Discussant: Morgan E. Levine, *Yale University School of Medicine, New Haven, Connecticut, United States*

This symposium presents early results on epigenetic, transcriptomic and other aging biomarkers such as telomere length and mitochondrial DNA copy number from the Health and Retirement Study that allows a detailed examination of the biological pathways through which socioeconomic conditions influence the human aging process. In 2016 HRS collected 6 tubes of blood from people who completed the 2016 interview, had been in the sample at the prior wave and were not in a nursing home (n=9,973) to maintain a nationally-representative sample. These blood samples were analyzed for novel biomarkers of aging that included global methylation arrays, whole transcriptome sequencing, telomere length and mitochondrial DNA copy number among other biomarkers that were shown to be related to both social and economic circumstances and health outcomes at older ages. This level of integration of biological data to address social disparities hasn't been accomplished before on a large nationally-representative sample of Americans and will provide a unique opportunity to understand the biological mechanisms through which social disparities affect human health. The symposium will describe the utility of measuring novel age related biomarkers in a nationally representative population study such as HRS and the potential research opportunities that can be pursued using this publicly available resource. It will provide an overview of the measurement and distribution of epigenetic, transcriptomic and telomere length and mitochondrial DNA copy number as novel aging biomarkers. It will also describe the utility of these biomarkers in further understanding the biological underpinnings of socioeconomic differences in health and mortality.

NOVEL AGING BIOMARKERS IN THE HRS

Eileen Crimmins[1], *1. Davis School of Gerontology, University of Southern California, Los Angeles, California, United States*

In addition to the broad panel of aging related biomarkers available in HRS, we will describe measurement of novel aging biomarkers such as telomere length and mitochondrial DNA copy number in 4000 HRS participants. Both these biomarkers were measured in DNA obtained from whole unsorted blood using quantitative real time polymerase chain reaction (PCR) and were adjusted for individual cell composition measured from flow cytometry. We will describe the relationship between these two biomarkers and other measures of biological age available in HRS. Differences in these two novel aging biomarker by socioeconomic status, race/ethnicity, and exposure to early life hardships will be presented to clarify the value of the data to further unravel how social factors get under the skin to affect the process of aging.

TRANSCRIPTOMIC AGING IN THE HRS

Bharat Thyagarajan[1], *1. Department of Laboratory Medicine and Pathology University of Minnesota; Minneapolis, Minnesota, United States*

Since age related perturbations in gene expression profiles have been described and transcriptomic changes in specific biological pathways have been implicated in the aging process, we performed whole transcriptome sequencing on 4000 HRS participants using RNA obtained from Paxgene tubes collected during the 2016 interview. We will describe design and implementation of innovative quality control procedures to minimize technical variability in transcriptomic measurements and monitor analytical variation in large population studies such as HRS. We will also report the distribution of transcriptomic profiles according to various demographic characteristics (age, sex, racial/ethnic and socioeconomic differences) and describe the prevalence of previously reported aging related transcriptomic signatures in HRS. We will describe the associations between transcriptomic profiles and other measures of biological aging in HRS and report how changes in cell composition can affect transcriptomic profiles observed in population studies such as HRS.

EPIGENETIC AGING IN THE HRS

Jessica Faul[1], *1. University of Michigan, Ann Arbor, Michigan, United States*

Biological aging can be characterized by molecular, cellular, and epigenetic changes that in addition to being related to chronologic age, are also associated with social disadvantage and associated morbidity and mortality. These biological markers can help explain at a biological level why socially disadvantaged individuals are at greater risk of aging-related disease and premature death. From DNA extracted from venous blood collected from over 4,000 HRS participants we measured array based DNA methylation. These assessments were made from unsorted cells, but are adjusted for individual cell composition measured from flow cytometry. We present genome-wide methylation differentials by age, race/ethnicity and SES using the largest, nationally representative sample with these data available to date. Understanding basic biological changes related to age and social disadvantage is essential for identifying translational opportunities to improve health.

SESSION 2265 (SYMPOSIUM)

NOVEL FINDINGS TWO DECADES FOLLOWING COGNITIVE TRAINING: FINDINGS FROM THE ACTIVE TRIAL

Chair: Alden L. Gross, *Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, United States*
Co-Chair: George W. Rebok, *Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, United States*
Discussant: Walter Boot, *Florida State University, Tallahassee, Florida, United States*

Although the only demonstrated panacea against cognitive decline, behavioral cognitive training usually fails to demonstrate transfer either to untrained cognitive abilities or to distal outcomes like everyday functioning. No such trials, however, have leveraged more than a decade of follow-up to adapt life-course perspectives. The Advanced Cognitive Training for Independent and Vital Elderly (ACTIVE) study remains the largest NIA-funded clinical trial of cognitively normal older adults. Efforts to re-invigorate the cohort after 20 years with external data linkages have coalesced around renewed interests in how training-related cognitive improvements affect long-term dementia risk, health care utilization and costs, credit scores, and active years in later life. The first presentation by Rebok overviews ACTIVE and its 20-year follow-up plans. Next, Gross and colleagues tested whether cognitive training attenuates the relationship between IADL difficulty and mortality; negative findings suggest proposed relationships between cognition and IADL difficulty are