Subject: Re: accounting clustering effects of women's data when using baby-based analysis

Posted by Reduced-For(u)m on Sat, 28 Sep 2013 21:52:08 GMT

View Forum Message <> Reply to Message

So I'm guessing the big concern here is that using an RE model you get "significant" results, and using clustering you don't. My honest opinion - I'd believe the clustering p-values above the RE ones. On the other hand, in Epi all previous results have p-values from RE models, so you'd be subjecting your results to a tougher test than is common. Common is probably wrong in Epi (meaning that my experience is most of their SE estimates are too small in general), but it is also the baseline. So which results you decide to go with is totally up to you.

As for why this is happening - well, since clustering imposes less structure on the data (and to repeat what I said above) and so almost always produces larger SEs than RE models. In your case, that causes the 90% CI to go from excluding 0 to including it. That sucks for you, but is probably more "right". Notice that the point estimates are exactly the same, so all that is changing is that when you don't impose structure on your residuals, your residuals (within-group) tell a different story about precision.

So I guess my point is: clustering will lead to larger SEs than RE models, but these SEs are probably more "correct" or closer to "correct" (meaning produce reliable rejection rates) than the RE estimates.

One last thing - how many "clusters" do you have? If it is less than 50 or so, even these cluster SEs might be too small. Otherwise, they should be good.

Sorry to bear what I think is probably bad news for your research, but I also think your result is probably still really interesting, since I think of "statistical significance" as something much less important than other people do. Getting precision estimates right is important, but which side of a threshold it falls on is not that important (to me). Good luck. Let me know if I can help more.