Subject: Biomarkers / Malaria
Posted by kalfikirsisay@gmail.com on Fri, 10 Oct 2014 13:32:13 GMT
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Hi All, I am using Ethiopian DHS2011 data for my analysis involving bimarker data. I tried to see on the DHS recode map that variable HML32 (with subscrips)stands for malaria and bednet uses; neverthless, I couldnot trace out this variable in any of the child, HH, male, HHmemeber, and individual recodes. Can any one help where to find this and other biomrker indicators?
Reards,

Subject: Re: Biomarkers / Malaria
Posted by Liz-DHS on Fri, 10 Oct 2014 16:43:23 GMT
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Dear User,
The section on malaria and bed net use was not used in Ethiopia DHS 2011. Variable HML32 will only exist in a dataset when the bed net module is used in a country.

For other biomarkers variables used in Ethiopioa DHS 2011 please look at the following: (if the variable are N/A, they were not applicable in Ethiopia)
-Women biomarker variables HA0 HA70
-Children biomarker variables HC1 - HC70
-Men biomarker variables HB0 HB70

The HIV data sets are separate data sets from the main files and have their own variables and dictionary.
Thank you for your post.

Subject: Re: Biomarkers / Malaria
Posted by kalfikirsisay@gmail.com on Fri, 10 Oct 2014 19:29:18 GMT
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Many Thanks for your helps
Regards,
Kal

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

Subject: Re: Biomarkers / Malaria
Posted by Trevor-DHS on Mon, 13 Oct 2014 14:16:33 GMT

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Two problems:
1) rename hivline hv003 is renaming to the wrong variable. hv003 is the line number of the respondent to the household questionnaire, not the line number of the woman or man whose data you are interested in. You need to use

```
rename hivline ha0
```

where ha0 is the line number of the woman.
2) Your merge should be a 1:1 merge, not a many to one merge.

You will first need to merge the data with the women's biomarker data, then repeat the process using hb0 to merge with the men's biomarker data.

Subject: Re: Biomarkers / Malaria
Posted by kalfikirsisay@gmail.com on Fri, 17 Oct 2014 13:01:11 GMT

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Dear Trevors,

Many thanks for your usual helps,
Kalkidan