**Application number/Title:** 30252 - Overlap in aging-related phenotypes, genome and epigenome: toward a general factor of aging

**Applicant PI**: Dr. Kristen Fortney

**Application Institution:** BioAge Labs, Inc., Bioinformatics 1658 University Avenue, Berkeley CA 94703, United States

**Keywords provided by the Applicant PI to describe the research project:**

Aging, Comorbidity, Genetics, Epigenetics

**Application Lay Summary:**

1a: Understanding the factors that drive the aging process in humans is a fundamental problem in basic medical research. It is known that there are correlations between various pairs of age-related diseases, which suggests that these diseases may share a common cause. The goal of this research is to make progress on identifying this cause, if it exists, by determining the phenotypical characteristics that are most predictive of age-related diseases, and search the genome and epigenome for biomarkers associated with a large fraction of age-related diseases.

1b: Aging-related diseases comprise a large fraction of the disease burden in the developed world. Identifying factors upstream of multiple aging-related diseases holds promise of targeting these factors developing more efficient treatments.

1c: We will use factor analysis and network analysis, methods originally developed for the analysis of psychological data, to examine patterns in the correlations between aging-related diseases. Furthermore, we will find associations between such diseases and the genome or epigenome by using statistical methods which take into account pre-existing knowledge about the genetic and epigenetic basis of each disease. Finally, we will apply modern statistical methods suited for large datasets with complex structure such as regularized linear regression and Bayesian hierarchical modeling.

1d: The full cohort (~500k).