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Subject: Merging KR with PR

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Country: Nigeria

Survey:2018

Dataset: Child Recode (KR) and Household Member Recode(PR)

I am working on anemia, diarrhea, and malaria in under-5 children in Nigeria. The data on anemia and diarrhea is contained in the KR file while the data on malaria is contained in the PR file(I do not need the fever data in the KR file). The issue is how to merge the "HOUSEHOLD - Malaria: by Household Member" subset of the PR file to the KR file. I have adapted several codes I sourced on this platform but to no avail. I keep getting no observation after merging. I believe I can match the children in the KR file with the "Malaria: by Household Member" section of PR. In the PR file, I tabulated the "child's age in months" against "final result of malaria from blood smear test" and below is a sample of the output as evidence that children's malaria test results are in the PR file. I will appreciate any assistance in this regard to be able to match the children in KR with children in PR. Thanks.

child's age in months	final result of malaria from blood smear test		Total
	negative	positive	
6	141	31	172
7	114	34	148
8	128	23	151
9	129	21	150
10	100	21	121
11	132	16	148
12	159	24	183
13	164	39	203
14	129	25	154
15	148	35	183
16	116	32	148
17	130	28	158
18	134	24	158
19	110	21	131
20	109	32	141

Below is the most recent code I adapted:

```
use "C:\Users\ezpawm\Downloads\NG_2018_DHS_10132022_1330_145124\NGPR7BFL.DTA",  
clear
```

```
keep if hmhidx==1
gen cluster=hv001
gen hh=hv002
gen caretaker= hml30
sort cluster hh caretaker
save
"C:\Users\ezpawn\Downloads\NG_2018_DHS_10132022_1330_145124\NGPR7BFL_Temp.DTA"
, replace

use "C:\Users\ezpawn\Downloads\NG_2018_DHS_10132022_1330_145124\NGKR7BFL.dta",
clear
gen cluster=v001
gen hh=v002
gen caretaker=v003
sort cluster hh caretaker
merge cluster hh caretaker using
"C:\Users\ezpawn\Downloads\NG_2018_DHS_10132022_1330_145124\NGPR7BFL_Temp.DTA"

tab _merge

keep if _merge==3
save
"C:\Users\ezpawn\Downloads\NG_2018_DHS_10132022_1330_145124\NG_KR_PR_Merged.dta"
, replace

gen children_per_caretaker=1
collapse(sum) children_per_caretaker, by(cluster hh caretaker)

tab children
```

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