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 relevent 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!