Subject: Namibia 2013

Posted by imup on Sun, 15 Feb 2015 07:52:15 GMT

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Hi,

I am using the dataset from Namibia 2013.I would like to know how to reproduce the table 17.7.1 and 17.7.2of fasting blood glucose testing. The data set have 6 columns for blood glucose level with a lot of missing/notavailable data in the household part regarding that.(I am using R).
reply much appreciated.

Subject: Re: Namibia 2013

Posted by Trevor-DHS on Sat, 21 Feb 2015 18:11:58 GMT

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The key variable you need to use is sh336k which holds the blood glucose level. The missing values come for a number of reasons:
1) Blood glucose is only collected in a subsample of households. All members in households not selected for the sample will have a missing value.
2) Blood glucose is only collected for women and men age 35-64. All members other than those age 35-64 will have a missing value.
3) Blood glucose is only collected for women and men age 35-64 who consent to being tested. All other will have missing data.

The values in sh336k are recoded into the 4 groups presented in the tables. sh336k contains values per decilitre (dl) rather than per litre as shown in the table, so the recoding is into the following groups: 0-38 = below normal, 39-60 = normal, 61-69 = prediabetic, 70-222 = elevated, other higher values are consider invalid as are excluded.

Below is some simple code in R for tabulating the data:

```
install.packages("foreign")
install.packages("survey")
install.packages("car")
library(foreign)
library(survey)
library(car)

dta <- read.dta("C:/Data/DHS_stata/NMPR60FL.dta", convert.factors = FALSE)

dta$bg<-factor(recode(dta$sh336k,"0:38='1 below normal';39:60='2 normal';61:69='3
prediabetic';70:222='4 elevated';else=NA"))
dta$sex <-factor(recode(dta$hv104,"1='1 Male';2='2 Female';else=NA"))

DHSdesign<-svydesign(id=dta$hv021, strata=dta$hv022, weights=dta$hv005/1000000, data=dta)
bg.table <- svytable(~sex+bg, DHSdesign)
bg.table
prop.table(bg.table,1)*100
```

```
margin.table(bg.table,1)
```

The output results should look like:

```
> bg.table
        bg
sex       1 below normal   2 normal 3 prediabetic 4 elevated
  1 Male       111.24863  967.97756      76.83102   65.28731
  2 Female      79.05747 1570.28125     133.86968   89.82786
> prop.table(bg.table,1)*100
        bg
sex       1 below normal  2 normal 3 prediabetic 4 elevated
  1 Male        9.108702 79.255078      6.290692   5.345528
  2 Female      4.220819 83.836137      7.147202   4.795842
> margin.table(bg.table,1)
sex
  1 Male 2 Female
1221.345 1873.036
```

Subject: Re: Namibia 2013
Posted by imup on Tue, 24 Feb 2015 14:01:06 GMT

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Thanks thats very helpful.
however, I still don't get why many columns e.g. blood glucose sh336k there are sh336k.1sh336k.2...sh336k.6, is it different sample/visits for the same respondent or different samples from different members in the same household.?if so how do i figure which is for which?
I want to merge that with HIV results from HIV set but still I don't know how to explain the columns in the household set to get Male/female and BMI for example in R.

reply very much appreciated

Subject: Re: Namibia 2013
Posted by imup on Tue, 24 Feb 2015 17:05:31 GMT

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Thanks alot that was very helpful.

Subject: Re: Namibia 2013
Posted by Trevor-DHS on Mon, 16 Mar 2015 23:59:33 GMT

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I think you are looking at the household recode dataset, rather than the person's recode dataset. In the household recode dataset, there are entries for sh336k for up to 7 different household members - no household in the survey had more than 7 men and women age 35-64 who were eligible for the blood glucose test. In the person's recode dataset there is one record per person, and only one variable sh336k. See my example above, that tabulates sh336k by sex.