

Introduction: This submission provides SAS code for fitting a longitudinal logistic regression model in which a random intercept is included to induce a compound symmetry covariance structure for repeated measures on individual subjects.

Keyword Categories:

Clinical: Longitudinal Study
Genetics: Not Applicable (NA)
Statistical: Generalized Linear Mixed Models; NLMIXED procedure;
Longitudinal Data Analysis
Software: SAS 9.1
Related:

References:

Van Ness, PH, J. O'Leary, et al. (2004). "Fitting longitudinal mixed effect logistic regression models with the NLMIXED procedure." *Proceedings of the 29th Annual SAS® Users Group International Conference (SUGI 29)* **29**: 1-6 (www2.sas.com/proceedings/sugi29/190-29.pdf).

Fried T, Byers, AL, Gallo, WT, Van Ness, PH, Towle, VR, O'Leary, JR, Dubin, JA. Prospective study of health status preferences and changes in preferences over time in older adults. *Archives of Internal Medicine*. 2006;166:890-895.

Component Files:

- a. PDF file explaining the entire sample: NLMIXEDSummaryVanNess.pdf
- b. SAS program: NLMIXEDProgramVanNess.txt
- c. SAS data file: NLMIXEDDataVanNess.txt
- d. SAS output file: NLMIXEDOutputVanNess.txt

Optimal Use:

To run the macro one should first copy the NLMIXEDProgramVanNess.txt file and paste it into SAS software enhanced editor window. Next, save this newly created SAS program using the filename 'mixed_long_logit.inc'. Then, run the macro using the syntax provided in the annotations for the macro program.

Prerequisites:

One only needs the ability to run SAS programs, any recent version will be sufficient.

Potential Applications:

This macro program is intended for use with regression models of sufficiently large dimension, e.g., in which the number of covariates is expected to be a half dozen or more, such that failure to obtain successful convergence of estimating algorithms is a real problem. The program seeks to address this problem by providing good approximations for estimated parameters from a related GEE model fit with PROC GENMOD.

Acknowledgement:

This work was supported in part by grants from the Biostatistics Core of the Claude D. Pepper Older Americans Independence Center at Yale University School of Medicine (#2P30AG021342-06).