The groupwise Decomposition: Estimating Group-Specific Contributions to Life Table Functions

Eugenio Paglino

Department of Sociology
Population Studies Center
University of Pennsylvania

Introduction

The decomposition of demographic measures is a fundamental tool in a demographer's toolkit. Through decomposition of demographic measures, researchers can gain crucial insights into the importance of different mechanisms in producing demographic change. Most decomposition techniques focus on changes in demographic measures over time or, more generally, differences between demographic rates (Andreev, Shkolnikov, and Begun 2002; Arriaga 1984; Caswell 1989; Das Gupta 1978; Horiuchi, Wilmoth, and Pletcher 2008; Kitagawa 1964; Vaupel and Canudas-Romo 2002). However, fewer techniques are available to researchers needing to estimate the contribution of different subpopulations to the difference in a demographic measure, such as life expectancy, between a baseline population and the total population. Although some of the general decomposition techniques can be used for this purpose with some adjustments, I will show that they quickly become computationally inefficient even when few groups are involved. This paper thus develops a new decomposition technique which overcomes these limitations, discusses one practical application, and shows how the technique can be further extended.

Relationship

Given a population (T), a baseline subpopulation (B), and a partition of the population into mutually exclusive subgroups $(G_1, G_2, \ldots, G_N)$, indexed by i, such that $\square_n D_x^B + \sum_{i=1}^{N} \square_n D_x^i = \square_n D_x^T$ and $\square_n L_x^B + \sum_{i=1}^{N} \square_n L_x^i = \square_n L_x^T$, how can we compute the contribution of subgroups $G_1, G_2, \ldots G_N$ to the difference between the life table functions of the baseline population $(l_x^B, {}_n L_x^B, {}_n T_x^B, e_x^B)$ and those of the total population $(l_x^T, {}_n L_x^T, {}_n T_x^T, e_x^T)$? This paper proposes a decomposition method to answer this question and proves some of its properties. It then illustrates one practical application of the proposed decomposition.

We can define the problem formall as follows. Given a population (T), a baseline population (B), and a partition of the population excluding B into mutually exclusive subgroups $(G_1, G_2, \ldots, G_N)$, we want to find group-specific terms C^n that satisfy the following equation:

$$C^n \ (n = 1, \ 2, \ ..., \ N) \quad s.t. \quad \sum_{n=1}^{N} C^n = l(T) - l(B)$$

Where $l(\cdot)$ is a generic life table function which, as we will see, can be left unspecified.

A Decomposition for $N = 2$

Let us consider a population (T) that is composed of a baseline population (B) and two mutually exclusive

contributing groups (G_1, G_2). Let us also denote the population combining (G_1, G_2) as G. Finally, let us be as

general as we can and leave the life table function of interest unspecified. As in other general decomposition

techniques, we will see that computationally all that matters is that we can write the life table measure as a

function of a single input vector storing exposures and deaths counts (Andreev et al. 2002; Caswell 1989;

Horiuchi et al. 2008). We will denote with $l(A)$ the life table function for population A. To be precise, the

generic $l(\cdot)$ function takes as input a vector of age-specific death counts and exposures for population A

(stacked to form a single vector) and outputs the life table measure $l(A)$. We can trivially write the total

contribution of the two groups as:

$$C^G = l(T) - l(B)$$

Because both the exposures and the death counts involved in the computation of life tables combine

additively, we have that $l(B) = l(T - G)$. Equivalently, we could write $l(T) = l(B + G)$. The two previous

equations hold because once death counts and exposures for a population are stacked into a single vector, to

obtain the corresponding vector for the combined population we just need to sum the two subpopulation-

specific vectors. Together, these two equations allow us to write:

$$C^G = l(T) - l(B) = l(B + G) - l(B) = l(T) - l(T - G)$$

Looking at the equation above it is apparent that the total contribution of population G can equivalently be understood as an addition process starting from the baseline population $C^G = l(B + G) - l(B)$ or as a subtraction process starting from the total population $C^G = l(T) - l(T - G)$. It now becomes useful to introduce another layer of notation. We define $C^{G+} \equiv l(B + G) - l(B)$ and call it the "addition contribution" of G. We instead define $C^{G-} \equiv l(T) - l(T - G)$ and call it the "subtraction contribution" of G. Clearly, when a single contributing population is considered $C^{G+} = C^{G-}$. However, we will see that even in the case of two contributing subpopulations (G_1, G_2), $C^{1+} \neq C^{1-}$ and $C^{2+} \neq C^{2-}$ so that the notation I just introduced becomes useful. To see why these two inequalities arise, let us consider C^{1+} and C^{1-}. Suppose for the moment that both G_1 and G_2 contribute positively to the life table function we are considering, and more precisely that $C^{1+}, C^{1-}, C^{2+}, C^{2-} > 0$. When we compute C^{1-} we are then starting from a population T which already encapsulates the positive effect of population G_2. On the contrary, when we compute C^{1+} we are starting from the baseline population B that has not yet received the positive effect of population G_2. Furthermore, population B from which are starting in our calculations for C^{1+} is smaller than population $B + G_2$ from which we start in our calculations for C^{1-}. Consequently, the effect of G_1 will be larger when computed as C^{1+} than when computed as C^{1-} and $C^{1+} > C^{1-}$. A specular argument can be made for C^{2+}, C^{2-}. While the inequality $C^{1+} > C^{1-}$ depends on the assumption that both populations have a positive effect, it illustrates the general principle that leads to the inequality $C^{1+} \neq C^{1-}$.

The inequality above means that we now have two different measures of the contribution of each group. One way of solving this inconsistency is to introduce a third type of contribution $C^1 \equiv \frac{1}{2}(C^{1+} + C^{1-})$, which we call the "average contribution". It turns out that the average contributions have a nice property that both the addition and the subtraction contributions generally lack.

$$C^1 + C^2 = \frac{1}{2}(C^{1+} + C^{1-}) + \frac{1}{2}(C^{2+} + C^{2-})$$

$$= \frac{1}{2}[(l(B + G_1) - l(B)) + (l(T) - l(T + G_1)) + (l(B + G_2) - l(B)) + (l(T) - l(T + G_2))]$$

$$= \frac{1}{2}[2(l(T) - l(B)) + (l(B + G_1) - l(T - G_2)) + (l(B + G_2) - l(T - G_1))]$$

$$= (l(T) - l(B)) + \frac{1}{2}[(l(B + G_1) - l(T - G_2)) + (l(B + G_2) - l(T - G_1))]$$

$$= C^G + \frac{1}{2}[(l(B + G_1) - l(T - G_2)) + (l(B + G_2) - l(T - G_1))]$$

$$= C^G + \frac{1}{2}[(l(B + G_1) - l(B + G_1)) + (l(B + G_2) - l(B - G_2))]$$

$$= C^G$$

So, the two average contributions sum to the total contribution of G, which establishes C^1, C^2 as a legitimate decomposition of C^G or of the difference $l(T) - l(B)$. Note that the substitutions in the second last line hold because of the additivity of exposures and deaths so $l(T - G_2) = l(B + G_1 + G_2 - G_2) = l(B + G_1)$ and similarly $l(T - G_1) = l(B + G_2)$. Notice also that no special properties of the life table function were used in the proof, which establishes that this approach is valid for functions other than life expectancy as long as they can be written as a function of a vector of death counts and exposures.

Extending the Decomposition to the Case $N = 3$

The case of three groups (G_1, G_2, G_3) introduces a few additional complications which illuminate some properties of this decomposition and will allow us to find a general expression for any number of groups. The main difference with the $(N = 2)$ case is that our notation C^{n+}, C^{n-} for $n = 1,2,3$ is no longer sufficient to describe all possible ways of computing the contribution of group G_n to the life table function for the total population. Indeed, we now have four ways of computing the contribution of G_1:

1. $l(B + G_n) - l(B)$

2. $l(B + G_2 + G_1) - l(B + G_2)$

3. $l(B + G_3 + G_1) - l(B + G_3)$

4. $l(T) - l(B + G_2 + G_3)$

Number 1 and 4 are equal to C^{1+} and C^{1-}, but number 2 and 3 are outside of what we have seen so far. In the next section, I will introduce a more general notation to capture these cases. However, for the moment, let us focus on how to define the average contribution in this case. It turns out that the average contribution in this case assigns weights to each term that are inversely proportional to the number of groups $N = 3$ and to the number of contributions involving the same number of subpopulations. Notice that contributions 1 and 4 involve 1 and 3 subpopulations respectively, while contributions 2 and 3 each involve 2 subpopulations. As such, contributions 1 and 4 have weight $\frac{1}{N}\frac{1}{1} = \frac{1}{3}$, while contributions 2 and 3 have weight $\frac{1}{N}\frac{1}{2} = \frac{1}{3}\frac{1}{2} = \frac{1}{6}$. The use of these weights is equivalent to first averaging within contributions involving the same number of subpopulations and then averaging between contributions involving different numbers of subpopulations. While this might seem unintuitive, I will now show that it leads to a set of average contributions that sum to the total contribution as in the $N = 2$ case.

$$C^1 + C^2 + C^3 = \frac{1}{3}(l(B + G_1) - l(B)) + \frac{1}{6}\left(l(B + G_2 + G_1) - l(B + G_2)\right) + \frac{1}{6}\left(l(B + G_3 + G_1) - l(B + G_3)\right) + \frac{1}{3}\left(l(T) - l(B + G_2 + G_3)\right)$$

$$+ \frac{1}{3}(l(B + G_2) - l(B)) + \frac{1}{6}\left(l(B + G_1 + G_2) - l(B + G_1)\right) + \frac{1}{6}\left(l(B + G_3 + G_2) - l(B + G_3)\right) + \frac{1}{3}\left(l(T) - l(B + G_1 + G_3)\right)$$

$$+ \frac{1}{3}(l(B + G_3) - l(B)) + \frac{1}{6}\left(l(B + G_1 + G_3) - l(B + G_1)\right) + \frac{1}{6}\left(l(B + G_2 + G_3) - l(B + G_2)\right) + \frac{1}{3}\left(l(T) - l(B + G_1 + G_2)\right)$$

It is easy to see that one can take out of this complicated expression the target value $l(T) - l(B)$. We can then reorder the remaining terms and write:

$$C^1 + C^2 + C^3 = \left(l(T) - l(B)\right) + \frac{1}{3}\left(l(B + G_1) + l(B + G_2) + l(B + G_3)\right)$$

$$-\frac{1}{3}\left(l(B + G_1 + G_2) + l(B + G_1 + G_3) + l(B + G_2 + G_3)\right)$$

$$-\frac{1}{6}\left(2l(B + G_1) + 2l(B + G_2) + 2l(B + G_3)\right)$$

$$+\frac{1}{6}\left(2l(B + G_1 + G_2) + 2l(B + G_1 + G_3) + 2l(B + G_2 + G_3)\right)$$

From which one can easily verify that $C^1 + C^2 + C^3 = \left(l(T) - l(B)\right)$ as we wanted to prove. This result establishes (C^1, C^2, C^3) as a legitimate decomposition of C^G.

By comparing the computations involved in the case $N = 2$ to those for the case $N = 3$, becomes apparent that the computational requirement for this method increases very fast as the number of groups increases. However, the number of groups in the typical demographic application will not be too large and I will show that compared to alternative approached, this decomposition method is still very fast.

Generalizing the Decomposition to a Population with N subgroups

To study the general case of N contributing groups, it is useful to introduce a slightly more general notation. We define:

$$C^{n,m,i} = l(B + G_i^m + G_n) - l(B + G_i^m)$$

With $n = \{1,2,\dots,N\}, m = \{0,1,\dots,N-1\}, i = \{1,2,\dots,\binom{N-1}{m}\}$ and where G_i^m is the ith set of subpopulations G_k with $k \neq n$ such that $\#G_i^m = m$. In words, $C^{n,m,i}$ is the contribution of subgroup G_n to the life table function $l(\cdot)$ for the total population calculated as the difference between the value of $l(\cdot)$ for the population obtained by combining the baseline population, the ith subset of G_k's not including G_n, and G_n, $l(B + G_i^m + G_n)$, and the value of $l(\cdot)$ for the population obtained by combining the baseline population and

the ith possible subset of G_k's not including G_n, $l(B + G_i^m)$. This definition might seem confusing but it's just a generalization of the types of contributions we have seen in the cases $N = 2, 3$. Indeed, for $N = 2$, our familiar C^{1+} is simply $C^{1,0,1}$ while C^{1-} is $C^{1,1,1}$. For $N = 3$, we have the more interesting "internal" terms for which we had no notation so far. With this new notation we can write:

1. $l(B + G_2 + G_1) - l(B + G_2) = C^{1,1,1}$

2. $l(B + G_3 + G_1) - l(B + G_3) = C^{1,1,2}$

With these expressions, we can see why m should be bounded between 0 and $N - 1$ and i between 1 and $\binom{N-1}{m}$. With $m = 0$, we recover C^{1+}, when $m = 0$, there is no need for an index i, which we can conventionally set to 1. For $m = 1$, G_i^m contains only one element which we can choose out of the $N - 1$ groups that are not G_n. The first of these groups will be denoted as G_1^1, the second as G_2^1, and so on. The order in which we select the groups does not matter because addition is commutative. Notice that, for a general value m there will be $\binom{N-1}{m}$ of these groups, which explains the limits imposed on i. Finally, when we reach $m = N - 1$, we obtain C^{1-} because:

$$l(B + G_1^{N-1} + G_1) - l(B + G_1^{N-1}) = l(T) - l(T - G_1) = C^{1-}$$

Clearly, there is only one way of choosing $N - 1$ elements from a set of $N - 1$ elements.

As for the $N = 3$ case, we now need to find appropriate weights for each contribution $C^{n,m,i}$. The general principle is still the same, we need weights that are inversely proportional to the number of contribution types N and inversely proportional to the number of contributions for the specific type m. This consideration leads to a simple expression:

$$w^m = \frac{1}{N\binom{N-1}{m}}$$

Which is just a generalization of the weights we derived for $(N = 3)$. In the expression above, w^m denotes the weight for all terms $C^{n,m,i}$. These weights are equal for all m-type contributions and ensure that each set of m-contributions is collectively assigned the same weight $\frac{1}{N}$ while each of its members is also assigned the same weight $\frac{1}{N\binom{N-1}{m}}$. With our new notation and having defined appropriate weights, we can define the average contribution of group G_n as:

$$C^n = \sum_{m=0}^{N-1} \frac{1}{N} \sum_{i=1}^{\binom{N-1}{m}} \frac{1}{\binom{N-1}{m}} C^{n,m,i}$$

To establish that average contributions defined in this way form a valid decomposition of C^G into group-specific contributions, we need to prove that:

$$\sum_{n=1}^{N} C^n = l(T) - l(B)$$

We already saw that for $N = 2, 3$, the proof involves showing that all terms except $l(T)$ and $l(B)$ have weights summing to 0. This is harder to do directly now that we have many terms. However, we can start by recognizing that the life table function computed for a given population composed by a set of subgroups plus the baseline population can appear in two ways:

1. As a term of the form $l(B + G_i^m + G_n)$ in a contribution of the type $C^{n,m,i}$

2. As a term of the form $l(B + G_i^{m+1})$ in a contribution of the type $C^{k,m,i}$ where $k \neq n$.

In the first case, the life table function will have weight w^m and in the second case it will have weight $-w^{m+1}$. To understand what the final weight will be for each term $l(B + G_i^m + G_n)$, we just need to know how many times it will appear with weight w^m and how many times with weight w^{m+1}. For terms of the first type, we have $m + 1$ ways of choosing n while keeping the subgroups involved the same. On the other hand, terms of the second type can only appear in contributions involving the $N - (m + 1)$ excluded groups. With this information, we are now able to compute the weight associated with the life table function computed for each population:

$$w(l(B + G_i^m + G_n)) = (m + 1)w^m - (N - m - 1)w^{m+1}$$

$$= (m + 1)\frac{1}{N\binom{N-1}{m}} - (N - m - 1)\frac{1}{N\binom{N-1}{m+1}}$$

$$= (m + 1)\frac{(N - 1)!}{m!\,(N - 1 - m)!} - (N - m - 1)\frac{(N - 1)!}{(m + 1)!\,(N - 1 - m - 1)!}$$

$$= (m + 1)\frac{m!\,(N - 1 - m)!}{(N - 1)!} - (N - m - 1)\frac{(m + 1)!\,(N - 1 - m - 1)!}{(N - 1)!}$$

$$= \frac{(m + 1)!\,(N - 1 - m)!}{(N - 1)!} - \frac{(m + 1)!\,(N - 1 - m)!}{(N - 1)!}$$

$$= 0$$

Which proves that life table functions for all populations of the type $B + G_i^m + G_n$ cancel out. The only two exceptions are $l(B)$, which appears N times with weight $-\frac{1}{N}$, and $l(T)$, which appears N times with weight $\frac{1}{N}$. Thus, summing the average contributions for our N groups we obtain:

$$\sum_{n=1}^{N} C^n = l(T) - l(B)$$

as desired. This result shows that the average contributions provide a decomposition of the total contribution C^G even in the case of N subgroups.

Origins of the Decomposition and Notes on Its Interpretation

The basic idea for the decomposition method developed in this paper was originally proposed by Hendi and Ho (2021) to investigate the contribution of the foreign born population to the national life expectancy at age 1 in the United States (Hendi and Ho 2021). In that context, Hendi and Ho considered a total population T including all residents of the United States, a baseline population B including only US-born residents, and a single contributing group G including all foreign-born residents. They proposed to compute the contribution of the foreign-born population to the US life expectancy at age 1 as:

$$C^G = e_1^T - e_1^B$$

Where e_1^T is the life expectancy at age 1 for the total population and e_1^B is the life expectancy at age 1 for US-born residents (the baseline population). The logic behind this formula is clear, the difference between the life expectancy of all US residents and US-born residents must be explained by the contribution of the foreign-born population. However, it is important to highlight some possible difficulties in the interpretation of such contribution before moving forward. Using Hendi and Ho (2020) example, if x^{USB} is the vector of period age-specific mortality rates for US-born residents, x^{FB} is the vector of period age-specific mortality rates for the foreign-born residents, and x^T is the vector of age-specific mortality rates for the total population, and assuming $e_1^{FB} \geq e_1^{USB}$, there is no guarantee that:

$$e_1^{USB} \leq e_1(x^{FB}w^{FB} + x^{USB}w^{USB}) = e_1^T \leq e_1^{FB}$$

Where w^{FB} and w^{USB} are vectors of age-specific weights proportional to the share of the foreign-born and US-born in the population, respectively, and such that $w_i^{FB} + w_i^{USB} = 1 \; \forall i$. The two inequalities fail to hold because a priori:

$$\max\left(e_1^T(x^{FB}w^{FB} + x^{USB}w^{USB})\right) \; w.r.t. \; (w^{FB}, w^{USB}) = e_1(\min(x^{FB}, x^{USB}))$$

where $\min(x^{FB}, x^{USB})$ is the set of elementwise (age-specific) minimums and:

$$\min\left(e_1^T(x^{FB}w^{FB} + x^{USB}w^{USB})\right) \; w.r.t. \; (w^{FB}, w^{USB}) = e_1(\max(x^{FB}, x^{USB}))$$

where $\max(x^{FB}, x^{USB})$ is the set of elementwise (age-specific) maximums. Equivalently, as long as the two sets of mortality rates x^{FB}, x^{USB} cross at some point (i.e. $\exists i,j \; s.t. \; x_i^{FB} > x_i^{USB} \wedge x_j^{FB} < x_j^{USB}$), there will be a set of weights such that $e_1^T > \max(e_1^{FB}, e_1^{USB})$ and also a set of weights such that $e_1^T < \min(e_1^{FB}, e_1^{USB})$. The failure of e_1^T to be bounded by (e_1^{FB}, e_1^{USB}) has two consequences that affect how we think of the contribution of a group G to the total life-expectancy given a certain baseline population:

1. It can happen that $C^G = e_1^T - e_1^B > e_1^G - e_1^B$. In words, a group G could contribute more years to the total life expectancy than the difference between its life expectancy and that of the baseline population.

2. Suppose we exchange the role of the contributing group G and that of the baseline population B. We would then define: $C^B = e_1^T - e_1^G$. It is possible that both $C^B > 0$ and $C^G > 0$ even though B and G, by definition, form the total population T. Of course, it is also possible that $C^B < 0$ and $C^G < 0$.

Given these two facts, it is important to understand that the contribution of group G computed with the Hendi and Ho (2020) formula, and similar contributions computed with the technique developed in this paper, depend on the mortality rates of the baseline population and thus on the choice of a baseline. More precisely, the contribution C^G does not capture the effect of group G "in isolation" but also its interaction with the mortality conditions of the baseline population. Keeping this is mind, when the choice of a baseline does not have strong theoretical foundations, researchers should test the robustness of the results to the choice of a different baseline and, if mayor differences are found, discuss why it might be the case. While the choice of a baseline may seem intuitive in the case of two populations, it will become less obvious when multiple groups are considered, such as populations living in different Census Divisions, or in counties classified along the urban-rural continuum.

Use Cases

The decomposition developed in this paper can be used to investigate the contribution of any set of mutually exclusive groups to the values of a life table function for the total population. As mentioned before, the basic decomposition for the $N = 1$ case was introduced by Hendi and Ho (2021) to study how the foreign-born population contributes to the US life expectancy. However, the contributions subgroups of the foreign-born population, by origin or race/ethnicity for example, can be studied with the decomposition developed in this paper. Other interesting applications include the investigation of how different regions contribute to national life expectancy, how different countries contribute to the regional life expectancy, or how different educational groups contribute to the difference between the life expectancy of the lowest group and that of the total population.

Example Application: The Contribution of Counties along the Urban-Rural Classification to the Gap between Life Expectancy at Birth in Large Central Metro and in the United States

For this application, I use death counts and population data from the National Center for Health Statistics obtained through CDC WONDER. Deaths and population are classified by year (2017-2019), sex, five-year age groups (<1, 1-4, 5-9, …, 85+), and one of six urban-rural codes. The six codes schema classifies counties into four metropolitan categories and two non-metropolitan categories. The metropolitan categories are large central metro, large fringe metro, medium metro, and small metro. The non-metropolitan categories are micropolitan and noncore. Details on the classification criteria are available in the NCHS online documentation (NCHS 2023).

As can be seen in Figure 1, at the national level, large fringe metro counties have the highest life expectancy for males, followed by large central metro counties, medium metro counties, small metro counties, micropolitan counties, and noncore counties. The ordering is essentially the same for females, the only difference being that large central metro counties have the highest life expectancy, with large fringe metro counties coming second. Figure 2 shows the group-specific contributions to national life-expectancy using the groupwise decomposition. As we would have expected, all groups but large fringe metro counties contribute negatively to the national life expectancy. Micropolitan counties have the largest absolute contribution followed by noncore counties, medium metro counties, small metro counties, and large fringe metro counties. The size of each contribution is determined by the interaction of three factors: the population size of counties belonging to the specific group, the population's age distribution, and its age-specific mortality rates (which life expectancy conveniently summarizes).

As a further test of the validity of the groupwise decomposition, I adapted the three general decomposition methods (Andreev et al. 2002; Caswell 1989; Horiuchi et al. 2008) as implemented in the `DemoDecomp` package (Riffe 2019) to obtain a decomposition by group similar to the one developed in this paper. The results of the comparison between the results obtained with the groupwise decomposition and those obtained with each of the three methods are presented in Figure 3 and Figure 4 (in which the stepwise decomposition

is removed). They show that the groupwise decomposition produces result almost identical to those of the line-integral method (Horiuchi et al. 2008) and close to the ones of the life table response experiment (Caswell 1989). The stepwise decomposition fails to produce reasonable results. A legitimate question is why one should use the groupwise decomposition if both the line-integral and the life table response experiment methods provide similar results. One answer is that the groupwise decomposition is computationally very efficient compared with the alternatives. For the example presented above, where a very simple life table function is used (`LTabr` from `DemoDecomp`) the average execution time measured with the `microbenchmark` package (Mersmann et al. 2023), was 0.15 seconds for the groupwise decomposition, 68.59 for the line-integral method, and 249.30 for the life tables experiment, both of the latter as implemented in the `DemoDecomp` package. In this relatively simple application, the groupwise decomposition is thus about 460 times faster than the line-integral method and about 1670 times faster than the life table experiment method. The computational advantage increases when more complex functions are used and more groups are considered.

A Simple Extension: Combining Decomposition Techniques to Compute Age- and Group-Specific Contributions

Once we have seen how the decomposition works, we can quickly recognize two facts. First, while we only considered a function mapping vectors to scalars, nothing in the proof requires it. We can thus extend the decomposition to functions that take as input a vector of deaths counts and exposures and output a vector of contributions. Second, general decomposition techniques themselves are a useful class of vector-to-vector functions that satisfy this property. With these two realizations we see that we can easily combine other decomposition techniques with the groupwise decomposition to further decompose group-specific contributions by other dimensions.

Figure 5 shows the results of this extension, using age as the additional dimension. Figure 6 replicates the decomposition using the line-integral method and once again shows that the results are nearly identical. In this more complex application, the computational advantages of the groupwise decomposition are a bit smaller because the function being decomposed now outputs vectors rather than a scalar, while the computations for the line-integral decomposition remain the same. Again, using the `microbenchmark` package, I timed the mean execution time for the groupwise decomposition at 2.25 seconds compared with 94.77 seconds for the line-integral method as implemented in the `DemoDecomp` package (with the groupwise decomposition 42 times faster).

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Figure 1: Life Expectancy at Birth by Year, Sex, and Urban-Rural Category
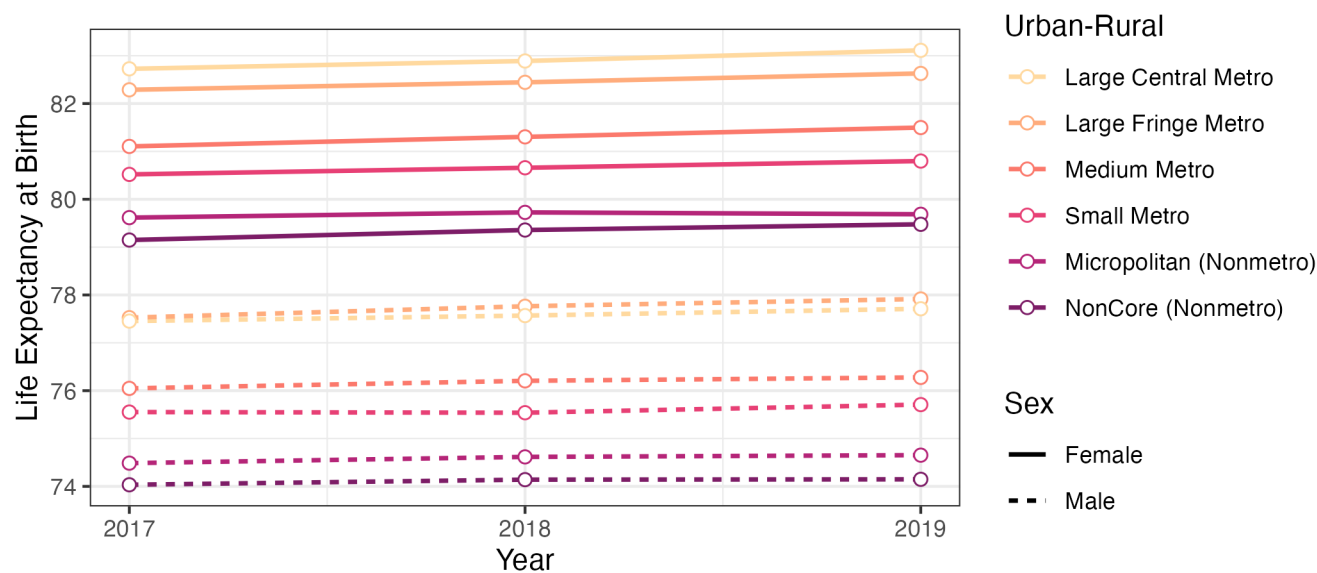

Figure 2: Decomposing the Contribution of Non-Large Central Metro Counties to National Life Expectancy by Urban-Rural Categories.
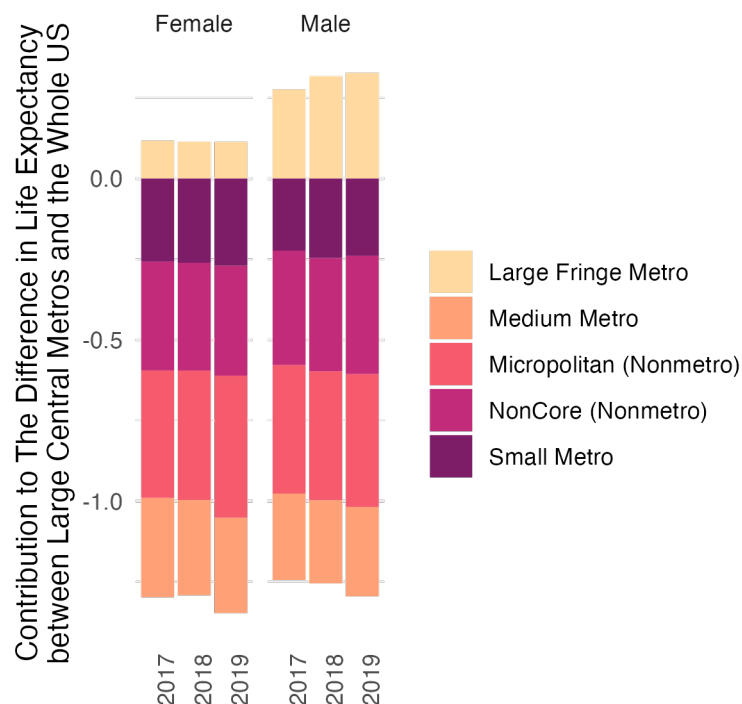
Figure 3: Comparing Decomposition Results from the groupwise decomposition with Those Obtained with Other General Decomposition Methods: Horiuchi, LTRE, and Step-Wise.
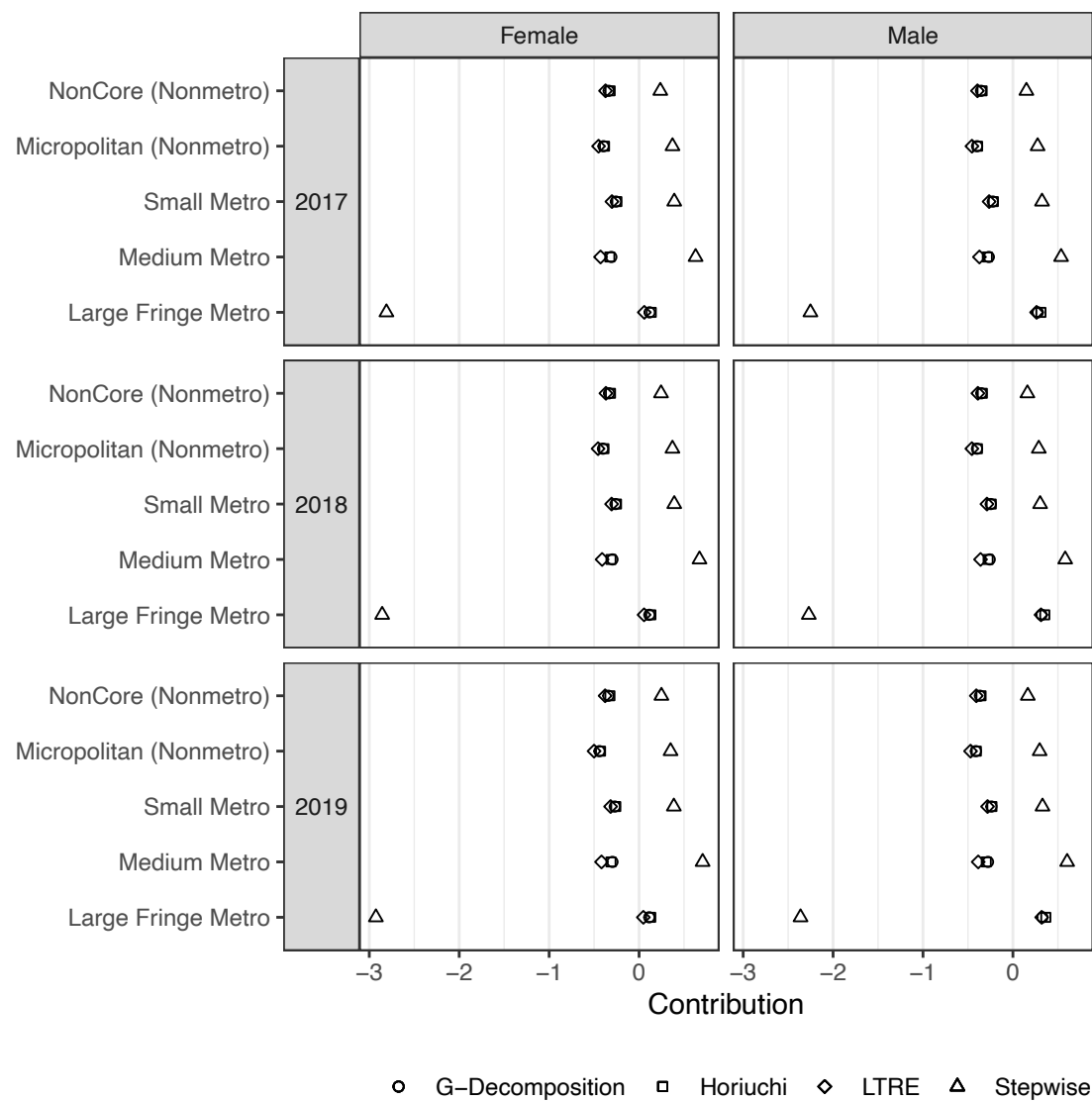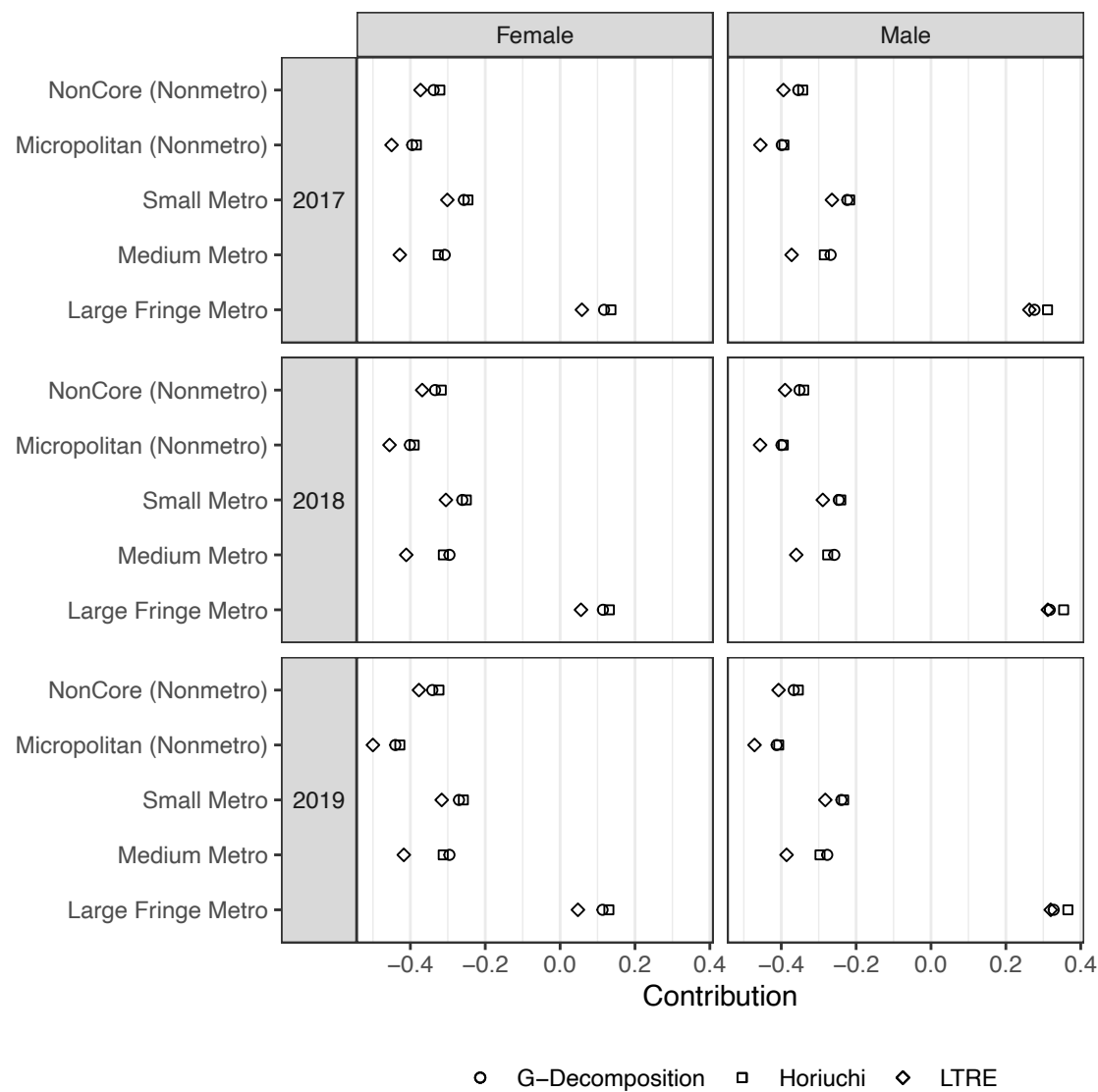
Figure 4: Comparing Decomposition Results from the groupwise decomposition with Those Obtained with the Horiuchi and LTRE General Decomposition Methods.

Figure 5: Decomposition of Contributions to National Life Expectancy by Metro Type and Age (2019) Using the groupwise decomposition.
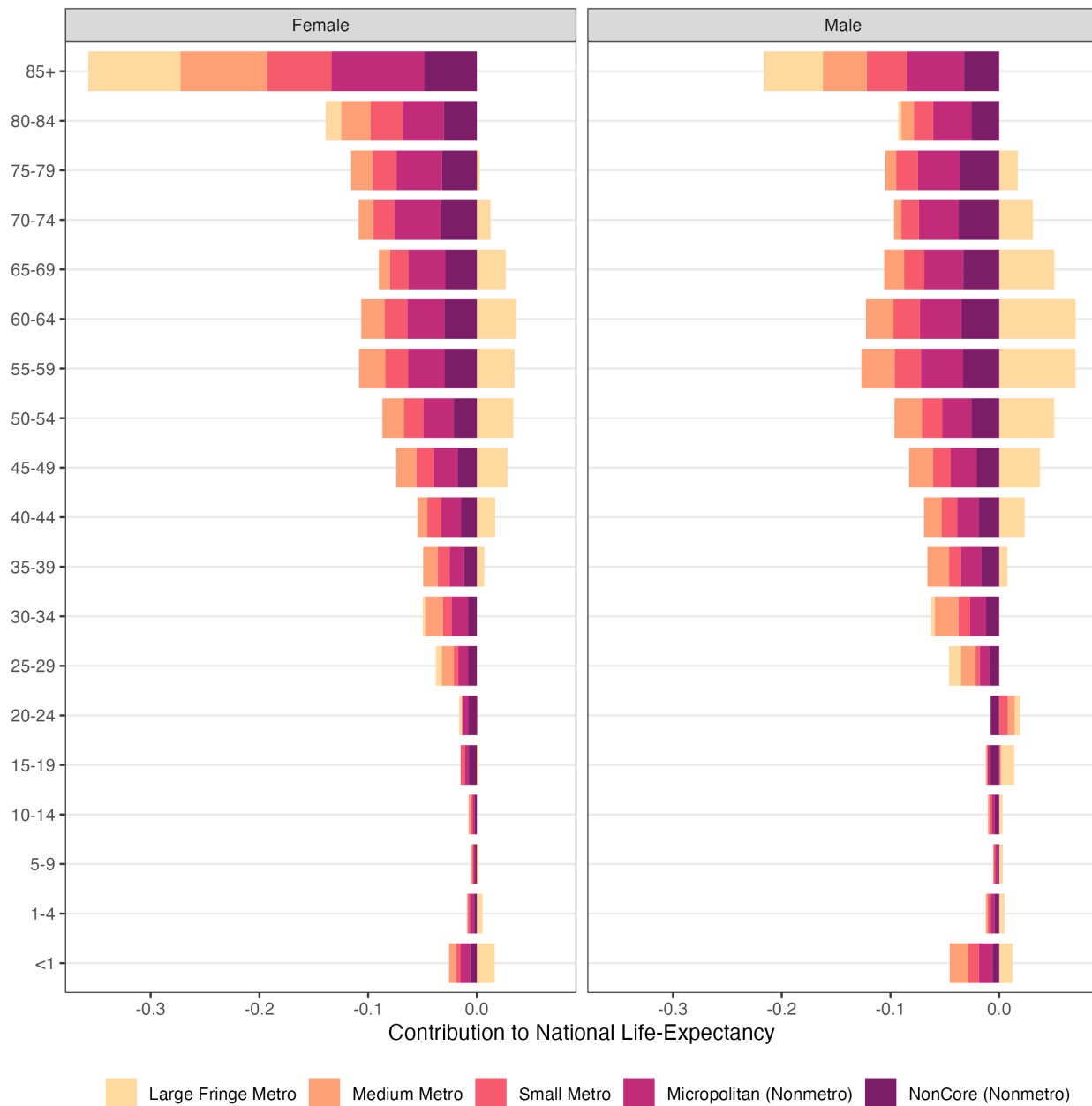
Figure 6: Decomposition of Contributions to National Life Expectancy by Metro Type and Age (2019) Using the Line-Integral Decomposition (Horiuchi et al. 2008).