1037-92-326 **Nathan J Markward*** (nathan.markward@pbrc.edu), 6400 Perkins Road, Baton Rouge, LA 70808. *Using Genomic Profile Data to Obtain Personalized Estimates of Disease Risk.* Preliminary report.

OBJECTIVE: Available computational tools in the genome and health sciences provide limited theoretical guidance as to how information on each individual's "personal genome" can be integrated into the disease risk assessment process. This presentation describes an approach that may help to fill this methodological void, demonstrating how measurement models from education and psychology can be used to extract personalized estimates of disease risk from genomic profile data. METHODS: Genomic and cardiovascular disease (CVD) information were downloaded from the CardioGenomics Program for Genomic Applications website at Harvard University. The data were submitted to Winsteps® for iterative scoring and phasing of alleles relative to disease status, scale construction, and assessment of fit to the measurement model. Model parameter estimates, fit statistics, and standard errors were successfully generated for persons, loci, and disease. RESULTS: Exponentiation of person measures yields probabilities of CVD that are specific to each individual and based solely on his or her unique genomic profile. CONCLUSIONS: The method appears to be applicable to any disease area of interest and, therefore, may prove to be a valuable addition to the mathematical arsenal of genetics and epidemiology. (Received February 05, 2008)