A response from Dr. Tom Pullum,
Quote:
Rather than comment on your steps I will just give you the lines that will accomplish what you
want to do. You will need to modify the paths. I am using the old version of the merge command,
which for me is less error prone than the new version. Note that in the merged file you should use
hiv05 as the weight.

```
set more off
use e:\DHS\DHS_data\AR_files\GMAR60FL.dta, clear
rename hivclust v001
rename hivnumb v002
rename hivline v003
drop hiv01 hiv02
sort v001 v002 v003
save e:\DHS\DHS_data\scratch\GMARtemp.dta, replace

use e:\DHS\DHS_data\IR_files\GMIR60FL.dta, clear
keep v*
gen sex=2
save e:\DHS\DHS_data\scratch\GMIRtemp.dta, replace

use e:\DHS\DHS_data\MR_files\GMMR60FL.dta, clear
keep mv*
rename mv* v*
gen sex=1
append using e:\DHS\DHS_data\scratch\GMIRtemp.dta
sort v001 v002 v003
merge v001 v002 v003 using e:\DHS\DHS_data\scratch\GMARtemp.dta
tab _merge
keep if _merge==3
tab sex hiv03 [iweight=hiv05/1000000], row
```