
Subject: Re: 2017 Ghana Maternal Health Survey
Posted by [Imallick](#) on Mon, 19 Aug 2019 19:50:43 GMT
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Then I would try to collapse the BQ file to what would be the caseid in an IR file: qhclust qhnumber qline using a count of each of the dummy pregnancy variables that you could create using the line above.

Does this help:

use GHBQ7IFL.DTA, clear

gen wt = qweight/1000000

```
ta pregout, gen(pregout_dummy)
sort qhclust qhnumber qline
collapse (count) live = pregout_dummy1 ///
  still = pregout_dummy2 ///
  miscar = pregout_dummy3 ///
  abor = pregout_dummy4 ///
  , by(qhclust qhnumber qline)
```

save GHpregout.dta, replace

use GHIQ7IFL.dta, clear

merge 1:1 qhclust qhnumber qline using GHpregout

Once merged, you could create a binary variable for ever had an abortion (Y/N) if abor is greater than or equal to 1. Then you could cross tab with q578_1.
