Further applications and clarification of the multistate life table decomposition method

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Abstract

Background: A recently proposed method allows for the decomposition of differentials in multistate life tables into contributions from initial state distributions and each transition between states. An extension of this approach further enables decomposition by population subgroups defined by time-fixed characteristics (e.g., sex or education at older ages). However, existing methods face important limitations. First, when the state space includes an absorbing state, typically mortality, the contribution of transitions to this state cannot be directly decomposed. Second, subgroup decomposition is restricted to time-invariant characteristics, limiting its application to contexts where subgroups vary over time (e.g., morbidity or marital status).

Objectives: This paper extends the current decomposition framework to broaden its applicability within the multiple multistate modeling framework. Specifically, our approach allows for the decomposition of mortality effects and accommodates population subgroups defined by both time-invariant and time-varying characteristics.

Data and Application: To demonstrate the added value of our method, we replicate and extend previous analyses using data from the Health and Retirement Study. We present three applications: (1) a three-state life table with mortality, (2) a three-state model with education-based subgroups, and (3) a multiple multistate model incorporating morbidity and disability.

Conclusion: The extended decomposition method provides researchers with a more comprehensive tool to disentangle the relative contributions of initial population structure and transition dynamics to differences in state-specific life expectancies. By explicitly incorporating mortality and allowing for time-varying subgroup characteristics, the method enhances interpretability and flexibility. This facilitates more nuanced analyses, both within health research and in other fields, and offers a clearer link between multistate decompositions and traditional Sullivan-based perspectives.

Keywords: Multistate life table, Decomposition, Formal demography, Population composition, mortality

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Introduction

Understanding the sources of variation in life expectancy and related measures is a central concern in demography and population health. Decomposition methods provide a powerful means to disentangle these differences, revealing how population structure and transition dynamics contribute to disparities in outcomes such as healthy life expectancy.

Two main approaches are used to estimate healthy life expectancy: Sullivan's method and the multistate life table. Sullivan's method decomposes differences in healthy life expectancy into components attributable to mortality and health prevalence (Andreev et al., 2002; Luy et al., 2019; Nusselder & Looman, 2004; Sauerberg & Canudas-Romo, 2022). In contrast, multistate life tables explicitly model transitions between health or functional states, capturing the full dynamics of population change. The decomposition of a multistate life table thus reflects both the initial distribution of individuals across states and the age-specific transition rates between them (Shen et al., 2023).

Existing decomposition methods for multistate life expectancy, however, have important limitations. Shen et al. (2023) fail to explicitly disentangle the effect of transitions to mortality in their decomposition method, despite mortality often being a major driver of population differences. Moreover, existing method (Shen et al., 2025) only allow subgroup decompositions based on characteristics that are fixed at baseline, such as sex or education. This limits their applicability in contexts where subgroup membership may change during the life course—for example, transitions in health, marital status, or other time-varying attributes.

In this paper, we extend current decomposition methods within the multiple multistate method (MMM) framework (Shen et al., 2024). Our approach explicitly incorporates mortality into the decomposition, enabling direct estimation of its contribution alongside other state transitions. It also accommodates both time-fixed and time-varying subgroup characteristics, enhancing flexibility and relevance for life course analyses. We illustrate the method using data from the Health and Retirement Study, through three applications: (1) a three-state model with mortality as the absorbing state, (2) a three-state model stratified by educational attainment, and (3) a multiple multistate model combining morbidity and disability. Together, these examples demonstrate how our extended decomposition method clarifies the respective roles of population structure, transition dynamics, and mortality in shaping differences in health and longevity.

Method

In Shen et al. (2023), the multistate temporary life expectancy, ${}_{\beta-\alpha}\mathbf{e}_{\alpha}$, is expressed in terms of the survival matrix, $\mathbf{l}_x$, as

$$ {}_{\beta-\alpha}\mathbf{e}_{\alpha} = \frac{\mathbf{l}_{\alpha}}{2} + \sum_{x=\alpha+1}^{\beta-1} \mathbf{l}_x + \frac{\mathbf{l}_{\beta}}{2}. \tag{1} $$

This survival matrix, $\mathbf{l}_x$, can be calculated based on the transition probabilities as

$$ \mathbf{l}_x = \mathbf{l}_{x-1}\mathbf{P}_{x-1} = \mathbf{l}_{\alpha} \prod_{k=\alpha}^{x-1} \mathbf{P}_k \,, \tag{2} $$

where $\mathbf{P}_x$ is the matrix of transition probabilities at a given age and $\mathbf{l}_{\alpha}$ is a diagonal matrix of initial proportion of people at each state at the *radix* age of the multistate life table (the product operator $\prod_{k=\alpha}^{x-1} \mathbf{P}_k$ invokes matrix products). Substituting Eq. (2) into Eq. (1), ${}_{\beta-\alpha}\mathbf{e}_{\alpha}$ essentially consists of $\mathbf{l}_{\alpha}$ and $\mathbf{P}_x$. To be clear, $\mathbf{l}_{\alpha} = \begin{bmatrix} l_{\alpha}^1 & 0 & \cdots & 0 \\ 0 & l_{\alpha}^2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & l_{\alpha}^n \end{bmatrix}$, where l_{α}^i are the initial proportion of people at state i at the *radix* age ($\sum_{i=1}^{n} l_{\alpha}^i = 1$), and $\mathbf{P}_x = \begin{bmatrix} p_x^{11} & p_x^{12} & \cdots & p_x^{1n} \\ p_x^{21} & p_x^{22} & \cdots & p_x^{2n} \\ \vdots & \vdots & \ddots & \vdots \\ p_x^{n1} & p_x^{n2} & \cdots & p_x^{nn} \end{bmatrix}$, where p_x^{ij} represents the transition probability from state i to j between ages x and $x+1$.

With derivation detailed in the original paper, the differential of the multistate temporary life expectancy, with a dot on top of a function to denote the derivative either with respect to time or between population comparison, can be calculated as the derivative for each of the additive components

$$ {}_{\beta-\alpha}\dot{\mathbf{e}}_{\alpha} = \dot{\mathbf{l}}_{\alpha} \cdot {}_{\beta-\alpha}\mathbb{e}_{\alpha} + \sum_{x=\alpha}^{\beta-1} \mathbf{l}_x \dot{\mathbf{P}}_x \left(\frac{\mathbb{I}}{2} + {}_{\beta-x-1}\mathbb{e}_{x+1} \right), \tag{3} $$

where $\mathbb{I}$ is an identity matrix and ${}_{\beta-x}\mathbb{e}_{x}$ is a weight function (Shen et al. 2023). Therefore, the differential in multistate life expectancy has two components: the proportion resulting from differences in initial state distribution $\dot{\mathbf{l}}_\alpha \cdot {}_{\beta-\alpha}\mathbb{e}_\alpha$, and the proportion resulting from differences in transitions probabilities at each age $\mathbf{l}_x\dot{\mathbf{P}}_x \left(\frac{\mathbb{I}}{2} + {}_{\beta-x-1}\mathbb{e}_{x+1}\right)$. Another recent paper (Shen et al., 2025) follows this logic and extends Eq. (3) with subpopulations

$$ {}_{\beta-\alpha}\dot{\mathbf{e}}_\alpha = \sum_k \dot{c}_\alpha^k \cdot {}_{\beta-\alpha}\mathbf{e}_\alpha^k + c_\alpha^k \dot{\mathbf{l}}_\alpha^k \cdot {}_{\beta-\alpha}\mathbb{e}_\alpha^k + c_\alpha^k \sum_{x=\alpha}^{\beta-1} \mathbf{l}_x^k \dot{\mathbf{P}}_x^k \left(\frac{\mathbb{I}}{2} + {}_{\beta-x-1}\mathbb{e}_{x+1}^k\right), \tag{4} $$

where k represent the sub-population and c_α^k is the population proportion of the subnational population at *radix* age. The restriction is that the subgroups are exclusive, and individuals stay in the same subgroups from age α to β.

To this point, we merely reiterate the existing papers. The main purpose of this paper is to allow the decomposition of effects from the different characteristics of the population to the overall differential in multistate life expectancy. In other word, we would decompose the effect from both components in Eq. (3) by these characteristics.

In this paragraph, we discuss the first component, $\dot{\mathbf{l}}_\alpha \cdot {}_{\beta-\alpha}\mathbb{e}_\alpha$. If we consider subgroups k and states i in $\mathbf{l}_\alpha^k$ in Eq. (4) as two characteristics, Eq. (4) provides an initial attempt to separate the subgroup effect in the first component into the effect from subgroups k, $\dot{c}_\alpha^k \cdot {}_{\beta-\alpha}\mathbf{e}_\alpha^k = \dot{c}_\alpha^k \mathbf{l}_\alpha^k \cdot {}_{\beta-\alpha}\mathbb{e}_\alpha^k$, and state distribution, $c_\alpha^k \dot{\mathbf{l}}_\alpha^k \cdot {}_{\beta-\alpha}\mathbb{e}_\alpha^k$. According to the matric calculus (Caswell, 2008), the derivative of a matrix is the derivative of each element in the matrix. Writing out each element, we have $\dot{l}_\alpha^i = \dot{c}_\alpha^k l_\alpha^{k,i} + c_\alpha^k \dot{l}_\alpha^{k,i}$. The procedure can be formally interpreted as a multiplicative decomposition of the joint frequency distribution. In the two-dimensional case, l_α^i is expressed as the product of a marginal distribution, c_α^k, and an interaction term conditional on this margin, $l_\alpha^{k,i}$. Alternatively, the decomposition of a 2-dimension joint frequency table can be specified using both marginal distributions and an interaction term defined with respect to these margins.

When the number of dimensions increases, the structure of the decomposition becomes more complex due to the presence of higher-order interactions. In this context, researchers may specify which marginal distributions and interaction terms to decompose explicitly, with the remaining effects absorbed into a composite interaction term. Furthermore, if we wish to eliminate the explicit interaction term, we could also redistribute its effect into the decomposed components proportionally or uniformly. The choice of decomposition strategy should be informed by the research question, theoretical considerations, and the desired level of parsimony. In practice, it is advisable to align the number of decomposed components with the substantive characteristics of interest. This facilitates a more interpretable representation of the data structure, ideally involving only a single interaction term, while absorbing residual variation into the main effects.

For the calculation of multistate life expectancy, all the elements would be arranged diagonally into one expended matrix of $\dot{\mathbf{l}}_\alpha$ and it is expressed as

$$\dot{\mathbf{l}}_\alpha = \dot{\mathbf{l}}_\alpha^{(1)}\mathbf{l}_\alpha^{(2)} \dots \mathbf{l}_\alpha^{(n)} + \mathbf{l}_\alpha^{(1)}\dot{\mathbf{l}}_\alpha^{(2)} \dots \mathbf{l}_\alpha^{(n)} + \dots + \mathbf{l}_\alpha^{(1)}\mathbf{l}_\alpha^{(2)} \dots \dot{\mathbf{l}}_\alpha^{(n)}, \tag{5}$$

with (n) characteristics explaining the effect from initial population distribution. Substituting Eq. (5) into Eq. (3), we obtain the effect of each component to the differential of the overall multistate temporary life expectancy, ${}_{\beta-\alpha}\dot{\mathbf{e}}_\alpha$.

Similarly, we also decompose the effect in $\mathbf{l}_x\dot{\mathbf{P}}_x\left(\frac{\mathbb{I}}{2} + {}_{\beta-x-1}\mathbb{e}_{x+1}\right)$ into different components of characteristic. Instead of decomposing the matrix of $\dot{\mathbf{P}}_x$, we focus on the derivative of each element in the matrix, $\dot{p}_x^{gh}$, the effect from a specific transition probability from origin state g to destination state h at age x. The multiple multistate method (MMM) is designed to separate the coevolution between different time-varying variables into several interconnected multistate models, thereby allowing greater modeling flexibility (Shen et al., 2024). The authors show that a *recursive MMM* can replicate the results of a complex multistate model that includes all possible combinations of the time-varying variables in its state space. A key advantage of the MMM is that it allows us to ignore some interactions between variables while still producing expectancy estimates that are very close to those obtained from the full model. In this paper, we apply this *reduced-form* MMM approach to compute expectancies and perform the decomposition analysis. The decomposition procedure for a *recursive* MMM is conceptually comparable to that of a *reduced-form* MMM, but it involves additional conditioning on the outcome states of the other multistate models. As the number of characteristics increases, the number of conditioning variables also grows. To keep the analysis tractable and the results more interpretable, we therefore use the *reduced-form* MMM rather than the fully recursive version.

In the MMM (Shen et al., 2024), the origin state g is kept the same with all possible combinations of the time-varying variables. The destination state h, by contrast, is factorized into n components corresponding to each variable. For instance, in an MMM with two variables, if h is A_1B_1, so $h^{(1)} = A_1$ and $h^{(2)} = B_1$. The transition probability from g to h can be expressed as the product of the transition probabilities from g to each component of h: $p_x^{gh} = p_x^{gh^{(1)}} p_x^{gh^{(2)}}$. More generally, for (n) characteristics, the differential of the transition probability can be written as

$$\dot{p}_x^{gh} = \dot{p}_x^{gh^{(1)}} p_x^{gh^{(2)}} \dots p_x^{gh^{(n)}} + p_x^{gh^{(1)}} \dot{p}_x^{gh^{(2)}} \dots p_x^{gh^{(n)}} + \dots + p_x^{gh^{(1)}} p_x^{gh^{(2)}} \dots \dot{p}_x^{gh^{(n)}}, \tag{6}$$

where each term represents the marginal contribution of a single characteristic to the total change in the transition probability.

If death is included as a destination, h cannot be factorized in the same way and is instead assigned to one of the variables, with the remaining variables conditioned on survival in the MMM method. Alternatively, we may choose to condition all variables on survival, which introduces an additional survival component into the decomposition in Equation (6). This allows us to explicitly account for survival as a separate factor alongside the other time-varying variables.

According to the relationship in Shen et al. (2023), the differential of each transition probability, $\dot{p}_x^{gh}$, has an effect on the differential in life expectancy in state j,

$$_{gh}\lambda_x^{\cdot j} = \sum_{i=1}^{n} \frac{l_x^{ig} \dot{p}_x^{gj}}{2} + l_x^{ig} \dot{p}_x^{gh} \; _{\beta-x-1}\varepsilon_{x+1}^{hj}. \tag{7}$$

Therefore, we can substitute Eq. (6) in Eq. (7) to compute the contribution of each component, (n), on the differential of the multistate temporary life expectancy, $_{\beta-\alpha}\dot{\mathbf{e}}_\alpha$. In sum, we decompose the effect from both components in Eq. (3) by characteristics with the reconstruction of $\dot{\mathbf{l}}_\alpha$ in Eq. (5) and $\dot{p}_x^{gh}$ in Eq. (6). We further demonstrate how these equations are operationalized in the following section.

Applications

We replicate multistate life tables from three previously published studies to illustrate the application of our decomposition method. In the first application, we focus on demonstrating how to separate the effect of mortality from each transition probability. The second application shows how the decomposition can be performed when one of the characteristics is time-invariant. Finally, the third application illustrates how the method can be applied when two characteristics are time-varying.

Example 1: Three-state model with mortality

In example 1, we examine the sex differential in disability-free (HLE) and disabled life expectancy (ULE) between ages 55 and 105 in the United States based on the setup in Shen et al. (2023). This differential is decomposed into contributions from initial population health structure and from differences in transition probabilities between health states. Using data from the Health and Retirement Study (2021), disability is defined based on difficulty with Activities of Daily Living (ADLs). The state space consists of two transient states (disability-free, "H", and disabled, "U",) and one absorbing state (death, "D") as shown in Figure 1, Panel a, and the transition probabilities from time t to $t+1$ are specified in Table 1a. The initial population health remains the same because it has no morality in $\mathbf{l}_\alpha$, so we only focus on the transition probabilities in this example.

[Figure 1 about here]

We modify the state space in to Figure 1, Panel b, where there are two systems of transition. The first part (i) is the survival probability by health state, and the second part (ii) is the transition probabilities from time t to $t+1$ between disability-free and disabled conditioned on survival of that health state in Table 1b. For example, the probability of remaining disability-free and alive is $p_x^{hh|s} = \frac{p_x^{hh}}{1-p_x^{hd}} = \frac{p_x^{hh}}{p_x^{hh}+p_x^{hu}}$, and thus $p_x^{hh|s} + p_x^{hu|s} = 1$. In Shen et al. (2023), effects of transitions to mortality, p_x^{hd} and p_x^{ud}, on HLE and ULE are embedded within the other transitions hence not shown in Figure 2, Panel a. However, in this paper, we explicitly disentangle the effects of transitions to mortality by conditioning health transitions on survival. Therefore, our transition probability matrix and the original approach has this relationship, $\mathbf{P}_x = \begin{bmatrix} p_x^{hh} & p_x^{hu} \\ p_x^{uh} & p_x^{uu} \end{bmatrix} = \begin{bmatrix} p_x^{hh|s} \cdot (1-p_x^{hd}) & p_x^{hu|s} \cdot (1-p_x^{hd}) \\ p_x^{uh|s} \cdot (1-p_x^{hd}) & p_x^{uu|s} \cdot (1-p_x^{hd}) \end{bmatrix}$.

[Table 1 about here]

Figure 2 presents the comparison the between original method (panel a) and the MMM method (panel b). The most striking difference lies in the terms p^{hd} and p^{ud} in panel b. These do not represent the effect of mortality directly but rather its complement—the effect of survival. The sex gap in p^{hd} and p^{ud} are contributing to a higher sex gap in both HLE and ULE reflecting the fact that women, whether healthy or unhealthy, have higher survival rates than men at every age. This survival advantage contributes to a larger sex gap in both HLE and ULE: survival of healthy women (p^{hd}), contributes more to the gap in HLE, while survival of unhealthy women (p^{ud}) contributes more to the gap in ULE, particularly at older ages (around 80 to 90).

[Figure 2 about here]

In the original approach, mortality is integrated into the health transition process itself: individuals transition between healthy and unhealthy states, and these transitions inherently determine their survival. By contrast, our approach first conditions on survival, and then examines transitions between health states only among those who remain alive. Survival is hence treated as given, and the analysis focuses on how individuals move between healthy and unhealthy states over time. This perspective aligns more closely with the logic of Sullivan's method and its decomposition (Andreev et al., 2002; Nusselder & Looman, 2004; Sullivan, 1971), in which health expectancies are calculated conditional on being alive (i.e., person-years lived) at each age. Neither approach is inherently superior; rather, they offer different ways of conceptualizing the relationship between health and mortality. However, conditioning on survival provides a more intuitive interpretation from the decomposition standpoint and greater flexibility, particularly when the focus of the model extends beyond health to other subpopulations, such as educational groups in example 2 and morbidity groups in example 3.

Another noticeable difference is that the p^{hh} becomes negative after conditioning on survival. In the original method, women had a higher probability of remaining healthy partly because they were more likely to survive. However, when we condition on survival—focusing only on those who remain alive—the relative advantage shifts. Among survivors, a smaller proportion of women stay healthy compared to men, leading p^{hh} to be negative in Panel b. This illustrates how separating survival from health transitions provides a more nuanced picture of what drives differences in healthy and unhealthy life expectancy between men and women.

A further note on p^{hu} and p^{uu} helps explain why these transitions contribute positively to HLE. As shown in Eq. (7), the contribution to HLE or ULE depends on the destination state j at the end of the equation, not on the superscript "u" in p^{hu} or p^{uu} as it is only acting as a passage for later ages. This means that their contribution is determined by the last transition, not the intermediary state. Because women have higher probabilities of p^{hu} or p^{uu} than men, part of their higher HLE is due to going through these transitions at earlier ages. In Panel b, the contribution of p^{uu} on HLE is noticeably smaller compared to Panel a. This is because, in the original approach, the positive effect largely came from unhealthy women being more likely to survive, allowing them to continue contributing to HLE at later ages. Once we condition on survival, that survival advantage is already accounted for, leaving a smaller effect from p^{uu}.

Example 2: Three-state model with education subgroups

In this example, we reformulate the decomposition of disability-free life expectancy (HLE) by educational attainment presented in Shen et al. (2025) within the framework of the Multiple Multistate Method (MMM). Shen et al. analyzed data from the U.S. Health and Retirement Study (2000–2020), comparing ten-year birth cohorts to assess how rising educational attainment influenced life expectancies among older Americans. Their original approach expressed population-level life expectancies as a weighted sum of four education-specific life tables, thereby separating the effects of (1) changes in the educational composition of the population, (2) differences in health status at initial ages across education groups, and (3) differences in health and mortality transitions at older ages. This method relies on a key assumption that that no individual changes their education at these ages.

Within the MMM framework, these educational weights are incorporated directly into the initial population structure. Specifically, the diagonal elements of the initial state matrix represent the joint distribution of individuals across educational attainment and health status—that is, the proportion of individuals in each education group who are disability-free or disabled at baseline,

$$\mathbf{l}_\alpha = \begin{bmatrix} c_\alpha^{<\mathrm{HS}} l_\alpha^{\mathrm{H}} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & c_\alpha^{<\mathrm{HS}} l_\alpha^{\mathrm{U}} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & c_\alpha^{\mathrm{HS}} l_\alpha^{\mathrm{H}} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & c_\alpha^{\mathrm{HS}} l_\alpha^{\mathrm{U}} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & c_\alpha^{\mathrm{Col}} l_\alpha^{\mathrm{H}} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & c_\alpha^{\mathrm{Col}} l_\alpha^{\mathrm{U}} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & c_\alpha^{\mathrm{Bac}} l_\alpha^{\mathrm{H}} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & c_\alpha^{\mathrm{Bac}} l_\alpha^{\mathrm{U}} \end{bmatrix}$$

The order in the diagonal can be changed, and each column would be the life expectancy of that state. For example, one can put all the “H” first on the left and then the “U” on the right. As long as the $\mathbf{P}_x$ also follow the same order, the results would be comparable with the new order.

[Table 2 about here]

In Table 2, we present the transition probability matrices for three subsystems: (i) survival by educational level and health states, (ii) disability transition conditional on survival, and (iii) educational transition conditional on survival. Because systems (ii) and (iii) represent conditional probabilities, the rows of each corresponding matrix sum to one. In particular, for the education subsystem, 100% of surviving individuals remain in their original education group, as education is assumed to be time-invariant beyond early adulthood. Following the structure of $\mathbf{l}_\alpha$, the overall transition probability matrix is of dimension 8×8, corresponding to the combinations of four educational groups and two health states (disability-free or disabled),

$$\mathbf{P}_x = \begin{bmatrix} s_x^{1.h} p_x^{1.h.h} & s_x^{1.h} p_x^{1.h.u} & 0 & 0 & 0 & 0 & 0 & 0 \\ s_x^{1.u} p_x^{1.u.h} & s_x^{1.u} p_x^{1.u.u} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & s_x^{2.h} p_x^{2.h.h} & s_x^{2.h} p_x^{2.h.u} & 0 & 0 & 0 & 0 \\ 0 & 0 & s_x^{2.u} p_x^{2.u.h} & s_x^{2.u} p_x^{2.u.u} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & s_x^{3.h} p_x^{3.h.h} & s_x^{3.h} p_x^{3.h.u} & 0 & 0 \\ 0 & 0 & 0 & 0 & s_x^{3.u} p_x^{3.u.h} & s_x^{3.u} p_x^{3.u.u} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & s_x^{4.h} p_x^{4.h.h} & s_x^{4.h} p_x^{4.h.u} \\ 0 & 0 & 0 & 0 & 0 & 0 & s_x^{4.u} p_x^{4.u.h} & s_x^{4.u} p_x^{4.u.u} \end{bmatrix}$$

The first cell represents the probability that an individual who is both disability-free and has less than a high school education (<HS) remains in the same combined state at the next age interval. This probability is the product of (1) the probability of survival, (2) the probability of remaining disability-free conditional on survival, and (3) the probability of remaining in the same education

group conditional on survival (which is 1). Many elements in the matrix are zero, reflecting structural constraints on educational mobility at these ages. For instance, the probability of transitioning from “<HS” to “HS” is set to zero, implying that the product of transition probabilities across these components is also zero.

[Figure 3 about here]

Figure 3 illustrates the decomposition of changes in partial life expectancies among females aged 60–69 between the 1936–1945 and 1946–1955 birth cohorts. As shown in row 1, disability-free life expectancy (HLE) increased in the more recent cohort, whereas disabled life expectancy (ULE) changed very little. The decomposition results from the two methods are identical with respect to the educational composition (row 2) and the initial health distribution by education (row 3). There is no effect of educational transition, as both approaches assume that education remains fixed over age. The key distinction lies in the decomposition of the health-related component: in the original method, the H-effect (row 4) represents the combined impact of health transitions and mortality. In the MMM framework, this component is further disaggregated into a health transition effect (H-effect, row 4) and a mortality effect (M-effect, row 5). Accordingly, rows 4 and 5 in panel b sum to row 4 in panel a when stratified by life expectancy and education group.

The results indicate that improvements in survival (the M-effect) have contributed to longer HLE and marginally longer unhealthy life expectancy (ULE), particularly among individuals with lower educational attainment. The H-effect (row 4) remains broadly comparable between the two methods, except for total life expectancy (TLE), where most of the cohort change is attributable to mortality reduction. Furthermore, after conditioning on mortality, the negative contribution of the H-effect to HLE among lower-educated individuals (<HS and HS) becomes more pronounced in the MMM-based decomposition.

Example 3: Morbidity and disability in multiple multistate

Shen and Payne (2023) examined cohort changes in health expectancies by disability and morbidity in the United States using data from the Health and Retirement Study (2021) and a multistate life table approach. In their framework, disability was defined based on limitations in activities of daily living (ADL), while morbidity was measured by whether individuals had ever been diagnosed with any of five chronic diseases. Their analysis compared four successive birth cohorts and found little compression of disability but a clear expansion of morbidity. The findings suggest a dynamic equilibrium, in which the relationship between chronic morbidity and disability has weakened across cohorts. Shen et al. (2024) replicated the study to demonstrate that MMM method without the interaction can produce almost the same health expectancies. In this example, we apply the MMM method to compute these health expectancies and then decompose the cohort change of women between 1934-1934 and 1924-1933 at ages 70-79 by the change in morbidity dimension and the change in disability dimension. Appendix 1 shows the health expectancies across these two cohorts by disability status. There is almost no change in disabled life expectancy (DLE) and very small increase in disability-free life expectancy (DFLE).

We first partition the initial state distribution, $\mathbf{l}_\alpha$, into the morbidity and disability components. In this example, we use a specification that includes the two marginal components and their interaction term, $\mathbf{l}_\alpha = \begin{bmatrix} l_\alpha^{\mathrm{MF}} l_\alpha^{\mathrm{DF}} l_\alpha^{int.1} & 0 & 0 & 0 \\ 0 & l_\alpha^{\mathrm{M}} l_\alpha^{\mathrm{DF}} l_\alpha^{int.2} & 0 & 0 \\ 0 & 0 & l_\alpha^{\mathrm{MF}} l_\alpha^{\mathrm{D}} l_\alpha^{int.3} & 0 \\ 0 & 0 & 0 & l_\alpha^{\mathrm{M}} l_\alpha^{\mathrm{D}} l_\alpha^{int.4} \end{bmatrix}$. Specifically, l_α^{MF} denotes the proportion of individuals who are morbidity-free at age α, l_α^{DF} represents the proportion who are disability-free, and $l_\alpha^{int.1}$ captures the two-way interaction between morbidity and disability. Note that the interaction terms differ for each cell in the corresponding frequency table.

[Table 3 about here]

Table 3 presents the transition probability matrices for three subsystems: (i) survival by morbidity and disability at time t, (ii) morbidity transition conditional on survival and morbidity, and (iii) disability transition conditional on survival and morbidity. The transition probability is the product of these three systems based on their status at $t+1$ for each row,

$$\mathbf{P}_x = \begin{bmatrix} s_x^1 p_x^{1.mf} p_x^{1.df} & s_x^1 p_x^{1.m} p_x^{1.df} & s_x^1 p_x^{1.mf} p_x^{1.d} & s_x^1 p_x^{1.m} p_x^{1.d} \\ s_x^2 p_x^{2.mf} p_x^{2.df} & s_x^2 p_x^{2.m} p_x^{2.df} & s_x^2 p_x^{2.mf} p_x^{2.d} & s_x^2 p_x^{2.m} p_x^{2.d} \\ s_x^3 p_x^{3.mf} p_x^{3.df} & s_x^3 p_x^{3.m} p_x^{3.df} & s_x^3 p_x^{3.mf} p_x^{3.d} & s_x^3 p_x^{3.m} p_x^{3.d} \\ s_x^4 p_x^{4.mf} p_x^{4.df} & s_x^4 p_x^{4.m} p_x^{4.df} & s_x^4 p_x^{4.mf} p_x^{4.d} & s_x^4 p_x^{4.m} p_x^{4.d} \end{bmatrix}.$$

With $\mathbf{l}_\alpha$ and $\mathbf{P}_x$ specified, we can compute healthy life expectancy (DFLE) and subsequently decompose the contribution of each component. Figure 4 presents the decomposition of the total gap in DFLE and disabled life expectancy (DLE) into seven components. The baseline effect is further partitioned into three parts, corresponding to the three terms in the product of $\mathbf{l}_\alpha$. Changes in morbidity contribute to a slight reduction in DFLE and a substantial increase in DLE, while changes in disability similarly decrease DFLE and increase DLE. The interaction between morbidity and disability, however, exhibits the opposite pattern—raising DFLE and lowering DLE. This interaction can be interpreted as capturing the extent to which the co-occurrence of morbidity and disability differs across cohorts; in other words, it reflects how strongly morbidity is associated with disability in the population.

[Figure 4 about here]

Turning to the transition probability matrix, $\mathbf{P}_x$, we can analogously decompose it into three multiplicative components. For analytical and illustration purpose, we summarize this as four effects: (1) morbidity transition, (2) disability transition conditional on being morbidity-free at time t ("Disability|MF"), (3) disability transition conditional on being morbid at time t ("Disability|M"), and (4) mortality. As shown in Table 3, System iii, p_x^1 and p_x^3 correspond to disability transitions among the morbidity-free, while p_x^2 and p_x^4 correspond to disability transitions among the morbid. Accordingly, the disability effect is divided between rows 1 and 3, and rows 2 and 4, in the transition probability matrix. This example illustrates that the way we summarize decomposition results within the MMM framework is flexible and can be tailored to specific analytical or substantive interests.

The results indicate that morbidity transitions have minimal impact on DFLE or DLE. By contrast, disability transitions substantially improve DFLE and reduce DLE, with the effect being even stronger among those with existing morbidities, suggesting that the likelihood of becoming disabled has decreased for individuals already with chronic conditions. Mortality reduction contributes positively to both DFLE and DLE, and this effect can be further disaggregated by health state at time t, analogous to Example 1, or by morbidity a time t, analogous to disability effect.

Summary

The three applications illustrate the methodological flexibility and analytical power of the MMM framework in decomposing changes in multistate life expectancy. The approach enables users to determine which components to decompose, with different specification available for the initial state distribution, $\mathbf{l}_\alpha$, and the option to include or exclude mortality decomposition within the transition probability matrix, $\mathbf{P}_x$. Consistency between the origin states (row) destination states (columns) of $\mathbf{l}_\alpha$ and $\mathbf{P}_x$ is essential for accurate reconstruction of the life table matrices. Following decomposition, results can be summarized at different levels of aggregation depending on the analytical objective. Taken together, these features position the MMM as a robust and adaptable framework that affords researchers substantial flexibility and autonomy in examining the drivers of change in multistate life expectancy.

Conclusion

This paper extends decomposition methods for multistate life expectancy within the multiple multistate method (MMM) framework, providing a unified and flexible approach to analyzing differences in population health and longevity. By explicitly incorporating mortality transitions and allowing for both time-fixed and time-varying subgroup characteristics, the method broadens the scope of decomposition analyses beyond existing approaches. Applications using the Health and Retirement Study demonstrate how the extended decomposition captures the interplay between population structure, transition dynamics, and mortality, offering deeper insights into the mechanisms driving disparities in health expectancies. The framework's modular structure also facilitates the inclusion of additional time-varying dimensions, such as morbidity, disability, and other life-course processes. Overall, the extended MMM decomposition enhances both the analytical power and interpretability of multistate analyses, providing a transparent tool for studying the dynamics underlying differences in health and longevity across populations.

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Table 1a. Transition Probabilities of the state space in Figure 1(a)

$t\backslash t+1$	Healthy	Unhealthy	Dead
Healthy	p_x^{hh}	p_x^{hu}	p_x^{hd}
Unhealthy	p_x^{uh}	p_x^{uu}	p_x^{ud}
Dead	0	0	1

Table 1b. Transition Probabilities of the MMM state space of example 1 in Figure 1(b)

i. Survival matrix

$t\backslash t+1$	Survival
Healthy	$1-p_x^{hd}$
Unhealthy	$1-p_x^{ud}$

ii. Transition matrix conditioned on survival

$t\backslash t+1$	Healthy	Unhealthy
Healthy	$p_x^{hh\|s}$	$p_x^{hu\|s}$
Unhealthy	$p_x^{uh\|s}$	$p_x^{uu\|s}$

Table 2. Transition Probabilities of the MMM state space of Example 2

i. Survival matrix

$t\backslash t+1$	Survival
< HS & H	$s_x^{1.h}$
< HS & U	$s_x^{1.u}$
HS & H	$s_x^{2.h}$
HS & U	$s_x^{2.u}$
Col & H	$s_x^{3.h}$
Col & U	$s_x^{3.u}$
Bac & H	$s_x^{4.h}$
Bac & U	$s_x^{4.u}$

ii. Transition matrix of disability status conditioned on survival

$t\backslash t+1$	H	U
< HS & H	$p_x^{1.h.h}$	$p_x^{1.h.u}$
< HS & U	$p_x^{1.u.h}$	$p_x^{1.u.u}$
HS & H	$p_x^{2.h.h}$	$p_x^{2.h.u}$
HS & U	$p_x^{2.u.h}$	$p_x^{2.u.u}$
Col & H	$p_x^{3.h.h}$	$p_x^{3.h.u}$
Col & U	$p_x^{3.u.h}$	$p_x^{3.u.u}$
Bac & H	$p_x^{4.h.h}$	$p_x^{4.h.u}$
Bac & U	$p_x^{4.u.h}$	$p_x^{4.u.u}$

iii. Transition matrix of educational group conditioned on survival

$t\backslash t+1$	< HS	HS	Col	Bac
< HS & H	1	0	0	0
< HS & U	1	0	0	0
HS & H	0	1	0	0
HS & U	0	1	0	0
Col & H	0	0	1	0
Col & U	0	0	1	0
Bac & H	0	0	0	1
Bac & U	0	0	0	1

Table 3. Transition Probabilities the MMM state space of Example 3

i. Survival matrix

$t\backslash t+1$	Survival
MF & DF	s_x^1
M & DF	s_x^2
MF & D	s_x^3
M & D	s_x^4

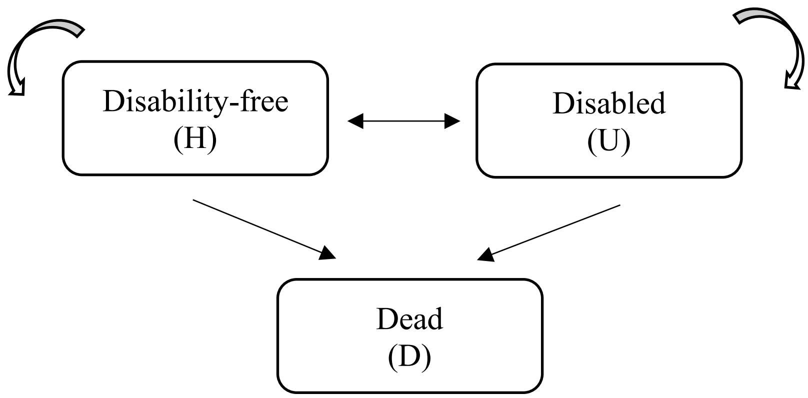
ii. Transition matrix of morbidity status conditioned on survival

$t\backslash t+1$	MF	M
MF & DF	$p_x^{1.mf}$	$p_x^{1.m}$
M & DF	$p_x^{2.mf}$	$p_x^{2.m}$
MF & D	$p_x^{3.mf}$	$p_x^{3.m}$
M & D	$p_x^{4.mf}$	$p_x^{4.m}$

iii. Transition matrix of disability status conditioned on survival

$t\backslash t+1$	DF	D
MF & DF	$p_x^{1.df}$	$p_x^{1.d}$
M & DF	$p_x^{2.df}$	$p_x^{2.d}$
MF & D	$p_x^{3.df}$	$p_x^{3.d}$
M & D	$p_x^{4.df}$	$p_x^{4.d}$

Panel a. Original method



Panel b. MMM method

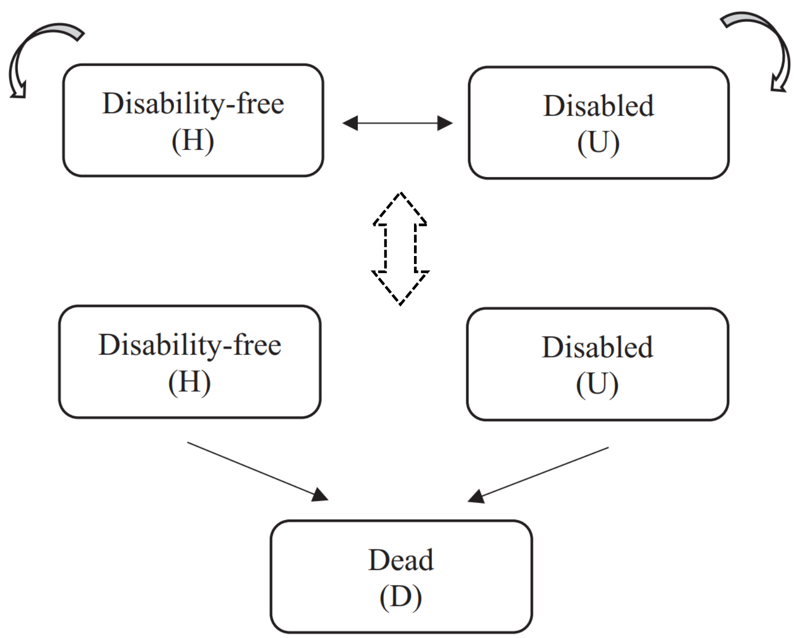


Figure 1. Example of state space in different modeling framework

Sex gap in	**Panel a**. Original method	**Panel b**. MMM method
HLE		
ULE		

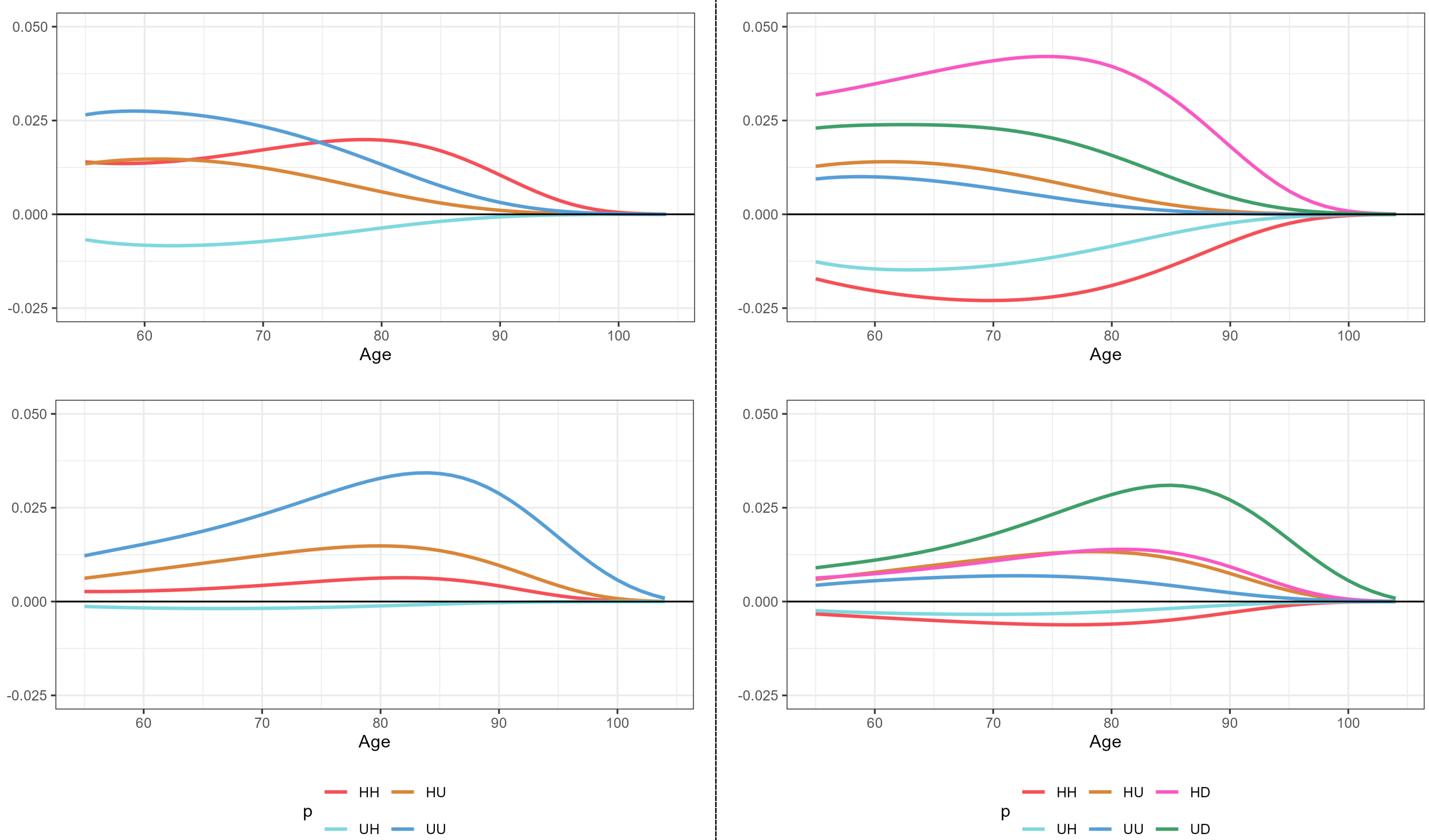


Figure 2. Effects from each transition probability by age to the difference in remaining HLE at age 55 between women and men --- Comparison between original method and MMM method with separated mortality effect

Source: Authors' own calculations based on the Health and Retirement Study (2021) and results in Shen et al. (2023)

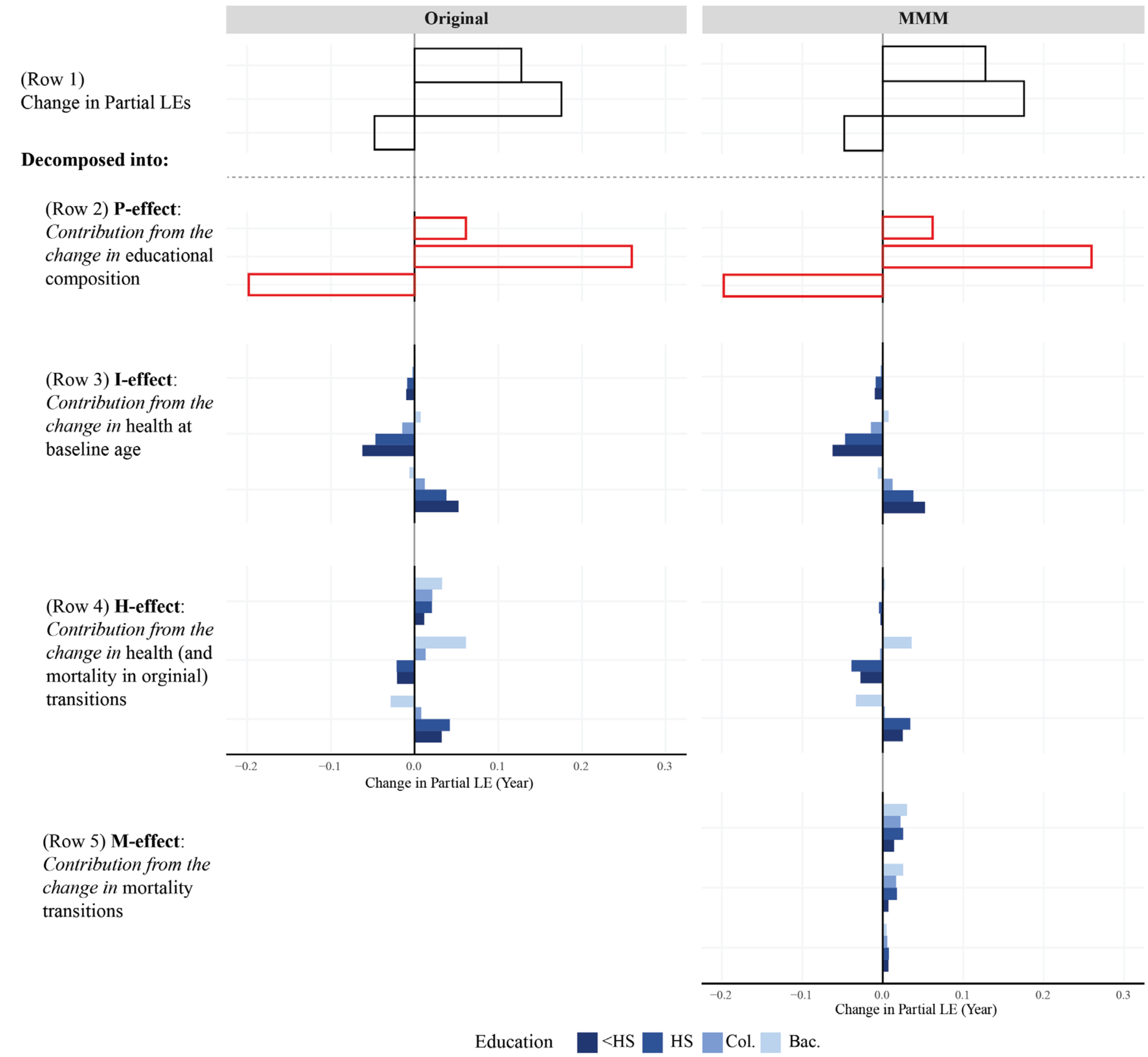


Figure 3. 10-year change in women's partial cohort life expectancy (ages 60-69) between cohorts 1946-1955 and 1936-1945, and contributions from different components by educational attainment --- Comparison between original method and MMM method with separated mortality effect

Note: Red-bars of the P-effect are aggregated by all education. TLE = 10-year partial total life expectancy; HLE = 10-year partial disability-free life expectancy; ULE = 10-year partial disabled life expectancy; <HS = Below high school; HS = High school; Col.= Some college; Bac. = Bachelor's degree or higher.

Source: Authors' own calculations based on the Health and Retirement Study (2024) and results in Shen et al. (2025)

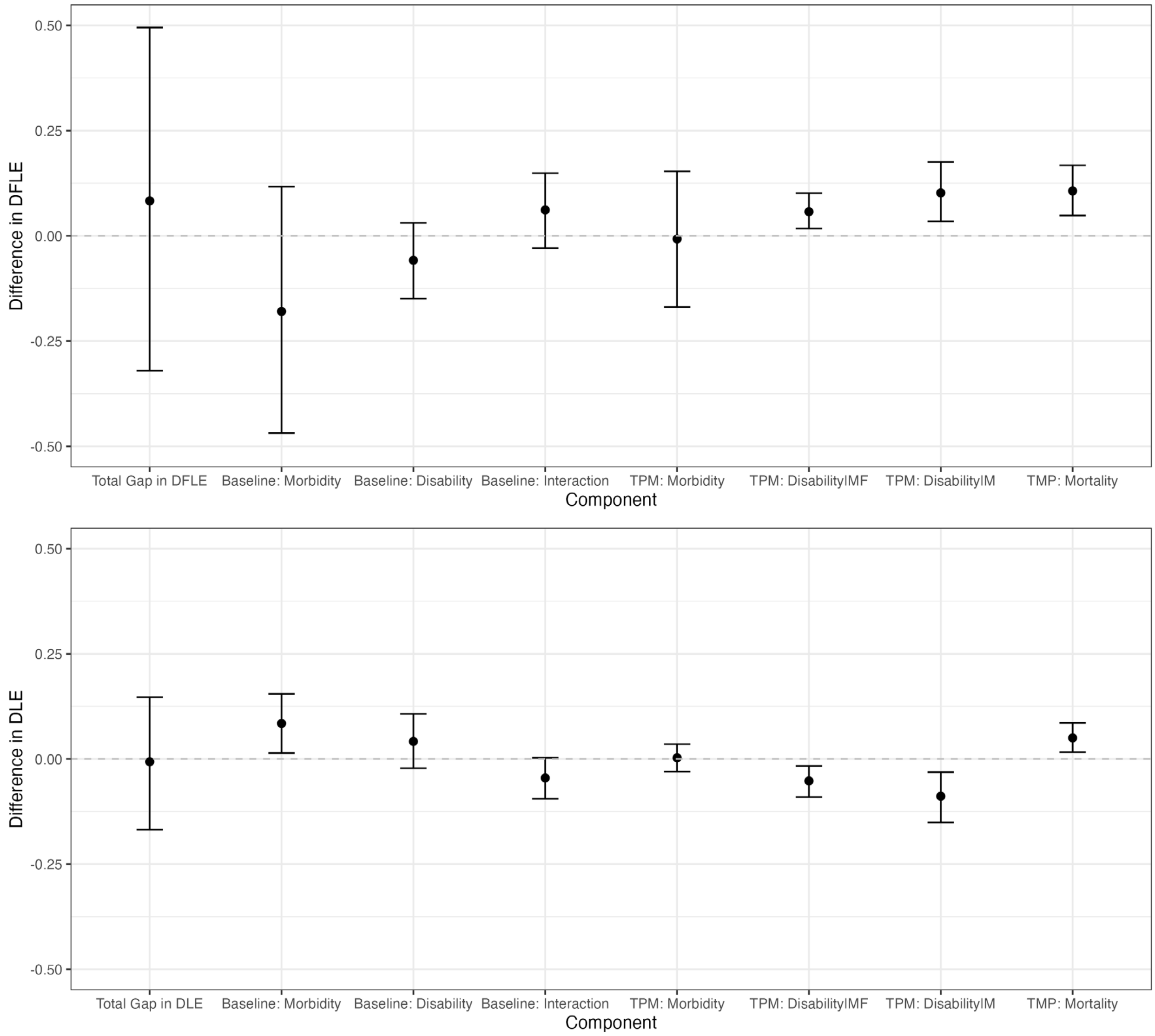
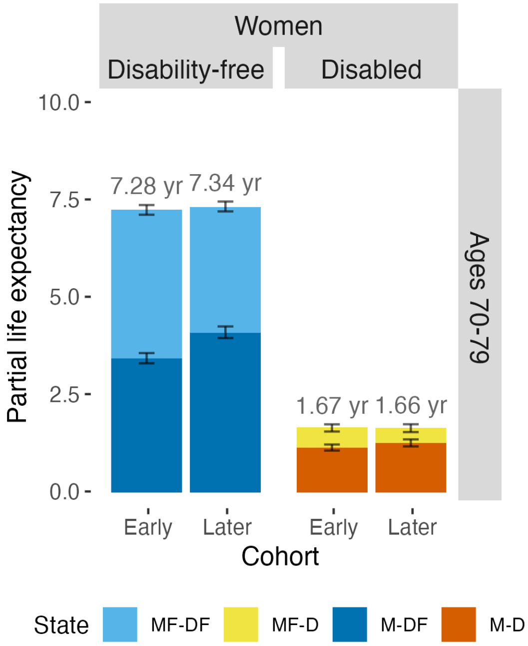


Figure 4. 10-year change in women's partial cohort life expectancy (ages 70-79) between cohorts 1934-1934 and 1924-1933, and contributions from different components with 95% confidence interval

Note: TMP = Transition probability matrix

Source: Authors' own calculations based on the Health and Retirement Study (2021)



Appendix Figure 1. Estimated women partial cohort health expectancies across birth cohorts 1924-1933 (Early) and 1934-1934 (Later) with 95% CI.

Source: MMM *(reduced-form)* in Shen et al. (2024)