Subject: Contraceptive prevalence rate
Posted by cyk3121 on Wed, 11 Dec 2024 18:31:51 GMT
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Hello, I am trying to calculate the mCPR using BDHS 2022, but my estimate does not match the report. I am getting 36.5% while the report says 54.7%. I have downloaded the data multiple times but can't seem to match the report. Has anyone else had this issue? Are there special considerations for Bangladesh that don't apply to other countries? I have calculated it for 14 other countries correctly except for Bangladesh.

Thanks!

Subject: Re: Contraceptive prevalence rate
Posted by Bridgette-DHS on Fri, 13 Dec 2024 12:39:48 GMT
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Following is a response from Senior DHS staff member, Tom Pullum:

I opened BDIR81FL.dta in Stata and entered the following line:

```
tab v313 if v501==1 [iweight=v005/1000000]
```

Here is the result:

The results include the 54.7% given in table 7.1.1 for the mCPR. This is the standard way to get the mCPR. I wonder what you were doing differently for the other surveys where you say you were getting a match.

The Bangladesh surveys only include ever-married women in the IR file but that should not affect the calculation of the mCPR, which is defined for currently married women.

File Attachments
1) v313.png, downloaded 388 times

Subject: Re: Contraceptive prevalence rate
Posted by cyk3121 on Mon, 16 Dec 2024 17:43:55 GMT
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Thank you for your response! I was using the FP module code on GitHub which generated an fp_cruse_mod variable from v313.

I see now that the Bangladesh data has missing values in v313 whereas the other countries in my analysis do not have missing data in this variable so that affected my denominator. Appreciate your insight.

```
*** Current use of contraceptive methods ***

//Currently use any method
gen fp_cruse_any = (v313>0 & v313<8)
label var fp_cruse_any "Currently used any contraceptive method"

//Currently use modern method
gen fp_cruse_mod = v313==3
label var fp_cruse_mod "Currently used any modern method"
```

Subject: Re: Contraceptive prevalence rate

Posted by Bridgette-DHS on Tue, 17 Dec 2024 12:20:55 GMT

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

Whenever I see a substantial number of cases with a dot (for Not Applicable or NA) on a key variable, I enter "lookfor select" to see if there is a selection variable for a subsample. One of the variables that comes up in this survey if you do that is "seligbm":

```
seligbm         byte    %8.0g      SELIGBM    hh selected for biomarker and long/short woman qre
```

which has the following distribution:

```
        hh selected for biomarker and |
                 long/short woman qre |      Freq.     Percent        Cum.
--------------------------------------+-----------------------------------
household selected for biomarker and fu |     10,053       33.42       33.42
household selected for full woman quest |      9,934       33.03       66.45
household selected for short woman ques |     10,091       33.55      100.00
--------------------------------------+-----------------------------------
                                Total |     30,078      100.00
```

It appears that there was indeed subsampling in this survey. 10,091 women were in households selected for a "short" women's questionnaire that omitted questions about contraceptive use. That is, women with seligbm=3 are NA on v313 (and many other variables). Those women must be ignored for the calculation of the mCPR. This subsampling may affect other variables in your analysis.

This sort of thing is one of the hazards of using DHS data and the GitHub programs. Someone could say that analysts should read about the sampling design before starting to use the data but we (you and I!) usually just plunge in and then find these exceptional features the hard way. The good thing is that you tried to calibrate your estimate against the report and found a discrepancy, and it led to the evidence of subsampling. That's good practice. Subsampling is one of the main reasons why users cannot match reports.