

**Introduction:**

This document ties together the four different files that make up the GRASP example for Little's test for missing completely at random (MCAR) on data drawn from the Cardiovascular Health Study (CHS). CHS is a population-based study designed to identify risk factors for cardiovascular disease in individuals aged 65 or older. In 1989, 5,201 participants were enrolled, and a supplemental cohort of 687 African Americans was added in 1992-1993. The participants were a random sample of Health Care Financing Administration eligibility lists and persons living in their households.

**Keyword Categories:**

Clinical: Longitudinal study, Cardiovascular Health Study

Genetic: Not Applicable

Statistical: Missing Data, missing completely at random (MCAR), imputation

Software: SAS

Related:

**References:**

Little RJA. A test of missing completely at random for multivariate data with missing values. *J Am Stat Assoc* 1988; 83:1198-1202.

Van Ness PH, Murphy TE, Araujo KLB, et al. The use of missingness screens in clinical epidemiologic research has implications for regression modeling. *J Clin Epidemiol* 2007; 60:1239-1245.

**Component Files:**

- a. SAS program: McarProgramNing.txt
- b. SAS data sample: McarDataNing.txt
- c. Mplus output: McarOutputNing.txt
- d. PDF file explaining entire example: McarSummaryNing.pdf (file you are reading)

**Optimal Use:**

1. Read this Summary file completely; Component d listed above.
2. Run the SAS program in concert with the data files; Components a & b above.
3. Generate output that should appear like that shown in the output.txt file; Component c listed above.

**Prerequisites:**

To run the example you must have a working knowledge of SAS that allows you to compile the SAS program, load the data file, and finally get results. The online SAS Help provides a number of step by step examples that can get you up to speed to run this example.

**Potential Applications:**

The contents here may be useful to folks performing Little's test for MCAR for issues on missing data/imputation. Any feedback on how to make this submission more useful is welcome. Log into the main GRASP page, i.e.

<http://grasp.med.yale.edu>

and choose the "forum" link in the upper menu on the right to enter feedback on any GRASP submission. Please refer to the specific file names when commenting so we can appropriately steer your suggestions.