EXAMPLE ANALYSES

DATA: NSFG 6 Female and Pregnancy files

Note: For the purposes of this exercise, we will ignore the sampling design of NSFG.

<u>Female file</u>
The Female Respondent file contains one record for each of the 7,643 women in the survey and includes most information from the questionnaires. It is structured like this example:

CASEID	VAR1	VAR2	VAR3
0001	1	5	0
0002	1	2	0
0003	0	3	1
0004	0	.	1
0005	1	1	0

A Stata data file including the following variables has been created:

caseid	respondent identification number
age	age at interview
marstat	marital status [1=married, 2=cohabiting, 3=widowed, 4=divorced, 5=separated, 6=never married]
hisprace	race/Hispanic ethnicity [1=Hispanic, 2=non-Hisp. white, 3=non-Hisp. Black, 4=non-Hisp. other]

<u>Pregnancy file</u>
The Female Interval (pregnancy) file contains one record for each of the 13,593 pregnancies (current and past), along with other related characteristics. It is structured like this example:

CASEID	PREGORDR	VARA	VARB
1	1	1	1
1	2	2	1
1	3	2	0
4	1	1	1
5	1	5	1
5	2	6	0

A data file including the following variables has been created. The pregnancy file has been turned into a female-level file using the "reshape" command in Stata. [reshape wide fmarcon, i(caseid) j(pregordr)] Once this has been done, the pregordr variable is deleted. (For more help with reshaping, see me or the Stata help menu)

caseid	respondent identification number
pregordr	pregnancy order
fmarcon1-fmarcon19	marital status at conception [1=married, 2=divorced, 3=widowed, 4=separated, 5=never married]

Action	**Command**
Set memory	set memory 5m
Begin log	log using "E:\feb5.smcl"
Open female data	use "E:\female.dta", clear
Create dummy variable coded [1=less than 18 years] [0=18 years or older]	generate lt18 = 1 if age<18 replace lt18 = 0 if age>=18
Recode "marstat" into dummy variables using "generate"	tab(marstat), gen(mardum)
Recode "hisprace" using xi	xi i.hisprace
Recode "hisprace" using xi so that no categories are omitted	xi i.hisprace, noomit
Create interaction term for "marstat" and "hisprace" using xi	xi i.marstat*i.hisprace, noomit
Save data as new dataset	save "E:\female1.dta"
Open pregnancy data file	use "E:\preg.dta", clear
Sort pregnancy file by caseid	sort caseid
Save the sorted data	save "E:\pregsort.dta"
Open female data file	use "E:\female1.dta", clear
Sort female file by caseid	sort caseid
Merge the files	merge caseid using "E:\pregsort.dta"
Check _merge variable	tab _merge
Drop cases where there was not data from both files	drop if _merge==1
Close log	log close