Replicating Williams' Simulations for "Using Heterogeneous Choice Models To Compare Logit and Probit Coefficients Across Groups"

Purpose: This shows how to replicate the simulations presented in Table 4 of

Williams, Richard. 2009. "Using Heterogeneous Choice Models To Compare Logit and Probit Coefficients Across Groups" *Sociological Methods & Research* 37(4): 531-559. A pre-publication version is available at http://www.nd.edu/~rwilliam/oglm/RW_Hetero_Choice.pdf .

Programs needed: `sim30.ado`, `complogitx.ado`, `complogitml.ado` (these use Allison's original code); and/or `sim31.ado`, `complogity.ado`, and `oglm` (`oglm` is downloadable from SSC). The simulations reported in the paper use `sim30` with a seed of 125 but, for new analysis (where you do not need to perfectly replicate the published results), it may be better to use `oglm` and `sim31` (you are less likely to have failed simulations).

Instructions:

1. The programs `sim30` and `sim31` create simulated data sets and then call programs to analyze them. Modify these programs if you don't like their current defaults. Both `sim` programs include the lines

```
syntax [, b11(real 1.00)]

local b0_0 = 1
local b1_0 = 1
local b2_0 = 1

local b0_1 = 1
local b1_1 = `b11'
local b2_1 = 2.0
local sigma1 = 1
```

This does the following:

- Sets the constants (b0_0 and b0_1) for both groups at 1
- Sets Beta 1 (b1_0) for group 0 at 1; Beta 1 for group 1 (b1_1) is specified by the user when the program is called (see below)
- Sets Beta 2 for group 0 (b2_0) at 1; sets Beta 2 for group 1 (b2_1) at 2
- Sets the sigma for group 1 (sigma1) at 1, i.e. there are no differences in residual variation. Note that sigma0 is automatically fixed at 1 in Allison's model.

Hence, the betas differ between groups, but the sigmas are the same.

The programs also include calls to `complogitx` or `complogity`. Somebody interested in a different sort of analysis may wish to use different calls. If so, make sure you understand how information gets saved when doing simulations.

2. So, suppose you want to run 1000 simulations with Beta 1 for group 1 set at 1.5. From within Stata, type:

```
simulate, reps(1000) seed(125): sim30, b11(1.5)
```

You can make reps smaller (you probably want to until sure that all is well).
Quite a bit of information is saved from each simulation. The critical parts are

gddelta: The value of delta when betas are assumed to be equal
resid_sig: Equals 1 if residual variances significantly differed, 0 otherwise
coef_sig: Equals 1 if the coefficients significantly differed, 0 otherwise
gsdelta: The value of delta when you add the interaction term
gsintr: The value of the interaction term

As noted in the paper, the way these simulations are set up, the true conditions are that gddelta equals 0; resid_sig should equal 0; coef_sig should equal 1; gsdelta should equal 1; and gsintr should equal 1. If Allison's method is working well, any deviations should just be due to sampling variability.

3. Run `summarize`.

4. You may want to save the data set at the end. I recommend giving it a name that will remind you how you set the optional parameters or otherwise keeping some record of how the simulation was done. [NOTE: the data set contains the summary statistics from the simulations, not the simulated data itself.]

5. Example. Here is a complete run. The files mentioned above must be in the current directory. (The version 9.2 command is required to perfectly replicate the results in the paper if you are not running under Stata 9).

```
. version 9.2

. simulate, reps(1000) seed(125): sim30, b11(1.5)

. sum gddelta resid_sig coeff_sig gsdelta gsintr

    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
     gddelta |      1000     .802184    .2641022   .1527157   2.008015
   resid_sig |      1000        .984    .1255379          0          1
   coeff_sig |      1000        .355    .4787528          0          1
     gsdelta |      1000    .5222734    .2826083  -.1237167   1.700472
      gsintr |      1000    .3589203    .2445751  -.3988463    1.35899

. save b11_150.dta
```

In this simulation, the hypothesis that the residual variances were the same was incorrectly rejected 98.4% of the time. The hypotheses that the betas differed was (correctly) rejected only 35.5% of the time. The hypothesis that the interaction term was 0 was (correctly) rejected only 35.9% of the time. In short, Allison's procedure does not work well with this simulation.