Subject: Re: Merging HIV data with Couples recode
Posted by Trevor-DHS on Mon, 24 Mar 2014 18:13:42 GMT
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Hi Tewodros,

First, a basic tenant of science is that your results must be reproducible. If you are using a point and click approach then your results are difficult to reproduce. Users are expected to use syntax to produce their analysis and to permit others to be able to reproduce the analysis. For the information you provide me it is impossible for me to tell what you have done exactly. From your description, I am assuming that you have a made a mistake with which file is your base file when merging, but I can't tell from the description. I highly recommend that you switch to using syntax files and use the syntax that I provided as a basis.

In answer to your questions:
1. Yes, you probably made a mistake in the merging steps, but I can't tell what mistake.
2. Learn to use syntax files for your analysis.
3. The unit of analysis will be the unit of analysis from your base dataset. The order in which you use the files in your merging steps is very important and will affect the unit of analysis. As I suspect you have an error in the merging, you probably do not have the right unit of analysis, but I can't tell from the information you provide.