Subject: Re: Biomarkers / Malaria

Posted by kalfikirsisay@gmail.com on Sun, 12 Oct 2014 15:32:52 GMT

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Hi Liz,
one more question,
I need to merge the HHmember recode (where ha0, hb and hcs are) with HIV separate data set. I followed the following commands.
first I renamed the identifiers :

```
rename hivclust hv001
rename hivnumb hv002
rename hivline hv003
sort hv001 hv002 hv003
```

I oppened the master file(HH member) and use the command

```
merge m:1 hv001 hv002 hv003 using HIV data set.
```

I obtained this table

```
 Result                           # of obs.
    -----------------------------------------
    not matched                       36,306
        from master                   18,674  (_merge==1)
        from using                    17,632  (_merge==2)

    matched                           59,070  (_merge==3)
    -----------------------------------------
```

which shows that 36,306 osbervations are not matched.I highly doubted if I have used the propoer merging, and worried why this is so. My unit of analysis is individula(women, men and children)
would you please extend your usual supports quickly
Regards
Kal