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Subject: Re: Merge BDSQ7RDT and BDVA7RDT with the household data file  
Posted by [Bridgette-DHS](#) on Thu, 01 Feb 2024 16:04:03 GMT

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

I recommend that you think of this as merging the SQ and PR data with the VA data. When you use the VA data, your interest is in the children (up to 8) for whom the mother provides information. The lines given below will do the merge, with one record per mother, as in the VA data. Your next step would probably be to reshape this file into a file that has one record per child.

It is not necessary to include "m:1" or 1:m" in the merge command. Let us know if you have questions.

\* BD7R: Merge the PR, VA, and SQ files

\* Specify workspace

```
cd e:\DHS\DHS_data\scratch
```

\* Prepare SQ file for merge

```
use "...BDSQ7RFL.DTA", clear
```

```
gen cluster=coclust
```

```
sort cluster
```

```
save SQtemp.dta, replace
```

\* Prepare PR file for merge

```
use "...BDPR7RFL.DTA", clear
```

```
gen cluster=hv001
```

```
gen hh=hv002
```

```
gen line=hvidx
```

```
sort cluster hh line
```

```
save PRtemp.dta, replace
```

\* Open the VA file and prepare for merge

\* The VA file has up to 8 records per mother, 1 for each reference child,

```
use "...BDVA7RFL.DTA", clear
```

```
gen cluster=qnccluster
```

```
gen hh=qnhnumber
```

```
gen line=qnmother
```

```
sort cluster hh line
```

```
merge cluster hh line using PRtemp.dta
```

\* Reduce to the mothers who are in both the VA and PR file

```
tab _merge
```

```
keep if _merge==3
```

```
drop _merge
```

\* Prepare for merge with the SQ file, which has one record per cluster  
sort cluster  
merge cluster using SQtemp.dta  
tab \_merge  
keep if \_merge==3  
drop \_merge

\* Save this file, which has one record per mother, and reshape for one record per child

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