NIH Award from the National Institute on Aging

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- Project: GENORM: Collection of Genotypic Data for the NIH Toolbox Norming Sample
- Start Date: September 30, 2009
- Total Award Amount: $415,490

How the results of this project will benefit society:
Benefits of the proposed study include: 1) providing a unique and otherwise unavailable resource that can be used to increase future knowledge about associations between genetics and motoric, cognitive, sensory and emotional health, and 2) creating one of the largest genetic datasets of Spanish-speaking subjects in the United States. This will be a valuable resource for future studies to explore genetic and phenotypic data, and has the potential to significantly impact health care policy for maintenance of neurological health and function.

The problem the project is trying to solve:
The proposed study, GENORM, will capitalize on, and extend, the NIH Toolbox for the Assessment of Neurological and Behavioral Function (a Blueprint for Neuroscience Research initiative), by adding the collection and storage of DNA to the planned and already-funded Toolbox norming phase. Combining the phenotypic information already being collected by the Toolbox project in a geographically and ethnically diverse sample with future state-of-the-art genotypic methods will be invaluable for the testing of future hypotheses regarding a broad range of neurological function.

How the project will work:
During Toolbox norming, measures of cognitive, emotional, motor and sensory function will be administered to a large community-based probability sample (N=5600; 3000 children and 2600 adults) ranging from 3-85 years of age. The sample will be equally divided between English- and Spanish-speaking residents of the United States. The Toolbox instruments assess 48 different aspects of these 4 functional areas and the data generated will provide the value of the Toolbox and Toolbox data to both the public and to the scientific community. We are seeking GO grant support for this additional activity. Specifically, we propose collecting a saliva sample from all 5600 participants at their initial assessment, extracting the DNA, and storing this sample so that it will be available for future research. This genetic material, when combined with the phenotypic data provided by the already-funded NIH Toolbox activities, will be the foundation for a future phenotype and genotype data archive.

This award is funded under the American Recovery and Reinvestment Act of 2009, NIH Award number: 1RC2AG036498-01.