

**Subnational contribution to life expectancy and life span variation changes  
Evidence from the United States**

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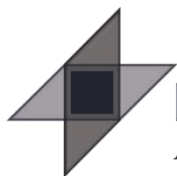
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This publication is part of the Special Collection in the Memory of Professor James W Vaupel (1945–2022), founder and long-time publisher of Demographic Research. The Special Collection is edited by Jakub Bijak, Griffith Feeney, Nico Keilman, and Carl Schmertmann.

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## **Subnational contribution to life expectancy and life span variation changes: Evidence from the United States**

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### **Abstract**

#### **BACKGROUND**

The US life expectancy has been stagnating in recent decades, and along with this, the time trends of life span variation have shown stagnation and even increases with respect to historical levels.

#### **OBJECTIVE**

We aim to disentangle contributions from subnational levels (US regions) to national changes in life expectancy and life span variation in 2010–2019 and 2019–2020.

#### **METHODS**

A decomposition of the change in the national life expectancy and life disparity into the contribution of changing mortality and population structure among subnational regions is presented. The US Census regions are the Midwest, Northeast, South, and West.

#### **RESULTS**

From 2010 to 2019, the South substantially contributed to the life span variation increase due to increasing mortality contributions. The old-age survival improvements across all regions further contributed to increasing life span variation at the national level. Different population growth patterns across regions, especially at older ages, are a further source of change in national life span variation and life expectancy. From 2019 to 2020, during

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the COVID-19 pandemic, an increase in life span variation and a decrease in life expectancy across all regions were observed.

## **CONTRIBUTION**

We present continuous-time decompositions for changes in life expectancy and life span variation. When decomposing subnational contributions to national changes, we also demonstrate the role of the composition effect through subnational–national growth differences. This paper quantifies and highlights the specific contributions of regions and age groups to the national mortality increase in the United States between 2010 and 2019, as well as between 2019 and 2020.

## **1. Introduction**

The United States is facing challenges in increasing life expectancy. The reasons are multifactorial, with the opioid epidemic (Case and Deaton 2021; Woolf and Schoemaker 2019), cardiovascular diseases (Mehta, Abrams, and Myrskylä 2020), violence and accidents, especially firearm-related deaths (Galea and Abdalla 2022; Goldstick et al. 2019; Schwandt et al. 2021; Shkolnikov et al. 2011), deaths related to the health care system (Dwyer-Lindgren et al. 2016; Fisman 2022; Nolte and McKee 2012), obesity (Preston and Stokes 2012), and more recently the COVID-19 pandemic (Aburto et al. 2021; Aburto et al. 2022; Schöley et al. 2022; Woolf, Masters, and Aron 2022) all thought to be contributing. As a result, life expectancy has stagnated and even fallen in recent years (Denney et al. 2013; Harper, Riddell, and King 2021), putting the United States in a disadvantaged position compared to other high-income countries that experienced continuous increases in life expectancy up until the COVID-19 pandemic (Avendano and Kawachi 2014; Ho and HENDI 2018; Ho and Preston 2010; Ni et al. 2021; Woolf, Masters, and Aron 2022).

Life expectancy at birth is the average number of years a synthetic cohort of newborns is expected to live if they were to experience the mortality rates observed in a given year over their life spans. Hence life expectancy, as an indicator of average longevity, does not convey information on the variation in life spans across individuals, which can be substantial (van Raalte, Sasson, and Martikainen 2018). Life span variation is a complementary indicator to life expectancy that expresses how spread out ages at death are at the population level or, alternatively, how predictable (or uncertain) the timing of death is at the individual level. This variation is important to monitor for various reasons: (1) Individual perceptions of the uncertainty in the timing of deaths may affect life course decisions (Heimer, Myrseth, and Schoenle 2019; Nepomuceno et al. 2021; Scott-Sheldon et al. 2010); (2) A higher degree of life span variation is often associated

with unusually high mortality at younger to middle ages in a population (Aburto et al. 2020; van Raalte and Caswell 2013); (3) Rising life span variation signals growing heterogeneity in population health (Edwards 2011; Edwards and Tuljapurkar 2005).

Several studies document differences in life span variation between the United States and other high-income countries. They show that the United States is experiencing higher life span variation than other high-income countries (De Ramos, Auchincloss, and Bilal 2022; Gillespie, Trotter, and Tuljapurkar 2014; Hiam, Minton, and McKee 2021; Rogers et al. 2020). Furthermore, life span variation in the United States has increased rapidly in recent years, starting around 2010 (Brown, Lariscy, and Walker 2023; Acciai and Firebaugh 2019). This stands in sharp contrast to other high-income countries (Jasilionis et al. 2023). This higher and increasing variation is mainly driven by higher premature mortality, with the United States experiencing particularly high levels of externally caused mortality from drug overdoses and firearms (Barbieri 2018; Galea and Abdalla 2022; Goldstick et al. 2019).

Previous paragraphs have outlined the mortality of the United States at the national level. Subnationally, life expectancies among US states have followed a divergent trajectory since 1985, a trend that has intensified in the 21st century (Brown, Lariscy, and Walker 2023; Couillard et al. 2021; Montez et al. 2020; Woolf 2023). At the same time, within the United States, trends in life span variation are diverging across multiple subnational dimensions, including geographic location (Couillard et al. 2021; Walker and Brown 2022; Xu, Engelman, and Fletcher 2021), education/socioeconomic status (Sasson 2016), and race/ethnic group (Aburto, Kristensen, and Sharp 2021; Aburto et al. 2022; Firebaugh et al. 2014; Lariscy et al. 2015). Research has shown that life span variation is higher for disadvantaged populations in the United States (such as Black Americans and those of low socioeconomic status) and geographic areas with lower economic development. Moreover, state-level mortality levels and patterns cluster within broader geographic regions, such as the US Census regions (Brown, Lariscy, and Walker 2023; Xu, Engelman, and Fletcher 2021; Woolf 2023). Southern states exhibited higher levels of life span variation and lower life expectancy compared to the national average while other parts of the United States experienced lower life span variation and higher life expectancy in 2019 (Brown, Lariscy, and Walker 2023).

On top of that, the global COVID-19 pandemic has had an effect on the worsening mortality across the globe since the start of 2020, including in the United States (Schöley et al. 2022; Aburto et al. 2021). Studies have indicated that on the national level during 2019–2020, the age profile of mortality in the United States underwent changes due to the impact of the COVID-19 pandemic. It is important to note that the changes in the mortality age profile during this period were not uniform across all subpopulations in the United States (Aburto et al. 2022). For instance, Hispanics suffered higher mortality at working ages compared to their non-Hispanic white counterparts in the United States in

2020, while Black Americans have suffered higher mortality at ages on average older than their white counterparts (Aburto et al. 2022).

Yet how the divergent levels and trends in subnational mortality (e.g., US regions or states) contribute to the national trends in life expectancy and life span variation was not made explicit in previous studies. This is important because mortality rates as well as population age structures trend differently between subnational groups, and both of these components of change aggregate to the overall national level. For instance, previous studies that have focused on the regional divergence between US states and regions (e.g. Brown, Lariscy, and Walker 2023; Xu, Engelman, and Fletcher 2021) have not explicitly examined the impact of these dynamics at the national level. Understanding how mortality inequalities aggregate to national-level changes through subpopulation-specific results will help contextualize previous studies.

In our study, we focus on larger geographic regions within the United States (census regions). For the United States, these geographic areas vary in terms of economic development, social connection, environmental factors, and regional policy on health services. These factors have been shown to exert a substantial influence on the lives of individuals and to contribute to distinct regional mortality patterns and experiences (Boing et al. 2020; Fenelon 2013; Vierboom, Preston, and Hendi 2019).

In this paper we extend the continuous-time decomposition methods developed by James W. Vaupel and colleagues over the past decades, with a focus on the impact of regional mortality divergence on national-level trends in life span variation over the periods 2010–2019 and 2019–2020 (Aburto et al. 2020; Vaupel and Canudas-Romo 2002; Vaupel and Canudas-Romo 2003; Zhang and Vaupel 2009). Vaupel worked at the forefront of life span variation research, beginning around the early 1980s (Vaupel 1986; Vaupel and Canudas-Romo 2003; Vaupel, Zhang, and van Raalte 2011; Colchero et al. 2016). He also pioneered explorations into how subpopulations and their mortality experiences can affect mortality at the national level (Vaupel 2010; Vaupel and Carey 1993; Vaupel and Yashin 1985).

To summarize, we extend previous decomposition methods on changes in life disparity and life expectancy at the national level (Vaupel, Zhang, and van Raalte 2011; Wagner 2010; Zhang and Vaupel 2009) to understand how different subnational populations contribute to the overall levels of these indicators. As an illustration, we quantify the contribution of changes at the subnational level to changes in US life expectancy and life span variation between 2010 and 2020.

## **2. Data**

The data used comprise mortality rates in single-age intervals and mid-year population counts for each US state. The age-specific death rates for each state in the United States were taken from the US Mortality Database (USMD 2023). The USMD uses a protocol similar to that of the high-quality Human Mortality Database (HMD); that is, the mortality data are smoothed at older ages with the Kannisto model to age 110+ (HMD 2023; Wilmoth et al. 2021). Data are available from 1959 to 2020, with life tables for each state. The mid-year population data from 2010 to 2020 for each state were obtained from the CDC Wonder database (NCHS 2023). The latter data come in single-year age groups up to the open age interval at 85+. To match population data and mortality data across all ages, the penalized composite link model (PCLM) was used to extend and smooth the population counts to age 110+ (Rizzi, Gampe, and Eilers 2015). State information was then grouped into four US Census regions (Midwest, Northeast, South, and West), which were compared across time. (Details on the regions are included in Appendix 1.) Life tables at the regional and US national levels for both males and females used in this study were constructed using standard life table methods (Preston, Heuveline, and Guillot 2001) from the age-disaggregated data for mortality and populations mentioned above.

## **3. Life span variation**

Life span variation measures the dispersion of the age at death in a population. It has been proposed that life span variation should be monitored regularly, along with life expectancy, to provide timely information on the outlook of population health (van Raalte et al. 2018). There are various highly correlated life span variation indices, each with its own mathematical and statistical properties (van Raalte and Caswell 2013; Vaupel, Zhang, and van Raalte 2011; Wilmoth and Horiuchi 1999). These indices include life disparity (Aburto and Beltrán-Sánchez 2019; Aburto and van Raalte 2018; Vaupel and Canudas-Romo 2003; Vaupel, Zhang, and van Raalte 2011), life table entropy (Keyfitz 1977; Leser 1955), the Gini coefficient (Peltzman 2009; Shkolnikov, Andreev, and Begun 2003), life table standard deviation (Canudas-Romo 2008; Edwards and Tuljapurkar 2005; Horiuchi et al. 2013; Tuljapurkar 2010), and the Theil index (Allison 1978; Permanyer and Scholl 2019), among others.

For our analysis, we chose life disparity for its mathematical properties. Life disparity (denoted as  $e^\dagger$ ) measures the average life expectancy lost due to death or the life table variation at the age at death in years (Vaupel 1986; Vaupel and Canudas-Romo



2003; Vaupel, Zhang, and van Raalte 2011). Life disparity tends to decrease as life expectancy increases (Colchero et al. 2016; Vaupel, Zhang, and van Raalte 2011).

## 4. Methods

The mathematical expression of life disparity at birth is  $e^+(0, t) = \int_0^\omega f(x, t)e(x, t) dx$ , where  $f(x, t)$  and  $e(x, t)$  stand for the life table distribution of deaths and remaining life expectancy at age  $x$  and time  $t$ .

Let a dot over a variable denote the derivative with respect to time. The changes in life disparity at birth over time  $\dot{e}^+$  can be expressed mathematically as:

$$\dot{e}^+(0, t) = - \int_0^\omega \dot{\mu}(x, t)W(x, t)dx, \quad (1)$$

where  $\mu(x, t)$  corresponds to the age-specific force of mortality at age  $x$  and time  $t$ . The component  $W(x, t) = \ell(x, t)[e^+(x, t) + e(x, t)(H(x, t) - 1)]$ , where  $\ell(x, t)$  stands for the life table survival function and  $H(x, t)$  for the cumulative hazard, can be seen as the weight that reflects the age-specific impact of survival improvements on life disparity (Zhang and Vaupel 2009, and Appendix 2).

Mortality improvements at any age translate into life expectancy gains. Unlike life expectancy, life span variation indicators react differently depending on where improvements occur. This component creates a unique threshold age that distinguishes life disparity changes due to premature mortality changes (premature mortality contributions) from life disparity changes due to old-age mortality changes (old-age survival contributions) (Wagner 2010; Zhang and Li 2020; Zhang and Vaupel 2009). While the decrease in mortality at young ages contributes to reducing life disparity, old-age survival improvements in mortality contribute positively and increase life disparity, and at times can offset the premature mortality contributions (Aburto et al. 2019; Aburto et al. 2022; Gillespie, Trotter, and Tuljapurkar 2014).

To incorporate subnational contributions into the changes in national life disparity, a relation between the national age-specific force of mortality, denoted by  $\mu(x, t)$ , and the subnational age-specific force of mortality, denoted by  $\mu(x, t, i)$ , where  $i$  represents subpopulation  $i$ , is used. Torres, Canudas-Romo, and Oeppen (2019) have shown that mortality at the national level can be expressed as the weighted sum of the subnational-specific mortality and the population proportion at each age, as  $\mu(x, t) = \sum_i \mu(x, t, i)c(x, t, i)$ , where  $c(x, t, i)$  is the population composition or proportion of the subnational population  $i$  at age  $x$  and time  $t$  with respect to the national level. The

derivative of the national force of mortality written in this form can be separated into two components, corresponding to subnational specific changes as

$$\dot{\mu}(x, t) = \sum_i \dot{\mu}(x, t, i)c(x, t, i) + \sum_i \mu(x, t, i)\dot{c}(x, t, i). \quad (2)$$

By substitution, the decomposition in Equation (1) can be rewritten as

$$\dot{e}^+(0, t) = - \int_0^\omega \sum_i \dot{\mu}(x, t, i)c(x, t, i)W(x, t) + \mu(x, t, i)\dot{c}(x, t, i)W(x, t) dx. \quad (3)$$

For life expectancy, the methodology developed by Torres, Canudas-Romo, and Oeppen (2019) allows us to decompose its change over time as

$$\dot{e}(0, t) = - \int_0^\omega \sum_i \dot{\mu}(x, t, i)c(x, t, i)T(x, t) + \mu(x, t, i)\dot{c}(x, t, i)T(x, t)dx, \quad (4)$$

where the notation  $T(x, t) = \ell(x, t)e(x, t)$  refers to the life table person-years lived after age  $x$  at time  $t$ .

The first component in Equations (3) and (4) stands for the contribution from mortality changes at each subnational level  $i$  to changes in national life disparity and life expectancy, respectively. This component is also referred to as the mortality component.

The second component, also known as the composition effect, can be interpreted as the contribution from the changes in population composition in each subnational level  $i$  to the changes in the national life disparity or life expectancy. The population composition adds up to 100% nationwide at each age, and if a region gains population by a certain percentage, another is forced to lose the same percentage (or that percentage can be distributed among several other regions). When these changes in population percentages are weighted by the mortality rates of their respective populations, the composition effect is the result of these changes canceling each other out at each age. This interpretation is also presented by Torres, Canudas-Romo, and Oeppen (2019) and Shkolnikov et al. (2003, 2006), among others.

Here we illustrate an alternative interpretation of the composition component that involves the interaction between population growth and mortality at each subnational level. The second component of Equation (2), at each subnational level  $i$ , is the difference in subpopulation and national population growth weighted by region-specific mortality. This relationship can be expressed by rewriting the composition elements within the second component in Equation (2) as  $\dot{c}(x, t, i) = c(x, t, i)[r(x, t, i) - r(x, t)]$ , where  $r(x, t, i)$  and  $r(x, t)$  represent the subnational and national age-specific growth rates, respectively. We can then write Equation (3) as:

$$\begin{aligned} \dot{e}^\dagger(0, t) = & - \int_0^\omega \sum_i \dot{\mu}(x, t, i) c(x, t, i) W(x, t) dx \\ & - \int_0^\omega \sum_i \mu(x, t, i) [r(x, t, i) - r(x, t)] c(x, i, t) W(x, t) dx. \end{aligned} \quad (5)$$

The composition component here works by offsetting/reinforcing the mortality changes at each subnational level. For example, given a scenario in which mortality is decreasing (improving) and the difference in  $[r(x, t, i) - r(x, t)] < 0$ , which signifies a subpopulation that is growing slower than the national level at a specific age, the composition effect reinforces the mortality component, with fewer people exposed to mortality relative to the national level. Meanwhile, when the difference  $[r(x, t, i) - r(x, t)] > 0$ , which signifies a subpopulation that is growing faster than the national level, the composition effect offsets the mortality component, signifying that more people are exposed to mortality. This mechanism is reversed in a mortality-increasing (worsening) scenario. A detailed derivation and elaboration of the equation can be found in Appendix 2.

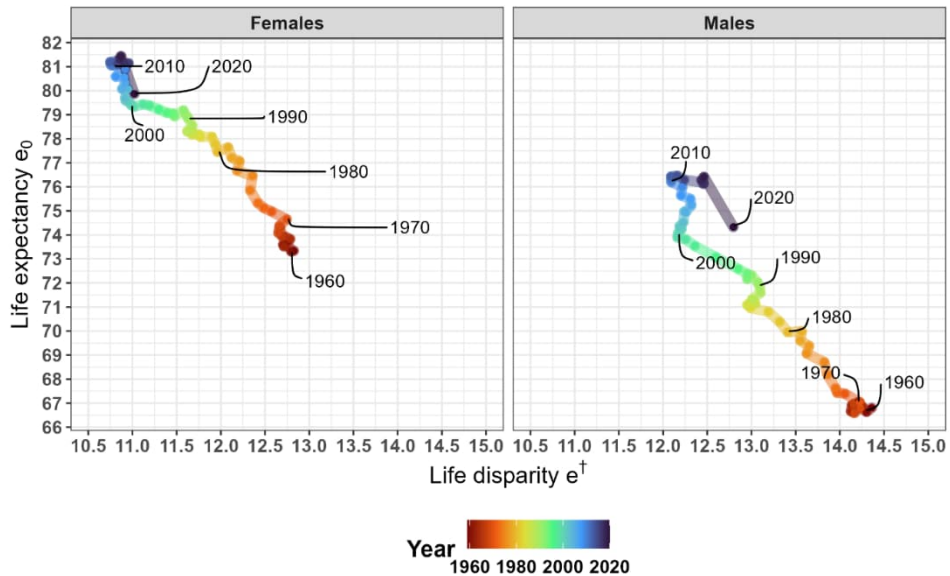
All the calculations in this study (estimation details in Appendix 2) were carried out using R software (R Core Team 2021), and commented R code is included in the repository: [OSF Link](#).

## 5. Results

### 5.1 National and subnational trends

The dynamics of life expectancy and life disparity change over time in the United States is a story of progressions that were halted occasionally along the way, until recent years. Figure 1 shows such dynamics across time (1959–2020) for both females and males, with life expectancy improving from low to high values (bottom to top) and life disparity reducing from high to low values (right to left). After 2000, the life disparity decline came to a halt. Life expectancy increases first slowed and then stagnated up until 2019 for both females and males before declining sharply in 2020. Our study focus on the recent ten years (2010–2020) in the United States. Since the substantive story of national and subnational mortality change does not appear to be sex-specific (though it is more pronounced among males), the rest of our results will focus on US males. Results for US females can be found in Appendix 3.

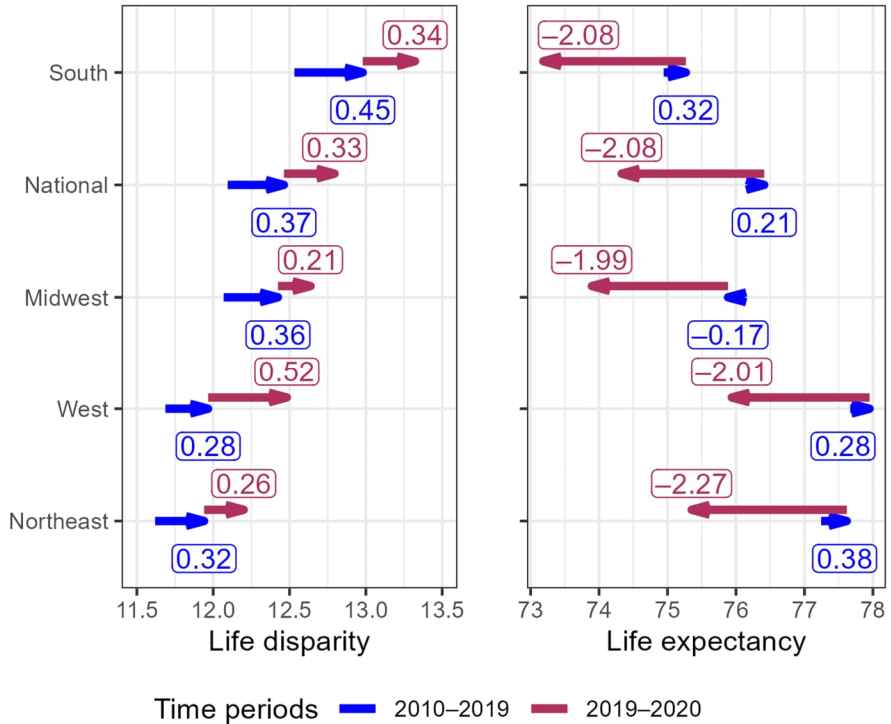
**Figure 1: US life disparity and life expectancy time trajectories, 1959–2020**



Source: Authors' calculation based on USMD (2023).

Figure 2 shows the levels and changes in life expectancy and life disparity of these recent ten years among US males in four census regions and at the national level. Since the COVID-19-induced changes were large, abrupt, and at least in part owing to different social determinants (for example, a region's international connectedness), we separated dynamics into the pre-COVID-19 pandemic period and the first COVID-19 pandemic year. Life disparity increased in all four regions during the periods 2010–2019 and 2019–2020. Among these increases, the Northeast and West regions started with a life disparity lower than the national level (11.6 and 11.7 years, respectively, compared to 12.1 years), while the Midwest and South regions had a similar or higher level compared to the national level (12.1 and 12.5 for the Midwest and the South, respectively). All regions apart from the Midwest experienced minor increases in life expectancy over the period 2010–2019. The COVID-19 pandemic disrupted these increases, and all regions experienced a drop in life expectancy during 2019–2020.

**Figure 2: US national and regional life disparity and life expectancy and their changes, males 2010–2020**



Notes: Blue represents changes in both life disparity and life expectancy during 2010–2019, and maroon represents the changes during 2019–2020. Labels illustrate the changes during the period with respect to the starting year. The figure is ordered from highest to lowest life disparity.

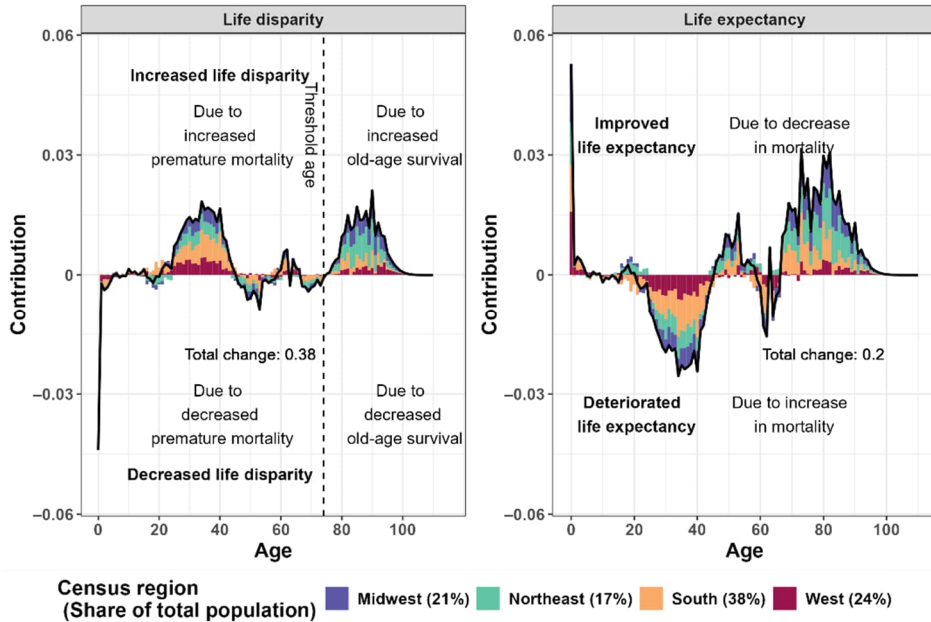
Source: Authors' calculation based on USMD (2023) and NCHS (2023).

## 5.2 Linking subnational and national changes, 2010–2020

The reversals in life disparity and life expectancy to levels observed a quarter century earlier are assessed with regional and age decompositions of the national change in life disparity (shown in the left panels of Figures 3 and 4) and life expectancy (right panels). The results show the changes and contributions from 2010 to 2019 in Figure 3 and from 2019 to 2020 in Figure 4. Contributions below zero represent decreased life disparity/life expectancy, and contributions above zero represent increased life disparity/life

expectancy. The threshold age of life disparity is visible in the left panels by the crossing-over age-specific contributions.

**Figure 3: Age and region contributions to changes in life disparity and life expectancy, US males 2010–2019**



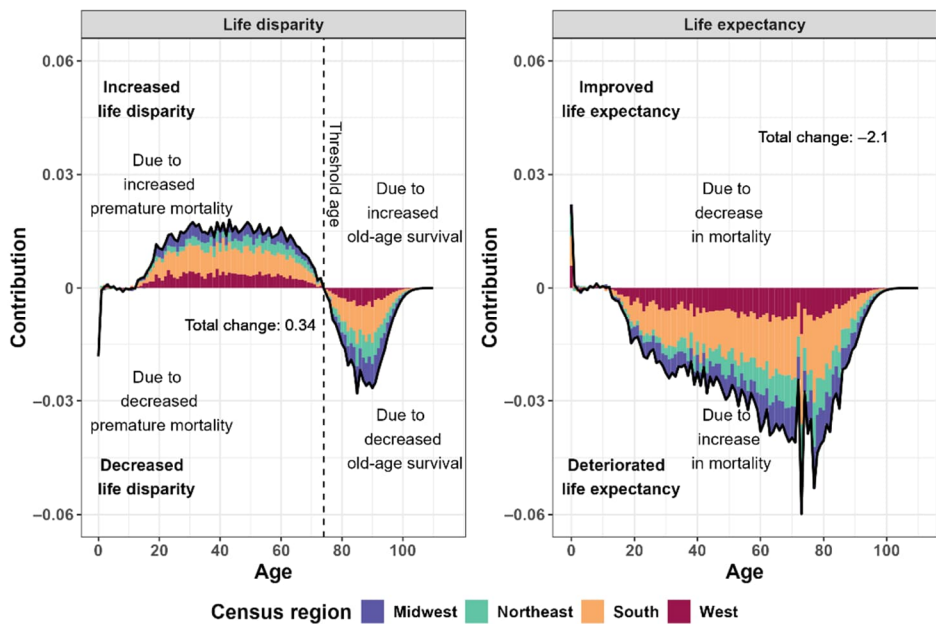
Notes: The mean proportions of the four regions with respect to the US national population during 2010–2019 are shown in parentheses in the legend. Dark solid lines represent total contribution at each age.  
 Source: Authors' calculations based on data from USMD (2023) and NCHS (2023).

The reversal of life disparity from 2010 to 2019 to a higher level was the combination of multiple subnational contributions from different age groups. Of all the contributions from the four regions in the United States, the Midwest and the South had the highest contributions to the 0.38-year increase during 2010–2019 (contributing 0.09 and 0.13 years, respectively, amounting to 58% of the national change). The Northeast (0.08 years) and the West (0.08 years) contributed the remainder. For noticeable age groups, the West region contributed around 17% (0.06) and the South around 26% (0.10) to the 0.38-year changes between the ages of 20 and 45. These two regions held the largest population shares in the nation during 2010–2019 (38% and 24% for the South and West, respectively). After the threshold age of 74, the Midwest and Northeast contribute most to the life disparity changes via the extension of old-age survival (around 0.16 years of

the total 0.22 years of increase in old-age contributions), with the other regions contributing only 0.06 years.

The change in life expectancy from 2010 to 2019 was mostly attributed to the Northeast (0.18 years of the national 0.21-year increase). The Midwest region contributed 0.10 years to the national change, while the West and the South opposed the national increase in life expectancy contributing with  $-0.07$  years.

**Figure 4: Age and region contributions to changes in life disparity and life expectancy, US males 2019–2020**



Notes: Dark solid lines represent the total contribution at each age.  
 Source: Authors' calculations based on data from USMD (2023) and NCHS (2023).

Figure 4 shows the decompositions of the change in life disparity and life expectancy during 2019–2020. For the increase in life disparity amid the first year of the COVID-19 pandemic, the South contributed the highest amount of 0.17 years (50% of the total change), followed by the West (0.11 years) and the Midwest and Northeast for the remaining 0.06 years. The contribution from the infant stage was negative, as seen in 2010–2019, corresponding to declines in infant mortality. However, over adult ages, positive contributions before the threshold age of 73 indicate an increase in premature

mortality across these ages, contributing to the increase in life disparity. The South had the highest contribution of 0.32 years in this age group, followed by the West with 0.18 years and 0.26 years from the Midwest and Northeast combined. At the same time, the positive contribution to life disparity change from the old-age survival extension observed in 2010–2019 is reversed in 2020. This negative component from ages 73 and above indicates increases in mortality in this age group.

A similar story is observed in changes in life expectancy between 2019 and 2020. Apart from the positive contributions to life expectancy from improvements in mortality in the first year of life, all ages were impacted by the COVID-19 pandemic in 2020, with different intensities. (In total the South contributed –0.85 years and the other three regions each contributed between –0.37 to –0.45 years.)

### **5.3 Contribution of mortality versus composition components**

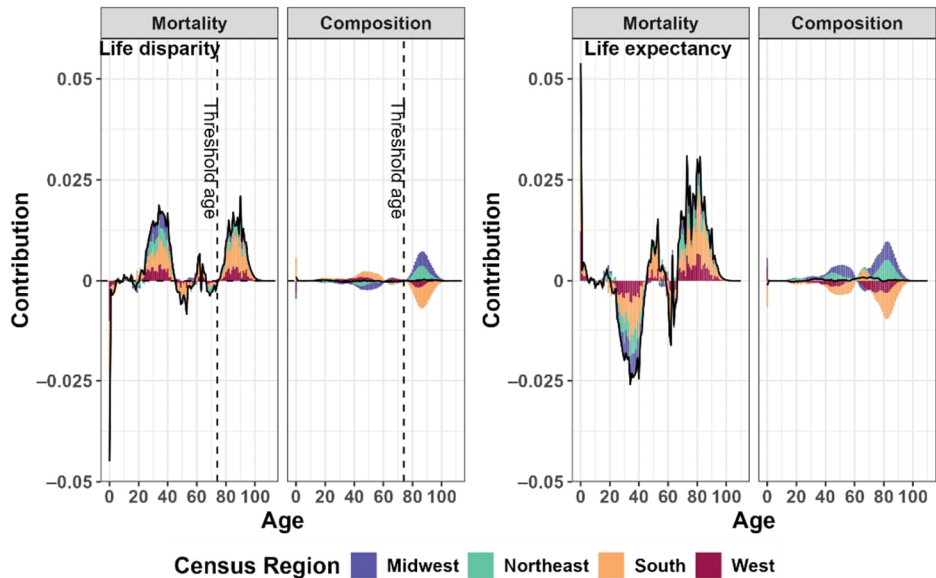
The contributions from each US region to the national changes in both life disparity and life expectancy presented above are the combination of mortality and composition components. Figure 5 further disaggregates the dynamic into those two components during 2010–2019. As mentioned earlier, the composition components cancel each other out when all regions are added. However, when we examine the contribution of each subnational level, the composition component plays an important role in shaping the regional age contributions, especially at older ages.

For life disparity, the South contributed 0.17 years (45% of total changes) from the mortality component and –0.04 years from the composition component (or 0.13 years of total contribution). The negative composition components arise from the South having growth rates higher than the national level from 2010 to 2019, which offset the mortality components, indicating that more people are exposed to mortality in these regions. In the Midwest, Northeast, and West, the mortality contribution to the national change was 0.06 to 0.08 years and the compositional contribution was 0.01 to 0.02 years, for total contributions of 0.09, 0.08, and 0.08, respectively. The positive composition components in this case are due to population growth lower than the national level in these regions. This dynamic can also be found in contributions to life expectancy changes. The South and West had negative contributions due to smaller positive mortality components (0.11 and 0.05 years, respectively) and bigger negative composition components (–0.14 and –0.08). Meanwhile, the Midwest and Northeast were quite the opposite (positive contributions = negative/smaller mortality component + bigger positive composition component). Details on the subnational–national growth differences within the United States can be found in Appendix 3.



In the 2019–2020 period, life expectancy and life disparity changes were overwhelmingly driven by the mortality components, as regional differences in population change were minimal. Detailed contributions from both the mortality and composition components of each region during 2010–2019 and 2019–2020 can be found as tables and figures in Appendix 3.

**Figure 5: Decomposition of changes in life disparity and life expectancy into mortality and composition components, as well as age and region contributions, US males 2010–2019**



Notes: The age pattern observed in Figure 3 is the sum of the values across ages from both mortality and composition components. Dark solid lines represent the total contribution from each component at each age.

Source: Authors' calculations based on data from USMD (2023) and NCHS (2023).

## **6. Discussion**

### **6.1 Regional mortality contributions to US mortality changes**

In recent years, higher mortality in the young to middle ages has been observed in the United States compared to other high-income countries, which lowers life expectancy and increases life span variation (Hiam, Minton, and McKee 2021; Ho and Preston 2010; Ho and Hendi 2018; Shkolnikov et al. 2011; Palloni and Yonker 2016). According to our results, US life expectancy stagnated during the first analysis period (2010–2019) while life disparity increased by 0.38 years. All regions in the United States contributed to an increase in life span variation during this period, although at different intensities. The South and West regions, in particular, were the main drivers of the increase in US life span variation due to rising premature mortality, especially at ages 20 to 45. Meanwhile, the Northeast and Midwest also contributed to the increase in life span variation via old-age mortality decline.

The mortality divergence that we found across US regions during 2010–2019 has been extensively studied (Brown, Lariscy, and Walker 2023; Fenelon 2013; Graetz and Elo 2022; Walker and Brown 2022; Vierboom, Preston, and Hendi 2019; Woolf and Schoemaker 2019; Xu, Engelman, and Fletcher 2021). Specifically, in the paper by Brown, Lariscy, and Walker, southern states have consistently higher life disparity compared to the national average during the period 2015–2019. This coincides with our results on the South's pronounced contribution to national-level changes. Certain northeastern and western states also have life span variation consistently lower than the national average (around one year) (Brown, Lariscy, and Walker 2023), although in our results, these regions also contributed to the increase in life span variation during 2010–2019. This mortality divergence, with different levels of life disparity among US regions, could indicate that Americans are likely to have different experiences in loss of kin (children, siblings, parents) not only across different geographic locations throughout their lives but also in comparison to their European peers.

Leading theories for this mortality divergence include diverging within-region levels of socioeconomic inequality (Dwyer-Lindgren et al. 2016; Montez et al. 2019; Roy et al. 2020; Shkolnikov et al. 2011) and economic development (Couillard et al. 2021; Chetty et al. 2016). For instance, southern states with lower median household income have higher levels of life span variation and lower life expectancy (Brown, Lariscy, and Walker 2023; Schwandt et al. 2022). Compositional change by race and ethnicity may also be contributing to regional divergence in mortality. For example, the South has a higher proportion of Black Americans and the West has a higher proportion of Hispanics (results from US Census Bureau 2022). This regional difference in race/ethnic composition may also affect the disparity in mortality within the United States owing to

increased mortality for Black Americans from adverse living conditions (Riddell et al. 2018) and the health advantage observed among Hispanic Americans at older ages (Lariscy et al. 2015). Furthermore, a combination of regional differences in smoking patterns (Fenelon and Preston 2012), differential opioid crisis impacts (Case and Deaton 2021; Vierboom, Preston, and Hendi 2019; Mattson et al. 2021), and differences in violent deaths (particularly serious in the Southeast; see Wintemute 2015) may have caused the South to lag behind other regions, particularly the Northeast.

Our results complement the recent findings of Brown, Lariscy, and Walker (2023) on diverging regional trends in life span variation. We estimated the impact of this divergence within the United States on national-level mortality changes and extended the results to include the impact of the first year of COVID-19 on regional and national mortality patterns. As life expectancy decreased and life span variation increased in the United States as a whole during 2019–2020, regional contributions varied once more, with the South again driving the changes. This phenomenon could be the exacerbation of the pre-pandemic determinants mentioned above being amplified by the pandemic (see, e.g., Aburto et al. 2021; Aburto et al. 2022; Andrasfay and Goldman 2021; Arias and Tejada-Vera 2023; Goldman and Andrasfay 2022; Woolf, Masters, and Aron 2022), on top of the case fatalities associated with the pandemic.

At the national level, we anticipate that the COVID-19 pandemic will further exacerbate ongoing mortality challenges in the United States, particularly during the years 2020–2021, following the initial shock in 2020. We derived national-level results from the HMD, which employs the same methodology as the USMD dataset. In the United States there has been a continued increase in life span variation, with an additional 0.56 years for males and 0.60 years for females. At the same time, life expectancy further declined by 0.72 years for males and 0.50 years for females during the period 2020–2021, building upon trends observed in the preceding period, 2019–2020. At the subnational level, we anticipate a similar trend in life span variation during 2020–2021 as was witnessed in 2019–2020. This is influenced by various factors, including the varying response policies of states, some of which have been slow and reluctant in certain regions. Additionally, the overall burden on the health care system in the United States was substantial during COVID-19 (Montez et al. 2020; Montez 2020). The persistent and disproportionate heavy impact of COVID-19 on the mortality of different minority race and ethnic groups, in comparison to non-Hispanic white Americans, also plays into the regional contribution at the local level (Aburto et al. 2021; Andrasfay and Goldman 2021; Luck et al. 2023). Based on our findings, we also expect that during 2020–2021, if the trends observed in 2019–2020 continue, the southern region will make a more significant contribution to changes in life span variation compared to regions exhibiting similar age patterns.

Overall, we found that within-region mortality change was a more important contributor to national-level age trends than population composition changes. At the same time, we found that population composition effects had a non-negligible and generally overlooked impact on national-level trends in mortality in the United States, especially at older ages. We anticipate that the share of life expectancy and life disparity changes resulting from regional compositional change will increase in the future for the United States. This is mainly because of the increasing regional divergence in age-specific population growth (Franklin 2014; Glaeser and Tobio 2008). As the baby boom cohorts age, the compositional contributions to life expectancy and life disparity changes will be driven increasingly by divergence in regional population growth at older ages (Canudas-Romo, Shen, and Payne 2021; Lee 2011; Preston and Vierboom 2021).

## **6.2 Methodological considerations and future outlook**

In this study, we measured the impact of mortality divergence across geographic locations within the United States on national averages with decomposition methods. Our subnational groups were defined in terms of geography, but the groups could be defined in terms of other characteristics as long as they are exhaustive. Examples include socioeconomic indicators (income quantile, education level, occupational class), race, and ethnicity.

In our analysis, we aggregated our results into four US Census regions. However, like other studies that use geographic areas as the basis for analysis, our study is affected by the modifiable area unit problem (MAUP; see Openshaw 1984): our results reflect only the overall situation of each census region and may not capture variations within regions in terms of contributions from smaller geographical areas (e.g., census divisions and states; for an empirical example, see, e.g., Boing et al. 2020). For example, within the southern United States, our further analysis disaggregated by state shows that certain states, such as Florida and Texas, contributed a dominating proportion to the contributions from the South region, while other southern states contributed a lesser proportion. Similar patterns are observed in other regions as well. (See Figure A-4 in Appendix 3 for results by US state.) States with pronounced contributions also have relatively higher shares of the total US population. This might signify that although groups are defined by broader geographic boundaries, our method still captures contributions to changes in life span variation and life expectancy from the population majority within those regions.

Our decomposition method is sensitive to the proportion of the population size within subpopulations (see Appendix 2: “Methodological supplements”). When a subpopulation comprises a larger proportion of the national population, it yields a more

significant influence on national-level changes in life expectancy and life span variation compared to subpopulations with relatively smaller sizes. To illustrate this, consider the case of males from Florida (within the South region) and Alaska (within the West region). Florida, with a considerably larger population size compared to Alaska, plays a more substantial role in driving national-level changes than Alaska, as indicated by their contributions of 0.044 and 0.001, respectively, to life disparity changes between 2010 and 2019 for males in our decomposition. This is despite both states having similar mortality levels (refer to Brown, Lariscy, and Walker 2023). This suggests that subpopulations with similar mortality patterns may affect national-level trends differently based on their relative population sizes. However, population size is just one part of the equation of the contribution to the national trend, and the mortality component can oppose or contribute similarly to the compositional trends.

Shkolnikov et al. (2003, 2006) proposed a method with a purpose similar to ours. It utilized the idea of stepwise replacement, commonly found in computer science, to disentangle subpopulation contributions to life expectancy. This method has been applied to high-income countries to examine the effect of educational composition changes (Enroth et al. 2022; Luy et al. 2019) or regional population composition changes (Timonin et al. 2016). Our method differs from the Shkolnikov approach by adopting a continuous-time framework, yet we expect the two to yield broadly similar results, as is generally found in comparisons of discrete and continuous decompositions (Pollard 1988). One advantage of continuous approaches in comparison to stepwise replacement methods is that continuous approaches do not require an ordering of the covariates, whereas in the stepwise replacement framework, there are small changes in contributions depending on the order in which covariates are introduced. While a young-to-old ordering makes logical sense for age-specific decompositions, there is no natural ordering for covariates such as region, as in our example.

Our proposed method is further strengthened by an additional explicit interpretation of compositional effect in terms of differences in age-specific growth rates between subnational and national levels. The subnational–national difference in age-specific growth rates itself is a function of past regional divergence in fertility, internal and international migration, and survival (Arthur and Vaupel 1984; Lee and Zhou 2017; Preston and Coale 1982; Preston and Stokes 2012; Canudas-Romo, Shen, and Payne 2022). Thus, if rich long-term historical data were available, an extension to the method proposed here could further split the compositional change contributions into these even more elementary components.

## **7. Conclusion**

In conclusion, this study highlights the regions and age groups that contributed to the stagnation in life expectancy and the increase in life disparity in the United States during 2010–2020. By extending the continuous-time decomposition methods developed by Vaupel and colleagues to quantify subnational mortality and compositional change contributions, we show that regional differences in age-specific growth rates can have a major impact on national-level change in life expectancy and life disparity, even if they are generally smaller than regional differences in mortality.

James W. Vaupel and his colleagues regularly demonstrated that summary measures conceal the intricate demographic processes at play underneath. This article is dedicated to Vaupel's pursuit of simple equations that can have profound and meaningful demographic interpretations.

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Jim Vaupel's commitment to the future of demography can be seen in this paper written by 3 generations of his PhD students. Jim was the main supervisor of Vladimir and Alyson. Vladimir and Alyson, together with Jim, went on to supervise Jose Manuel. Now we have continued the legacy of Jim Vaupel's love for demography by mentoring Wen. This reflects the reach and contributions of Jim's school, and we dedicate this paper to him.

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## Appendices – Subnational contribution to life expectancy and life span variation changes: Evidence from the United States

### Appendix 1 – Data backgrounds

#### US Census regions

**Table A-1: US Census regions and their constituting states**

Census Region	Midwest	Northeast	South	West
US States	Indiana	Connecticut	Delaware	Arizona
	Illinois	Maine	District of Columbia	Colorado
	Michigan	Massachusetts	Florida	Idaho
	Ohio	New Hampshire	Georgia	New Mexico
	Wisconsin	Rhode Island	Maryland	Montana
	Iowa	Vermont	North Carolina	Utah
	Nebraska	New Jersey	South Carolina	Nevada
	Kansas	New York	Virginia	Wyoming
	North Dakota	Pennsylvania	West Virginia	Alaska
	Minnesota		Alabama	California
	South Dakota		Kentucky	Hawaii
	Missouri		Mississippi	Oregon
			Tennessee	Washington
			Arkansas	
			Louisiana	
			Oklahoma	
			Texas	

Source: US Census Bureau, 2021.

#### Population data and mortality data

The mid-year population data are compiled by the US Census Bureau for the period 2010–2020 for all US states. The data are available from age 0 to age 85+ in the single-age interval. The PCLM has been performed on the 85+ category for all states to obtain a prudent estimation of populations aged 85–110 (Rizzi, Gampe, and Eilers 2015; Rizzi et al. 2016).

The mortality at the US national level is calculated as the weighted sum of states' age-specific mortality and population composition at each age, based on smoothed counts. The life table statistics based on the weighted sum mortality rates show no significant deviation from the life table statistics calculated from the US mortality database (close to zero).

We attempted to incorporate data from 2020–2021. In our study we used state-level mortality data from the USMD, which is available only until 2020. We performed a similar analysis for 2021 data from the number of deaths and the mid-year population count extracted from the CDC Wonder database. However, these results should be taken with caution since the mortality data preparation process is different from the standard

USMD and HMD procedures. We have taken the CDC Wonder data for both population and number of deaths and smoothed it with a PCLM model to calculate a mortality age schedule (Rizzi et al. 2015). This is in contrast to USMD and HMD, which extrapolate old-age mortality using a Kannisto model among other data adjustment procedures (see method protocol for HMD by Wilmoth et al. 2021).

Many death counts are omitted and not shown on the raw data file at the state level within the CDC database, on which our calculation is based. The data are omitted when the death count is smaller than 16 or there is no certainty that this is the accurate number. The changes in e-dagger and life expectancy derived from CDC Wonder therefore are noticeably different than the HMD estimates at the national level. CDC Wonder shows a notable increase in life span variation (0.80 years for females and 0.82 years for males in terms of life disparity), along with a decrease in life expectancy (0.33 years for females and 0.56 years for males); HMD reports changes in life span disparity of 0.56 for males and 0.60 for females, with life expectancy showing a decline of 0.50 years for females and 0.72 years for males during the period 2020–2021. Because of these concerns regarding validity, we have chosen to present only national-level data from the HMD for the period 2019–2020.

## Appendix 2 – Methodological supplements

### Disaggregating the age-specific mortality rate

The decomposition method is an adaptation of the method used by Torres, Canudas-Romo, and Oeppen (2019). Let  $D(a, t)$  and  $P(a, t)$  be the national total number of deaths and mid-year population for age  $a$  at time  $t$ , respectively. The observed age-specific death rate, denoted  $m(a, t)$ , can be written as the ratio of  $D(a, t)$  over  $P(a, t)$  but also as a combination of multiple subnational mortality and composition levels as

$$m(a, t) = \frac{D(a, t)}{P(a, t)} = \frac{\sum_i D(a, t, i)}{P(a, t)} = \sum_i \mu(a, t, i) c(a, t, i),$$

where  $i$  denotes the subnational-specific education level, here representing subnational education levels. For the expression above,  $\mu(a, t, i) = \frac{D(a, t, i)}{P(a, t, i)}$  and  $c(a, t, i) = \frac{P(a, t, i)}{P(a, t)}$  are the age-specific death rate and population composition at age  $a$  for subnational level  $i$ , respectively.

Let a dot on top of a variable denote the derivative with respect to time. The derivative of the population composition, or  $\dot{c}(a, t, i)$ , can be rewritten as:

$$\dot{c}(a, t, i) = c(a, t, i)[r(a, t, i) - r(a, t)], \quad (\text{A-1})$$

where  $r(a, t, i) = \frac{\dot{P}(a, t, i)}{P(a, t, i)}$  and  $r(a, t) = \frac{\dot{P}(a, t)}{P(a, t)}$  represent the age-specific growth rate of the subpopulation  $i$  and the national population, respectively.

### Decomposition of life disparity

The life disparity  $e^\dagger$  at birth can be expressed mathematically as:

$$e^\dagger(0, t) = \int_0^\omega e(x, t)f(x, t)dx = \int_0^\omega \ell(x, t)H(x, t)dx, \quad (\text{A-2})$$

where  $e(x, t)$  stands for the remaining life expectancy,  $f(x, t)$  stands for the life table death distribution,  $\ell(x, t)$  corresponds to the life table survival function, and  $H(x, t)$  represents the cumulative hazard, or  $H(x, t) = \int_0^x \mu(a, t)da = -\log(\ell(x, t))$ , all at age  $x$  at time  $t$ .

The decomposition with respect to time  $t$  of the life disparity at birth is written as:

$$\dot{e}^\dagger(0, t) = \int_0^\omega -\ell(x, t)H(x, t)\dot{H}(x, t) + \ell(x, t)\dot{H}(x, t)dx \quad (\text{A-3})$$

$$= \int_0^\omega \ell(x, t)[1 - H(x, t)] \int_0^x \dot{\mu}(a, t)dadx. \quad (\text{A-4})$$

Reversing the integral gives the following equation:

$$= \int_0^\omega \dot{\mu}(a, t) \int_a^\omega \ell(x, t)(1 + \log(\ell(x, t))) dx da. \quad (\text{A-5})$$

Equation (A-3) can also be found in Aburto et al. (2019). Based on the works of Wagner (2010) and Aburto et al. (2019), and the results section of Zhang and Vaupel (2009), Equation (A-5) can be further reduced with the changing of the sign for the equation

$$\dot{e}^\dagger = - \int_0^\omega \dot{\mu}(a, t)\ell(a, t) \int_a^\omega \left[ \frac{\ell(x, t)}{\ell(a, t)} (-1 - \log(\ell(x, t))) \right] dx da \quad (\text{A-6})$$

$$= - \int_0^\omega \dot{\mu}(a, t)\ell(a, t) \int_a^\omega \frac{\ell(x, t)}{\ell(a, t)} \left( -\log(\ell(a, t)) - 1 - \log\left(\frac{\ell(x, t)}{\ell(a, t)}\right) \right) dx da \quad (\text{A-7})$$

$$= - \int_0^\omega \dot{\mu}(a, t)\ell(a, t)[e^\dagger(a, t) + e(a, t)(H(a, t) - 1)] da, \quad (\text{A-8})$$

where, as shown in Aburto et al. (2019), the life disparity beyond age  $x$  is defined as  $e^\dagger(a, t) = -\frac{1}{\ell(a, t)} \int_a^\omega \ell(x, t) \log\left(\frac{\ell(x, t)}{\ell(a, t)}\right) dx$ .

Equation (A-8) is analogous to variance decomposition, where the variance of a variable can be decomposed into two components: the between-group component and the within-group component. The between-group component (the term  $-\int_0^\omega \dot{\mu}(a, t)\ell(a, t)e(a, t)((H(a, t) - 1))da$ ) measures the changes weighted by the average life span, which is the remaining life expectancy  $e(a, t)$ . The within-group component (the term  $-\int_0^\omega \dot{\mu}(a, t)\ell(a, t)e^\dagger(a, t) da$ ) measures changes that can be attributed to the variability in age at death, which is characterized by  $e^\dagger(a, t)$ . We used Equation (A-8) in the discrete approximation to get better estimates of the threshold age and the corresponding premature mortality and old-age survival contributions.

### Alternative illustration of decomposition

Equations (3) and (4), presented in the methods section in the main text, can be expressed in the form of the rate of mortality improvement ( $\rho(x, t, i) = -\frac{\dot{\mu}(x, t, i)}{\mu(x, t, i)}$ ) and the differences between the subnational and national age-specific growth rate ( $\Delta r(x, t, i) = r(x, t, i) - r(x, t)$ ). Take life disparity in the methods section as an example; the decomposition can be written as:

$$\dot{e}^\dagger(0, t) = -\int_0^\omega \sum_i [\dot{\mu}(x, t, i) + \mu(x, t, i)[r(x, t, i) - r(x, t)]]c(x, t, i) W(x, t) dx,$$

with  $W(x, t) = \ell(x, t)[e^\dagger(x, t) + e(x, t)(H(x, t) - 1)]$ . Our method shows that the changes in life disparity on the national level depend on not only mortality and population growth relative to the national level but also the share of the subpopulation (the component  $c(x, t, i)$ ).

This can also be rewritten as:

$$\begin{aligned} \dot{e}^\dagger(0, t) &= \int_0^\omega \sum_i \rho(x, t, i)\mu(x, t, i)c(x, t, i) W(x, t) \\ &\quad - \sum_i \Delta r(x, t, i)\mu(x, t, i) c(x, t, i)W(x, t)dx, \end{aligned}$$

where the top component represents the mortality component and the bottom component represents the composition component. This equation above further elaborates the relationship of composition effect offset mortality effect, mentioned in the methods section in the main text. Meanwhile, in the case of life disparity, it's important to note that the weight function  $W(x, t) = \ell(x, t)[e^{\dagger}(x, t) + e(x, t)(H(x, t) - 1)]$  changes from negative to positive after the threshold age. For life expectancy, no such threshold age exists:

$$\dot{e}(0, t) = \int_0^{\omega} \sum_i \rho(x, t, i) \mu(x, t, i) c(x, t, i) T(x, t) - \sum_i \Delta r(x, t, i) \mu(x, t, i) c(x, t, i) T(x, t) dx,$$

with the notation  $T(x, t) = \ell(x, t)e(x, t)$  referring to the life table person-years lived after age  $x$  at time  $t$ .

### Discrete approximation

Let the dot on top of a variable represents the derivative with respect to time, with the assumption of the constant change over a certain time interval. The discrete approximation for a derivative denoted  $\dot{v}(x, t + \frac{h}{2}, i)$  is shown as:

$$\dot{v}(x, t + \frac{h}{2}, i) \approx \frac{\ln\left[\frac{v(x, t+h, i)}{v(x, t, i)}\right]}{h} v(x, t + \frac{h}{2}, i).$$

At the same time, the midpoint of a variable across time,  $v(x, t + \frac{h}{2}, i)$  is shown as:

$$v(x, t + \frac{h}{2}, i) \approx [v(x, t, i)v(x, t + h, i)]^{\frac{1}{2}}.$$

This procedure is consistent with Vaupel and Canudas-Romo (2003).

### Appendix 3 – Results supplements

**Table A-1: Contributions to changes from mortality and composition components in life disparity for US males by region, 2010–2020**

Region	Midwest	Northeast	South	West	Total
2010–2019					
Contributions to change	0.09	0.08	0.13	0.08	0.38
Mortality component	0.08	0.06	0.17	0.07	0.38
Composition component	0.02	0.02	–0.04	0.01	0.00
Life disparity is 12.09 years in 2010 and 12.46 years in 2019 for males at the US national level					
2019–2020					
Contributions to change	0.04	0.02	0.17	0.11	0.34
Mortality component	0.04	0.02	0.17	0.11	0.34
Composition component	0.00	0.00	0.00	0.00	0.00
Life disparity is 12.46 years in 2019 to 12.80 years in 2020 for males at the US national level					

Notes: Calculations based on data from USMD (2023) and NCHS (2023). Small discrepancies are the result of discrete estimation procedures and rounding.

**Table A-2: Contributions to changes from mortality and composition components in life expectancy for US males by region, 2010–2020**

Region	Midwest	Northeast	South	West	Total
2010–2019					
Contributions to change	0.10	0.18	–0.03	–0.04	0.21
Mortality component	–0.03	0.06	0.11	0.05	0.19
Composition component	0.13	0.11	–0.14	–0.08	0.01
Life expectancy is 76.20 years in 2010 and 76.41 years in 2019 for males at the US national level					
2019–2020					
Contributions to change	–0.43	–0.37	–0.85	–0.45	–2.09
Mortality component	–0.44	–0.38	–0.83	–0.44	–2.09
Composition component	0.01	0.01	–0.02	–0.01	0.00
Life expectancy is 76.41 years in 2019 and 74.33 years in 2020 for males at the US national level					

Notes: Calculations based on data from USMD (2023) and NCHS (2023). Small discrepancies are the result of discrete estimation procedures and rounding.

**Table A-3: Contributions to changes from mortality and composition components in life disparity for US females by region, 2010–2020**

Region	Midwest	Northeast	South	West	Total
2010–2019					
Contributions to change	0.04	0.01	0.04	–0.01	0.09
Mortality component	0.03	0.02	0.04	0.00	0.09
Composition component	0.01	–0.01	0.00	–0.01	0.00
Life disparity is 10.79 years in 2010 and 10.87 years in 2019 for females at the US national level					
2019–2020					
Contributions to change	0.01	–0.02	0.11	0.06	0.16
Mortality component	0.00	–0.02	0.11	0.06	0.16
Composition component	0.01	0.00	–0.01	0.00	0.00
Life disparity is 10.87 years in 2019 to 11.02 years in 2020 for females at the US national level					

Notes: Calculations based on data from USMD (2023) and NCHS (2023). Small discrepancies are the result of discrete estimation procedures and rounding.

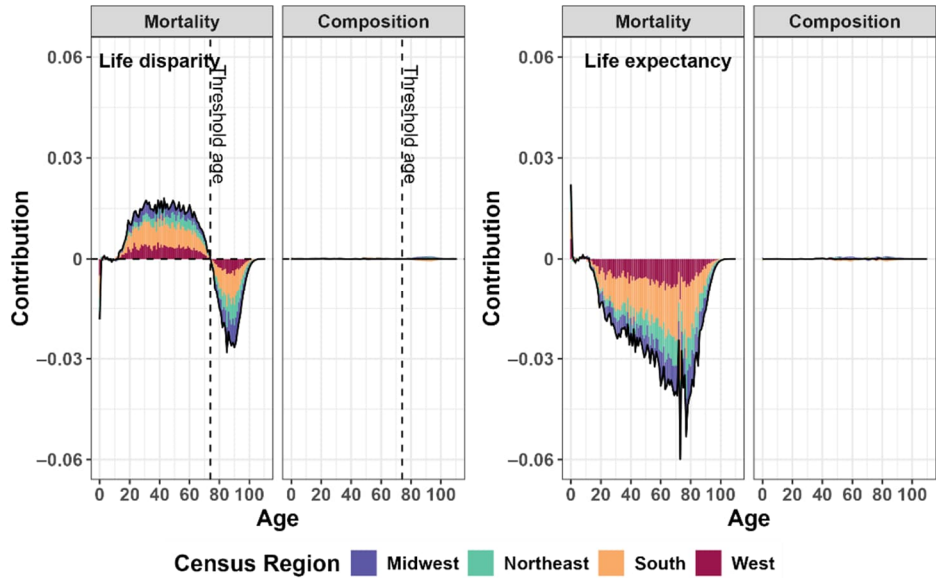
**Table A-4: Contributions to changes from mortality and composition components in life expectancy for US females by region, 2010–2020**

Region	Midwest	Northeast	South	West	Total
2010–2019					
Contributions to change	0.12	0.22	0.02	0.03	0.38
Mortality component	–0.01	0.11	0.16	0.12	0.37
Composition component	0.13	0.11	–0.14	–0.10	0.00
Life expectancy is 81.05 years in 2010 and 81.43 years in 2019 for females at the US national level					
2019–2020					
Contributions to change	–0.33	–0.28	–0.67	–0.30	–1.57
Mortality component	–0.34	–0.29	–0.65	–0.29	–1.57
Composition component	0.01	0.02	–0.02	–0.01	0.00
Life expectancy is 81.43 years in 2019 and 79.87 years in 2020 for females at the US national level					

Notes: Calculations based on data from USMD (2023) and NCHS (2023). Small discrepancies are the result of discrete estimation procedures.

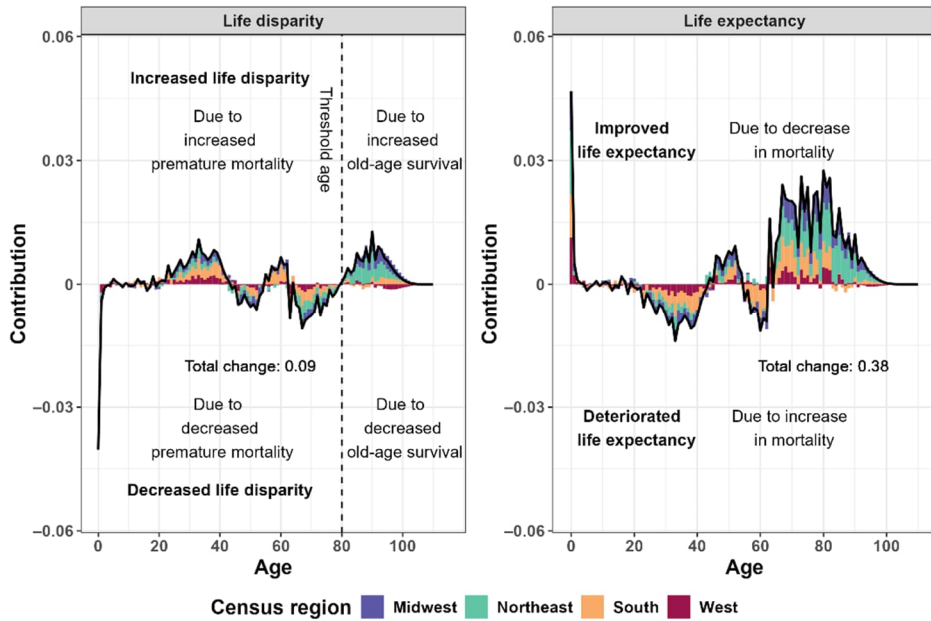


**Figure A-1: Decomposition to changes in life disparity and life expectancy into mortality and composition components as well as age and region contributions, US males 2019–2020**



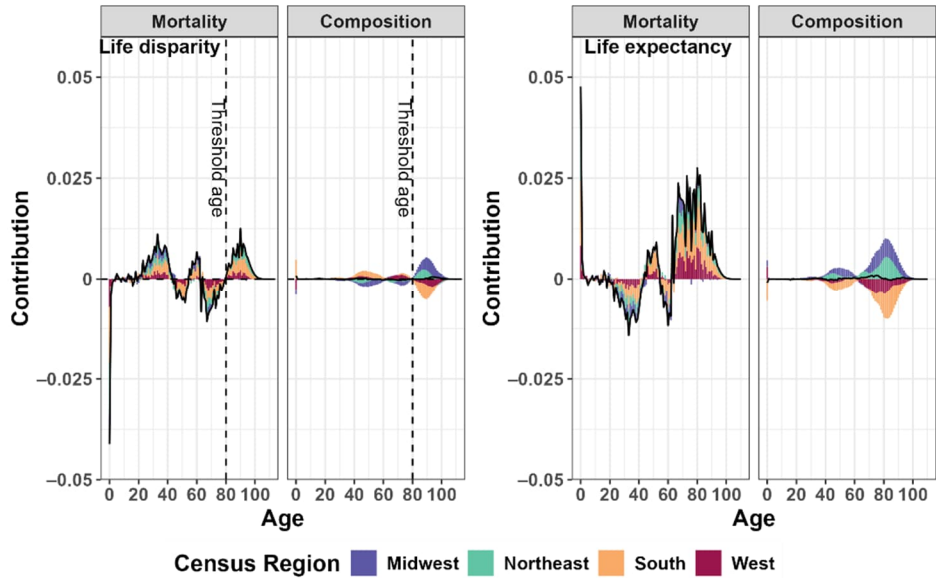
Notes: Dark solid lines represent total contribution at each age.  
Source: Calculations based on data from USMD (2023) and NCHS (2023).

**Figure A-2: Age and region contributions to changes in life disparity and life expectancy, US females 2010–2019**



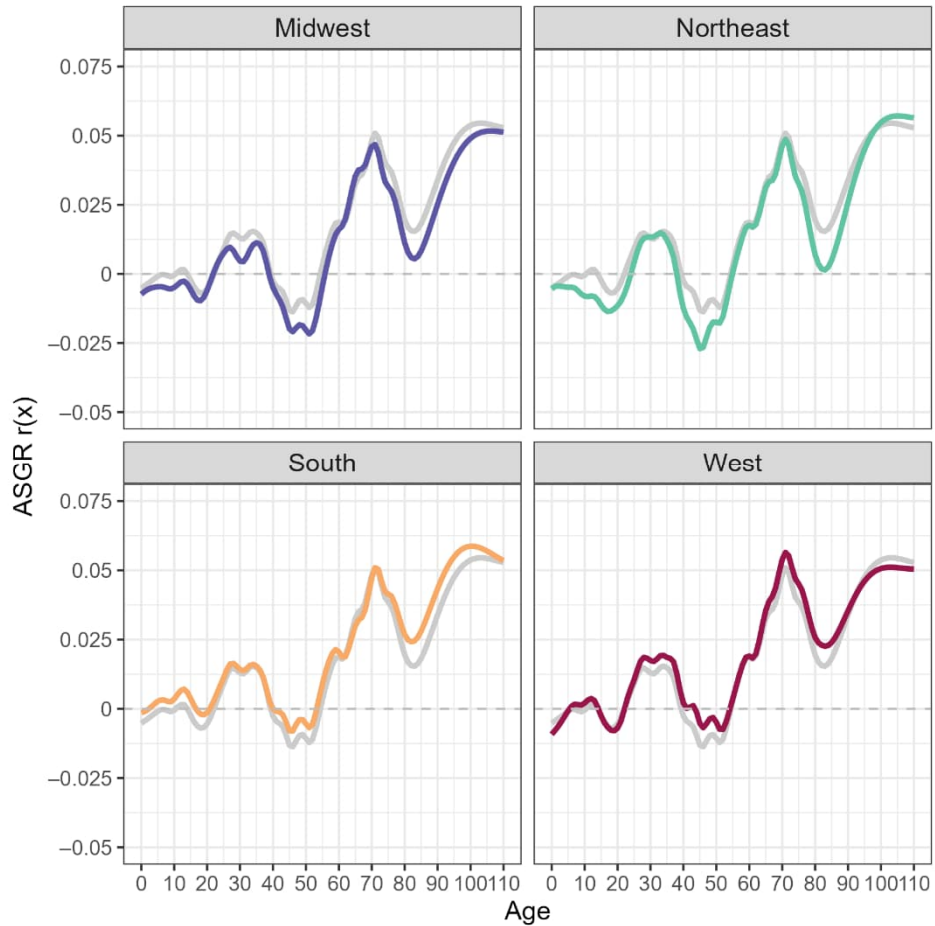
Notes: Dark solid lines represent total contribution at each age.  
 Source: Calculations based on data from USMD (2023) and NCHS (2023).

**Figure A-3: Decomposition of changes in life disparity and life span disparity into contributions from mortality and composition component, as well as age and region, US females 2010–2019**



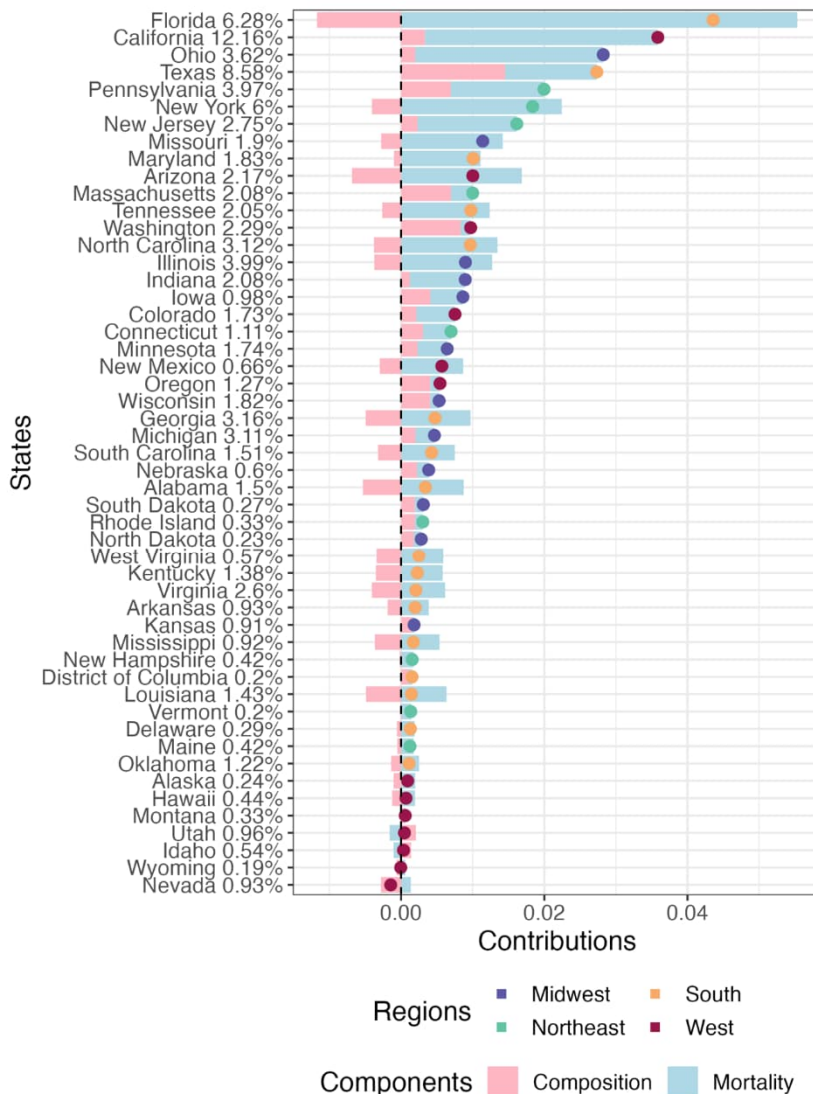
Notes: Dark solid lines represent total contribution from each component at each age.  
 Source: Calculations based on data from USMD (2023) and NCHS (2023).

**Figure A-4: Trends in age-specific growth rate (ASGR) between the US national level (gray line) and census divisions (colored line), US males 2010–2019**



Source: Calculations based on data from NCHS (2023).

**Figure A-5: State contributions to changes in national life span variation with components of mortality and composition for US males, 2010–2019**



Notes: The y-axis is arranged by highest to lowest total contributions by US states and the District of Columbia. The dots mark the total contributions for each state while the colored bars represent the two components aggregating to the total contributions. Dot color corresponds to census region.

Source: Authors' calculations based on USMD (2023).