Aging is the largest risk factor for most major chronic diseases, yet heterogeneity exists between tissues and organisms when it comes to the rate of biological changes over time. As a result, estimates of biological age can facilitate risk stratification, provide clinical endpoints for intervention trials, and inform our mechanistic understanding of underlying drivers of aging. This talk will describe some of the most successful biological age measures—often referred to as epigenetic clocks. Using data from DNA Methylation these aging proxies can be calculated to estimate aging in nearly any tissue and/or cell type.