ABSTRACT: Alzheimer’s disease (AD) is the most common type of dementia that affects 3-5 million people in the United States and costs ~$25 billion each year for health care and an additional $36 billion for lost productivity. AD is characterized by gradual but extensive brain atrophy which may take up ten years. Patients gradually lose cognitive functions including memory, speech, and executive functions, and becomes incapacitated and completely dependent upon caregivers.

In this talk I present two genomics approaches we have been taking to study the molecular mechanism of AD. The first half of my talk concerns gene expression changes in brain aging and AD and other neurodegenerative disorders. We developed algorithms that can estimate the age of an individual using gene expression profiles, and novel approaches that detect modifications and predict functional classes of non-coding RNAs using RNA-seq data. Using these algorithms, we showed that neurodegenerative disorders demonstrate transcriptomic changes similar to accelerated aging, and identified extensive changes in many non-coding RNA classes.

The second half of my talk provides an overview of Alzheimer's Disease Genetics Consortium (ADGC) and National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site (NIAGADS), two initiatives established by the National Institute on Aging (NIA) in the United States for Alzheimer's disease genetics research. The ADGC project is a multi-institutional collaboration in the United States to conduct GWA studies and high throughput sequencing experiments to identify genes associated with risk of developing Late Onset AD. The NIAGADS data repository is a data repository established by NIA to facilitate access by qualified investigators to genotypic data in order to promote the study of the genetics of AD.