**Abstract:**

These two talks will focus primarily on the Kaiser Permanente Northern California Research Program on Genes, Environment and Health (RPGEH), and the Genetic Epidemiology Research on Adult Health and Aging (GERA) cohort derived therefrom. This multi-ethnic cohort, established in 2005, is representative of Northern California and contains over 100,000 individuals with comprehensive electronic health record data that dates back over 20 years for most individuals. In 2009, genome-wide genotype and telomere length data were added through an NIH Grand Opportunity Award, facilitating genetic epidemiologic research on a large scale.

In the first of the two lectures, we will focus on the demographic structure of this cohort, which contains a large number of spouse, parent-child and sibling pairs. We show the relationship between how individuals self-identify in terms of race/ethnicity/nationality and their genetic ancestry, and also mating patterns that have and continue to determine the population genetic structure of the sample.

In the second of the two lectures, we will focus on the application of the genome-wide genotype and telomere data to a number of disease and clinical trait outcomes. The resource includes all aspects of care, including laboratory tests, pathology reports, physiologic tests and pharmacy prescription data, in addition to clinical diagnoses. Through examples, we demonstrate the power of this clinically homogeneous resource for gene discovery, as well as gene characterization through longitudinal analyses based in the EHR data. We also provide examples of cross-ethnic analyses, pleiotropy, pharmacogenetics and heritability.