Subject: Re: MM9 in the NGIR7BFL dataset of NDHS is from MM9\$01 - MM9\$20 (maternal mortality) Posted by Janet-DHS on Thu, 03 Oct 2024 18:18:28 GMT View Forum Message <> Reply to Message

Following is a response from DHS staff member, Tom Pullum:

You can calculate the number of siblings with these lines (in Stata), before reshaping the IR file: use "C:\Users\26216\ICF\Analysis - Shared Resources\Data\DHSdata\NGIR7BFL.DTA", clear

rename \*\_0\* \*\_\*

\* Calculate the number of siblings each woman has

gen nsibs=0

forvalues lsibs=1/20 {

replace nsibs=nsibs+1 if mm1\_`lsibs'<.

}

tab nsibs

tab nsibs [iweight=v005/1000000]

```
summarize nsibs [iweight=v005/1000000]
```

The weighted mean is 5.23 siblings. Note that you have to allow for the possibility of 0 siblings. This can be modified to give the number of siblings who are males, females, still alive, etc. I am repeating the Stata lines I gave earlier, because what I pasted the first time omitted m7. The full program is below--but it does not include the lines to calculate the adult and maternal mortality rates. Those lines are on our GitHub site.

use "C:\Users\26216\ICF\Analysis - Shared Resources\Data\DHSdata\NGIR7BFL.DTA", clear

rename \*\_0\* \*\_\*

```
* Calculate the number of siblings each woman has
gen nsibs=0
forvalues lsibs=1/20 {
replace nsibs=nsibs+1 if mm1_`lsibs'<.
}
```

tab nsibs

tab nsibs [iweight=v005/1000000]

```
summarize nsibs [iweight=v005/1000000]
```

\* For this example just keep mm1 and mm7 and mm9

```
keep v001 v002 v003 mm1_* mm7_* mm9_*
```

reshape long mm1\_ mm7\_ mm9\_, i(v001 v002 v003) j(index)

rename \*\_ \*

tab mm1, m

\* Drop the lines that go beyond the woman's actual number of siblings

drop if mm1==.

tab mm9 if mm1==2 & mm7>=15 & mm7<=49,m