

Research Use Statement for GAW16

Note to Applicants: You can use this Research Use Statement as is or you may modify as you see fit.

We plan to use GAW16 Problem Set [2 and/or 3] to conduct methodological genetics research to further our knowledge of appropriate methods in genome-wide studies, using longitudinal data collected on pedigrees. Such investigation is sorely needed to promote the proper conduct of research that evaluates genetic factors associated with the development of disease in such studies, including the joint effects of genes and environment.

1. Research objectives

- Promote the application of efficient methods for the study of the effects of genome-wide (GW) single nucleotide polymorphisms (SNPs) on the development of disease and associated risk factors, collected longitudinally in pedigrees
- Enhance the development of novel analytical strategies for the study of GW genotyping for evaluation of genetic determinants of quantitative and qualitative traits, collected longitudinally in pedigrees
- Further our knowledge of the genetic components involved in the development of coronary heart disease and its associated risk factors

2. Study design

- Longitudinal Pedigree Study, focusing on the development of coronary heart disease and its associated risk factors
- Phenotype data derived from the Framingham Heart Study, collected at 4 exams in the Original Cohort, 4 exams in the Offspring Cohort and 1 exam in the Third Generation
- Genetic data: ~550,000 SNPs genotyped by Affymetrix
- ~7000 subjects with genotype and phenotype data

3. Analysis plan

- A variety of analyses will be conducted to compare the efficiency, validity of existing methods or to develop novel methods

4. Explanation of how the proposed research is consistent with *Use Restrictions* for the requested dataset(s),

- Only subjects who have approved general use of their data are included in the dataset. All subjects have provided informed consent to promote genetics research in the Framingham Heart Study