
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
