NACC Project #2016-JI-01 (secondary analysis of NACC data)

Predicting and quantifying Alzheimer’s disease risk

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Project description
Late-onset Alzheimer’s disease (AD), the most common form of dementia, places a large emotional and economic burden on patients and society. With increasing health care expenditures among cognitively impaired elderly, identifying individuals at risk for developing AD is of utmost importance for potential preventative and therapeutic strategies. Integrating genome-wide detected genetic variants into a genetic epidemiology framework, we have recently developed and validated a novel polygenic hazard score for predicting the age-associated risk for developing AD (Desikan et al., under review).

In this proposal, our objective is to combine our recently developed polygenic hazard score with clinical and neuropathological variables from the NACC database to identify older non-demented individuals at greatest risk for AD and to develop a novel multidimensional risk score for AD. Our central hypothesis is that our polygenic hazard score will predict the time to progress to clinical AD and that cardiovascular, clinical, and genetic variables can be integrated into a prediction score for determining the risk associated with developing AD.

We expect that our polygenic risk score will identify nondemented older individuals at greatest risk for AD and that a combination of genetic, clinical, and cognitive variables will provide a powerful method for predicting age-associated AD onset.

Contact information
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