
Subject: Re: Biomarkers / Malaria

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

[View Forum Message](#) <> [Reply to Message](#)

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 opened 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 observations are not matched. I highly doubted if I have used the proper merging, and worried why this is so. My unit of analysis is individual (women, men and children) would you please extend your usual supports quickly

Regards

Kal
