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Research Article

Two-dimensional contour decomposition: Decomposing mortality differences into initial difference and trend components by age and cause of death

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Abstract

BACKGROUND

Conventional decomposition analysis identifies contributions from differences in covariates in total between-population difference, but does not address the question of the historical roots of the differences. To close this gap, the contour decomposition method was proposed. Since 2017, when it was published, this method has been successfully applied in several papers. Nevertheless, it has an important limitation: causes of death cannot be included in the analyses.

OBJECTIVE

Conventional decomposition analysis provides insight into the reasons for a difference in an aggregate index. It can be either the difference between two populations at a given time or a temporal change for one population. However, it does not consider the origin of this difference. Contour decomposition is the only method that does. We extend the contour decomposition method by adding one more dimension that can be used to estimate the contribution of an additional component; e.g., causes of death or educational structure.

METHODS

We use a step-wise replacement algorithm.

CONTRIBUTION

The proposed discrete method for decomposition is an extension of the earlier general algorithm of stepwise replacement and contour decomposition and permits a difference in an aggregate measure at a final time point to be split into cause-specific additive

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components that correspond to the initial differences in the event-rates of the measure and differences in trends in these underlying event-rates.

1. Introduction

A contour decomposition method is based on the methodological foundations of the decomposition of differences between two aggregated demographic measures. One of the first methods of decomposition was developed by Kitagawa (1955). It is devoted to a simple decomposition of differences between crude death rates (CDR) in two populations or at two time points into the contributions of (a) differences in mortality and (b) differences in age composition. This method was further extended in the 1990s (Das Gupta 1991, 1994) to a multidimensional case. Nevertheless, even the modified method can only be applied to linear functions; i.e., the (demographic) indicator under comparison should be a linear function of covariates – for example, age-specific death rates. While the decomposition of linear functions is a relatively simple mathematical task, the non-linearity significantly complicates decomposition tasks. The majority of demographic indicators, including any life table functions, are non-linear. For example, life expectancy is a non-linear function of age-specific death rates. The decomposition of difference in life expectancy is non-symmetrical and non-transitive (path-dependent) concerning the populations being compared (Horiuchi, Wilmoth, and Pletcher 2008). But the result of the decomposition task should always be additive; i.e., the sum of covariate contributions is equal to the total difference between the aggregated measures. For example, age-specific contributions of mortality differences at each age group should be equal to the total difference in life expectancy at birth. Thus, a classical goal of decomposition is to split the difference in the aggregate index into contributions from the covariates. The main challenge is that such additive decomposition is not straightforward for non-linear indicators.

The first formulae for the decomposition of non-linear functions concerned the decomposing differences in life expectancy and were proposed by four independent authors in the 1980s (Andreev 1982; Arriaga 1984; Pollard 1982; Pressat 1985). The decomposition became a standard tool in demography in the 2000s when new formulae for the decomposition of life-table-based measures of dispersion such as the Gini coefficient, standard deviation, lifetime disparity, variance, and life table entropy were proposed (Vaupel and Canudas Romo 2003; Shkolnikov, Andreev, and Begun 2003; Edwards and Tuljapurkar 2005; Zhang and Vaupel 2009; Nau and Firebaugh 2012; van Raalte and Caswell 2013; Gillespie, Trotter, and Tuljapurkar 2014).

At the same time, two more general frameworks for a universal method of decomposition of aggregated measures were proposed. Andreev, Shkolnikov, and Begun (2002) introduced a stepwise replacement algorithm for decomposition of changes in aggregate demographic measures. Horiuchi, Wilmoth, and Pletcher (2008) developed another universal method based on the continuous transition between two populations. While the latter method was practically realized as a numerical integration, the former used a more practical procedure presenting the total change in the dependent aggregate index as a sum of the effects of the sequential (stepwise) replacement of event rates at each age.

More recent methodological advances in the area of demographic decomposition concern a novel contour decomposition method that splits the difference in an aggregate measure at the time of observation into age-specific (a) additive components corresponding to the initial difference (at a certain time point in the past) and (b) additive components accounting for the differences in time trends between this time point in the past and the time of observation (Jdanov et al. 2017).

The contour decomposition operates in the framework of the stepwise replacement approach. Nevertheless, the idea that the current difference between the two populations depends on initial (starting) conditions and the trends (evolution during the considered time frame) might also be applied to the continuous framework.

Further steps in advancing contour decomposition by including causes of death were inspired by the corresponding extensions of the Andreev-Arriaga decomposition methods. The current study extends the stepwise contour decomposition method by adding one more dimension as an additional covariate. Such additional covariates may include causes of death, education, or other population characteristics; i.e., the method is also applicable (without any modifications) to any two-dimensional combination of event rates. Thus, in the same way as contour decomposition adds a retrospective trend to the conventional stepwise replacement decomposition, the propoposed method adds a trend to decomposition by age and cause of death (Shkolnikov, Andreev, and Begun 2003; Preston, Heuveline, and Guillot 2000). Using the same notations as in the article by Jdanov et al. (2017) and age-specific mortality data for the USA and England and Wales for 1980–2010, we provide an empirical example of the age- and cause-specific decomposition of the differences in life expectancy at birth in 2010 into the contributions of (a) the initial differences observed in 1980 and (b) the contributions of age- and cause-specific trends during 1980–2010.

2. Methods

2.1 Decomposition task

Let us assume that the demographic index of interest $f(.)$ for a population *A* is a function of a matrix of age- and cause-specific event rates:

$$E = f(\boldsymbol{M}_A),$$

where

$$\boldsymbol{M}_A = (m_A(x_{i,j})) = \begin{bmatrix} m_A(x_{1,1}) & m_A(x_{1,2}) & \cdots & m_A(x_{1,c-1}) & m_A(x_{1,c}) \\ \vdots & & \ddots & \vdots & \\ m_A(x_{n,1}) & m_A(x_{n,2}) & \cdots & m_A(x_{n,c-1}) & m_A(x_{n,c}) \end{bmatrix},$$

where $m(x_{i,j})$ are age- and cause-specific death rates at age group *i* from the cause of death *j*, and *n* and *c* are numbers of age groups and causes of death respectively. The age intervals $[x_{i,.}, x_{i+1,.})$ are designated by the starting age $x_{i,.}$. The difference in measure $E = f(.)$ between the two populations *A* and *B* is

$$\Delta_{AB} = f(\boldsymbol{M}_A) - f(\boldsymbol{M}_B). \quad (1)$$

This difference can be decomposed by age

$$\Delta_{AB} = \sum_{i=1}^{n} \Delta_{AB}^{i,.} \quad (2)$$

or by cause of death

$$\Delta_{AB} = \sum_{j=1}^{c} \Delta_{AB}^{.,j} \quad (3)$$

or by both age and cause of death

$$\Delta_{AB} = \sum_{i=1}^{n} \sum_{j=1}^{c} \Delta_{AB}^{i,j} \ , \quad (4)$$

where age- and cause-specific contributions $\Delta_{AB}^{i,.}$ and $\Delta_{AB}^{.,j}$ are defined as follows:

$$\Delta_{AB}^{i,.} = \sum_{j=1}^{c} \Delta_{AB}^{i,j} \tag{5}$$

and

$$\Delta_{AB}^{j,.} = \sum_{i=1}^{n} \Delta_{AB}^{i,j} \ . \tag{6}$$

The current difference between populations (say at time *T*) is (1) a legacy of the past (e.g., at least partly attributable to the difference between populations at some time in the past *t*) and (2) a result of differences in (mortality) changes during the period *T*-*t*. Thus, we may further decompose age- and cause-specific components to account for the influence of the initial difference and trends:

$$\Delta_{AB} = \sum_{i=1}^{n}\sum_{j=1}^{c}(Initial^{i,j} + Trend^{i,j}) = \sum_{i=1}^{n}\sum_{j=1}^{c}(\Delta^{i,j} + \delta^{i,j}), \tag{7}$$

$$\sum_{j=1}^{c} Initial^{i,j} + \sum_{j=1}^{c} Trend^{i,j} = \Delta^{i} + \delta^{i} = \Delta_{AB}^{i}, \qquad i = 1, \dots, n \tag{8}$$

where Δ^{i} and δ^{i}denote the initial difference component and trend component for age group *i*, respectively, and $\Delta^{i,j}$ and $\delta^{i,j}$ are the initial difference and trend components for age group *i* and cause of death *j*. The initial difference components represent the contribution of starting conditions at time *t*; i.e., the extent to which currently observed difference depends on a legacy of the past. The trend components refer to the contributions of changes that occurred during a specified period *T*-*t*. This component is the sum of trends A and B. Its effect on the difference in considering measures may be positive or negative, depending on which population was more successful regarding the respective changes in mortality by age group and cause of death.

2.2 Contour replacement method

Thus, we decompose the difference between two populations A and B at time *T* by age and cause of death conditioned on the past difference between *a* and *b* and the temporal

changes from *a* to *A* and from *b* to *B*. Here we denote populations *A* and *B* at time *t* as *a* and *b*.

The main idea of the stepwise replacement algorithm is to calculate factor-specific contributions by replacing the respective elements in the first matrix with elements from the second matrix. Nevertheless, there is a question about the order of such replacements. There is a conventional agreement that age-specific replacements should be gradually implemented from the youngest to the oldest ages. Unfortunately, this is not applicable to the second dimension (e.g., causes of death), because prioritizing any direction is hardly justifiable. Thus, for the second direction we should consider all possible options and use an average of components as an estimated value of the contribution to the total difference between the aggregated measures.

First, we consider a simplified example with two age groups and two causes of death. Using a stepwise replacement (i.e., replacement of one age- and cause-specific rate at each step), matrix **A** can be transformed into matrix **B** as follows:

$$\begin{aligned}\mathbf{A} = &\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}a_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}b_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow\\ &\begin{bmatrix}B_{1,1} & a_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & b_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & B_{1,2}\\ a_{2,1} & A_{2,2}\end{bmatrix} \rightarrow\\ &\begin{bmatrix}B_{1,1} & B_{1,2}\\ b_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & B_{1,2}\\ B_{2,1} & A_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & B_{1,2}\\ B_{2,1} & a_{2,2}\end{bmatrix} \rightarrow \begin{bmatrix}B_{1,1} & B_{1,2}\\ B_{2,1} & b_{2,2}\end{bmatrix} \rightarrow\\ &\begin{bmatrix}B_{1,1} & B_{1,2}\\ B_{2,1} & B_{2,2}\end{bmatrix} = \mathbf{B}\end{aligned} \tag{9}$$

Here we go from the young to the old age group and from the first to the second cause of death. The contribution of age group and cause of death is calculated as the difference between the rates calculated using matrices differing only in the corresponding element. For example, the contribution of the first cause of death of the first age group might be estimated as follows:

$$\widehat{\Delta}^{1,1}_{AB|A} = f\left(\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right).$$

The order of replacement for age groups is conventional and follows the logic of the aging process. Unfortunately, a fixed order of causes of death cannot be justified because we cannot prioritize any cause of death. Following Shkolnikov, Andreev, and Begun (2003), we suggest considering all possible combinations of replacements of cause-specific rates and using the average as a final estimate. In our example with two causes of death the only alternative to transformation (9) is

$$\begin{aligned}\mathbf{A} = &\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}A_{1,1} & a_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}A_{1,1} & b_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}A_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to\\ &\begin{bmatrix}a_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}b_{1,1} & b_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix} \to \begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & a_{2,2}\end{bmatrix} \to\\ &\begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & b_{2,2}\end{bmatrix} \to \begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & B_{2,2}\end{bmatrix} \to \begin{bmatrix}B_{1,1} & B_{1,2}\\ a_{2,1} & B_{2,2}\end{bmatrix} \to \begin{bmatrix}B_{1,1} & B_{1,2}\\ b_{2,1} & B_{2,2}\end{bmatrix} \to\\ &\begin{bmatrix}B_{1,1} & B_{1,2}\\ B_{2,1} & B_{2,2}\end{bmatrix} = \mathbf{B}\end{aligned} \tag{10}$$

In this case, the contribution of the first cause of death of the first age group might be estimated as follows:

$$\overleftarrow{\Delta}^{1,1}_{AB|A} = f\left(\begin{bmatrix}A_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right).$$

The final estimate should be an average of $\overrightarrow{\Delta}^{1,1}_{AB|A}$ and $\overleftarrow{\Delta}^{1,1}_{AB|A}$:

$$\begin{aligned}\Delta^{1,1}_{AB|A} = &\frac{1}{2}\left[f\left(\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) + f\left(\begin{bmatrix}A_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) -\right.\\ &\left. f\left(\begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right]\end{aligned} \tag{11}$$

Let us now consider the first row of (9) and calculate changes at each step of the transformation:

$$\begin{aligned}&\left\{f\left(\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}a_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\} + \left\{f\left(\begin{bmatrix}a_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}b_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\}\\ &+ \left\{f\left(\begin{bmatrix}b_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{matrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{matrix}\right)\right\}\\ &= f\left(\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{matrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{matrix}\right)\end{aligned}$$

Here the first and third terms might be considered as a contribution of (mortality) trends because by replacing *A* with a and *b* with *B* we go back and forth in time. The second term is about the difference in historical conditions and can be attributed to difference due to initial conditions. The same is applicable to (10). Similar to (11), using an average of two permutations, the final estimates of the trend and initial components of contribution of first cause of death in the first age group are calculated as follows:

$$Trend^{1,1} = \delta_{ab|B}^{1,1} = \delta_{Aa|B}^{1,1} - \delta_{bB|B}^{1,1} \tag{12}$$

$$\begin{aligned}\delta_{Aa|A}^{1,1} = {} & \frac{1}{2}\left\{f\left(\begin{bmatrix}A_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}a_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\} \\ & + \frac{1}{2}\left\{f\left(\begin{bmatrix}A_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}a_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\},\end{aligned} \tag{13}$$

$$\begin{aligned}\delta_{bB|A}^{1,1} = {} & \frac{1}{2}\left\{f\left(\begin{bmatrix}B_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}b_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\} \\ & + \frac{1}{2}\left\{f\left(\begin{bmatrix}B_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}b_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\},\end{aligned} \tag{14}$$

$$\begin{aligned}Initial^{1,1} = {} & \Delta_{ab|A}^{1,1} \\ = {} & \frac{1}{2}\left\{f\left(\begin{bmatrix}a_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}b_{1,1} & A_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\} \\ & + \frac{1}{2}\left\{f\left(\begin{bmatrix}a_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right) - f\left(\begin{bmatrix}b_{1,1} & B_{1,2}\\ A_{2,1} & A_{2,2}\end{bmatrix}\right)\right\}\end{aligned} \tag{15}$$

We considered a transformation that refers to a sequence of replacements over the contour *A→a→b→B.* Another option is to consider the reverse direction *B→b→a→;* i.e., the case where age- and cause-specific death rates in population *B* are replaced by the corresponding rates in population *B* using elements *b* and *a.* Despite the absolute total difference not depending on the direction

$$\Delta_{AB} = f(\mathbf{A}) - f(\mathbf{B}) = -\big(f(B) - f(A)\big) = -\Delta_{BA} \ ,$$

the components may differ. All components are calculated as the difference between the respective elements of transformation (9) or (10). The intermediate matrices are contingent on the chosen direction. Thus, the resulting contributions should be calculated as an average of the respective estimates of these two contours. Below we provide an algorithm for the case with *n* age groups and *c* causes of death.

Let us consider the matrix of age- and cause-specific rates

$$\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},s]} = \begin{bmatrix} m_A(x_{1,1}) & \dots & m_A(x_{1,c}) \\ \vdots & \ddots & \vdots \\ m_A(x_{i-1,1}) & \dots & m_A(x_{i-1,c}) \\ m_{AB}^{\boldsymbol{k},1}(x_{i,1}) & \dots & m_{AB}^{\boldsymbol{k},c}(x_{i,c}) \\ m_B(x_{i+1,1}) & \dots & m_B(x_{i+1,c}) \\ \vdots & \ddots & \vdots \\ m_B(x_{n,1}) & \dots & m_B(x_{n,c}) \end{bmatrix}, \tag{16}$$

$$m_{AB}^{K,j}(x_{i,j}) = \begin{cases} m_A(x_{i,j}), j \in \{k(1), \dots, k(s)\} \\ m_B(x_{i,j}), j \notin \{k(1), \dots, k(s)\} \end{cases}, \; s = 1, \dots, c, \; \boldsymbol{M}_{AB}^{[0,\dots]} = \boldsymbol{M}_B$$

where $\boldsymbol{k}$ is a vector of permutations without the repetition of dimension *c*. In other words, this is a matrix $\boldsymbol{M}_B$ where elements of rows from 1 to *i*–1 are replaced by the corresponding rates of matrix *A*. The *i*th row is a combination of rates from both populations defined by the first *s* elements of $\boldsymbol{k}$. The vector of permutation $\boldsymbol{k}$ defines the order of replacements of cause-specific death rates in the *i*th row. For example, $\boldsymbol{k} = \{1,2,\dots,c\}$ means that all elements will be replaced in order starting from the first element. In this case, elements of the *i*th row of the matrix $\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},s]}$ can be defined as follows:

$$m_{AB}^{\boldsymbol{k},j}(x_{i,j}) = \begin{cases} m_A(x_{i,j}), j \le s \\ m_B(x_{i,j}), j > s \end{cases}, \; s = 1, \dots, c \; .$$

For the vector with *c* elements, we may have *c*! permutations without repetitions. Thus, we may have *c*! different vectors of $\boldsymbol{k}$. We will denote $\boldsymbol{K}$ as the set of all possible values of $\boldsymbol{k}$.

The main equation of the stepwise replacement algorithm can be written as follows:

$$f(\boldsymbol{M}_A) - f(\boldsymbol{M}_B) = \sum_{i=1}^{n} \sum_{j=1}^{c} \Delta_{AB}^{i,j} \; . \tag{17}$$

$$\Delta_{AB}^{i,j} = \frac{1}{c!} \sum_{\boldsymbol{k} \in \boldsymbol{K}, s: k(s)=j} \left[f\left(\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},s]}\right) - f\left(\boldsymbol{M}_{AB}^{[i-1,\boldsymbol{k},c]}\right) \right]. \tag{18}$$

In other words, the age- and cause-specific contribution $\Delta_{AB}^{i,j}$ is an average change by replacing $m_B(x_{i,j})$ with $m_A(x_{i,j})$ over the whole set $\boldsymbol{K}$. It is easy to check that this definition fits conditions (4)–(6).

Using a simple algebraic trick, we may rewrite the terms in (18) as follows:

$$\begin{aligned} f\left(\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{AB}^{[i-1,\boldsymbol{k},c]}\right) \\ = \left[f\left(\boldsymbol{M}_{A(b)B}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{AB}^{[i-1,\boldsymbol{k},c]}\right)\right] \\ + \left[f\left(\boldsymbol{M}_{A(a)B}^{[i,\boldsymbol{k},s]}\right) - f\left(\boldsymbol{M}_{A(b)B}^{[i,\boldsymbol{k},s]}\right)\right] \\ + \left[f\left(\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},s]}\right) - f\left(\boldsymbol{M}_{A(a)B}^{[i,\boldsymbol{k},s]}\right)\right], \qquad i = 1, \dots, n, \end{aligned} \tag{19}$$

where

$$\boldsymbol{M}_{A(a)B}^{[i,\boldsymbol{k},s]} = \begin{bmatrix} m_A(x_{1,1}) & \dots & m_A(x_{1,c}) \\ \vdots & \ddots & \vdots \\ m_A(x_{i-1,1}) & \dots & m_A(x_{i-1,c}) \\ m_{A(a)B}^{\boldsymbol{k},1}(x_{i,1}) & \dots & m_{A(a)B}^{\boldsymbol{k},c}(x_{i,c}) \\ m_B(x_{i+1,1}) & \dots & m_B(x_{i+1,c}) \\ \vdots & \ddots & \vdots \\ m_B(x_{n,1}) & \dots & m_B(x_{n,c}) \end{bmatrix}, \tag{20}$$

$$m_{A(a)B}^{K,j}(x_{i,j}) = \begin{cases} m_A(x_{i,j}), j \in \{k(1), \dots, k(s-1)\} \\ m_a(x_{i,j}), j = k(s) \\ m_B(x_{i,j}), j \notin \{k(1), \dots, k(s)\} \end{cases}, \; s = 1, \dots, c,$$

$$\boldsymbol{M}_{AB}^{[0,.,.]} = \boldsymbol{M}_B$$

In (20), instead of directly replacing $m_B(x_{i,j})$ with $m_A(x_{i,j})$ (B→A), we replace $m_B(x_{i,j})$ consecutively with $m_a(x_{i,j})$, $m_b(x_{i,j})$, and then $m_A(x_{i,j})$ (B→b→a→A).

The first and the third additive terms of (19) are elements of the trend component. They are produced by temporal mortality changes in populations *B* (former *b*) and *A* (former *a*), respectively. Following (18), we define the trend components as an average over the set $\boldsymbol{K}$:

$$\delta_{bB|B}^{i,j} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}_{A(b)B}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{AB}^{[i-1,\boldsymbol{k},c]}\right)\right], i = 1,\dots,n; j = 1,\dots,c, \tag{21}$$

$$\delta_{Aa|B}^{i,j} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}_{AB}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{A(a)B}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right)\right], \quad i = 1,\dots,n; j = 1,\dots,c. \tag{22}$$

The second additive term in (19) is the initial difference component. The average of all possible permutations is the contribution of the initial difference:

$$\Delta_{ab|B}^{i} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}_{A(a)B}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{A(b)B}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right)\right], \quad i = 1,\dots,n; j = 1,\dots,c. \tag{23}$$

Formulae (18)–(23) describe a replacement that transforms population *B* into population *A*. In other words, this transformation refers to a sequence of replacements over the contours *B*→*b*→*a*→*A*. Another option is to consider the reverse direction *A*→*a*→*b*→*B;* i.e., the case where age-specific death rates in population *A* are replaced by the corresponding rates in population *B* using elements *a* and *b* (the same procedure as provided in our example at the beginning of this section). Both directions are equivalent and the final contributions should be based on averaging these two options.

For an alternative replacement path *A*→*a*→*b*→*B*, Equation (19) can be rewritten as follows:

$$\begin{aligned} f\left(\boldsymbol{M}_{BA}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{BA}^{[i-1,\boldsymbol{k},c]}\right) &= \left[f\left(\boldsymbol{M}_{B(a)A}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{BA}^{[i-1,\boldsymbol{k},c]}\right)\right] \\ &+ \left[f\left(\boldsymbol{M}_{B(b)A}^{[i,\boldsymbol{k},s]}\right) - f\left(\boldsymbol{M}_{B(a)A}^{[i,\boldsymbol{k},s]}\right)\right] \\ &+ \left[f\left(\boldsymbol{M}_{BA}^{[i,\boldsymbol{k},s]}\right) - f\left(\boldsymbol{M}_{B(b)A}^{[i,\boldsymbol{k},s]}\right)\right], \quad i = 1,2,\dots n. \end{aligned} \tag{24}$$

The corresponding contributions reflecting the trend and initial difference components are

$$\delta_{aA|A}^{i} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}_{B(a)A}^{[i,\boldsymbol{k},\boldsymbol{s}]}\right) - f\left(\boldsymbol{M}_{BA}^{[i-1,\boldsymbol{k},c]}\right)\right], \quad i = 1,\dots,n, \tag{25}$$

$$\delta^{i}_{Bb|A} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}^{[i,\boldsymbol{k},\boldsymbol{s}]}_{BA}\right) - f\left(\boldsymbol{M}^{[i,\boldsymbol{k},\boldsymbol{s}]}_{B(b)A}\right)\right], \qquad i = 1, \dots, n, \tag{26}$$

$$\Delta^{i}_{ba|A} = \frac{1}{c!} \sum_{\boldsymbol{k}\in\boldsymbol{K},s:k(s)=j} \left[f\left(\boldsymbol{M}^{[i,\boldsymbol{k},\boldsymbol{s}]}_{B(b)A}\right) - f\left(\boldsymbol{M}^{[i,\boldsymbol{k},\boldsymbol{s}]}_{B(a)A}\right)\right], \qquad i = 1, \dots, n. \tag{27}$$

The final trend components are averages of the two equally possible contour paths defined by Equations (21)–(23) and (25)–(27):

$$\delta^{i,j}_{Aa|AB} = \frac{1}{2}\left[\delta^{i,j}_{Aa|B} - \delta^{i,j}_{aA|A}\right], \tag{28}$$

$$\delta^{i,j}_{Bb|AB} = \frac{1}{2}\left[\delta^{i,j}_{Bb|B} - \delta^{i,j}_{bB|A}\right]. \tag{29}$$

Formulae (28) and (29) refer to components contributed by temporal trends within each of the two populations. The total trend component produced by the difference in temporal changes is

$$Trend^{i,j} = \delta^{i}_{ab|AB} = \delta^{i}_{Aa|AB} - \delta^{i}_{Bb|AB} \tag{30}$$

Similarly, the initial difference component is

$$Initial^{i,j} = \Delta^{i,j}_{ab|AB} = \frac{1}{2}\left[\Delta^{i,j}_{ab|B} - \Delta^{i,j}_{ba|A}\right] \tag{31}$$

Equations (21)–(23) and (25)–(31) determine the algorithm of contour decomposition by age and cause of death.

2.3 Example: Mortality development of the USA and England and Wales in 1980–2010

Following the original study introducing the contour decomposition method by Jdanov et al. (2017), we illustrate the application of the extended method by performing age and cause decomposition of the difference in life expectancy at birth between the USA and England and Wales in 2010. The decomposition provides age- and cause-specific contributions to the differences in life expectancy at birth in 2010 attributable to (a) the

initial differences in age- and cause-specific death rates in 1980 and (b) the differences in trends in age- and cause-specific death rates during 1980–2010.

For this empirical exercise, we use age-, sex-, and cause-specific death counts from the WHO mortality database (WHO 2023) and population exposures from the Human Mortality Database (HMD 2023). To avoid comparability issues due to possible differences in coding practices, we use only five large groups of causes of death: (1) cardiovascular diseases (CVD), (2) trachea, bronchus, and lung (TBL) cancer, (3) other cancers, (4) external causes of death, and (5) other causes of death. The data and R scripts used for decomposition are available in the GitHub repository (Jdanov 2024).

Life expectancy at birth in the USA in 1980 was 70.0 and 77.5 years for males and females respectively. For the same year, England and Wales showed slightly higher life expectancy at birth for males (70.7 years), whereas the female life expectancy of 76.8 years lagged behind the United States. Between 1980 and 2003, both countries experienced overall improvements in general mortality stemming from progress in reducing the burden of chronic causes of death (Shkolnikov et al. 2011). However, the difference in life expectancy between the two countries became more pronounced due to more systematic and faster progress in the United Kingdom. From 1980 to 2010 the difference in life expectancy at birth between England and Wales and the USA increased from 0.7 to 2.3 years for males and reversed for females to reach 1.4 years in favor of England and Wales.

Using the contour decomposition method, Jdanov et al. (2017) decomposed the gap in life expectancy in 2010 into the age-specific initial differences component and age-specific trend contributions from 1980. We further decompose these components by cause of death. The results for life expectancy are displayed in Figures 1a (males) and 1b (females). Detailed results are provided in Table A-1 in the Appendix. The final difference (red bars in each top left panel) is the sum of orange and blue bars; i.e., initial and trend components. Although the age shape of the final difference is quite similar for both sexes, their initial and trend components are quite different. The total contribution (sum across all ages) of the initial component is 0.0 years for males and 1.4 years for females. Trend components contributed –2.2 years for males and –2.8 years for females to the total life expectancy difference in 2010, suggesting that trends were more favorable in the United Kingdom. The initial excess in mortality at ages below 65 in the USA contributed to its life expectancy disadvantage in 2010, but the lower initial level of mortality at ages 65+ partially counterbalanced this difference. The trend contributions were unfavorable for the United States across almost all ages for both sexes. The only favorable age-specific trend component is for the age range 15 to 39 years.

All components are further split by cause of death. The initial differences in CVD mortality observed in 1980 were favorable for the United States across almost all age groups except the last open-ended age interval 85+. The reverse situation can be observed

for the trend component, suggesting less favorable CVD mortality changes in the United States leading to substantial contributions to an increase in the longevity gap in 2010 (in favor of England and Wales). It can also be noted that although external causes played a minor role for females, they were important contributors to the longevity difference among males. Figure 1a suggests that unfavorable initial conditions in the United States were not fully compensated by slightly faster progress in reducing external cause mortality during 1980–2010. In addition, the USA had an advantage in the initial difference in cancer and other cause mortality at old ages, which was counterbalanced by higher rates at younger ages and slower progress in reducing cancer mortality at older ages during 1980–2010.

Figure 1a.: Decomposition of the difference in life expectancy between the USA and England and Wales in 2010 into initial difference component and trend contributions, 1980 to 2010, by age and cause of death, males

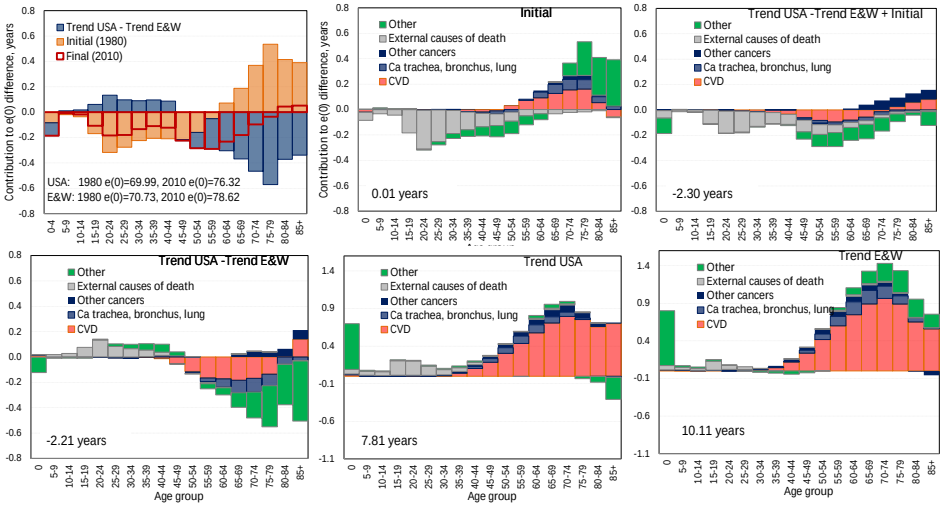
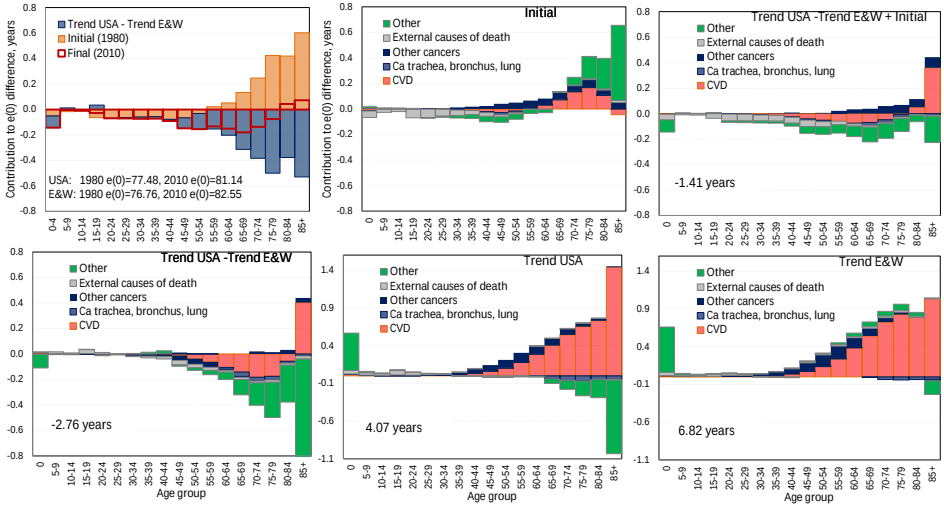


Figure 1b: Decomposition of the difference in life expectancy between the USA and England and Wales in 2010 into initial difference component and trend contributions, 1980 to 2010, by age and cause of death, females



3. Discussion

This paper presents a further advance of the contour decomposition method. The original method allows performing a one-dimensional decomposition of the difference in aggregated measures into the age-specific contributions of initial conditions and trend components. Since 2017 this method has been successfully applied in several papers. For example, Leon, Jdanov, and Shkolnikov (2019) analyzed the growing mortality disadvantage of England and Wales from 2011 to 2019 if compared to other selected developed countries. van Raalte et al. (2020) decomposed the difference in life expectancy between German regions from 1980 to 2014. Abrams, Myrskylä, and Mehta (2021) used contour decomposition in sensitivity analysis to re-estimate a growing rural–urban divide in life expectancy in the USA.

The conventional decomposition methods identify the contributions of event-specific rates to either the total difference in the aggregated measure between populations at a certain time point or to the change in event-specific rates between two time points within one population. The contour decomposition method allows measuring the impact of the past origins of this difference. For example, the high contribution of young adult ages to the observed difference in life expectancy between men in the United Kingdom

and the United States stems from the high impact of excess US mortality in the past, whereas the trend component contributes to the diminishing gap between the two countries (Jdanov et al. 2017).

The current study extends the contour method by adding a second covariate beyond age. This covariate may refer to causes of death or other characteristics such as socioeconomic status. We provide an empirical application of this method using death rates by cause of death. This is an important characteristic for understanding the main drivers of longevity divergences. In our example, we demonstrated that the main driver of the increasing difference between the USA and England and Wales was cardiovascular mortality.

Cause-specific contour decomposition could be a useful tool for analyzing the effects of COVID-19 on mortality. This newly developed method can be used to estimate the extent to which longevity disparities between countries in the pandemic year depend on age- and cause-specific mortality disparities observed before the pandemic (initial conditions) and age- and cause-specific mortality changes between pre-pandemic and pandemic year (trend component).

The proposed method has several limitations. First, this method inherited all the limitations of the original contour decomposition. In particular, it depends on an arbitrary pre-defined period. The initial and trend components will differ if we change the period under consideration. Moreover, this method is, in general, not additive concerning the selected period: two consequent decompositions for periods t_1 to t_2 and t_2 to t_3 will produce somewhat different initial and trend components compared to decomposing directly over the period t_1 to t_3. The method depends on the path of mortality change and indirectly assumes a linear change over time. As result, the sum over a sequence of decompositions calculated relying on a (real) non-linear trend will produce somewhat different initial and trend components when compared to decomposing the change between the beginning and end of the period.

Second, the algorithm is sensitive to computational capacity. If we have n age groups and c cause-of-death groups then the indicator function will be calculated $2 \times n \times c!$ times. Thus, the practical use of the algorithm is limited to 6–8 groups of causes of death. This is enough for the vast majority of empirical analyses, taking into account that using more specific and larger numbers of causes of death may lead to comparability issues due to changes in ICD classification and coding practices. Nevertheless, this limitation might be solved if we refuse a complete permutation of the causes of death (as we did for the first dimension, age). For example, we could use only the first 10,000 randomly selected permutations instead of the complete set of permutations.

In this study we presented a new method, using cause-specific contour decomposition. Nevertheless, all equations in the paper are presented in a form that might be considered a description of a general two-dimensional contour decomposition. This

method could be used to decompose by SES group, birth order, or any other demographic or epidemiologic characteristic instead of causes of death.

R scripts for contour decomposition and the data used in the paper are available on GitHub (Jdanov 2024).

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Appendix: Results of the contour decomposition

Table A-1: Results of the decomposition of the difference in life expectancy between the USA and England and Wales in 2010 into initial difference component and trend contributions from 1980 to 2010 by age and cause of death, females

	Final	Trend USA					
Age		All causes	CVD	Ca trachea bronchus, lung	Other cancers	External	Other
Females							
0	–0.14	0.57	0.02	0.00	0.01	0.05	0.49
5–9	0.00	0.06	0.00	0.00	0.01	0.03	0.02
10–14	–0.01	0.04	0.00	0.00	0.00	0.02	0.01
15–19	–0.03	0.08	0.00	0.00	0.01	0.06	0.01
20–24	–0.07	0.05	0.00	0.00	0.01	0.04	0.01
25–29	–0.07	0.03	0.01	0.00	0.01	0.02	0.00
30–34	–0.07	0.03	0.00	0.00	0.02	0.00	0.00
35–39	–0.07	0.05	0.01	0.00	0.03	–0.01	0.00
40–44	–0.09	0.09	0.03	0.01	0.05	–0.01	0.01
45–49	–0.15	0.12	0.06	0.01	0.07	–0.02	0.00
50–54	–0.16	0.19	0.10	0.02	0.10	–0.01	–0.01
55–59	–0.13	0.29	0.18	0.01	0.11	0.00	–0.01
60–64	–0.15	0.38	0.28	0.00	0.11	0.01	–0.02
65–69	–0.18	0.40	0.40	–0.04	0.09	0.01	–0.06
70–74	–0.13	0.45	0.54	–0.06	0.08	0.01	–0.11
75–79	–0.07	0.44	0.65	–0.07	0.05	0.01	–0.20
80–84	0.05	0.47	0.73	–0.05	0.03	0.00	–0.24
85+	0.22	0.42	1.44	–0.05	0.01	–0.01	–0.98
Males							
0	–0.19	0.70	0.02	0.00	0.01	0.06	0.61
5–9	–0.01	0.08	0.00	0.00	0.01	0.05	0.02
10–14	–0.02	0.07	0.00	0.00	0.01	0.05	0.01
15–19	–0.11	0.22	0.00	0.00	0.01	0.19	0.01
20–24	–0.19	0.21	0.00	0.00	0.01	0.19	0.01
25–29	–0.18	0.15	0.00	0.00	0.01	0.12	0.01
30–34	–0.14	0.10	0.01	0.00	0.01	0.07	0.02
35–39	–0.11	0.14	0.04	0.01	0.02	0.05	0.02
40–44	–0.12	0.20	0.10	0.03	0.03	0.03	0.02
45–49	–0.23	0.28	0.18	0.05	0.03	0.00	0.01
50–54	–0.29	0.43	0.30	0.08	0.05	0.00	0.00
55–59	–0.29	0.59	0.43	0.10	0.06	0.01	0.00
60–64	–0.23	0.81	0.58	0.11	0.07	0.02	0.04
65–69	–0.19	0.96	0.71	0.08	0.09	0.02	0.05
70–74	–0.09	1.00	0.80	0.06	0.09	0.02	0.03
75–79	–0.04	0.82	0.75	0.02	0.07	0.01	–0.03
80–84	0.05	0.63	0.65	0.00	0.05	0.01	–0.08
85+	0.12	0.51	0.70	–0.01	0.02	0.00	–0.29

Table A–1: (Continued)

Age	Final	Initial					
		All causes	CVD	Ca trachea, bronchus, lung	Other cancers	External causes of death	Other
Females							
0	–0.14	–0.05	–0.02	0.00	0.01	–0.05	0.01
5–9	0.00	–0.02	0.00	0.00	0.00	–0.02	0.01
10–14	–0.01	–0.01	0.00	0.00	0.00	–0.02	0.01
15–19	–0.03	–0.06	0.00	0.00	0.00	–0.07	0.00
20–24	–0.07	–0.07	0.00	0.00	0.00	–0.07	–0.01
25–29	–0.07	–0.06	0.00	0.00	0.00	–0.05	–0.01
30–34	–0.07	–0.06	–0.01	0.00	0.01	–0.04	–0.02
35–39	–0.07	–0.06	–0.01	0.00	0.02	–0.03	–0.03
40–44	–0.09	–0.08	–0.02	–0.01	0.02	–0.03	–0.04
45–49	–0.15	–0.06	–0.03	–0.02	0.04	–0.02	–0.04
50–54	–0.16	–0.03	–0.02	–0.01	0.05	–0.01	–0.04
55–59	–0.13	0.03	0.00	0.00	0.06	0.00	–0.03
60–64	–0.15	0.05	0.03	0.01	0.04	0.00	–0.02
65–69	–0.18	0.14	0.07	0.01	0.05	0.00	0.01
70–74	–0.13	0.25	0.13	0.01	0.04	0.01	0.06
75–79	–0.07	0.41	0.17	0.01	0.05	0.01	0.17
80–84	0.05	0.40	0.11	0.01	0.03	0.01	0.24
85+	0.22	0.61	–0.04	0.00	0.05	0.02	0.59
Males							
0	–0.19	–0.08	–0.02	0.00	0.00	–0.06	0.00
5–9	–0.01	–0.02	0.00	0.00	0.00	–0.03	0.01
10–14	–0.02	–0.04	0.00	0.00	0.00	–0.04	0.01
15–19	–0.11	–0.18	0.00	0.00	0.00	–0.18	0.01
20–24	–0.19	–0.32	0.00	0.00	0.00	–0.31	–0.01
25–29	–0.18	–0.28	0.00	0.00	0.00	–0.25	–0.03
30–34	–0.14	–0.22	–0.01	0.00	0.00	–0.18	–0.04
35–39	–0.11	–0.21	–0.02	0.00	0.00	–0.14	–0.05
40–44	–0.12	–0.21	–0.02	–0.01	0.00	–0.11	–0.07
45–49	–0.23	–0.21	–0.01	–0.02	0.00	–0.09	–0.09
50–54	–0.29	–0.16	0.03	–0.02	0.00	–0.07	–0.10
55–59	–0.29	–0.04	0.07	0.01	0.00	–0.05	–0.07
60–64	–0.23	0.07	0.09	0.04	0.01	–0.03	–0.05
65–69	–0.19	0.18	0.13	0.07	0.02	–0.03	0.00
70–74	–0.09	0.34	0.15	0.08	0.03	–0.02	0.10
75–79	–0.04	0.47	0.16	0.08	0.03	–0.02	0.26
80–84	0.05	0.36	0.05	0.05	0.01	–0.01	0.30
85+	0.12	0.31	–0.06	0.02	0.00	–0.01	0.37

Table A–1: (Continued)

	Final	Trend E&W					
Age		All causes	CVD	Ca trachea, bronchus, lung	Other cancers	External	Other
Females							
0	–0.14	0.66	0.01	0.00	0.01	0.04	0.60
5–9	0.00	0.05	0.00	0.00	0.01	0.02	0.02
10–14	–0.01	0.04	0.00	0.00	0.00	0.01	0.02
15–19	–0.03	0.04	0.00	0.00	0.01	0.03	0.01
20–24	–0.07	0.05	0.01	0.00	0.01	0.02	0.01
25–29	–0.07	0.04	0.01	0.00	0.01	0.02	0.01
30–34	–0.07	0.04	0.01	0.00	0.03	0.01	0.00
35–39	–0.07	0.06	0.02	0.00	0.05	0.01	–0.01
40–44	–0.09	0.11	0.04	0.01	0.06	0.01	–0.01
45–49	–0.15	0.21	0.07	0.01	0.11	0.02	0.01
50–54	–0.16	0.32	0.14	0.02	0.14	0.02	0.01
55–59	–0.13	0.45	0.24	0.01	0.16	0.02	0.02
60–64	–0.15	0.58	0.38	0.01	0.12	0.02	0.04
65–69	–0.18	0.72	0.54	–0.01	0.10	0.02	0.06
70–74	–0.13	0.83	0.72	–0.04	0.06	0.02	0.06
75–79	–0.07	0.92	0.83	–0.04	0.03	0.02	0.08
80–84	0.05	0.82	0.79	–0.04	0.00	0.02	0.05
85+	0.22	0.81	1.03	–0.03	–0.02	0.01	–0.18
Males							
0	–0.19	0.80	0.00	0.00	0.01	0.06	0.73
5–9	–0.01	0.07	0.00	0.00	0.02	0.03	0.02
10–14	–0.02	0.05	0.00	0.00	0.01	0.02	0.02
15–19	–0.11	0.15	0.00	0.00	0.01	0.12	0.02
20–24	–0.19	0.08	0.00	0.00	0.02	0.06	0.00
25–29	–0.18	0.05	0.01	0.00	0.01	0.04	0.00
30–34	–0.14	0.02	0.01	0.00	0.01	0.00	–0.02
35–39	–0.11	0.04	0.04	0.00	0.02	0.00	–0.03
40–44	–0.12	0.12	0.12	0.01	0.03	0.00	–0.04
45–49	–0.23	0.29	0.24	0.04	0.04	0.01	–0.03
50–54	–0.29	0.56	0.42	0.07	0.06	0.01	0.00
55–59	–0.29	0.84	0.60	0.13	0.06	0.02	0.04
60–64	–0.23	1.11	0.75	0.17	0.07	0.02	0.09
65–69	–0.19	1.33	0.89	0.18	0.07	0.02	0.17
70–74	–0.09	1.43	0.96	0.16	0.05	0.02	0.24
75–79	–0.04	1.33	0.89	0.11	0.03	0.01	0.29
80–84	0.05	0.94	0.65	0.05	–0.01	0.01	0.24
85+	0.12	0.70	0.56	0.01	–0.06	0.00	0.18