
Subject: Anthropometric z scores_Ethiopia DHS2011

Posted by [Bubbu](#) on Fri, 08 Mar 2019 19:57:00 GMT

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Hi all,

Please look at the following case and help me!

NB: I use mac book

I am working on anthropometric z scores using Ethiopia DHS 2011.

I have various data sets in "/Users/mes/Documents/ET_2011_DHS_messu/" directory. From the DHS data sets in this directory, I have one data set with variables: hv001, hv002, hvidx, gender, age_months, ageunit, weight, height, oedema, measure, sw, hv120 which are relevant to calculate anthropometry Z scores. The dataset is saved in "/Users/mes/Documents/WHO igrowup STATA/WHO igrowup workdata/ETH11_survey.dta"

I ran the following syntax as guided in WHO Anthro files (from <https://www.who.int/childgrowth/software/en/>) for STATA.

*THIS RUNS THE ANTHRO ADO FILE FROM WHO *

```
clear
```

```
set more 1
```

```
/* Higher memory might be necessary for larger datasets */
```

```
set memory 20m
```

```
set maxvar 10000
```

```
/* Example: survey_standard.do using survey.dta */
```

```
/* Indicate to the Stata compiler where the igrowup_standard.ado file is stored*/
```

```
adopath + "/Users/mes/Documents/WHO igrowup STATA/"
```

```
/* Load the data file */
```

```
use "/Users/mes/Documents/WHO igrowup STATA/WHO igrowup workdata/ETH11_survey.dta",
```

```
clear
```

```
/* generate the first three parameters reflib, datalib & datalab */
```

```
gen str60 reflib="/Users/mes/WHO igrowup STATA"
```

```
lab var reflib "Directory of reference tables"
```

```
gen str60 datalib="/Users/mes/Documents/WHO igrowup STATA/WHO igrowup workdata"  
lab var datalib "Directory for datafiles"
```

```
gen str30 datalab="ETH11_survey"  
lab var datalab "Working file"
```

```
/* check the variable for "sex" 1 = male, 2=female */  
desc gender  
tab gender
```

```
/* check the variable for "age" */  
ren age_months agemons  
desc agemons  
summ agemons
```

```
/* define your ageunit */  
*gen str6 ageunit="months" /* or gen ageunit="days" */  
*lab var ageunit "=days or =months"
```

```
/* check the variable for body "weight" which must be in kilograms*/  
/* NOTE: if not available, please create as [gen weight=.]*/  
desc weight  
summ weight
```

```
/* check the variable for "height" which must be in centimeters*/  
/* NOTE: if not available, please create as [gen height=.]*/  
desc height  
summ height
```

```
/* check the variable for "measure"*/  
/* NOTE: if not available, please create as [gen str1 measure=" " ]*/  
desc measure  
tab measure
```

```
/* check the variable for "headc" which must be in centimeters*/  
/* NOTE: if not available, please create as [gen headc=.]*/  
gen headc=.  
desc head  
summ head
```

```
/* check the variable for "armc" which must be in in centimeters*/  
/* NOTE: if not available, please create as [gen armc=.]*/  
gen muac=.
```

```
desc muac
summ muac
```

```
/* check the variable for "triskin" which must be in millimeters*/
/* NOTE: if not available, please create as [gen triskin=.]*/
gen triskin=.
desc tri
summ tri
```

```
/* check the variable for "subskin" which must be in millimeters*/
/* NOTE: if not available, please create as [gen subskin=.]*/
gen subskin=.
desc sub
summ sub
```

```
/* check the variable for "oedema"*/
/* NOTE: if not available, please create as [gen str1 oedema="n"]*/
desc oedema
tab oedema
```

```
/* check the variable for "sw" for the sampling weight*/
/* NOTE: if not available, please create as [gen sw=1]*/
desc sw
summ sw
```

```
/* Fill in the macro parameters to run the command */
igrowup_standard reflib datalib datalab gender agemons ageunit weight height measure head
muac tri sub oedema sw
```

However, I got the following error message:

```
<<Please wait, programme is running.....
```

```
.....
file /Users/mes/igrowup_stata\weianthro.dta not found r(601);
```

```
end of do-file
```

```
r(601);>>
```

And I checked back that weianthro.dta exists in the directory: "/Users/mes/Documents/WHO igrowup STATA/". Yet I see the above error message.

Please help me get it right!
