Subject: Merging of SA DHS 2016 HIV dataset ZAAR and ZAPR
Posted by mnyahuma on Tue, 14 May 2024 09:24:36 GMT
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I would like help with the merging of HIV dataset and the ZAPR dataset for SA 2016. I would like to find out if there is an alternative way to combine the HIV data set with ZAPR or combining HIV dataset with both IR and MR so that I can be able to analyses the relationship between HIV and associated risk factors in the survey. I managed to append HIV data with IR and then merged it with MR in order to determine the number of males and females who are positive but I am struggling to combine the datasets in order to determine relationship between HIV and the associated risk factors. Your help is greatly appreciated

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Subject: Re: Merging of SA DHS 2016 HIV dataset ZAAR and ZAPR
Posted by Janet-DHS on Thu, 16 May 2024 13:42:16 GMT
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Following is a response from DHS staff member, Tom Pullum:

There are various ways to do this merge. The following lines will work. You need to specify a workspace and your path to the data.

```
* merge_AR_IR_MR_PR_do_15May2024

* South Africa 2016 DHS, ZA71



* specify workspace

cd e:\DHS\DHS_data\scratch



* specify path to the data with a scalar

scalar spath="C:\Users\26216\ICF\Analysis - Shared Resources\Data\DHSdata"

local lpath=spath



* Prepare the four data files

use "`lpath'\ZAAR71FL.DTA", clear

gen cluster=hivclust

gen hh=hivnumb
```

```
gen line=hivline
gen wt=hiv05/1000000
gen in_AR=1
tab in_AR
save ARtemp.dta, replace

use "`lpath'\ZAPR71FL.DTA", clear
gen cluster=hv001
gen hh=hv002
gen line=hvidx
keep if hv117==1 | hv118==1
save PRtemp.dta, replace

use "`lpath'\ZAIR71FL.DTA", clear
gen cluster=v001
gen hh=v002
gen line=v003
save IRtemp.dta, replace

use "`lpath'\ZAMR71FL.DTA", clear
rename mv* v*
gen cluster=v001
gen hh=v002
gen line=v003
```

```
save MRtemp.dta, replace


* Append IR and MR
use IRtemp.dta, clear
append using MRtemp.dta
save IRMRtemp.dta, replace


* Merge AR with PR
use ARtemp.dta, clear
merge 1:1 cluster hh line using PRtemp.dta
keep if in_AR==1
drop _merge


* Merge with IR+MR
merge 1:1 cluster hh line using IRMRtemp.dta
keep if in_AR==1
drop _merge


* Confirm that we have all the cases in the AR file
tab in_AR,m
```

Subject: Re: Merging of SA DHS 2016 HIV dataset ZAAR and ZAPR
Posted by mnyahuma on Fri, 17 May 2024 13:15:17 GMT
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Thank you very much