

ARIC MANUSCRIPT PROPOSAL FORM

Manuscript #243b

1. Title (length 26 characters):

Multivariate change

Full Title: Analysis of predictors of associations with change in a multivariate outcome when baseline variable is subject to measurement error

2. Writing Group (list individual with lead responsibility first):

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3. Timeline:

The paper is finished.

4. Rationale:

MS243 analyzed change in IMT over 4 ARIC visits, as a function of risk factors and baseline IMT. Since baseline IMT was measured with error, ordinary least squares estimates of model coefficients are seriously biased, so estimates must be corrected for this bias. There are theoretical papers in the statistical literature on how this correction might be done for multivariate outcome variables, but there was a need to explicate these methods in a more applied manner.

5. Main Hypothesis/Study Questions:

This is a methodology paper, explicating the methods needed to correct for measurement error in baseline when the outcome is a multivariate change variable. ARIC data are used in examples applying the methods, and serve in a simulation study as hypothetical "true" measurements to which "error" is generated and added, for the purpose of giving an example with realistic data to show the size of the bias caused from ignoring the problem of measurement error.

6. Data (variables, time window, source, inclusions/exclusions):

Data from ARIC visits 1-3, including only IMT, HDL, hypertension, sex, race, time between visits, fibrinogen, age, BMI, and LDL.

7.a. Will the data be used for non-CVD analysis in this manuscript? NO

b. If Yes, is the author aware that the file ICTDER02 must be used to exclude persons with a value RES_OTH = "CVD Research" for non-DNA analysis,
and for DNA analysis RES_DNA = "CVD Research" would be used?

(This file ICTDER02 has been distributed to ARIC PIs, and contains the responses to consent updates related to stored sample use for research.)

8.a. Will the DNA data be used in this manuscript? NO

b. If yes, is the author aware that either DNA data distributed by the Coordinating Center must be used, or the file ICTDER02 must be used to exclude those with value RES_DNA = "No use/storage DNA"?