
Subject: Re: Selecting appropriate weights when IR and MR files are pooled

Posted by [Bridgette-DHS](#) on Mon, 24 Apr 2023 12:07:00 GMT

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

Your results looked ok but the only way I could confirm was by doing it myself. I'll paste the Stata lines below because they could be useful to others. I get the same results.

* Specify workspace

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

```
use "...ETAR71FL.DTA", clear
```

```
gen cluster=hivclust
```

```
gen hh=hivnumb
```

```
gen line=hivline
```

```
sort cluster hh line
```

```
save ARtemp.dta, replace
```

```
use "...ETIR71FL.DTA", clear
```

```
gen sex=2
```

```
save IRtemp.dta, replace
```

```
use "...ETMR71FL.DTA", clear
```

```
gen sex=1
```

```
rename mv* v*
```

```
append using IRtemp.dta
```

```
gen cluster=v001
```

```
gen hh=v002
```

```
gen line=v003
```

```
sort cluster hh line
```

```
merge 1:1 cluster hh line using ARtemp.dta
```

```
tab _merge
```