with vcov = "HC1"!
    - If you use "HC1" in both, you'll get identical results.
  - This is only about the structure of the error term. Not the coefficients.

Possion vs quasi-poisson (note the similar standard errors with HC1 for poisson)

```r
# Poisson with HC1
summary(feglm(months_in_poverty ~ h_male + h_age, data = df, family = "poisson", vcov = "HC1"))
```

```
## GLM estimation, family = poisson, Dep. Var.: months_in_poverty
## Observations: 4,609
## Standard-errors: Heteroskedasticity-robust
##              Estimate Std. Error   t value   Pr(>|t|)
## (Intercept)  1.456020   0.092210 15.790222  < 2.2e-16 ***
## h_male      -0.277845   0.057268 -4.851679 1.2242e-06 ***
## h_age        0.001255   0.001487  0.844145 3.9859e-01
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Log-Likelihood: -17,506.6   Adj. Pseudo R2: 0.00303
##            BIC:  35,038.6     Squared Cor.: 0.004978
```

```r
# quasipoisson
summary(feglm(months_in_poverty ~ h_male + h_age, data = df, family = "quasipoisson"))
```

```
## GLM estimation, family = quasipoisson, Dep. Var.: months_in_poverty
## Observations: 4,609
## Standard-errors: IID
##              Estimate Std. Error   t value   Pr(>|t|)
## (Intercept)  1.456020   0.091127 15.977892  < 2.2e-16 ***
## h_male      -0.277845   0.059249 -4.689409 2.8192e-06 ***
## h_age        0.001255   0.001429  0.878563 3.7968e-01
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##   Squared Cor.: 0.004978
```

Doesn't have to be integers!

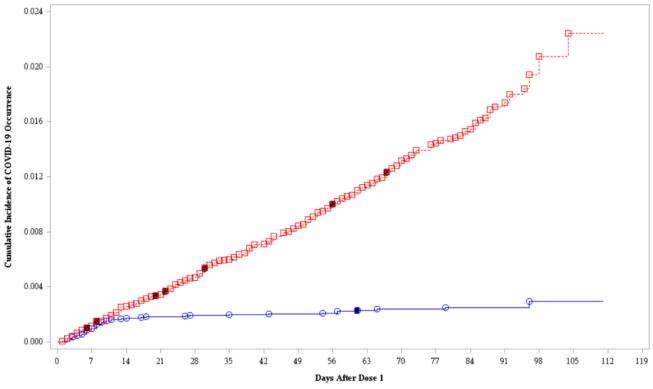
- You can use poisson for non-integer outcomes, too!
  - It's just a distribution
  - It's often used for integer outcomes because it's a count distribution
- Jeff Wooldridge is a huge proponent of using (quasi) poisson
- Two really nice things: it is robust and has an easy interpretation

- These models are used for *duration* data
  - i.e. time until an event occurs or a state changes
  - e.g. time until death after being diagnosed with cancer, time until a person leaves poverty, time until a person gets a job, until contracting a disease, etc.

- You need a very specific kind of data for this...
  - We want to know what kinds of variables predict the occurence of some event (e.g. death).

- **Warning:** I am not an expert on survival models. I will give you a brief overview, but you should consult a textbook for more information.

Figure 13 Cumulative Incidence Curves for the First COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population



- Let's use the package survival in R.
  - It has a dataset set up for us, called diabetic

```
library(survival)
# dataset with "high-risk" diabetic retinopathy patients
head(diabetic)
```

```
##   id laser age   eye trt risk  time status
## 1  5 argon  28  left   0    9 46.23      0
## 2  5 argon  28 right   1    9 46.23      0
## 3 14 xenon  12  left   1    8 42.50      0
## 4 14 xenon  12 right   0    6 31.30      1
## 5 16 xenon   9  left   1   11 42.27      0
## 6 16 xenon   9 right   0   11 42.27      0
```

- Note: this is a *panel* dataset
  - Each row is a patient (id)
  - Each patient has multiple observations (time)
  - Interested in loss of sight (status $= 1$)

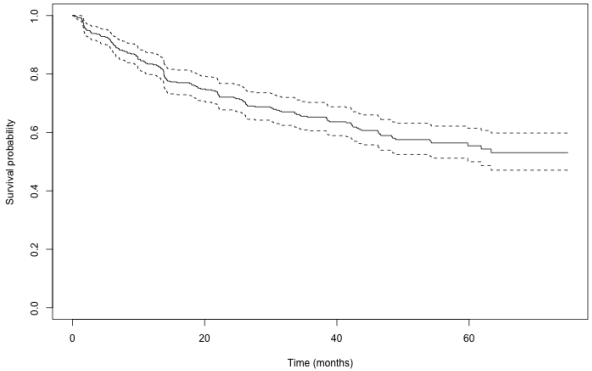
Survival function

- Let's first look at the survival function
  - This is the probability of surviving past a certain time
  - We're going to use the Kaplan-Meier estimator

```
KM <- survfit(Surv(time = time, event = status) ~ 1, data = diabetic)
# note that Surv() is necessary here. It's a function that creates a survival object.
# The ~ 1 means this is for EVERYONE.
```

Survival curve

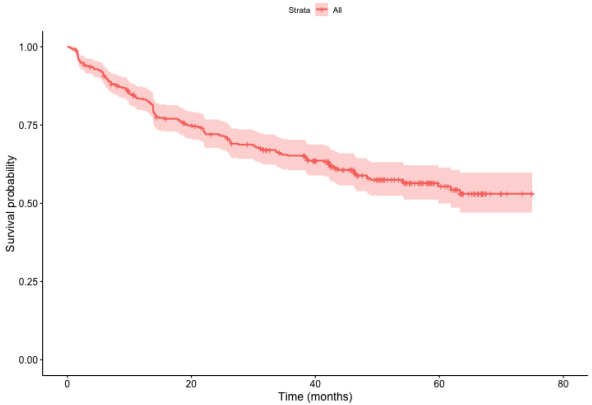
```
KM <- survfit(Surv(time = time, event = status) ~ 1, data = diabetic)
plot(KM, ylab = "Survival probability", xlab = "Time (months)")
```



Comparing survival curves based on treatment

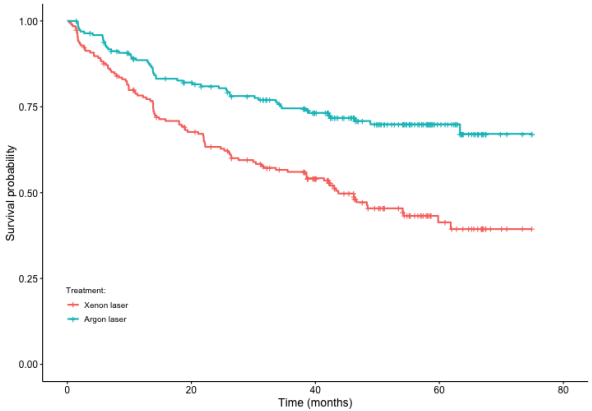
- Base R has ugly plots. We can use survminer to make it work with ggplot.

```
library(survminer)
KM <- survfit(Surv(time = time, event = status) ~ 1, data = diabetic)
ggsurvplot(KM) +
  labs(y = "Survival probability", x = "Time (months)")
```



Comparing survival curves based on treatment

```
KM <- survfit(Surv(time = time, event = status) ~ trt, data = diabetic)
ggsurvplot(KM)$plot +
  labs(y = "Survival probability", x = "Time (months)") +
  scale_color_discrete("Treatment:", labels = c("Xenon laser", "Argon laser")) +
  theme(legend.position = c(0.1, 0.2))
```



Comparing survival curves based on treatment, empirically

```r
survdiff(Surv(time = time, event = status) ~ trt, data = diabetic)
```

```
## Call:
## survdiff(formula = Surv(time = time, event = status) ~ trt, data = diabetic)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## trt=0 197      101     71.8      11.9      22.2
## trt=1 197       54     83.2      10.3      22.2
##
##  Chisq= 22.2  on 1 degrees of freedom, p= 2e-06
```

```r
# changes the weighting (more weight on earlier time points); doesn't matter here! Huge differences.
survdiff(Surv(time = time, event = status) ~ trt, data = diabetic, rho = 1)
```

```
## Call:
## survdiff(formula = Surv(time = time, event = status) ~ trt, data = diabetic,
##     rho = 1)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## trt=0 197     80.3     57.6      8.95      20.7
## trt=1 197     43.1     65.8      7.84      20.7
##
##  Chisq= 20.7  on 1 degrees of freedom, p= 6e-06
```

- Plotting two survival curves with a simply treatment dummy is straightforward.
  - But what if we want to add more covariates?
  - For example, the `diabetic` dataset has age at diagnosis and which eye the problem is. Does this matter?

- We can use a Cox proportional hazards model to do this.
  - This is a semi-parametric model that is very popular in survival analysis.
  - It is a *proportional hazards* model, which means that the hazard ratio is constant over time.
  - Its nature means we do not estimate the baseline hazard function.
    - Instead, we compare across variables

Adding more covariates

```
coxph(Surv(time = time, event = status) ~ age + as_factor(eye) + trt, data = diabetic)
```

```
## Call:
## coxph(formula = Surv(time = time, event = status) ~ age + as_factor(eye) +
##     trt, data = diabetic)
##
##                           coef exp(coef)  se(coef)      z        p
## age                   0.003321  1.003326  0.005463  0.608   0.5433
## as_factor(eye)right   0.350484  1.419754  0.162537  2.156   0.0311
## trt                  -0.812522  0.443738  0.169412 -4.796 1.62e-06
##
## Likelihood ratio test=27.59  on 3 df, p=4.421e-06
## n= 394, number of events= 155
```

- Note that treatment is randomized, so we *shouldn't* see large changes in the coefficient on treatment when we add covariates.
  - More on this next week!

Some warnings

- Note that all these methods have assumptions that can sometimes be important
- Given our time, I am purposefully just showing you the basics
  - If any of these specific methods interest you, I suggest doing more in-depth readings. I can provide some suggestions.