New methods of interpretation using marginal effects for nonlinear models

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Road map for talk

Goals
1. Demonstrate new methods for using marginal effects
2. Exploit the power of margins, factor syntax, and gsem
3. Illustrate the SPost13 m* commands

Outline
1. Statistical background
   - Binary logit model
   - Standard definitions of marginal effects
   - Generalizations of marginal effects
2. Stata commands
   - Estimation: factor notation, storing estimates, and gsem
   - Post-estimation: margins and lincom
   - SPost13’s m* commands
3. Example: explaining the occurrence of diabetes

Logit model

Probability as outcome
1. Nonlinear in probabilities
   \[ \pi(x) = \frac{\exp(x'\beta)}{1 + \exp(x'\beta)} = \Lambda(x'\beta) \]
2. Interpretation with marginal effect: additive change in \( \pi \) for change in \( x_k \) holding other variables at specific values

Odds as outcome
3. Multiplicative in odds
   \[ \Omega(x) = \frac{\pi(x)}{1 - \pi(x)} = \exp(x'\beta) \]
4. Interpretation with odds ratio: multiplicative change in \( \Omega(x) \) for change in \( x_k \) holding other variables constant

Marginal and discrete change

1. Marginal change: instantaneous rate of change in \( \pi(x) \)
2. Discrete change: change in \( \pi(x) \) for discrete change in \( x \)

Definition of discrete change

1. \( x_k \) changes from start to end
2. \( x = x^* \) contains specific values of other variables
3. Discrete change of \( x_k \)
   \[ DC(x_k) = \frac{\Delta \pi(x)}{\Delta x_k (\text{start} \rightarrow \text{end})} = \frac{\pi(x_k = \text{end}, x = x^*) - \pi(x_k = \text{start}, x = x^*)}{\Delta x_k} \]
4. Interpretation
   For a change in \( x_k \) from start to end, the probability changes by \( DC(x_k) \), holding other variables at the specified values.
Examples of discrete change

1. At observed values for observation \( i \)
   \[
   \frac{\Delta \pi(x_i)}{\Delta x_k(x_k \to x_k + 1)} = \pi(x_k = x_k, x_i) - \pi(x_k = x_k + 1, x_i)
   \]

2. At representative values \( x^* \)
   \[
   \frac{\Delta \pi(x^*)}{\Delta x_k(0 \to 1)} = \pi(x_k = 1, x^*) - \pi(x_k = 0, x^*)
   \]

3. Since \( \Delta \pi / \Delta x_k \) depends on where it is evaluated, how should the effect of \( x_k \) be summarized?

Common summary measures of discrete change

Discrete change at the mean (DCM)
\[
DCM(x_k) = \frac{\Delta \pi(x)}{\Delta x_k(\text{start} \to \text{end})} = \pi(x_k = \text{end}, x) - \pi(x_k = \text{start}, x)
\]

For someone who is average on all variables, increasing \( x_k \) from start to end changes the probability by \( DCM(x_k) \).

Average discrete change (ADC)
\[
ADC(x_k) = \frac{1}{N} \sum_{i=1}^{N} \frac{\Delta \pi(x = x_i)}{\Delta x_k(\text{start} \to \text{end})}
\]

On average, increasing \( x_k \) from start to end changes the probability by \( ADC(x_k) \).

Comparison for computing discrete change

* indicates generalization of standard methods

<table>
<thead>
<tr>
<th>Conditional and average change</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Conditional effects</strong></td>
</tr>
<tr>
<td>At observed values</td>
</tr>
<tr>
<td>At mean values</td>
</tr>
<tr>
<td>At representative values</td>
</tr>
<tr>
<td><strong>Average effects</strong></td>
</tr>
<tr>
<td>Average in full sample</td>
</tr>
<tr>
<td>Average in sub-sample *</td>
</tr>
</tbody>
</table>

| Amount of change               |
| Additive change                |
| Proportional change *          |
| Changes as function of predictors * |
| Change a component in multiplicative measure * |

| Number of variables changed   |
| One variable                  |
| Two or more variables *       |

Comparing discrete changes

Comparisons within a model

- Effects of different variables
  - \( H_0: DC(\text{gender}) = DC(\text{age}) \)
  - One variable’s effect at different locations
    - \( H_0: DC(\text{age} | \text{age} = 50, x^*) = DC(\text{age} | \text{age} = 65, x^*) \)

Comparisons across models

- Different samples or groups
  - \( DC(\text{weight}) \) for whites compared to non-whites
- Model specifications
  - \( DC(\text{weight}) \) in different model specifications

Stata: Overview

1. Requires Stata 12 or later; some examples need Stata 14
2. Assumes spost13_ado package is installed
3. Estimation uses factor syntax
   - Logit model used but examples generalize
   - Survey estimation can be used
4. Post-estimation with margins and lincom
5. In Stata, search eusmex2016 to download
   - eusmex2016-effects-scott-long.do and dataset
   - PDF of slides from talk
   - In the slides, [:xx:] points to locations in the do-file

Stata: Estimation

1. Fitting a logit model
   \[
   \text{logit dependent independent [ , options ]}
   \]
2. Factor variable syntax
   - \text{i.var}: categorical predictor (e.g., \text{i.female})
   - \text{c.var}: continuous predictor (e.g., \text{c.age})
   - \text{c.var1#c.var2}: product (e.g., c.age#c.age \equiv c.age*c.age)
3. Regression estimates are stored for later use
   \text{estimates store ModelName}
4. To replace current estimates with previously stored estimates
   \text{estimates restore ModelName}
Stata: post-estimation

1. `margins` estimates functions of predictions from regressions
2. `margins, post` stores these estimates to `e(b)` and `e(V)`
3. `lincom` estimates linear functions of `e(b)`
4. `mchange`, `mtable`, `mgen` and `mlincom` are SPost13 wrappers to generate complex `margins` commands and improve output

Example

1. Health and Retirement Survey\(^1\): cross-sectional data on health
2. Outcome is patient’s report of having diabetes
3. Begin with standard marginal effects to introduce Stata tools
4. Use these tools to compute more complex marginal effects
5. Demonstrate methods for statistically comparing effects

---

Variables and descriptive statistics

```
. use hrs-gme-analysis2, clear
     (hrs-gme-analysis2.dta | Health & Retirement Study GME sample | 2016-04-08)
```

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>diabetes</td>
<td>.205</td>
<td>0</td>
<td>1</td>
<td>Respondent has diabetes?</td>
</tr>
<tr>
<td>white</td>
<td>.772</td>
<td>0</td>
<td>1</td>
<td>Is white respondent?</td>
</tr>
<tr>
<td>bmi</td>
<td>27.9</td>
<td>10.6</td>
<td>82.7</td>
<td>Body mass index</td>
</tr>
<tr>
<td>weight</td>
<td>174.9</td>
<td>73</td>
<td>400</td>
<td>Weight in pounds</td>
</tr>
<tr>
<td>height</td>
<td>66.3</td>
<td>48</td>
<td>89</td>
<td>Height in inches</td>
</tr>
<tr>
<td>age</td>
<td>69.3</td>
<td>53</td>
<td>101</td>
<td>Age</td>
</tr>
<tr>
<td>female</td>
<td>.568</td>
<td>0</td>
<td>1</td>
<td>Is female?</td>
</tr>
<tr>
<td>hsdegree</td>
<td>.762</td>
<td>0</td>
<td>1</td>
<td>Has high school degree?</td>
</tr>
</tbody>
</table>

Body mass index: \( \text{BMI} = \frac{\text{weight}_g}{\text{height}_m^2} = \frac{703 \times \text{weight}_b}{\text{height}_m^2} \)

---

Models of diabetes: estimate and store

1. Two models are fit \[#02\]
2. Model `Mbmi` measures body mass with the BMI index
   
   ```
   logit diabetes c.bmi i.white c.age##c.age i.female i.hsdegree
   estimates store Mbmi
   ```
3. Model `Mwt` measures body mass with height and weight
   
   ```
   logit diabetes c.weight c.height i.white c.age##c.age i.female i.hsdegree
   estimates store Mwt
   ```

---

Models of diabetes: odds ratios and p-values

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mbmi</th>
<th>Mwt</th>
</tr>
</thead>
<tbody>
<tr>
<td>bmi</td>
<td>1.1046*</td>
<td>1.1046*</td>
</tr>
<tr>
<td>weight</td>
<td>1.0165*</td>
<td>1.0165*</td>
</tr>
<tr>
<td>height</td>
<td>0.9299*</td>
<td>0.9299*</td>
</tr>
<tr>
<td>white</td>
<td>0.5412*</td>
<td>0.5313*</td>
</tr>
<tr>
<td>White</td>
<td>0.5412*</td>
<td>0.5313*</td>
</tr>
<tr>
<td>age</td>
<td>1.3091*</td>
<td>1.3093*</td>
</tr>
<tr>
<td>c.age##c.age</td>
<td>0.9983*</td>
<td>0.9983*</td>
</tr>
<tr>
<td>female</td>
<td>0.7848*</td>
<td>0.8743#</td>
</tr>
<tr>
<td>women</td>
<td>0.7848*</td>
<td>0.8743#</td>
</tr>
<tr>
<td>hsdegree</td>
<td>0.7191*</td>
<td>0.7067*</td>
</tr>
<tr>
<td>HS degree</td>
<td>0.7191*</td>
<td>0.7067*</td>
</tr>
<tr>
<td>_cons</td>
<td>0.0000*</td>
<td>0.0001*</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mbmi</th>
<th>Mwt</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Change</td>
<td>p-value</td>
</tr>
<tr>
<td>white</td>
<td>-0.099</td>
<td>0.000</td>
</tr>
<tr>
<td>White vs Non-white</td>
<td>-0.099</td>
<td>0.000</td>
</tr>
<tr>
<td>bmi</td>
<td>+SD</td>
<td>0.997</td>
</tr>
</tbody>
</table>

(output omitted)

Note: # significance at .05 level; * at the .001 level.

---

Summarizing effects with average discrete change

1. `mchange` from SPost13 is a great first step for assessing effects \[#03\]
   
   ```
   . estimates restore Mbmi
   . mchange, amount(sd)
   logit: Changes in Pr(y) | Number of obs = 16071
   ```
   
<table>
<thead>
<tr>
<th>white</th>
<th>White vs Non-white</th>
<th>Change</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>White</td>
<td>-0.099</td>
<td>0.000</td>
</tr>
<tr>
<td></td>
<td>Non-white</td>
<td>+SD</td>
<td>0.997</td>
</tr>
</tbody>
</table>

2. Interpretation
   
   On average the probability of diabetes is .099 less for white respondents than non-white respondents.

   Increasing BMI by one standard deviation on average increases the probability of diabetes .097.

3. Where did these numbers come from?
Tool: margins, at( ... ) and atmeans

1. By default, margins
   1.1 Computes prediction for each observation
   1.2 Then it averages these predictions
2. Average prediction assuming everyone is white
   margins, at(white=1)
3. Two average predictions
   margins, at(white=1) at(white=0)
4. Prediction if white with means for other variables
   margins, at(white=1) atmeans

ADC for binary x_k: ADC(white)

5. The post option saves the average probabilities
   . matlist e(b)
   | 1.   2. |
   | _at   _at |
   | .2797806 .1805306 |
6. lincom computes ADC as difference in predictions in e(b)
   . lincom _b[2._at] - _b[1._at]
   \begin{array}{c}
   (1) \\
   -.09925
   \end{array}
   \begin{array}{c}
   .0082362
   \end{array}
   \begin{array}{c}
   -12.05
   \end{array}
   \begin{array}{c}
   .0000
   \end{array}
   \begin{array}{c}
   -.1153927
   \end{array}
   \begin{array}{c}
   -.0831073
   \end{array}
7. Interpretation
   On average, being white decreases the probability of diabetes by .099 (p < .001).

Tool: mlincom simplifies lincom

1. lincom requires column names from e(b) that can be complex
   lincom (_b[2._at#1.white] - _b[1._at#1.white]) ///
   - (_b[2._at#0.white] - _b[1._at#0.white])
2. mlincom uses column numbers which are rows in margins output
   mlincom (4-2) - (3-1)

ADC for continuous x_k: ADC(bmi)

1. Compute probabilities at observed bmi and observed+sd
   . quietly sum bmi
   . local sd = r(sd)
   . margins, at(bmi = gen(bmi)) at(bmi = gen(bmi + `sd'))
2. ADC(bmi+sd)
   . mlincom 2-1, stats(all)
   \begin{array}{cccc}
   | lincom & se & svalue & pvalue & ll & ul |
   \hline
   1 | .097 & .004 & 27.208 & .000 & .090 & .104 |
   \end{array}
   On average, increasing BMI by one standard deviation, about 6 points, increases the probability of diabetes by .097 (p < .001).
Tool: mtable wrapper for margins

1. margins output is complete, not compact
2. mtable executes margins, then simplifies output (and more)
   ▶ mtable, commands lists the margins commands used
   ▶ mtable, detail shows margins output and mtable output

DCM for continuous $x_k$: DCM(bmi)

1. Let bmi increase from mean to mean+SD
   . qui sum bmi
   . local mn = r(mean)
   . local mnplus = r(mean) + r(sd)
2. Option atmeans holds other variables at their means
   . margins, atmeans at(bmi = `mn´) at(bmi = `mnplus´) post
   Expression : Pr(diabetes), predict() 
   _at : bmi = 27.89787
   0.white = .2284239 (mean)
   1.white = .7715761 (mean)
   age = 69.29276 (mean)
   0.female = .4315226 (mean)
   1.female = .5684774 (mean)
   0.hsdegree = .2375086 (mean)
   1.hsdegree = .7624914 (mean)

2. Alternatively, mtable runs margins and reformats the results
   . mtable, atmeans at(bmi = `mn´) at(bmi = `mnplus´) post
   Expression : Pr(diabetes), predict()
   bmi Pr(y)
   1 27.9 0.210
   2 33.7 0.320

3. DCM(bmi+sd)
   . mlincom 2 - 1
   lincom pvalue ll ul
   1 0.111 0.000 0.102 0.119

For an average person, increasing BMI by one standard deviation increases the probability of diabetes by .111 ($p < .001$).

Proportional change in $x_k$: changing weight

1. Body mass be measured with height and weight
   logit diabetes c.weight c.height ///
   i.white c.age##c.age i.female i.hsdegree, or estimates store Mwt
2. ADC(weight) increases weight by a constant, say 25 pounds
3. A 25 pound increase in weight means different things
   ▶ A 25% increase from 100 pounds
   ▶ At 14% increase from average weight
   ▶ An 8% increase from 300 pounds
4. The effect of a percentage increase could be more useful than the effect of a 25 pound increase

Proportional change in $x_k$: ADC(weight+25)

1. Computing ADC(weight+25)
   . estimates restore Mwt
   . mtable, at(weight = gen(weight)) at(weight = gen(weight + 25)) post
   Expression: Pr(diabetes), predict()
   Pr(y)
   1 0.205
   2 0.271
   . quietly mlincom 2 - 1, rowname(ADC add) clear
**Proportional change in $x_k$: ADC(weight*1.14)**

2. A simple change to `gen()` computes proportional change
   ```
   . mtable, gen(PRpct) at(weight=gen(weight)) at(weight=gen(weight*1.14)) post
   Expression: Pr(diabetes), predict()
<table>
<thead>
<tr>
<th></th>
<th>Pr(y)</th>
<th>pvalue</th>
<th>ll</th>
<th>ul</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.205</td>
<td>0.000</td>
<td>0.062</td>
<td>0.071</td>
</tr>
<tr>
<td>2</td>
<td>0.273</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
   ```

3. The average effects are close, but is the average a good summary?

**Tool: margins, generate()**

1. margins, gen(stub) creates variables containing predictions for each observation (help margins generate)

2. For example, to save probabilities for 16,071 cases and average them
   ```
   . margins, gen(Prob) at(weight = gen(weight))
   Predictive margins
   Number of obs = 16,071
   Expression: Pr(diabetes), predict()
   |       | Delta-method | Margin | Std. Err. | z    | P>|z|   | [95% Conf. Interval] |
   |-------|--------------|--------|-----------|------|-------|---------------------|
   | _cons | .2047166     |        | .0030316  | 67.53| 0.000 | .1987747            |
   ```

3. Note that `gen()` is used two ways

**Proportional change in $x_k$: generating variables**

1. For ADC(weight*1.14) compute effect and and create variables
   ```
   . mtable, gen(PRadd) at(weight=gen(weight)) at(weight=gen(weight+25)) post
   Expression: Pr(diabetes), predict()
   Predictive margins
   Number of obs = 16,071
   Delta-method
<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prob1</td>
<td>16,071</td>
<td>.2047166</td>
<td>.1229016</td>
<td>.0123593</td>
<td>.9067207</td>
</tr>
</tbody>
</table>
   ```

2. Compute DC(weight*1.14) for each observation
   ```
   . generate DCpct = PRpct2 - PRpct1
   . label var DCpct "DC for 14 percent increase in weight"
   ```

3. Similarly, ADC(weight + 25)
   ```
   . stable, gen(PRadd) at(weight=gen(weight)) at(weight=gen(weight+25)) post
   (output omitted)
   . generate DCadd = PRadd2 - PRadd1
   . label var _DCadd "DC for 25 pound increase"
   ```

4. DC(weight*1.14) and DC(weight+25) have quite different distributions

**Discrete change with polynomials**

1. A standard discrete change allows only one variable to change

2. With polynomials multiple variables must change together
   ```
   ▶ You can’t change age, holding age-squared constant
   ```

3. For example,
   ```
   \[
   \frac{\Delta \pi(x)}{\Delta \text{age}(50 \rightarrow 60)} = \pi(\text{age} = 60, \text{agesq} = 60^2) - \pi(\text{age} = 50, \text{agesq} = 50^2)
   \]
   ```

4. This can be computed two ways
   ```
   4.1 Automatically with factor syntax
   4.2 Explicitly with at(...) = gen(...)
   ```

5. Average effects are close, but individual effects can differ greatly

---

**Proportional change in $x_k$: comparing ADCs**

5. Average effects are close, but individual effects can differ greatly
Discrete change with polynomials

1. With $x$ and $x^2$ only values on the blue curve are mathematically possible

2. Changes in the probability reflect linked changes in $x$ and $x^2$

3. The probability can increase and decrease as $x$ and implicitly $x^2$ change

**Tool:** factor notation for polynomials

Without factor notation

1. Generate age-squared
   
   ```
   generate agesq = age * age
   ```

2. Model specification
   
   ```
   logit diabetes c.age c.agesq ...
   ```

With factor notation

1. `c.age##c.age` with two #s does three things (you must include `c. `)
   1.1 Adds `c.age` to the model
   1.2 Create `c.age#c.age ≡ c.age*c.age`
   1.3 Adds `c.age#c.age` to the model

2. Model specification
   
   ```
   logit diabetes c.age##c.age ...
   ```

3. When `c.age` changes, `margins` automatically changes `c.age#c.age`

Correct ADC with factor notation

1. age and age#age automatically change together [##08]

   ```
   . logit diabetes c.age##c.age c.bmi i.white i.female i.hsdegree, or
   (output omitted)
   . mtable, at(age = gen(age)) at(age = gen(age+10)) post
   Expression: Pr(diabetes), predict()
   |   |   |   |
   | Pr(y) | 1  | 0.205 |
   |       | 2  | 0.223 |
   . mlincom 2 - 1, rowname(FV right)
   |   |   |   |
   | lincom  prvalue  ll  ul |
   | FV right | 0.018 0.000 0.011 0.024 |
   ```

2. Why is the effect of age so small?

Incorrect ADC without factor notation

1. age and agesq are distinct variables

   ```
   . logit diabetes c.age c.agesq c.bmi i.white i.female i.hsdegree, or
   (output omitted)
   . mtable, at(age = gen(age)) at(age = gen(age+10)) post
   Expression: Pr(diabetes), predict()
   |   |   |   |
   | Pr(y) | 1  | 0.205 |
   |       | 2  | 0.744 |
   . mlincom 2 - 1, rowname(noFV wrong)
   |   |   |   |
   | lincom  prvalue  ll  ul |
   | noFV wrong | 0.540 0.000 0.445 0.634 |
   ```

2. When `margins` changes `age`, variable `agesq` does not change
Discrete change with age & age^2

Correct ADC without factor notation

1] \[ \logit \text{diabetes} \ c.age \ c.ageq \ c.bmi \ i.white \ i.female \ i.hsdegree, \ or \]
(output omitted)

2] \[ \text{mtable, at(} \text{age} = \text{gen(age)} \text{) \ agesq = gen(ageq)} \text{) \ ///} \]

3] > \[ \text{at(age) = gen(age+10) \ agesq = gen((age+10)^2)) \ post} \]
(output omitted)

4] \[ \text{mlincom} \ 2 - 1, \ \text{rname(noFV \ right)} \]
(output omitted)

The power of \text{at( gen() )}

1. With factor syntax you do not need \text{at(...=gen())}

2. However, \text{at(...=gen())} allows complex links among variables

Associated variables: ADC(height, weight)

1. Regress weight on height and height squared

\[ \text{regress weight c.height##c.height, noci} \]
(output omitted)

\begin{tabular}{lrrr}
 & weight & Coef. & Std. Err. & t & P>|t| \\
height & -6.338708 & 1.61073 & -3.94 & 0.000 \\
c.height#c.height & .0855799 & .0120867 & 7.08 & 0.000 \\
_cons & 217.5991 & 53.5548 & 4.06 & 0.000 \\
\end{tabular}

2. Save estimates

\[ \text{scalar b0 = } _b[\_cons] \]

\[ \text{scalar b1 = } _b[\text{height}] \]

\[ \text{scalar b2 = } _b[\text{c.height##c.height}] \]

Associated variables: ADC(height, weight)

3. \text{margins, gen()} changes weight based on a 6" change in height

\[ \text{mtable, at(height = gen(height) /// observed height} \]

\[ \text{at(height = gen(height+6) /// +6 inches} \]

\[ \text{at(weight = gen(b0 + b1* \ (height+6) /// +estimated weight} \]

Expression: \text{Pr(diabetes), predict()} \]

\begin{tabular}{lrrrr}
 & Pr(y) & \\
1 & 0.205 & \\
2 & 0.208 & \\
\end{tabular}

4. Interpretation

\text{There is no evidence that being physically larger without greater body mass contributes to the incidence of diabetes.}

Summary measures of change: ADC and DCM

1. ADC and DCM are common summaries of a variable’s effect

2. Each uses the mean to summarize a distribution

3. ADC: average discrete change

\[ \text{ADC(x)} = \frac{1}{\bar{x}} \sum \left[ \frac{\Delta \pi}{\Delta \pi | x = x_i} \right] \]

4. DCM: discrete change at the mean

\[ \text{DCM(x)} = \frac{\Delta \pi}{\Delta \pi | x = \bar{x}} \text{ where } \bar{x} = \frac{1}{\bar{x}} \sum x_i \]

5. Hypothetical data shows why means can be misleading

Summary measures of change: ADC and DCM

Hypothetical data

\[ \text{Pr(diabetes), Age} \]

\[ 0 \ 1 \ 2 \]

\[ 55 \ 60 \ 65 \ 70 \ 75 \ 80 \ 85 \ 90 \ 95 \ 100 \]
Summary measures of change: distribution of effects

1. To evaluate ADC(age), look at the distribution of DC(age_i)
2. Create a variable with the DC for each observation
   1] margins, generate(PRage) ///
   2] at(age = gen(age)) at(age = gen(age+10))
   3] gen DCage10 = PRage2 - PRage1
   4] lab var DCage10 "DC for 10 year increase in age"

3. The average effect of age is small, but is large and negative for some people and large and positive for others

Summary measures of change: distribution of effects

3. ADC and DCM are more useful than odds ratios
2. In nonlinear models, summary measure can be very misleading
3. The distribution of effects is valuable for assessing a variable’s effect and is simple with margins, generate()
   ▶ Long and Freese (2014) do this before the gen() option was added
4. The best summary is the one that explains the process being modeled
5. For age, multiple DCRs are more useful than ADC or DCM
   ▶ I use DCR to introduce methods for comparing effects

Comparing effects within a model

Examples
1. Compare DCRs for one variable at different values
   ▶ Is the effect of age the same at 60 as at 80?
2. Compare ADCs for two variables
   ▶ Does BMI have a larger impact than race?
3. Compare ADCs for two sub-samples
   ▶ Does BMI have a larger effect for whites than non-whites?

Comparing DCR(age) at different ages

1. Are the DCR(age) significantly different at different ages?

Other variables held at means

<table>
<thead>
<tr>
<th>Age</th>
<th>Pr(diabetes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>55</td>
<td>0.03</td>
</tr>
<tr>
<td>60</td>
<td>0.06</td>
</tr>
<tr>
<td>65</td>
<td>0.09</td>
</tr>
<tr>
<td>70</td>
<td>0.12</td>
</tr>
<tr>
<td>75</td>
<td>0.15</td>
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<td>80</td>
<td>0.18</td>
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<td>85</td>
<td>0.21</td>
</tr>
<tr>
<td>90</td>
<td>0.24</td>
</tr>
<tr>
<td>95</td>
<td>0.27</td>
</tr>
<tr>
<td>100</td>
<td>0.30</td>
</tr>
</tbody>
</table>

Comparing DCR(age) at different ages

2. Compute probabilities at 4 ages with other variables at means

   . mtable, at(age=(60(10)90)) post atmeans
   Expression: Pr(diabetes), predict()

<table>
<thead>
<tr>
<th>age</th>
<th>Pr(y)</th>
</tr>
</thead>
<tbody>
<tr>
<td>60</td>
<td>0.150</td>
</tr>
<tr>
<td>70</td>
<td>0.213</td>
</tr>
<tr>
<td>80</td>
<td>0.227</td>
</tr>
<tr>
<td>90</td>
<td>0.183</td>
</tr>
</tbody>
</table>

   Specified values of covariates

<table>
<thead>
<tr>
<th>bmi</th>
<th>white</th>
<th>female</th>
<th>hsdegree</th>
</tr>
</thead>
<tbody>
<tr>
<td>27.9</td>
<td>.772</td>
<td>.568</td>
<td>.762</td>
</tr>
</tbody>
</table>

3. DCRs at different ages

   . mlincom 2-1, clear rowname(DCR60)
   . mlincom 3-2, add rowname(DCR70)
   . mlincom 4-3, add rowname(DCR80)
Comparing DCR(age) at different ages

4. Test differences in DCRs
   . mlincom (2-1) - (3-2), add rowname(DCR60 - DCR70)
   . mlincom (2-1) - (4-3), add rowname(DCR60 - DCR80)
   . mlincom (3-2) - (4-3), add rowname(DCR70 - DCR80)

5. Summarizing
   . mlincom, twid(14)

<table>
<thead>
<tr>
<th></th>
<th>lincom</th>
<th>pvalue</th>
<th>ll</th>
<th>ul</th>
</tr>
</thead>
<tbody>
<tr>
<td>DCR60</td>
<td>0.063</td>
<td>0.000</td>
<td>0.054</td>
<td>0.073</td>
</tr>
<tr>
<td>DCR70</td>
<td>0.014</td>
<td>0.004</td>
<td>0.004</td>
<td>0.023</td>
</tr>
<tr>
<td>DCR80</td>
<td>-0.043</td>
<td>0.000</td>
<td>-0.061</td>
<td>-0.026</td>
</tr>
<tr>
<td>DCR60 - DCR70</td>
<td>0.049</td>
<td>0.000</td>
<td>0.037</td>
<td>0.062</td>
</tr>
<tr>
<td>DCR60 - DCR80</td>
<td>0.107</td>
<td>0.000</td>
<td>0.083</td>
<td>0.130</td>
</tr>
<tr>
<td>DCR70 - DCR80</td>
<td>0.057</td>
<td>0.000</td>
<td>0.046</td>
<td>0.069</td>
</tr>
</tbody>
</table>

6. Interpretation
   The effects of a ten-year increase in age are significantly different at ages 60, 70, and 80 (p < .001).

Comparing ADC(white) and ADC(bmi)

3. Simultaneously compute components for ADC(white) and ADC(bmi)
   . quietly sum bmi
   . local sd = r(sd)
   . margins, at(white=(0 1)) at(bmi = gen(bmi)) at(bmi = gen(bmi + `sd´)) post

   Predictive margins
   Number of obs = 16,071
   Model VCE : OIM
   Expression : Pr(diabetes), predict()
   1._at : white = 0
   2._at : white = 1
   3._at : bmi = bmi + 5.770835041238605
   4._at : bmi = bmi + 5.770835041238605

   Delta-method

   |        | Margin | Std. Err. | z    | P>|z| | [95% Conf. Interval] |
   |--------|--------|-----------|------|-------|----------------------|
   | 1      | .2797806 | .0073107  | 38.27| 0.000 | .265452 .2941092 |
   | 2      | .1805306 | .0034215  | 52.76| 0.000 | .1738245 .1872367 |
   | 3      | .2047166 | .0030338  | 67.48| 0.000 | .1987704 .2106627 |
   | 4      | .3017056 | .005199   | 58.03| 0.000 | .2915159 .3118954 |

4. Compute effects and test equality
   . qui mlincom (2-1), rowname(ADC white) clear
   . qui mlincom (4-3), rowname(ADC bmi) add
   . mlincom (2-1) + (4-3), rowname(Sum of ADCs) add

   lincom  pvalue  ll   ul
   ADC female -0.099 0.000 -0.115 -0.083
   ADC bmi 0.097 0.000 0.090 0.104

   Sum of ADCs -0.002 0.809 -0.021 0.016

5. Conclusion
   The health cost of being non-white is equivalent to a standard deviation increase in body mass (p > .80).

Comparing ADC(bmi) by race

1. An ADC is typically averaged over the estimation sample
2. By averaging within groups, we can examine effects for different groups
   ▶ Is the average effect of BMI the same for whites and non-whites?
3. This requires margins, over()

Tool: margins, over()

1. By default, margins averages over all observations
2. Averages on subsamples are possible with if and over()
3. Averaging for the non-white subsample
   margins if white==0, ///
   at(bmi = gen(bmi)) at(bmi = gen(bmi+‘sd’))
4. For the white subsample
   margins if white==1, ///
   at(bmi = gen(bmi)) at(bmi = gen(bmi+‘sd’))
5. For both subsamples simultaneously
   margins, over(white) ///
   at(bmi = gen(bmi)) at(bmi = gen(bmi+‘sd’))
Comparing ADC(bmi) by race

1. Use over() to compute components for group specific ADC(bmi) \[\#13\]
   . margins, over(white) at(bmi = gen(bmi)) at(bmi = gen(bmi + `sd´)) post
   Expression: Pr(diabetes), predict()
   over: white
   1._at : 0.white
   bmi = bmi
   1.white
   bmi = bmi
   2._at : 0.white
   bmi = bmi + 5.770835041238605
   1.white
   bmi = bmi + 5.770835041238605

   Delta-method
   Margin Std. Err. z P>|z| [95% Conf. Interval]
   _at#white
   #Non-white .3097249 .0072773 42.56 0.000 .2954616 .3239881
   #White .173629 .0032892 52.79 0.000 .1671824 .1800757
   2#Non-white .4302294 .009226 46.63 0.000 .4121468 .448312
   2#White .2636564 .0054903 48.02 0.000 .2528955 .2744172

2. Computing ADC(bmi) by group
   . qui mlincom 4-2, clear rowname(White: ADC bmi)
   . mlincom 3-1, add rowname(Non-white: ADC bmi)
   lincom pvalue ll ul
   White ADC bmi 0.090 0.000 0.083 0.097
   Non-white ADC bmi 0.000 .000 .000 .000
   3. A second difference compares effects for the groups
   . mlincom (4-2) - (3-1), rowname(Difference: ADC bmi)
   lincom pvalue ll ul
   Difference ADC bmi -0.030 0.000 -0.034 -0.027

4. Interpretation
   The effect of BMI for non-whites is significantly larger than the effect for whites \(p < .001\).

TOOL: joint estimation in Stata

1. gsem simultaneously fits multiple equations
   1.1 Limited to GLM models
   1.2 margins behaves “normally”, but is slow
   1.3 Robust standard errors are not required but vce(robust) and vce(cluster clustvar) are available
   1.4 Some complex expressions() might not work...

2. suest combines stored estimates
   2.1 Works with most regression models
   2.2 margins computes \(x \hat{\beta}\); computing \(\hat{\pi}(x)\) is complicated
   2.3 Average effects for subsamples cannot be computed
   2.4 Robust standard errors must be used

3. Specialized commands like khb (Kohler et al., 2011) are available

Comparing ADCs across models: examples

Examples of comparing effects from different models

1. Different specifications of predictors
   ▶ Does DC(female) depend on how body mass is measured?

2. Different groups
   ▶ Does DC(bmi) differ for whites and nonwhites

Comparing ADC(female) across models

Does the effect of female depend on how body mass is measured?

1. Since female is a factor variables, margins, dydx(female) computes DC(female)

2. Computing ADC(female) for two models
   . qui logit diabetes c.bmi i.white c.age##c.age i.hsdegree
eq 0, clear rowname(ADC(female) with Mbmi) cl
   . qui logit diabetes c.weight c.height i.female i.white c.age##c.age i.hsdegree
eq 0, clear rowname(ADC(female) with Mwt) below

   Expression: Pr(diabetes), predict()
   d Pr(y)
   ADC(female) with Mbmi
   -0.036
   ADC(female) with Mwt
   -0.020

3. To test if they are equal, we compute the effects simultaneously

Tool: gsem for multiple equations

1. This does not estimate two models
   gsem ///
   (diabetes <- c.bmi i.female i.white c.age##c.age i.hsdegree, logit) ///
   (diabetes <- c.weight c.height i.female i.white c.age##c.age i.hsdegree, logit)
   since it is interpreted as
   gsem ///
   (diabetes <- c.bmi i.female i.white c.age##c.age i.hsdegree /// c.weight c.height, logit)

2. The solution is to create clones for each model
   . clonevar lhbm1 = diabetes /// outcome for bmi model
   . clonevar lhwt = diabetes /// outcome for weight height model
### Comparing ADC(female) across models

1. Estimating the models simultaneously
   ``` stata
   . gsem (lhsbmi <- c.bmi i.female i.white c.age##c.age i.hsdegree, logit) 
   > (lhswt <- c.weight c.height i.female i.white c.age##c.age i.hsdegree, 
   > logit) 
   > , vce(robust)
   
   Generalized structural equation model Number of obs = 16,071
   Response : lhsbmi
   Family : Bernoulli
   Link : logit
   Response : lhswt
   Family : Bernoulli
   Link : logit
   Log pseudolikelihood = -14914.007
   
   Robust
   Coef. Std. Err. z P>|z| [95% Conf.
   < Interval]
   
   lhsbmi <-
   bmi .099441 .003747 26.54 0.000 .092097 .1067851
   female Women -.2423701 .0413006 -5.87 0.000 -.3233177 -.1614225
   white .614614 .0480926 -12.77 0.000 -.3082738 -.3195263
   
   Robust
   Coef. Std. Err. z P>|z| [95% Conf.
   < Interval]
   
   lhswt <-
   weight .099441 .003747 26.54 0.000 .092097 .1067851
   height .099441 .003747 26.54 0.000 .092097 .1067851
   female Women -.2423701 .0413006 -5.87 0.000 -.3233177 -.1614225
   white .614614 .0480926 -12.77 0.000 -.3082738 -.3195263
   
   Note: dy/dx for factor levels is the discrete change from the base level.
   ```

2. Estimate ADC(female) for both models simultaneously
   ``` stata
   . qui est restore Mgsem
   . margins, dydx(female) post
   
   Average marginal effects Number of obs = 16,071
   Model VCE : Robust
   dy/dx w.r.t. : 1.female
   1._predict : Predicted mean (Respondent has diabetes?), predict(pr outcome(outcome(lhsbmi))
   2._predict : Predicted mean (Respondent has diabetes?), predict(pr outcome(lhswt))
   
   Delta-method
   dy/dx Std. Err. z P>|z| [95% Conf.
   < Interval]
   
   1.female
   _predict 1 -.0360559 .0061773 -5.84 0.000 -.0481631 -.0239487
   2 -.0199213 .0089687 -2.22 0.026 -.0374997 -.0023429
   
   Note: dy/dx for factor levels is the discrete change from the base level.
   ```

3. Testing if ADC(female) is the same in both models
   ``` stata
   . mlincom 1-2, stats(all)
   
   lincom se zvalue pvalue ll ul
   1 -0.016 0.006 -2.526 0.012 -0.029 -0.004
   
   4. Interpretation
   The effect of being female is significantly larger when body mass is measured with the BMI index ($p < .02$).
   ```

### Comparing effects across models

1. Jointly estimating models with `gsem` and computing effects with `margins` is a general approach for comparing effects across models (Mize et al., 2009)
2. `gsem`
   2.1 Fits the GLM class of models, but does not fit non-GLM models
   2.2 `margins` is slow (grumble, grumble)
3. `suest`
   3.1 Fits a much wider class of models
   3.2 `margins` is fast, but hard to use (grumble, grumble)
4. `suest` and `gsem` produce identical results

### Comparing groups: outcomes and marginal effects

#### Linear regression
1. Coefficients differ by group such as $\beta_W$ and $\beta_N$
2. Analysis focuses on Chow tests such as $H_0 : \beta_W = \beta_N$

#### Logit and probit
1. Coefficients differ by group such as $\beta_W$ and $\beta_N$
2. The coefficients combines
   2.1 The effect of $x_k$ which can differ by group
   2.2 The variance of the error which can differ by group
3. Since regression coefficients are identified to a scale factor, Chow-type tests of $H_0 : \beta_N = \beta_W$ are invalid (Allison, 1999)
4. Probabilities and marginal effects are identified (Long, 2009)

### Comparing groups: outcomes and marginal effects

#### Group differences can be examined two ways
1. Differences in probabilities
   $$H_0 : \pi_W(x = x^*) = \pi_N(x = x^*)$$
   *Is the probability of diabetes the same for white and non-white respondents who have the same characteristics?*
2. Differences in marginal effects
   $$H_0 : \frac{\Delta \pi_W}{\Delta x_k} = \frac{\Delta \pi_N}{\Delta x_k}$$
   *Is the effect of $x_k$ the same for whites and non-whites?*
3. These dimensions of difference are shown in the next graph
Comparing groups: outcome and marginal effects

Hypothetical data

Comparing groups: model estimation

1. Factor syntax allows coefficients to differ by `white`
   
   logit diabetes `ibn.white` ///
   `ibn.white##(i.female i.hsdegree c.age##c.age c.bmi)`, nocon

2. This is equivalent to simultaneously estimating
   
   logit diabetes `i.female i.hsdegree c.age##c.age c.bmi` if `white==1`
   logit diabetes `i.female i.hsdegree c.age##c.age c.bmi` if `white==0`

3. For example

   Variable | Whites | NonWhites
   --- | --- | ---
   female | 0.713 | 1.024
   hsdegree | 0.706 | 0.743
   age | 1.278 | 1.369

Group comparison of probabilities by age

1. `dydx(white)` computes DC(white)

   . `mtable, dydx(white)` at(age=(55(10)85)) atmeans stats(est p)

   Expression: Pr(diabetes), predict()

<table>
<thead>
<tr>
<th>age</th>
<th>d Pr(y)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>55</td>
<td>-0.078</td>
</tr>
<tr>
<td>2</td>
<td>65</td>
<td>-0.124</td>
</tr>
<tr>
<td>3</td>
<td>75</td>
<td>-0.129</td>
</tr>
<tr>
<td>4</td>
<td>85</td>
<td>-0.092</td>
</tr>
</tbody>
</table>

   Specified values of covariates

   | 0. 1. 1. 1. 1. |
   | white white female hsdegree bmi |
   | Current | .228 | .772 | .568 | .762 | 27.9 |

2. Example of interpretation

   The probability of diabetes is significantly larger for 55 year-old non-whites than whites who are average on other characteristics (p < .01).

3. Graphically we can show effects at multiple ages

Group comparison of effects: ADC or DCM?

1. ADC reflects the distribution of predictors
2. DCR is the effect at specific values

Comparing ADCs

1. ADCs reflect
   1.1 Differences in the probability curves
   1.2 Differences in distribution of variables
2. Group differences in ADCs reflect both components

Comparing DCRs

1. DCRs show differences in probability curves at a specific location
2. Group differences in DCRs do not depend on the distribution of variables

Which to use?

1. The answer depends on what you want to know?
Group comparison of effects: ADC(bmi+5)

1. To compute ADC(bmi + 5) by race

   mtable, over(white) at(bmi = gen(bmi)) at(bmi = gen(bmi+5)) post

   Expression: Pr(diabetes), predict()

   Pr(y)

   0.white#c.1 0.310
   1.white#c.1 0.174
   0.white#c.2 0.391
   1.white#c.2 0.257

   qui mlincom 3-1, rowname(ADC(bmi) non) stats(est p) clear
   qui mlincom 4-2, rowname(ADC(bmi) wht) stats(est p) add
   mlincom (4-2) - (3-1), rowname(Difference) stats(est p) add

   lincom

   pvalue

   ADC(bmi) non 0.082 0.000
   ADC(bmi) wht 0.083 0.000
   Difference 0.002 0.926

2. Conclusion

   The average effects of BMI are not significantly different for whites and non-whites (p=.83).

Group comparison of effects: DCR(age+10)

1. Since ADC(age) is not a useful measure, we compare DCR(age+10)

   1.1 Other variables are held at sample means

   1.2 Group specific means could be used (Long and Freese, 2014)

2. For example, DCR(age + 10) at 55

   mtable, at(age=55 white=(0 1)) at(age=55 white=(0 1)) atmeans post

   mlincom 3-1, rowname(DC nonwhite) stats(est p) clear
   mlincom 4-2, rowname(DC white) stats(est p) add
   mlincom (4-2) - (3-1), rowname(Dif at 55) stats(est p) add

   And so on, with the following results

55: DC non

   Pr(y)

   0.110 0.000
   0.064 0.000
   Difference 0.046 0.000

70: DC non

   Pr(y)

   0.005 0.000
   0.000 0.000
   Difference 0.005 0.000

85: DC non

   Pr(y)

   -0.109 0.000
   -0.049 0.000
   Difference 0.060 0.000

3. These comparisons do not depend on group differences in the distribution of age or other variables

* Decomposing BMI

1. The BMI index measures relative weight or body mass

   \[ BMI = \frac{weight_{lb}}{height_{in}^2} \]

2. Question 1: If BMI is in the model, can we compute the effect of increasing weight?

   ▶ DC(weight) is clearer to patients then DC(bmi)

3. Question 2: Does DC(weight) differ depending on how body mass is included in the model?

4. To do this we create BMI as a product variable

   \[ BMI = 703 \times \frac{weight_{lb}}{height_{in}^2} \]

Decomposing BMI: bmi as an interaction

1. Create components of BMI

   generate heightinv = 1/height
   label var heightinv "1/height"
   generate S = 703
   label var S "scale factor to convert from metric"

2. These models are identical

   logit diabetes c.bmi i.white c.age##c.age i.female i.hsdegree
   estimates store Mbmi

   logit diabetes c.S#c.weight#c.height_inv#c.height_inv ///
   c.age##c.age i.female i.hsdegree
   estimates store MbmiFV

3. The estimates are identical

   Variable MbmiFV Mbmi
   bmi 1.104553 1.104553
   white .5411742 .5411742
   weight 0.000 0.000

4. margins with factor syntax makes the rest trivial

5. ADC(weight) in MbmiFV changes only weight

   qui estimates restore MbmiFV
   mchange weight, amount(sd) delta(25)

6. ADC(weight) in Mbti is slightly larger

   qui estimates restore Mbti
   mchange weight, amount(sd) delta(25)

Decomposing BMI: ADC(weight)

4. ADC(weight) in MbtiFV changes only weight

   qui estimates restore MbtiFV
   mchange weight, amount(sd) delta(25)
   logit: Changes in Pr(y) | Number of obs = 16071
   Expression: Pr(diabetes), predict(pr)
   Change  p-value
   weight +25 0.065 0.000

6. ADC(weight) in Mbti is slightly larger

   qui estimates restore Mbti
   mchange weight, amount(sd) delta(25)
   logit: Changes in Pr(y) | Number of obs = 16071
   Expression: Pr(diabetes), predict(pr)
   Change  p-value
   weight +25 0.067 0.000
Decomposing BMI: summary

1. Factor variables and margins make the difficult decompositions trivial
2. Factor syntax understands interactions in model specifications
3. margins in turn understands interactions and handles the messy details

Comparing ADC(weight) in two models

1. To compare ADC(weight) requires joint estimation [%16]
   - clonevar lhsBMI = diabetes
   - clonevar lhswt = diabetes
   . gsem ///
   > (lhsBMI <- c.s#c.weight#c.height_inv#c.height_inv ///
   > i.white c.age##c.age i.female i.hsdegree, logit) ///
   > (lhswt <- c.weight c.height i.female i.white c.age##c.age i.hsdegree ///
   > i, logit) ///
   > , vce(robust)

Comparing ADC(weight) in two models

2. Computing the average predictions for both equations
   . margins, at(weight=gen(weight)) at(weight=gen(weight+25)) post

Predictive margins
Number of obs = 16,071
Model VCE : Robust

<table>
<thead>
<tr>
<th></th>
<th>_predict#_at</th>
<th>_predict#_at</th>
<th>_predict#_at</th>
<th>_predict#_at</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.1</td>
<td>0.2047166</td>
<td>0.2701404</td>
<td>0.2047166</td>
<td>0.271305</td>
</tr>
<tr>
<td>1.2</td>
<td>0.0030419</td>
<td>0.0044591</td>
<td>0.0030394</td>
<td>0.0044054</td>
</tr>
<tr>
<td>2.1</td>
<td>0.6730</td>
<td>0.6735</td>
<td>0.6158</td>
<td>0.6158</td>
</tr>
<tr>
<td>2.2</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
</tbody>
</table>

Delta-method
Marg: Std. Err.  z  P>|z|  [95% Conf. Interval]

Comparing ADC(weight) in two models

3. ADC(weight) for each model and their difference
   - qui mlincom 2-1, rowname(MBMI ADC) clear
   - qui mlincom 4-3, rowname(Mwt ADC) add
   - mlincom (4-3) - (2-1), rowname(Difference) add

<table>
<thead>
<tr>
<th></th>
<th>lincom</th>
<th>pvalue</th>
<th>ll</th>
<th>ul</th>
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<tr>
<td>MBMI ADC</td>
<td>0.065</td>
<td>0.000</td>
<td>0.061</td>
<td>0.070</td>
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<tr>
<td>Mwt ADC</td>
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<td>0.000</td>
<td>0.062</td>
<td>0.071</td>
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<tr>
<td>Difference</td>
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<td>0.029</td>
<td>0.000</td>
<td>0.002</td>
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</tbody>
</table>

4. Conclusion
   The effect of weight on diabetes are nearly identical whether body mass is measured with BMI or with height and weight (p = .03).

Conclusions: Stata, margins, and interpretation

Model interpretation and Stata
1. Too often interpretation ends with the estimated coefficients
2. Interpretations using predictions are more informative
3. Without margins what I suggested today (and more) would be impractical

Marginal effects is only one method
1. Marginal effects are more useful than odds ratios and should be routinely computed (mchange makes this trivial)
2. margins allow many extensions to standard marginal effects
3. The best measure is the one that answers your question and might not be a standard measure
4. Marginal effects are one method, not the only or best method. Tables and graphs are often more useful (Long and Freese, 2014)
5. The best interpretation must be motivated by your substantive question

Thanks to many people

Collaborators
Parts of this work were developed with Long Doan, Jeremy Freese, Trent Mize, and Sarah Mustillo. Jeff Pitblado and David Drukker provided valuable help. Mistakes are my own.

Relevant publications
There is a large literature on marginal effects and interpreting models. Long and Freese (2014) include many citations. The references directly related to this presentation are given below.

Thank you for listening


