Subject: Maternal Mortality in Ghana
Posted by Shine on Sun, 23 Apr 2023 16:54:44 GMT
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Dear All,

I am trying to calculate maternal mortality ratio for Ghana using the Ghana Maternal Health Survey (MHS) 2017 data. I read in the report that the MHS is the same as the Ghana DHS Special, however, I cannot run the the do-file provided in chapter 16 in the github page as the variables in MHS are coded differently, also, some of the variables in the DHS are not in the MHS. Can I get the do-file used in calculating maternal mortality using the MHS 2017?

Thank You.

Subject: Re: Maternal Mortality in Ghana
Posted by Janet-DHS on Wed, 26 Apr 2023 18:28:04 GMT
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Following is a response from DHS staff member, Tom Pullum:

If you open GHIQ7JFL.dta in Stata and enter "describe q8*_01" you will get a list of the variables from the sibling histories that were included in this survey. They can be recoded into the mm variables that would be in a standard DHS (you can get those by entering "describe mm*_01" for another survey, such as the Tanzania 2015-16 survey). It's not just a matter of changing the variable names. More recoding than that would be necessary to get mm9 from q819, q820, and q821, for example. After you have done these recodes you can apply the standard GitHub program.

Subject: Re: Maternal Mortality in Ghana
Posted by Shine on Tue, 02 May 2023 18:37:54 GMT
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Thank you very much Janet for the response.

Studying the GitHub dofile, I realized that variables v021-v023 are not present in the GHIQ data set. What do I do in this case?

Subject: Re: Maternal Mortality in Ghana
Posted by Janet-DHS on Fri, 05 May 2023 18:27:13 GMT
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Following is a response from DHS staff member, Tom Pullum:

The variables you are looking for actually are in GHIQ7JFL.dta or can be constructed. The cluster

ID, which is normally v001 v021 (they are duplicates) is qhclust. Normally v022 and v023 (they are duplicates) are the stratum ID code. I don't see it explicitly but you can construct it as combinations of region and type of place of residence with "egen stratum=group(qtype qregion)". The sample weight is normally v005 but here it is qweight (probably you had already seen it). So you do have everything you need for the svyset command.