Has the Overall Health of the United States Population Changed? Evidence from Biomarker Data

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Abstract

The overall health of a population can be viewed as an indicator of social welfare. Yet, individual health itself is complex and multidimensional, influenced by endogenous choices, as well as exogenous environmental and genetic factors. Moreover, defining a mapping from individual health to social welfare can involve onerous assumptions. This paper adopts a nonparametric approach to ranking individual health as a function of several biomarkers--Body Mass Index (BMI), glycohemoglobin (HbA1c), total cholesterol, alanine aminotransferase (ALT), serum creatinine, white blood cell counts (WBC), etc. With this ranking in hand, we use a nonparametric approach to map individual health into social welfare using minimal assumptions (e.g., monotonicity and concavity). Results show that the distribution of wellbeing became worse-off from 1988 to 2018, although there has been a slight rebound since 2009. Moreover, the distribution has widened: those prone to a higher health status have become better-off while those prone to poorer health have become worse-off which, thereby raising inequality and here policy implications need to be focused on. Finally, we construct counterfactual distributions of wellbeing to explore if the change in the distribution is attributed to socio-demographic factors. Findings show that age, gender and race/ethnicity cells combined with education can explain very little of the negative shift than the attributes without education while leaving a substantial portion unexplained.

Keywords: Health, wellbeing, biomarkers, inequality, nonparametric social welfare, decomposition analysis

JEL classification: I3, I14

1. Introduction

An individual's health and functioning can be influenced by a multitude of factors including genetics, life experiences, living environments, and exposure to challenges or stressful events which may accumulate as well as carry on over the life span (Weinstein & Willis, 2001). These factors may leave a mark on the overall individual wellbeing that could be influential to the mechanisms whereby mapping individual wellbeing to the social welfare. While these factors are not directly observables, biomarkers serve as a proxy for the well-being within health production functions. They are sensitive to specific dimensions of health and have a potential advantage over self-reported perception (Davillas & Pudney, 2017). It is an early warning system that predicts disability (Davillas & Pudney, 2020), risk of chronic conditions (Davillas & Jones, 2020) , adverse health outcomes (Li et al., 2021; NIEHS, 2023; Vasan, 2006), including mortality (Glei et al., 2014; Gruenewald et al., 2006; Willems et al., 2010) and are capable of informing physical and mental wellbeing (Seplaki et al., 2004) as well as overall population health status (Albert, 2011; Bodaghi et al., 2023). For instance, high C-reactive protein suggests inflammation (Albert, 2011), while an increased total cholesterol level indicates susceptibility to coronary heart disease and non-alcoholic fatty liver disease (Liu et al., 2014). Given the varying relevance of different biomarkers based on context and population, measuring inequality of individual health status using a single biomarker is challenging.

Throughout past decades, United States experienced improvement in life expectancy (Murray et al., 2018); total cholesterol level (Carroll et al., 2005, 2012) while some studies found lack of progress in health equity (Zimmerman & Anderson, 2019); increasing rate of ALT (Balali et al., 2022; Welsh et al., 2013), body mass index (BMI) (Flegal et al., 2010; Stokes et al., 2017), fasting plasma glucose level and glycohemoglobin A1c (Cheng et al., 2013; Menke et al., 2015; Neupane

et al., 2024), prediabetes (Bullard et al., 2013); and increasing rate of risk behaviors which are associated with consumption of alcohol, excessive smoking, physical inactivity etc. (King et al., 2009). Thus, if we take a closer look at different health outcomes, we see multiple dimensions of the trends. Our study focuses on biomarkers related to some common chronic diseases in the United States to assess population wellbeing from the perspective of social welfare[1], as according to the Center for Disease control and prevention (CDC), about 129 million population have at least one major chronic disease (Benavidez et al., 2024) and about 27.2 percent adults have multiple chronic conditions (Boersma et al., 2020). This prevalence has been steadily increasing over the past decades (Benavidez et al., 2024) and are responsible for seven out of ten deaths in the United States (CDC, 2014; Raghupathi & Raghupathi, 2018). As chronic conditions often do not exist in isolation, thus, with multiple measures of health (e.g., several biomarkers.), it is not always entirely clear which measure has the greatest influence on health outcomes. For example, how to compare an individual with high cholesterol with normal blood pressure to another person with normal cholesterol but high blood pressure? Considering this, our research question evolves, how can we map multiple dimensions of health into a single index while still satisfying basic assumptions about social welfare?

In social welfare, aspects of wellbeing are multidimensional in nature and sometimes, it is very difficult to rank and compare between them, although policy makers need a means of comparison. There are many approaches explaining aggregation, selecting weighting scheme, statistical methods, counting measures from the perspective of multidimensional wellbeing measurement, for example- equally weighted aggregation like Human Development Index (HDI) (Anand & Sen,

[1] Common chronic diseases are: coronary heart disease, diabetes, cancer, obesity, hypertension, high cholesterol, asthma, chronic kidney disease and depression (Benavidez et al., 2024)

1994), counting based measure specifying a cut-off point to find deprived or not in each dimension and then count the total deprivation like Alkire-Foster method (Alkire & Foster, 2011), Principal Component Analysis (PCA) (Filmer & Pritchett, 1999) etc. But little is known about the mechanism by which we can map overall wellbeing from the multidimensional biomarkers perspective. One approach practically implemented by Seeman and colleagues (1997) on the concept of allostatic load by creating a cumulative index from ten biological markers to predict health status[2]. Then, variation in allostatic load index was used to predict disability risk (Davillas & Pudney, 2020) and risk of chronic conditions (Davillas & Jones, 2020); assess food security (Pak & Kim, 2021); reducing cognitive skill, physical functioning and adverse cardiovascular disease (Gonzales et al., 2022; T. E. Seeman et al., 1997); and health inequality (Carrieri et al., 2020b). A number of studies also tried to link this allostatic load index with the socio-economic differentials specially measured by income, education, race/ethnicity (Howard & Sparks, 2016; Kubzansky et al., 1999; T. Seeman et al., 2008). Another approach (semiparametric) recently proposed by Carrieri and collogues (Carrieri et al., 2020b) to address curse of dimensionality in health inequality is finite mixture models combined with decomposition approached proposed by Carrieri & Jones (2018) to classify and rank population into latent classes without having any prior grouping, weighting or require distributional assumptions. The common concern of all these indices or latent class type estimation is what indicators should be included in the measurement of wellbeing and in what process they should be aggregated or weighted (Anderson et al., 2014). And

[2] Allostatic load is a cumulative risk factors index reflecting "wear and tear" on the cardiovascular, endocrine, and metabolic system: systolic and diastolic blood pressure, abdomen-hip ratio, serum high-density lipoprotein (HDL) and total cholesterol level, hemoglobin A1c, C-reactive protein, Body Mass Index,. each individual is assigned an index score based on the levels of each parameter and clinical cut-off points. Individuals with higher allostatic load scores are at increasing risk of deterioration in health independent of sociodemographic factors (Kubzansky et al., 1999)

also, this aggregation and counting approaches don't quantify how worst or good the individual's health outcome is.

A recent nonparametric approach developed by Anderson and colleagues (2011), addresses the multidimensionality issue and avoids choice of weights in aggregating and measuring wellbeing. They showed how two-sided bounds can be placed on each dimension on a welfare index for each individual following the assumptions that wellbeing is increasing (monotonically) and quasi-concave (weakly) with respect to its various dimensions. The region between two bounds within which true wellbeing function exists. They estimate a distance function which measures the amount by which an indicator needs to be scaled, so that it achieves some reference welfare level and also rank population overall wellbeing

This paper contributes to this growing literature by melding Anderson et.al (2011)'s approach with counting measure's intuition, to address multidimensional biomarkers' burden. This study estimates nonparametric welfare bounds by measuring distance from each biomarker for each individual to achieve the reference wellbeing reference level. After imposing upper and lower bounds, we consider midpoints of the bounds as our outcome of interest to proxy overall wellbeing and thereby rank all individuals from better off to worst off. If we see population get healthier over time, the change in the distribution might be the result of changes in efforts, technological advancement or changes in the genetical make-up of the United States. Hence, to assess how much of the wellbeing gap can be accounted for by the observable characteristics within population, we employ the non-parametric decomposition approach developed by DiNardo, Fortin and Lemieux (DFL) (DiNardo et al., 1996) to quantify and decompose disparity in wellbeing status[3]. While these

[3] Considering the decomposition of the source of inequality in health outcomes, recent literature of health equity separates out the associated contributing factors as-- circumstances i.e., observable factors beyond individual's control i.e., gender, race/ethnicity, age, parental background, genetical composition; and efforts i.e., individuals are responsible which is a remarkable source of inequality for example, diet, physical activity,

contributing factors are unobservable, differences in well-being patterns may emerge when comparing low-income disadvantaged population to the counterparts. We will also want to note, however, that our method doesn't work well when some values of the social welfare determinants can be zero, or binary. In poverty literature, this happens in many cases (Alkire & Foster, 2011). For example, do you have access to clean water? Which could be measured continuously as "how far are you from a clean water source?" Rather than focusing on any causal relationship between biomarkers and wellbeing, we are primarily interested in mapping the overall wellbeing of the population focusing on the disadvantaged population who are eligible to federal assistance programs such as SNAP, reduced school lunch program, and WIC to high income counterparts. In this study we embrace a social perspective of both circumstances and efforts, as well as draw on the socio-legal context of the US health system to define the source of inequality.

To our knowledge, no available study in the United States has explored the trends of individual's overall wellbeing distribution as well as ranked population health status in terms of multidimensional biomarkers using nonparametric social welfare approach. Also, this study contributes to the wellbeing literature by aggregating cardinal biological markers related to chronic diseases as they capture physiological responses that are associated with process through demographic, economic and social circumstances across the lifespan rather not using self-reported measures to proxy individual health.

Using data from multiple survey waves of National Health and Examination Survey (NHANES), we map overall wellbeing, rank the whole population and draw the wellbeing distribution. We find

smoking (Brunori et al., 2021; Carrieri & Jones, 2018; Davillas & Jones, 2020; Jusot et al., 2013; Rosa Dias, 2009). As efforts are particularly difficult to observe and measure, health appears to be a good option to quantify inequalities of outcomes being explained by circumstances not by efforts (Jusot et al., 2013). Thus, few studies have investigated the source of inequality and found correlation between metabolic and demographic factors such as age, race, gender; and also highlight the complexity of biomarker variations (Dong et al., 2012; Liu et al., 2014). But Seeman et al., (2008); Lantz et al., (2001); Burstrom et al., (2005) found specifically education and income negatively associated with cumulative biomarkers risk and source of the health inequality

wellbeing decreased significantly from 1988 to 2010 and then it again experienced a slight rebound from 2011 to 2018 but not in the same proportion as it was in 1988. The counterfactual estimates show that the change in the wellbeing distribution can be attributed to the composition of age, gender, race, ethnicity and education while a big portion remains unobserved. This paper proceeds with explaining theoretical framework in section two. We then motivate our approach in explaining data and biomarkers. The following section represents results including the population overall wellbeing ranking, the decomposition and counterfactual estimates. Finally, we conclude with mentioning policy implications in the last section.

2. Theoretical Framework

When there are multidimensional measurements, using any index or cumulative scoring (Caleyachetty et al., 2015) for example, z-score (Hickson et al., 2012) are very common aggregation method to assess social welfare. But aggregating multidimensional indicators in this way makes the comparison blurred as it is very hard to distinguish between two individuals with the same scores whether they might have different outcomes. Also, assigning different weights to each indicator exhibits matter of some dispute as which one should get more weight compared to others without having any prior knowledge. Besides, with the increase in number of dimensions, the results may not be robust (Anderson et al., 2014). Another challenge is to choose an appropriate functional form to estimate health production function using those indicators. But using a nonparametric approach which doesn't require any functional form or prior knowledge, and which is valid for all possible choices of aggregator, we can measure the distance of how far the individual from the threshold for each biomarker is. Our nonparametric empirical approach involves three steps.

2.1 Wellbeing Ranking

Firstly, to address the challenges of interpreting and aggregating biomarker indicators, a distance function *d* can be used to estimate the relative ranking of each individual's well-being by imposing nonparametric two-sided bounds across all biomarker dimensions[4]. Following Anderson et al., (2011), distance function d can be represented as[5]:

$$d(x, W) = \min \{d: W(dx) \geq W\} \qquad (1)$$

Considering $W(x_i)$ as a measure of aggregated welfare or wellbeing function associated with the *i'th* individual, where the level sets of *W* imply how the individual trades off benefits in one indicator for sacrificing in another one. The scalar *d* measures the "size" of amount needs to be scaled the Euclidian norm of the indicator vector $||x_i||$ relative to a reference wellbeing level W^*. The higher value of d implies higher wellbeing as compared to the reference value of W^* (i.e., d measures how far W is "above" the reference value of W*). This reference level is the welfare associated with the worst-off observation (the lowest value). The method is best described by figure 1 (figure 2 in Anderson et al., 2011), which displays two hypothetical biomarkers for health x_1 and x_2 for three individuals (i, j, and k). The idea is to ask, how could we rank these three individuals based on their observed values for x_1 and x_2? To do so, we invoke three assumptions on a welfare function *W*: (1) monotonicity[6]: social welfare is nondecreasing in its arguments (more is better), (2) quasi-concavity[7]: welfare is (weakly) increased by any reallocation that reduces inequality (downward sloping social indifference curves that are weakly bowed inward).

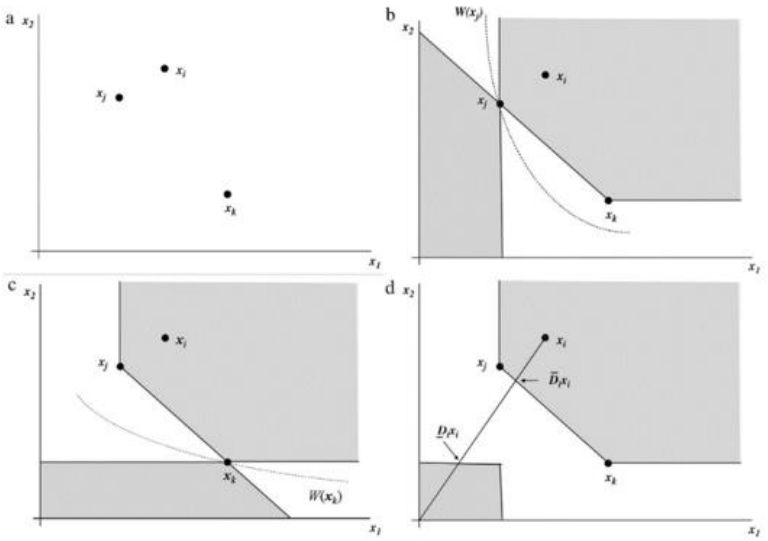
[4] Distance function is the dual representation of the welfare function which measures the smallest amount by which one has to scale the indicator vector of an individual to achieve some reference welfare level (Anderson et al., 2011).

[5] Distance (d) is increasing in W but decreasing in indicator x with homogenous degree of one in x (Anderson et al., 2011).

[6] Monotonicity: $W(\mathbf{x}) \geq W(\mathbf{y})$ if $\mathbf{x} \geq \mathbf{y}$ indicates wellbeing doesn't fall with increase in the measured indicators.

[7] Quasi-concavity: $W(\mathbf{x}) = W(\mathbf{y}) \leq W(\alpha\mathbf{x} + (1 - \alpha)\mathbf{y})$ for all $\alpha \in [0, 1]$ indicates wellbeing is weakly increased by any inequality reducing reallocation between individuals (Anderson et al., 2011).

Figure 1. A two-sided bounds approach on the distance function



Note: Adapted from Anderson et al. (2010)

In words, any social welfare function would rank observation i over both j and k, shown by panels (b) and (c) considering the reference welfare level W^* which is the worst-off welfare [8]:

$$W^* = \min_j \{W(x_j): x_j \in X \qquad (2)$$

However, as the distance function is bounded by two-sided bound on each dimension for each individual given W^*, it encompasses the entire set of wellbeing components consistent with monotonicity and quasi-concavity. Hence, they provide a region within which any parametric index satisfying the assumption can lie (Anderson et al., 2014). The bounds also provide a natural mapping into the wellbeing such that relatively higher distant bounds imply better off health status[9]. The set of inputs' variability can influence the width between bounds and also can lead changes in the wellbeing rankings.

[8] If we consider 1-d rather considering only d

[9] The gap between bounds is large in high wellbeing and small in low wellbeing. The span also increases with the increase in dimensionality.

This method is repeated for all observations resulting in nonparametric bounds on all possible relative rankings. Panel (d) in figure 1 shows the lower ($\underline{di}$) and upper ($\overline{di}$) bounds of the distance function for observation i. Here, we use the midpoint of these two bounds as our wellbeing measure and outcome of interest. The wellbeing index can be expressed as:

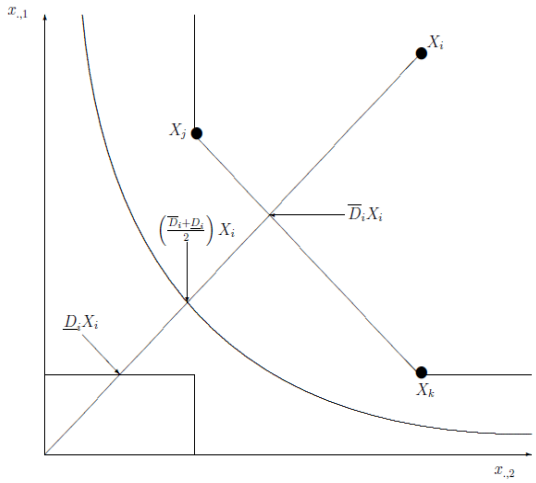
$$W(x) = \frac{\overline{di} + \underline{di}}{2} ||x_i||, \qquad (3)$$

And then the welfare reference point W^* indicates,

$$W^* = W(x_i) \left(\frac{\overline{di} + \underline{di}}{2}\right) \qquad (4)$$

or, $$W(x) = \frac{W^*}{\left(\frac{\overline{di} + \underline{di}}{2}\right)}$$

Figure 2. Two sided bounds and midpoint on the distance



Note: Adapted from (Anderson et al., 2014)

Figure 2 (figure 2 from Anderson et al., 2014) shows the midpoints on the welfare level. Following this above concept, we measure the scalar value of d from all biomarkers (x_i) for each individual. As we know deviation from the normal range implies lower wellbeing, the distant value from the reference W^* level is scaled down with small d and the nearest one is scaled with larger d. Hence, we consider higher the d, better off the wellbeing is, which forms our outcome of interest for the next steps.

2.2 Counterfactual and decomposition of the wellbeing gap

Secondly, we can think a health (wellbeing) production function is composed of individual's circumstances and effort indicators (Rosa Dias, 2009). Hence, if we witness a shift in the wellbeing distribution, there could be many reasons combined with circumstances and efforts factors. It could

be due to the change of the disease prevalence, healthcare accessibility, community factors, demographic factors, individual's diet and lifestyle etc. These factors which change over time within the population can explain observed changes in the distribution. But keeping all these factors constant, we are only interested in considering the changes in circumstances and changes in efforts. Following the recent literature on health inequality, we consider circumstance factors- age, gender, race/ethnicity (Carrieri & Jones, 2018; Davillas & Jones, 2020; Rosa Dias, 2009) and effort factors- education level (Rosa Dias, 2009), health insurance coverage (world bank, 2007).

To assess how much of the wellbeing gap can be accounted for by the observable characteristics within population, we employ the non-parametric decomposition approach developed by DiNardo, Fortin and Lemieux (DFL) (DiNardo et al., 1996). We focus on the overall distribution for the whole population as well as the lower and higher income group of the population. Unlike the familiar Oaxaca-blinder approach which considers counterfactual with mean characteristics and decomposes the differences at mean (Fortin et al., 2010), DFL decomposes across the overall distribution. Hence, we break down the observed differences of the distribution into components that could be accounted for by the observables and unexplained portion (residual).

Theoretically, DFL estimates counterfactual distribution $F_w^c(.)$ by replacing the marginal distribution of x for one period with the marginal distribution of x for another period using a reweighting factor $\psi(x)$. When the demographic composition is compared, the counterfactual for the entire distribution translates, what would be the distribution of wellbeing in 1988 look like had the same demographic characteristics of 1999-2010 or 2011-2018 prevailed in 1988-1994. Hence, let for each individual, our outcome of interest (wellbeing, w), time period (t) and the indicators (x) are assumed to have a joint distribution which means that if indicators observe more frequently, the outcome will also have same (Thompson & Suarez, 2015). No other parametric assumption we

place on the formation of wellbeing and the estimator allows inferences to be drawn along all points of the wellbeing distribution. At time t, the joint distribution of w and x is the conditional distribution F(w, x|t). Following DiNardo et al., (1996), the wellbeing density at one point in time $f_t(w)$, can be written as the integral of the wellbeing density conditional on set of demographic characteristics x, and on a date t_w, $f(w|x, t_w)$, over the distribution of demograph (5) ributes $F(x|t_x)$ at t_x:

$$f_t(w) = \int_{x \in \Omega x} f(w|z, t_w = \mathrm{t})\, dF(x|t_x = t)$$

$$= f(w;\ t_w = t,\ t_x = t)$$

Here Ω indicates the domain of the demographic characteristics. Now, if we assume the wellbeing density of population at 1988-94 had the same 1999-2010 attributes prevailed $F(w|t_x=99)$, the hypothetical counterfactual density $f(w, t_w=88, t_x=99)$ would have:

$$f_t(w, t_w = 88, t_x = 99\ ) = \int f(w|z, t_w = 88) dF(x|\ t_x = 99)$$

$$= \int f(w|z, t_w = 88)\ \Psi_x(x)\ dF(x|t_x = 99) \qquad (6)$$

The difference between actual and counterfactual distribution implies the effect of changes in the population characteristics. Where, the reweighting function $\Psi_x(x)$ can be defined as,

$$\Psi_x(x) = \frac{dF(x|t_x=99)}{dF(x|t_x=88)}$$

Applying Bay's formula, $\Psi_x(x)$ can be written as:

$$\Psi_x(x) = \frac{\Pr\,(t_x = 99|x)}{\Pr\,(t_x = 88|x)} . \frac{\Pr\,(t_x = 88)}{\Pr\,(t_x = 99)} \qquad (7)$$

For each individual, the predicted probability of being in period t given the x, can be estimated using probit model and the unconditional probability is equal to the weighted number of observations in 1988 divided by the weighted number of observations in both 1988 and 1999 (DiNardo et al., 1996). Thus, we can obtain $\Psi_x(x)$ which is similar to estimating propensity scores and reweights using inverse probability weighting where it forces estimates to be drawn from the common support across the two samples. Hence, it assigns zero weight to the observation that lack common support (Thompson & Suarez, 2015). According to DiNardo (2002), this weight $\Psi_x(x)$ allows to fold a multidimensional indicator problem into a one-dimensional indicator problem.

As DFL provides aggregated decomposition, the reweighting function doesn't differentiate between attributes x. We consider such demographic characteristics which are not endogenous in nature. The long-run components change of gender, race, age, race/ethnicity are plausibly exogenous (Beatty et al., 2014), hence there is also less possibility that the education and health insurance coverage are assumed uncorrelated with the unobservables which might affect the wellbeing pattern. Assuming ignitability, here we would like to explore how changes in the distribution of education and health insurance coverage might affect changes in the wellbeing distribution rather than any causal relationship between population wellbeing and education or health insurance coverage[10]. Hence, our counterfactual distribution estimation starts with considering age, gender, race or ethnicity and we obtain reweighting function Ψ_x. Next, we consider education, health insurance coverage separately as well as along with demographic attributes and get $\Psi_{x,e}$, $\Psi_{x,i}$, $\Psi_{x,e,i}$ respectively. As DFL estimator is sensitive to the order of the

[10] Ignorability is also known as unconfoundedness or selection on observables (Beatty et al., 2014)

attributes (DiNardo et al., 1996), hence, we also decompose by changing the order of the attributes to test the robustness of the estimation.

2.3 Stochastic Dominance

In the third step, once we get the distribution of wellbeing, we might see a change of the overall distribution positively or negatively. The change in the distribution intrigues us to explore the possibilities or reason of those changes. Hence, using the Stochastic Dominance (SD) testing method, we map the entire distribution of well-being and test if the shift of the distribution is significant or not. After estimating the counterfactual distribution, we also test if the explaining counterfactual distribution is significant or not. SD is a popular tool in economics to assess the distribution of income or wealth. It helps to zoom in to the distribution of the low-income population whose wellbeing is the specific focus of the policy makers.

3. Data

This study uses data from the National Health and Nutrition Examination Survey (NHANES): NHANES III (1988-1994) and ten waves from continuous NHANES (from 1999 to 2018) conducted by the National Center for Health Statistics (NCHS) of the Centers for Disease Control and Prevention. NHANES comprises cross-sectional, multistage, stratified, clustered probability, a nationally representative sample of the US civilian non-institutionalized population with laboratory components, interview, and clinical exam information. Our sample is restricted to the working aged population from 20 years to 64 years who were both interviewed and examined. After excluding individuals with missing biomarkers, income poverty ratio information our sample includes 47,822 for the wellbeing ranking estimation and further excluded individuals with missing demographic information (904 individuals).

Demographic attributes

We consider circumstance indicators: age, gender, race and ethnicity, health insurance coverage; efforts indicators: educational level background to assess the counterfactual analysis. Here we categorize education level as didn't attend high school, high school but no college, attended college. We also categorize race and ethnicity as, white non-Hispanic, Black non-Hispanic, Mexican American, and others. Among the race ethnicity category, "other" indicates self-reported Hispanic except Mexican American and non-Hispanic multiracial group. Race/ethnicity were reported by survey participants.

Biomarkers

Biomarkers are like checkpoints on the road to be a healthy individual. It plays an important role in precise diagnosis as well as reflect on risk hereby adopting remedy that improves the clinical outcomes (Gowda et al., 2010). Biomarkers definition working group defines biomarker as *"A defined characteristics that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes or pharmacologic responses to an exposure or intervention"* (Atkinson et al., 2001). In this study, rather than focusing on specific health outcomes, we assess the overall wellbeing by considering a subset of blood based biological indicators reflecting inflammatory, metabolic, and cardiovascular parameters. We focus on biomarkers related to some common chronic diseases in the United States such as cancer, diabetes, hypertension, coronary heart disease, obesity, arthritis, chronic kidney disease (CKD) etc. Hence, we consider six biomarkers: white blood cell count (WBC), BMI, Alanine Aminotransferase (ALT), total cholesterol (TC), serum creatinine, and glycohemoglobin (HbA1c). Five of these biomarkers, excluding BMI, are blood-based indicators linked to coronary, liver, immunity, inflammation, kidney and diabetes health. All of these biomarkers satisfy monotonicity condition

i.e., higher the value, the worse off the population are. These markers are independently or jointly linked with various risk factors. Table 1 in appendix provides descriptive statistics for all these biomarkers.

The level of cholesterol has a vital role in the coronary disease process. Hence, we consider total cholesterol an indicator of lipid levels measures cardiovascular health and associated with all-cause mortality (He et al., 2021) from the markers of lipid profile rather than considering Low Density Lipoprotein (LDL or High-Density Lipoprotein (HDL) separately. Although some studies mention LDL could be more appropriate to measure the health risk (Albert, 2011), others mention LDL alone is not an efficient marker to predict heart health (Field & Vasan, 2018). Triglycerides is also another important marker among the lipid profile, but the level fluctuates considerably from day to day and are highest 1 to 4 hours after meals where cholesterol levels are fairly constant (Cox & García-Palmieri, 1990).

To assess the liver health, we consider ALT as it is a specific indicator of liver cell injury than Aspartate Aminotransferase (AST) and it has been utilized frequently to detect patients with liver disease (Kaplan, 2002). BMI is an important well-known marker for the diagnosis of obesity and several health issues (Romero-Corral et al., 2008). We use measured BMI collected by the trained health professional due to concerns and ongoing debate about the accuracy and consistency of self-reported BMI (Flegal et al., 2019; Hill & Roberts, 1998; Olfert et al., 2018). Glycohemoglobin (HbA1c) measures blood sugar level over the 8-12 weeks before measurement and is considered as validated diagnostic test for diabetes (WHO, 2011). To address renal disease especially chronic kidney disease (CKD), we consider serum creatinine level as it is a most commonly used biomarker to evaluate (Van Veldhuisen et al., 2016) besides urea, uric acid and electrolytes. We standardize

serum creatinine value through the calibration suggested by NHANES analytic guideline to compare between the years (Selvin et al., 2007).

There are other markers linked to these same health conditions but not available in every survey wave, either have excessive missing responses or not representing the monotonicity fact. For example, C-reactive protein is also a marker for inflammation and satisfies monotonicity condition. But due to unavailability of the data, we are considering the alternate inflammation marker WBC which has similar diagnostic accuracy rate to C-reactive protein (Willems et al., 2010; Xharra et al., 2012). WBC indicatse infection, inflammation, or certain types of cancer. WBCs are produced in bone marrow and defend the body against disease and infection. Medical literature also mentions other markers, for example albumin (high risk if <3.8 g/dL) (Visser et al., 2005), thyroid stimulating hormone (TSH) (high risk if <0.35 or >4.50), iron and vitamin D (<25 ng/mL, (Alaunyte et al., 2015)) etc. to represent population wellbeing. But we cannot consider such biomarkers which do not follow monotonicity as we must assume utility is monotonic (with higher utility people are worse off).

Summary Statistics

After inspecting the distribution of each biomarker in figure (3), we could see most of them are skewed. To make normalized distribution, we apply winsorization at the 1st and 99th percentiles following Hoo et al. (2002) to address data outlier's issue. Figure 3 represents distribution along with the average value and the recommended range for each biomarker. Table (A1) and table (A2) in appendix show a detailed description of these biomarkers including the clinically defined normal ranges along with the summary statistics for different time periods. At the first stage, we combined the survey periods: (1988-1994), (1999-2002), (2003-2006), (2007-2010), and (2011-2014), (2015-2018) to explore the empirical cumulative distribution of each biomarker.

Figure 3. Biomarkers distribution with clinically recommended range

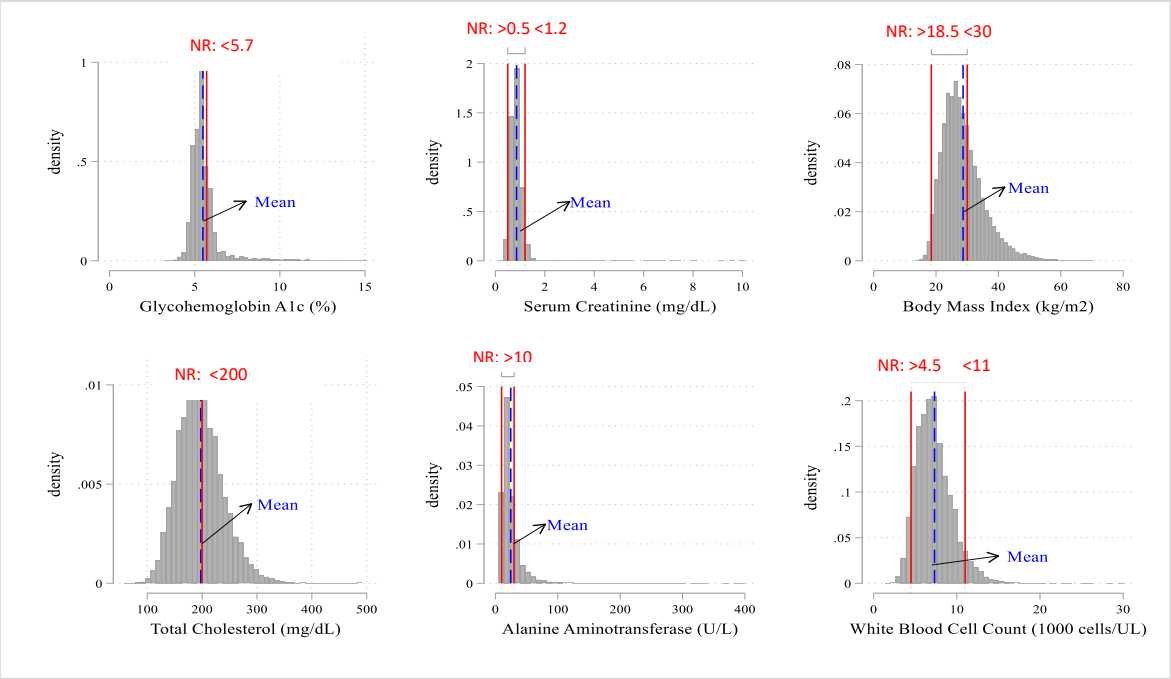


Figure (1) in the appendix depicts the distribution of each biomarker. Once we explore, it is evident that there is a large negative shift from 1988-1994 to 1999-2002 which continued declining in the case of BMI, WBC and HbA1c until 2007-2010 but total cholesterol and ALT rebounded after 2007-2010. Most of the population are within the clinically defined normal range except BMI and total cholesterol. With these multiple directions, it is very difficult to rank an individual's health status and measure overall wellbeing whether it is declining or improving for the whole population. Also, this change in the distribution made us conceptualize what could be the contributing factors behind these shifts, and how can we rank individuals' overall ranking.

Our analysis is stratified by two groups: 1) low income if population below 185 percent of the poverty guideline. This is a specific policy relevant threshold that acts as an upper bound for many federal assistance programs focused on nutrition. For example, WIC has a threshold of 185 percent whereas SNAP has a threshold of 130 percent. 2) everyone else (higher income). All the analysis is performed by incorporating complex survey design and analytical examination weights

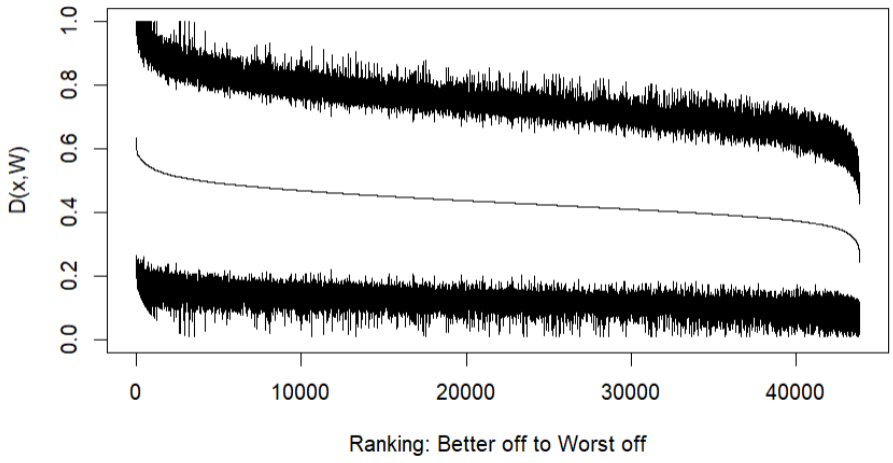
suggested by NHANES analytical guidelines to get robust inference and represent whole population. (CDC, 2024).

4. Results

4.1 Ranking population wellbeing

Using the nonparametric welfare ranking method, we estimate upper and lower bounds for each individual and rank everyone's wellbeing. The variation is the wellbeing score reflects the individual level differences in the values of all biomarkers. Figure (4) shows the mapping of the overall wellbeing for the whole population and individuals are ranked from better to worst off according to the mid-point of their distance bounds. Table (1) shows that the wellbeing (W), which is the midpoint of the two bounds ranges from 0.24 to 0.63, higher value indicates better health. The gap between upper and lower bound gets narrower when the overall wellbeing for an individual is worse compared to others.

Figure 4. Ranking of the population based on their wellbeing distance bounds from 1988-2018



Here, D indicates scaled down distance from the reference wellbeing level for each biomarker i.e., in our case, higher the distance better off the population is. The results indicate that the bounds on the distance measure are very informative about wellbeing comparisons across individuals and it

doesn't span the entire interval of 0 and 1. Here, in general the size of the gap is increasing in overall wellbeing, especially noticeable is that the bounds are narrowest for the worst-off population. With respect to wellbeing, to illustrate the correlation magnitude involved, if we plot all the biomarkers, we see a inverse relationship with all markers. Higher the values of each marker, lower the wellbeing level is.

Wellbeing distribution

Table 1 reports the summary statistucs of the wellbeing for the population as a whole and the individuals below and above 185 percent of the federal poverty line for each time periods in our sample. We find whole population experienced a 6.36 percent decline in the overall wellbeing since 1988-1994 to 2011-2018. Comparing to the most recent period to the initial period low income group population appear to have a 5.9 percent decline in the wellbeing. Similarly, high income population also experienced lowering the wellbeing level

Table 1. Summary statistics of wellbeing from 1988 to 2018

Population	All	1988-1994	1999-2010	2011-2018
Whole Population	0.431 (0.048) [0.242, 0.632] 43846	0.453 (0.050)[a] [0.273, 0.633] 10484	0.4289 (0.042) [0.251, 0.624] 19439	0.429 (0.045) [0.242, 0.618] 13923
Low Income Population (<= 185% poverty line)	0.434 (0.049) [0.251, 0.633] 19371	0.455 (0.067)[a] [0.251, 0.633] 4863	0.433 (0.054) [0.251, 0.624] 8143	0.432 (0.056) [0.255, 0.618] 6365
High Income Population (> 185% poverty line)	0.429 (0.046) [0.242, 0.632] 24475	0.452 (0.042)[a] [0.273, 0.633] 5621	0.428 (0.037)[b] [0.254, 0.624] 11296	0.428 (0.039)[b] [0.243, 0.616] 7558

Note: Standard deviations are in the parenthesis where Maximum and Minimum values are in the brackets.

[a]: the difference between time periods, compared each period to 2011-2018

[b]: the difference between low-income and high-income population

. After comparing low and high income population within year, we find that low income individuals have significantly lower wellbeing score in most recent years in the data, although in the 2007-2010 period, the average wellbeing gap between two groups is highest. The density of

wellbeing is fairly symmetric and unimodal (Figure A2 in appendix). Once we visualize the empirical cumulative distribution of wellbeing for each time period, we see there is a large shift between the distributions of 1988-94 and 1999-2002 in figure (5, 6) and from 2003 to 2018 there is little difference between the periods. Since 1988-94, overall wellbeing declined and continued to decline untill 2007-2010. But in the most recent period, we witness a slight rebound.

4.2.Counterfactual Analysis

Whole population

We see there is a large negative shift of wellbeing distribution between 1988 to 2010, and positive shift between 2010 to 2018 from our ECDF figure (7). This intrigues us to explore what could be the reasons for this negative outcome that are evolving over time within the population and can explain this decline. Calling the counterfactual density, our main point of concern is what would be the distribution of wellbeing in 1988-1994 if the population of 1988-1994 had the demographic characteristics remained at the level of 1999-2010 and population also had the 1988-94 wellbeing score. Looking over the population characteristics in table (A2), we see a clear declining pattern of younger and working aged population but a rise in the older population aged 45 to 64 years. The non-Hispanic white population also decreased while we see increasing rate of non-Hispanic Black as well as Mexican population. Considering education, the proportion of attending college population increased by 27 percent while we find the proportion of having health insurance coverage declined from 85 percent to 78 percent from 1988-94 to 1999-2010 time period. Our process starts with estimating equation (6) by constructing a counterfactual distribution to explore if the decrease is because of change in the composition of demographic characteristics such as age, gender, race and ethnicity.

Figure 5. Distribution of Wellbeing for the whole population

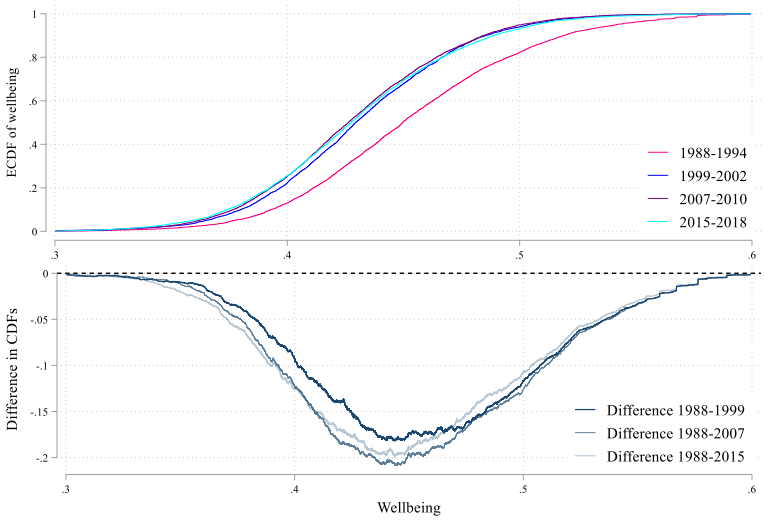
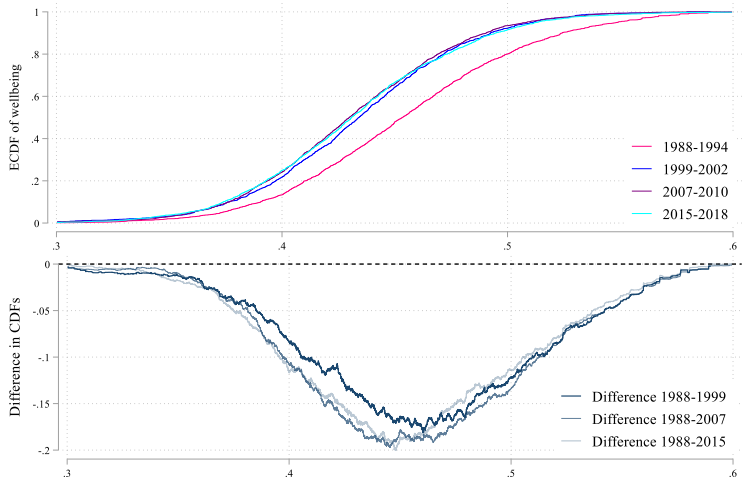
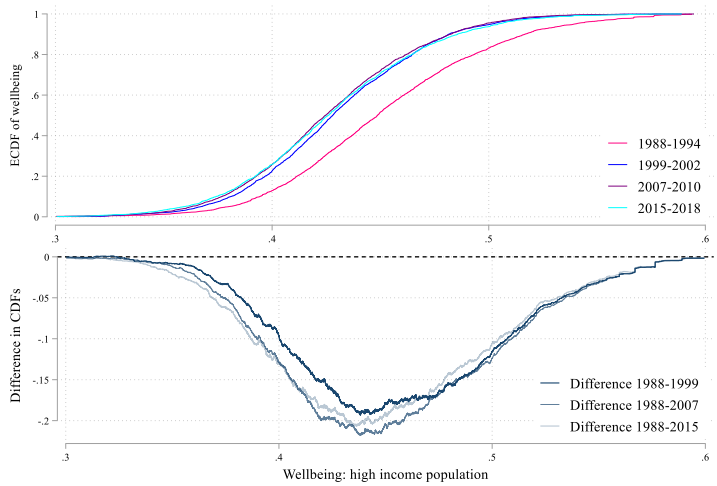


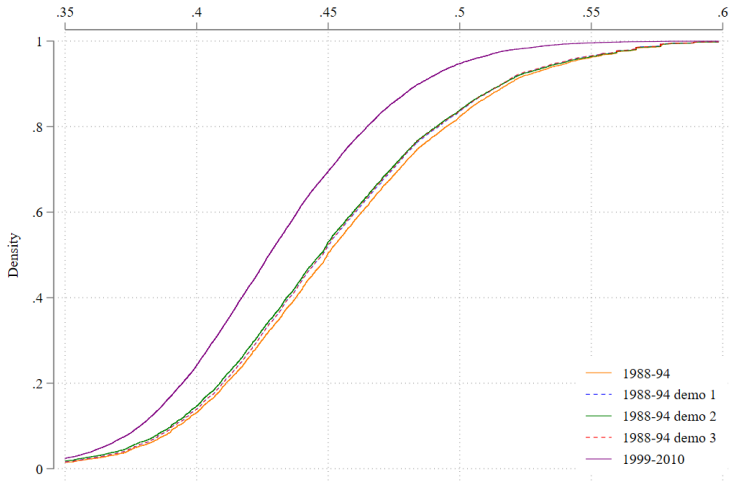
Figure 6. Distribution of Wellbeing by income group





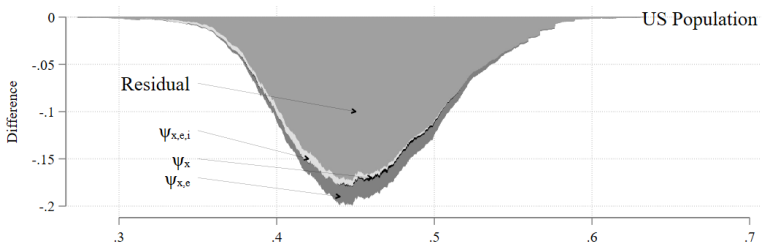
And next we consider how changes in the distribution of education and health insurance coverage affect changes in wellbeing. Figure (7) shows that if the initial period's population had the same demographic composition of the later period, wellbeing gets worse off for the whole population. We see that all of the counterfactual distribution curves lie everywhere to the left of the original 1988-94 distribution. And this shift is more explained by the counterfactual group without education and health insurance coverage in the lower tail of the wellbeing distribution holding other factors constant. In the shaded region of figure (7), we see the changes in the ECDF attributed to the demographic characteristics; education; health insurance; demographic characteristics combined with education and health insurance.

Figure 7. 1988-94 counterfactual distribution and observed 1999-2010 wellbeing distribution



Note: Demo 1 includes age, sex, race/ethnicity and education.
Demo 2 includes age, sex, race and ethnicity.
Demo 3 includes age, sex, race and ethnicity, education, health insurance.

Figure 8. Differences between 1988-94 counterfactual distributions and observed 1999-2010 distribution



Among all these combinations of the attributes, the landscape with education but no health insurance contributes better to the changes in the overall wellbeing distribution compared to the one including those. The better educated population became less healthy throughout this period. The proportion of these areas to the total area gives a scalar measure of the changes in each category. Without education and insurance, it contributes 36% of the total differences between 1988-94 and 1999-2010. Overall finding indicate that observable factors account for comparatively small portion of the wellbeing decline between periods, while leaving a substantial portion unexplained

Decomposition by income group

The counterfactual Figure for the whole population suggests that overall decline in the wellbeing is mostly attributed to the demographic attributes combined with education. It makes us interested to explore how the decline happened between the population who are qualified for different federal assistance programs and those who have higher income.

Figure 9. Differences between 1988-1994 counterfactual and observed 1999-2010 wellbeing distribution by income status

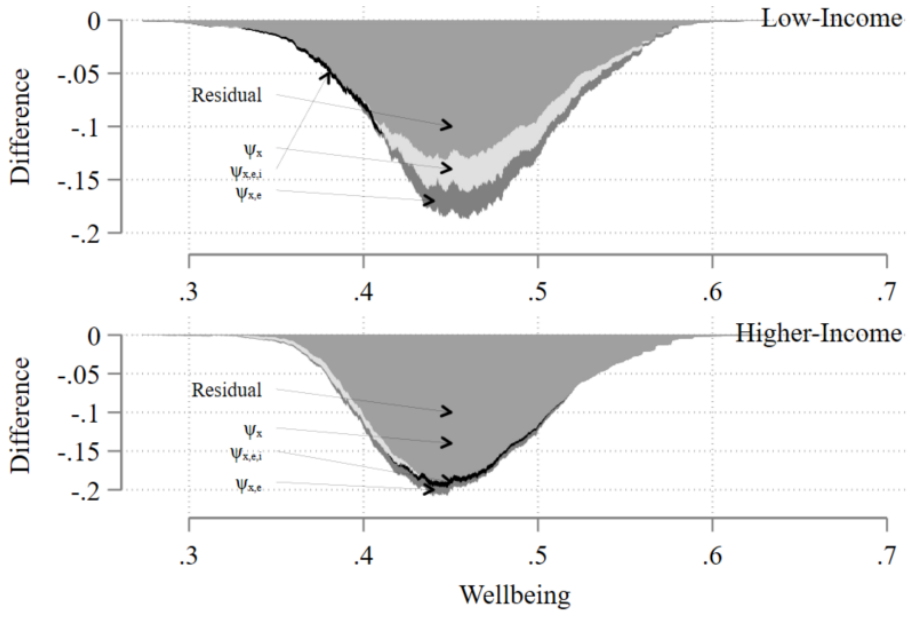


Figure (9) shows that in the lower half distribution, socio-demographic attributes combined with education contribute more to the composition of the wellbeing gap compared to the demographic attributes solely or including health insurance coverage for both income group. Almost 70 percent decline happened due to demographics combined with education. There is a larger variation in the contributing factors to the overall decline for the low-income group than the higher income group. Table (3) provides the scalar measure of changes. Our next task is to test stochastic dominance to explore if the differences and changes are significant.

Discussion and Conclusion

Using biomarkers data from NHANES, out preliminary results show the entire distribution of well-being became worse-off from 1988 to 1999. In the last twenty years (2000-2020), the distribution has also widened: those prone to higher health became better off while those prone to poorer health became worse off. There could be many reasons behind this wide gap, and as health inequality is a complex issue, it could be entangled with multiple endogenous factors. The population might get prone to unhealthy lifestyle, behavioral pattern could be changed, income and occupation combination and many other things might be the contributing factors. While it is difficult to control unobservable factors, we try to explore if the contributing factors behind this decline can be explained by demographic attributes, education and health insurance coverage. And we find that the more educated population are getting less healthy with the time period. While demographics, education and health insurance coverage explained a small portion of this decline, a large portion remains unexplained. Our next step would be to test if this shift and counterfactual contribution are significant or not using SD method. This widening disparity raises concerns about increasing inequality in health outcomes, those who need less help are getting better and the most vulnerable falling further behind where policy implications need to be focused on.

References

Alaunyte, I., Stojceska, V., & Plunkett, A. (2015). Iron and the female athlete: A review of dietary treatment methods for improving iron status and exercise performance. *Journal of the International Society of Sports Nutrition*, *12*(1), 1. https://doi.org/10.1186/s12970-015-0099-2

Albert, M. A. (2011). Biomarkers and Heart Disease. *Journal of Clinical Sleep Medicine : JCSM : Official Publication of the American Academy of Sleep Medicine*, *7*(5 Suppl), S9. https://doi.org/10.5664/JCSM.1342

Alkire, S., & Foster, J. (2011). Counting and multidimensional poverty measurement. *Journal of Public Economics*, *95*(7–8), 476–487. https://doi.org/10.1016/J.JPUBECO.2010.11.006

Anand, S., & Sen, A. (1994). Human development Index: Methodology and Measurement. *Human Development Occasional Papers (1992-2007)*. https://ideas.repec.org/p/hdr/hdocpa/hdocpa-1994-02.html

Anderson, G., Crawford, I., & Leicester, A. (2011). Welfare rankings from multivariate data, a nonparametric approach. *Journal of Public Economics*, *95*(3–4), 247–252. https://doi.org/10.1016/J.JPUBECO.2010.08.003

Anderson, G., Leo, T. W., & Anand, P. (2014). *Dealing with Increasing Dimensionality in Wellbeing and Poverty Measurement, Some Problems and Solutions*.

Atkinson, A. J., Colburn, W. A., DeGruttola, V. G., DeMets, D. L., Downing, G. J., Hoth, D. F., Oates, J. A., Peck, C. C., Schooley, R. T., Spilker, B. A., Woodcock, J., & Zeger, S. L. (2001). Biomarkers and surrogate endpoints: Preferred definitions and conceptual framework. *Clinical Pharmacology & Therapeutics*, *69*(3), 89–95. https://doi.org/10.1067/MCP.2001.113989

Balali, P., Nasserinejad, M., Azadnajafabad, S., Ahmadi, N., Delavari, F., Rashidian, L., Ghasemi, E., Dilmaghani-Marand, A., Fateh, S. M., Ebrahimi, N., Kazemi, A., Derouei, A. A., Djalalinia, S., Rezaei, N., & Delavari, A. (2022). Is elevated ALT associated with lifestyle risk factors? A population-based survey. *Journal of Diabetes and Metabolic Disorders*, *21*(2), 1743. https://doi.org/10.1007/S40200-022-01137-6

Beatty, T. K. M., Lin, B. H., & Smith, T. A. (2014). Is Diet Quality Improving? Distributional Changes in the United States, 1989–2008. *American Journal of Agricultural Economics*, *96*(3), 769–789. https://doi.org/10.1093/AJAE/AAT104

Benavidez, G. A., Zahnd, W. E., Hung, P., & Eberth, J. M. (2024). Chronic Disease Prevalence in the US: Sociodemographic and Geographic Variations by Zip Code Tabulation Area. *Preventing Chronic Disease*, *21*. https://doi.org/10.5888/PCD21.230267

Beydoun, M. A., Beydoun, H. A., Dore, G. A., Canas, J. A., Fanelli-Kuczmarski, M. T., Evans, M. K., & Zonderman, A. B. (2016). White blood cell inflammatory markers are associated with depressive symptoms in a longitudinal study of urban adults. *Translational Psychiatry*, *6*(9), e895. https://doi.org/10.1038/TP.2016.180

Bodaghi, A., Fattahi, N., & Ramazani, A. (2023). Biomarkers: Promising and valuable tools towards diagnosis, prognosis and treatment of Covid-19 and other diseases. *Heliyon*, *9*(2). https://doi.org/10.1016/J.HELIYON.2023.E13323

Boersma, P., Black, L. I., & Ward, B. W. (2020). Prevalence of multiple chronic conditions among US adults, 2018. *Preventing Chronic Disease*, *17*. https://doi.org/10.5888/PCD17.200130

Brunori, P., Trannoy, A., & Guidi, C. F. (2021). Ranking populations in terms of inequality of health opportunity: A flexible latent type approach. *Health Economics*, *30*(2), 358–383. https://doi.org/10.1002/HEC.4185

Bullard, K. M. K., Saydah, S. H., Imperatore, G., Cowie, C. C., Gregg, E. W., Geiss, L. S., Cheng, Y. J., Rolka, D. B., Williams, D. E., & Caspersen, C. J. (2013). Secular changes in U.S. prediabetes prevalence defined by

hemoglobin A 1c and fasting plasma glucose: National Health and Nutrition Examination Surveys, 1999-2010. *Diabetes Care*, *36*(8), 2286–2293. https://doi.org/10.2337/DC12-2563/-/DC1

Caleyachetty, R., Echouffo-Tcheugui, J. B., Muennig, P., Zhu, W., Muntner, P., & Shimbo, D. (2015). Association between cumulative social risk and ideal cardiovascular health in US adults: NHANES 1999–2006. *International Journal of Cardiology*, *191*, 296–300. https://doi.org/10.1016/J.IJCARD.2015.05.007

Carrieri, V., Davillas, A., & Jones, A. M. (2020a). A latent class approach to inequity in health using biomarker data. *Health Economics*, *29*(7), 808–826. https://doi.org/10.1002/HEC.4022

Carrieri, V., Davillas, A., & Jones, A. M. (2020b). A latent class approach to inequity in health using biomarker data. *Health Economics (United Kingdom)*, *29*(7), 808–826. https://doi.org/10.1002/hec.4022

Carrieri, V., & Jones, A. M. (2018). Inequality of opportunity in health: A decomposition-based approach. *Health Economics*, *27*(12), 1981–1995. https://doi.org/10.1002/HEC.3814

Carroll, M. D., Kit, B. K., Lacher, D. A., Shero, S. T., & Mussolino, M. E. (2012). Trends in Lipids and Lipoproteins in US Adults, 1988-2010. *JAMA*, *308*(15), 1545–1554. https://doi.org/10.1001/JAMA.2012.13260

Carroll, M. D., Lacher, D. A., Sorlie, P. D., Cleeman, J. I., Gordon, D. J., Wolz, M., Grundy, S. M., & Johnson, C. L. (2005). Trends in Serum Lipids and Lipoproteins of Adults, 1960-2002. *JAMA*, *294*(14), 1773–1781. https://doi.org/10.1001/JAMA.294.14.1773

CDC. (2014). *FastStats - Leading Causes of Death*. https://www.cdc.gov/nchs/fastats/leading-causes-of-death.htm

CDC. (2024). *NHANES Survey Methods and Analytic Guidelines*. https://wwwn.cdc.gov/nchs/nhanes/analyticguidelines.aspx

Cheng, Y. J., Imperatore, G., Geiss, L. S., Wang, J., Saydah, S. H., Cowie, C. C., & Gregg, E. W. (2013). Secular Changes in the Age-Specific Prevalence of Diabetes Among U.S. Adults: 1988–2010. *Diabetes Care*, *36*(9), 2690–2696. https://doi.org/10.2337/DC12-2074

Cox, R. A., & García-Palmieri, M. R. (1990). Cholesterol, Triglycerides, and Associated Lipoproteins. *Clinical Methods: The History, Physical, and Laboratory Examinations*. https://www.ncbi.nlm.nih.gov/books/NBK351/

Davillas, A., & Jones, A. M. (2020). Ex ante inequality of opportunity in health, decomposition and distributional analysis of biomarkers. *Journal of Health Economics*, *69*. https://doi.org/10.1016/J.JHEALECO.2019.102251

Davillas, A., & Pudney, S. (2017). Concordance of health states in couples: Analysis of self-reported, nurse administered and blood-based biomarker data in the UK Understanding Society panel. *Journal of Health Economics*, *56*, 87–102. https://doi.org/10.1016/J.JHEALECO.2017.09.010

Davillas, A., & Pudney, S. (2020). Biomarkers as precursors of disability. *Economics & Human Biology*, *36*, 100814. https://doi.org/10.1016/J.EHB.2019.100814

Deaton, A., & Muellbauer, J. (1980). Economics and Consumer Behavior. *Economics and Consumer Behavior*. https://doi.org/10.1017/CBO9780511805653

DiNardo, J., Fortin, N. M., & Lemieux, T. (1996). Labor Market Institutions and the Distribution of Wages, 1973-1992: A Semiparametric Approach. *Econometrica*, *64*(5), 1001. https://doi.org/10.2307/2171954

Dong, M. H., Bettencourt, R., Brenner, D. A., Barrett-Connor, E., & Loomba, R. (2012). Serum Levels of Alanine Aminotransferase Decrease with Age in Longitudinal Analysis. *Clinical Gastroenterology and Hepatology*, *10*(3), 285. https://doi.org/10.1016/J.CGH.2011.10.014

Farhangi, M. A., Keshavarz, S. A., Eshraghian, M., Ostadrahimi, A., & Saboor-Yaraghi Dr., A. A. (2013). White Blood Cell Count in Women: Relation to Inflammatory Biomarkers, Haematological Profiles, Visceral

Adiposity, and Other Cardiovascular Risk Factors. *Journal of Health, Population, and Nutrition*, *31*(1), 58. https://doi.org/10.3329/JHPN.V31I1.14749

Field, P. A., & Vasan, R. S. (2018). LDL-Cholesterol is not the only clinically relevant biomarker for Coronary Artery Disease or Acute Coronary Syndrome. *Clinical Pharmacology and Therapeutics*, *104*(2), 232. https://doi.org/10.1002/CPT.1126

Filmer, D., & Pritchett, L. (1999). The Effect of Household Wealth on Educational Attainment: Evidence from 35 Countries. *Population and Development Review*, *25*(1), 85–120. https://doi.org/10.1111/J.1728-4457.1999.00085.X

Flegal, K. M., Carroll, M. D., Ogden, C. L., & Curtin, L. R. (2010). Prevalence and Trends in Obesity Among US Adults, 1999-2008. *JAMA*, *303*(3), 235–241. https://doi.org/10.1001/JAMA.2009.2014

Flegal, K. M., Ogden, C. L., Fryar, C., Afful, J., Klein, R., & Huang, D. T. (2019). Comparisons of Self-Reported and Measured Height and Weight, BMI, and Obesity Prevalence from National Surveys: 1999-2016. *Obesity (Silver Spring, Md.)*, *27*(10), 1711–1719. https://doi.org/10.1002/OBY.22591

Fortin, N., Lemieux, T., & Firpo, S. (2010). *Decomposition Methods in Economics*.

Glei, D. A., Goldman, N., Rodríguez, G., & Weinstein, M. (2014). Beyond self-reports: Changes in biomarkers as predictors of mortality. *Population and Development Review*, *40*(2), 331–360. https://doi.org/10.1111/J.1728-4457.2014.00676.X

Gonzales, M. M., Wang, C. P., Short, M. I., Parent, D. M., Kautz, T., MacCarthy, D., Satizabal, C. L., González, D. A., Royall, D. R., Zare, H., O'Bryant, S., Maestre, G. E., Tracy, R. P., & Seshadri, S. (2022). Blood biomarkers for cognitive decline and clinical progression in a Mexican American cohort. *Alzheimer's & Dementia: Diagnosis, Assessment & Disease Monitoring*, *14*(1), e12298. https://doi.org/10.1002/DAD2.12298

Gowda, S., Desai, P. B., Kulkarni, S. S., Hull, V. V., Math, A. A. K., & Vernekar, S. N. (2010). Markers of renal function tests. *North American Journal of Medical Sciences*, *2*(4), 170. /pmc/articles/PMC3354405/

Gruenewald, T. L., Seeman, T. E., Ryff, C. D., Karlamangla, A. S., & Singer, B. H. (2006). Combinations of biomarkers predictive of later life mortality. *Proceedings of the National Academy of Sciences of the United States of America*, *103*(38), 14158–14163. https://doi.org/10.1073/PNAS.0606215103/SUPPL_FILE/06215FIG4.PDF

He, G. dong, Liu, X. cong, Liu, L., Yu, Y. ling, Chen, C. lei, Huang, J. yi, Lo, K., Huang, Y. qing, & Feng, Y. qing. (2021). A nonlinear association of total cholesterol with all-cause and cause-specific mortality. *Nutrition and Metabolism*, *18*(1), 1–11. https://doi.org/10.1186/S12986-021-00548-1/FIGURES/4

Hickson, D. A., Roux, A. V. D., Gebreab, S. Y., Wyatt, S. B., Dubbert, P. M., Sarpong, D. F., Sims, M., & Taylor, H. A. (2012). Social patterning of cumulative biological risk by education and income among African Americans. *American Journal of Public Health*, *102*(7), 1362–1369. https://doi.org/10.2105/AJPH.2011.300444

Hill, A., & Roberts, J. (1998). Body mass index: a comparison between self-reported and measured height and weight. *Journal of Public Health Medicine*, *20*(2), 206–210. https://academic.oup.com/jpubhealth/article/20/2/206/1555696

Hoo, K. A., Tvarlapati, K. J., Piovoso, M. J., & Hajare, R. (2002). A method of robust multivariate outlier replacement. *Computers & Chemical Engineering*, *26*(1), 17–39. https://doi.org/10.1016/S0098-1354(01)00734-7

Howard, J. T., & Sparks, P. J. (2016). Does allostatic load calculation method matter? Evaluation of different methods and individual biomarkers functioning by race/ethnicity and educational level. *American Journal of Human Biology : The Official Journal of the Human Biology Council*, *28*(5), 627–635. https://doi.org/10.1002/AJHB.22843

Jones, C. A., McQuillan, G. M., Kusek, J. W., Eberhardt, M. S., Herman, W. H., Coresh, J., Salive, M., Jones, C. P., & Agodoa, L. Y. (1998). Serum creatinine levels in the US population: third National Health and Nutrition Examination Survey. *American Journal of Kidney Diseases : The Official Journal of the National Kidney Foundation*, *32*(6), 992–999. https://doi.org/10.1016/S0272-6386(98)70074-5

Jusot, F., Tubeuf, S., & Trannoy, A. (2013). CIRCUMSTANCES AND EFFORTS: HOW IMPORTANT IS THEIR CORRELATION FOR THE MEASUREMENT OF INEQUALITY OF OPPORTUNITY IN HEALTH? *Health Economics*, *22*(12), 1470–1495. https://doi.org/10.1002/HEC.2896

Kaplan, M. M. (2002). Alanine aminotransferase levels: What's normal? *Annals of Internal Medicine*, *137*(1), 49–51. https://doi.org/10.7326/0003-4819-137-1-200207020-00012/ASSET/0003-4819-137-1-200207020-00012.FP.PNG_V03

King, D. E., Mainous, A. G., Carnemolla, M., & Everett, C. J. (2009). Adherence to healthy lifestyle habits in US adults, 1988-2006. *The American Journal of Medicine*, *122*(6), 528–534. https://doi.org/10.1016/J.AMJMED.2008.11.013

Kubzansky, L. D., Kawachi, I., & Sparrow, D. (1999). Socioeconomic status, hostility, and risk factor clustering in the normative aging study: Any help from the concept of allostatic load? *Annals of Behavioral Medicine*, *21*(4), 330–338. https://doi.org/10.1007/BF02895966

Li, X., Ploner, A., Wang, Y., Zhan, Y., Pedersen, N. L., Magnusson, P. K., Jylh, J., Av €, €, & Agg, S. H. €. (2021). Clinical biomarkers and associations with healthspan and lifespan: Evidence from observational and genetic data. *EBioMedicine*, *66*, 103318. https://doi.org/10.1016/j.ebiom.2021.103318

Liu, Z., Que, S., Xu, J., & Peng, T. (2014). Alanine Aminotransferase-Old Biomarker and New Concept: A Review. *International Journal of Medical Sciences*, *11*(9), 925. https://doi.org/10.7150/IJMS.8951

Menke, A., Casagrande, S., Geiss, L., & Cowie, C. C. (2015). Prevalence of and Trends in Diabetes Among Adults in the United States, 1988-2012. *JAMA*, *314*(10), 1021–1029. https://doi.org/10.1001/JAMA.2015.10029

Murray, C. J. L., Mokdad, A. H., Ballestros, K., Echko, M., Glenn, S., Olsen, H. E., Mullany, E., Lee, A., Khan, A. R., Ahmadi, A., Ferrari, A. J., Kasaeian, A., Werdecker, A., Carter, A., Zipkin, B., Sartorius, B., Serdar, B., Sykes, B. L., Troeger, C., … Murray, C. J. L. (2018). The State of US Health, 1990-2016: Burden of Diseases, Injuries, and Risk Factors Among US States. *JAMA*, *319*(14), 1444–1472. https://doi.org/10.1001/JAMA.2018.0158

Neupane, S., Florkowski, W. J., & Dhakal, C. (2024). Trends and Disparities in Diabetes Prevalence in the United States from 2012 to 2022. *American Journal of Preventive Medicine*. https://doi.org/10.1016/J.AMEPRE.2024.04.010

NIEHS. (2023). *National Institute of Environmental Health Sciences: Biomarkers*. NIEHS. https://www.niehs.nih.gov/health/topics/science/biomarkers

Olfert, M. D., Barr, M. L., Charlier, C. M., Famodu, O. A., Zhou, W., Mathews, A. E., Byrd-Bredbenner, C., & Colby, S. E. (2018). Self-Reported vs. Measured Height, Weight, and BMI in Young Adults. *International Journal of Environmental Research and Public Health*, *15*(10). https://doi.org/10.3390/IJERPH15102216

Pak, T. Y., & Kim, G. S. (2021). Association of Food Insecurity With Allostatic Load Among Older Adults in the US. *JAMA Network Open*, *4*(12), e2137503–e2137503. https://doi.org/10.1001/JAMANETWORKOPEN.2021.37503

Peters, S. A. E., Singhateh, Y., Mackay, D., Huxley, R. R., & Woodward, M. (2016). Total cholesterol as a risk factor for coronary heart disease and stroke in women compared with men: A systematic review and meta-analysis. *Atherosclerosis*, *248*, 123–131. https://doi.org/10.1016/J.ATHEROSCLEROSIS.2016.03.016

Prati, D., Taioli, E., Zanella, A., Della Torre, E., Butelli, S., Del Vecchio, E., Vianello, L., Zanuso, F., Mozzi, F., Milani, S., Conte, D., Colombo, M., & Sirchia, G. (2002). Updated definitions of healthy ranges for serum alanine aminotransferase levels. *Annals of Internal Medicine*, *137*(1), 1–9. https://doi.org/10.7326/0003-4819-137-1-200207020-00006

Raghupathi, W., & Raghupathi, V. (2018). An Empirical Study of Chronic Diseases in the United States: A Visual Analytics Approach to Public Health. *International Journal of Environmental Research and Public Health*, *15*(3). https://doi.org/10.3390/IJERPH15030431

Romero-Corral, A., Somers, V. K., Sierra-Johnson, J., Thomas, R. J., Collazo-Clavell, M. L., Korinek, J., Allison, T. G., Batsis, J. A., Sert-Kuniyoshi, F. H., & Lopez-Jimenez, F. (2008). Accuracy of Body Mass Index to Diagnose Obesity In the US Adult Population. *International Journal of Obesity (2005)*, *32*(6), 959. https://doi.org/10.1038/IJO.2008.11

Rosa Dias, P. (2009). Inequality of opportunity in health: evidence from a UK cohort study. *Health Economics*, *18*(9), 1057–1074. https://doi.org/10.1002/HEC.1535

Seeman, T. E., Singer, B. H., Rowe, J. W., Horwitz, R. I., & McEwen, B. S. (1997). Price of Adaptation—Allostatic Load and Its Health Consequences: MacArthur Studies of Successful Aging. *Archives of Internal Medicine*, *157*(19), 2259–2268. https://doi.org/10.1001/ARCHINTE.1997.00440400111013

Seeman, T., Merkin, S. S., Crimmins, E., Koretz, B., Charette, S., & Karlamangla, A. (2008). Education, Income and Ethnic Differences in Cumulative Biological Risk Profiles in a National Sample of US Adults: NHANES III (1988–1994). *Social Science & Medicine (1982)*, *66*(1), 72. https://doi.org/10.1016/J.SOCSCIMED.2007.08.027

Selvin, E., Manzi, J., Stevens, L. A., Van Lente, F., Lacher, D. A., Levey, A. S., & Coresh, J. (2007). Calibration of Serum Creatinine in the National Health and Nutrition Examination Surveys (NHANES) 1988-1994, 1999-2004. *American Journal of Kidney Diseases*, *50*(6), 918–926. https://doi.org/10.1053/j.ajkd.2007.08.020

Seplaki, C. L., Goldman, N., Weinstein, M., & Lin, Y. H. (2004). How Are Biomarkers Related to Physical and Mental Well-Being? *The Journals of Gerontology: Series A*, *59*(3), B201–B217. https://doi.org/10.1093/GERONA/59.3.B201

Stokes, A., Ni, Y., & Preston, S. H. (2017). Prevalence and Trends in Lifetime Obesity in the U.S., 1988–2014. *American Journal of Preventive Medicine*, *53*(5), 567–575. https://doi.org/10.1016/J.AMEPRE.2017.06.008

Thompson, J. P., & Suarez, G. A. (2015). Updating the Racial Wealth Gap. *Finance and Economics Discussion Series 2015-076.Washington: Board of Governors of the Federal Reserve System*, *Washington: Board of Governors of the Federal Reserve System*. https://doi.org/10.17016/FEDS.2015.076r1

Van Veldhuisen, D. J., Ruilope, L. M., Maisel, A. S., & Damman, K. (2016). Biomarkers of renal injury and function: diagnostic, prognostic and therapeutic implications in heart failure. *European Heart Journal*, *37*(33), 2577–2585. https://doi.org/10.1093/EURHEARTJ/EHV588

Vasan, R. S. (2006). Biomarkers of Cardiovascular Disease. *Circulation*, *113*(19), 2335–2362. https://doi.org/10.1161/CIRCULATIONAHA.104.482570

Visser, M., Kritchevsky, S. B., Newman, A. B., Goodpaster, B. H., Tylavsky, F. A., Nevitt, M. C., & Harris, T. B. (2005). Lower serum albumin concentration and change in muscle mass: the Health, Aging and Body Composition Study. *The American Journal of Clinical Nutrition*, *82*(3), 531–537. https://doi.org/10.1093/AJCN.82.3.531

Weinstein, M., & Willis, R. J. (2001). *Stretching Social Surveys to Include Bioindicators: Possibilities for the Health and Retirement Study, Experience from the Taiwan Study of the Elderly*. https://www.ncbi.nlm.nih.gov/books/NBK110037/

Welsh, J. A., Karpen, S., & Vos, M. B. (2013). Increasing Prevalence of Nonalcoholic Fatty Liver Disease Among United States Adolescents, 1988–1994 to 2007–2010. *The Journal of Pediatrics*, *162*(3), 496. https://doi.org/10.1016/J.JPEDS.2012.08.043

WHO. (2011). *Use of Glycated Haemoglobin (HbA1c) in the Diagnosis of Diabetes Mellitus Abbreviated Report of a WHO Consultation*.

Willems, J. M., Trompet, S., Blauw, G. J., Westendorp, R. G. J., & De Craen, A. J. M. (2010). White Blood Cell Count and C-Reactive Protein Are Independent Predictors of Mortality in the Oldest Old. *The Journals of Gerontology: Series A*, *65A*(7), 764–768. https://doi.org/10.1093/GERONA/GLQ004

Wirth, M. D., Sevoyan, M., Hofseth, L., Shivappa, N., Hurley, T. G., & Hébert, J. R. (2018). The Dietary Inflammatory Index is Associated with Elevated White Blood Cell Counts in the National Health and Nutrition Examination Survey. *Brain, Behavior, and Immunity*, *69*, 296. https://doi.org/10.1016/J.BBI.2017.12.003

Xharra, S., Gashi-Luci, L., Xharra, K., Veselaj, F., Bicaj, B., Sada, F., & Krasniqi, A. (2012). Correlation of serum C-reactive protein, white blood count and neutrophil percentage with histopathology findings in acute appendicitis. *World Journal of Emergency Surgery*, *7*(1), 1–6. https://doi.org/10.1186/1749-7922-7-27/TABLES/2

Zimmerman, F. J., & Anderson, N. W. (2019). Trends in Health Equity in the United States by Race/Ethnicity, Sex, and Income, 1993-2017. *JAMA Network Open*, *2*(6), e196386–e196386. https://doi.org/10.1001/JAMANETWORKOPEN.2019.6386

Appendix

Table A1. Summary statistics of biomarkers from 1988-2018, N= 43846

Biomarkers	Predictors	Clinically defined normal range	Mean (SD)	Min	Max
Hemoglobin A1c (%)	Diabetes	<5.7	5.437 (1.06)	3.2	15.1
Alanine Aminotransferase (ALT) (U/L)	Liver disease(Kaplan, 2002; Prati et al., 2002)	10-30	23.921 (19.914)	5	400
BMI (weight to height ratio, kg/m^2)	Obesity (Flegal et al., 2019)	<30.0	28.217 (6.842)	13.3	70.19
Total Cholesterol (mg/dL)	Heart disease (Peters et al., 2016)	<200	197.191 (42.189)	59	491
White Blood Cell Count (1000 cells/UL)	Inflammation or infection (Beydoun et al., 2016; Farhangi et al., 2013; Wirth et al., 2018)	4.5-11.0 x 10^9/L	7.296 (2.198)	1.4	30
Creatinine (mg/dL)	Renal disease (Jones et al., 1998)	0.5-1.2	0.851 (0.371)	0.104	10.1

Table A2. Summary Statistics for demographic attributes

	1988-1994	1999-2010	2011-2018
Age 20 - 29	0.259	0.222	0.227

	(0.010)	(0.005)	(0.008)
Age 30 - 44	0.427	0.367	0.327
	(0.010)	(0.006)	(0.007)
Age 45 - 64	0.315	0.412	0.446
	(0.009)	(0.007)	(0.008)
Non-Hispanic White	0.764	0.698	0.623
	(0.014)	(0.013)	(0.018)
Non-Hispanic Black	0.105	0.110	0.112
	(0.006)	(0.007)	(0.010)
Mexican American	0.052	0.085	0.094
	(0.004)	(0.007)	(0.010)
Other race/ethnicity	0.079	0.105	0.158
	(0.009)	(0.008)	(0.008)
Did not attend high school	0.077	0.049	0.039
	(0.000)	(0.002)	(0.003)
High school, no college	0.464	0.363	0.309
	(0.001)	(0.007)	(0.011)
Attended college	0.459	0.587	0.652
	(0.001)	(0.008)	(0.012)
Have insurance coverage	0.857	0.785	0.811
	(0.009)	(0.006)	(0.009)
Observation	10884	19439	13923

Note: Standard errors in parentheses
All numbers are represented as the percentage of the adult population in the US

Figure A1. Distribution of biomarkers from 1988 to 2018.