

---

Subject: Merging of SA DHS 2016 HIV dataset ZAAR and ZAPR

Posted by [mnyahuma](#) on Tue, 14 May 2024 09:24:36 GMT

[View Forum Message](#) <> [Reply to Message](#)

---

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

---

---

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

[View Forum Message](#) <> [Reply to Message](#)

---

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

[View Forum Message](#) <> [Reply to Message](#)

---

Thank you very much

---