Subject: Re: v001 v002 v003 doesnot uniquely identify observation
Posted by kalfikirsisay@gmail.com on Mon, 13 Oct 2014 15:43:52 GMT
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dear Trevor,
thanks for quick response
I tried using 1:1 merge command only to get simialr message from STATA as before. I couldnot figure out why this is so, the following was the exact code I used.

```
use "C:\Users\mademsei\Desktop\CSA data and reports\Biomaker manual\merging files for bio\HH member recode\ETPR61FL.DTA", clear
gen v001 = hv001
gen v002 = hv002
gen v003= hvidx
sort v002 v002 v003
merge 1:1 v001 v002 v003 using "C:\Users\mademsei\Desktop\birth 1 to 1 merge.dta"
variables v001 v002 v003 do not uniquely identify observations in the using data
```

The master file I am using is HH member and the using file is birthrecode. Neverthless, I used the 1:m merge and get matched data albeit many observations(over 66000) were not matched. This is the table I obtained from 1:m merge command.

```
merge 1:m v001 v002 v003 using "C:\Users\mademsei\Desktop\birth 1 to 1 merge.dta"

    Result                           # of obs.
    -----------------------------------------
    not matched                          66,848
        from master                      66,848  (_merge==1)
        from using                            0  (_merge==2)

    matched                              45,540  (_merge==3)
    -----------------------------------------
```

Is this the right way? I am a bit sceptic of the merging approach, I thought either m:1 or 1:1 to be proper, ofcourse I merged all observations in my using file and this what I need to appear in the maser file. your last comment on this is of prior value,Thanks in advance,
Kalkidan Sisay