

Preliminary Draft. Not for circulation.

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

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## 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 a demographic measure for 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 ( $T$ ) and a partition of the population into mutually exclusive subgroups ( $G_1, G_2, \dots, G_N$ ), how can we compute the contribution of subgroups  $G_1, G_2, \dots, G_N$  to life table functions ( $l_x, {}_nL_x, {}_nT_x, e_x$ ) starting from the life table of a baseline population ( $B$ )? 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.

The basic form of 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 national 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, 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:

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

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

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

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.  $\exists i, j \text{ s.t. } x_i^{FB} > x_i^{USB} \wedge x_j^{FB} < x_j^{USB}$ ), 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, depends 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 in 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 major 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.

Similar issues of ordering affecting the decomposition results arise in other decomposition techniques as well such as the Step-Wise decomposition (Andreev et al. 2002) and Arriaga's decomposition (Arriaga 1984). These issues have been usually solved by averaging over different orderings (Andreev 1982; Andreev et al. 2002; Pressat 1985) which however becomes computationally more challenging as the possible number of orderings to consider increases.

### **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  $l(A)$ . Hendi and Ho's expression for the total contribution of the two groups is still valid:

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

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 will lead 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 will 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.

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

So, the two average contributions sum to the total contribution of  $G$ , which establishes  $C^1, C^2$  as a legitimate decomposition of  $C^G$ . 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.

$$\begin{aligned}
C^1 + C^2 + C^3 &= \frac{1}{3}(l(B + G_1) - l(B)) + \frac{1}{6}(l(B + G_2 + G_1) - l(B + G_2)) + \frac{1}{6}(l(B + G_3 + G_1) - l(B + G_3)) + \frac{1}{3}(l(T) - l(B + G_2 + G_3)) \\
&\quad + \frac{1}{3}(l(B + G_2) - l(B)) + \frac{1}{6}(l(B + G_1 + G_2) - l(B + G_1)) + \frac{1}{6}(l(B + G_3 + G_2) - l(B + G_3)) + \frac{1}{3}(l(T) - l(B + G_1 + G_3)) \\
&\quad + \frac{1}{3}(l(B + G_3) - l(B)) + \frac{1}{6}(l(B + G_1 + G_3) - l(B + G_1)) + \frac{1}{6}(l(B + G_2 + G_3) - l(B + G_2)) + \frac{1}{3}(l(T) - l(B + G_1 + G_2))
\end{aligned}$$

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:



$$\begin{aligned}
C^1 + C^2 + C^3 &= (l(T) - l(B)) + \frac{1}{3}(l(B + G_1) + l(B + G_2) + l(B + G_3)) \\
&\quad - \frac{1}{3}(l(B + G_1 + G_2) + l(B + G_1 + G_3) + l(B + G_2 + G_3)) \\
&\quad - \frac{1}{6}(2l(B + G_1) + 2l(B + G_2) + 2l(B + G_3)) \\
&\quad + \frac{1}{6}(2l(B + G_1 + G_2) + 2l(B + G_1 + G_3) + 2l(B + G_2 + G_3))
\end{aligned}$$

From which one can easily verify that  $C^1 + C^2 + C^3 = (l(T) - l(B))$  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  $(N = 3)$ , it 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 approaches, this decomposition method is computationally 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  $i^{th}$  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  $i^{th}$  possible 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  $i^{th}$  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 just 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:

$$\begin{aligned}
 w(l(B + G_i^m + G_n)) &= (m + 1)w^m - (N - m - 1)w^{m+1} \\
 &= (m + 1) \frac{1}{N \binom{N-1}{m}} - (N - m - 1) \frac{1}{N \binom{N-1}{m+1}} \\
 &= (m + 1) \frac{(N - 1)!}{m! (N - 1 - m)!} - (N - m - 1) \frac{(N - 1)!}{(m + 1)! (N - 1 - m - 1)!} \\
 &= (m + 1) \frac{m! (N - 1 - m)!}{(N - 1)!} - (N - m - 1) \frac{(m + 1)! (N - 1 - m - 1)!}{(N - 1)!} \\
 &= \frac{(m + 1)! (N - 1 - m)!}{(N - 1)!} - \frac{(m + 1)! (N - 1 - m)!}{(N - 1)!} \\
 &= 0
 \end{aligned}$$

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.

## 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. 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 national life expectancy in the US. 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 or how different countries contribute to the regional life expectancy.

## Example Application: The Contribution of Counties along the Urban-Rural Classification to National Life Expectancy at Birth

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 G-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 G-decomposition, I adapted the three general decomposition methods (Andreev et al. 2002; Caswell 1989; Horiuchi et al. 2008) 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 G-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 G-decomposition produces result almost identical to those of the line-integral method and close to the ones of the life table response experiment. The stepwise decomposition fails to produce reasonable

results. A legitimate question is why one should use the G-decomposition if both the line-integral and the life table response experiment methods provide similar results. The answer is the G-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 G-decomposition, 68.59 for the line-integral method, and 249.30 for the life tables experiment. In this relatively simple application, the G-decomposition is thus about 460 times faster than the line-integral methods 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 G-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 G-decomposition are a bit smaller because the function being decomposed now outputs vector 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 G-decomposition at 2.25 seconds compared with 94.77 seconds for the line-integral method as implemented in the popular DemODEcomp package (with the G-decomposition 42 times faster).



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Figure and Tables

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

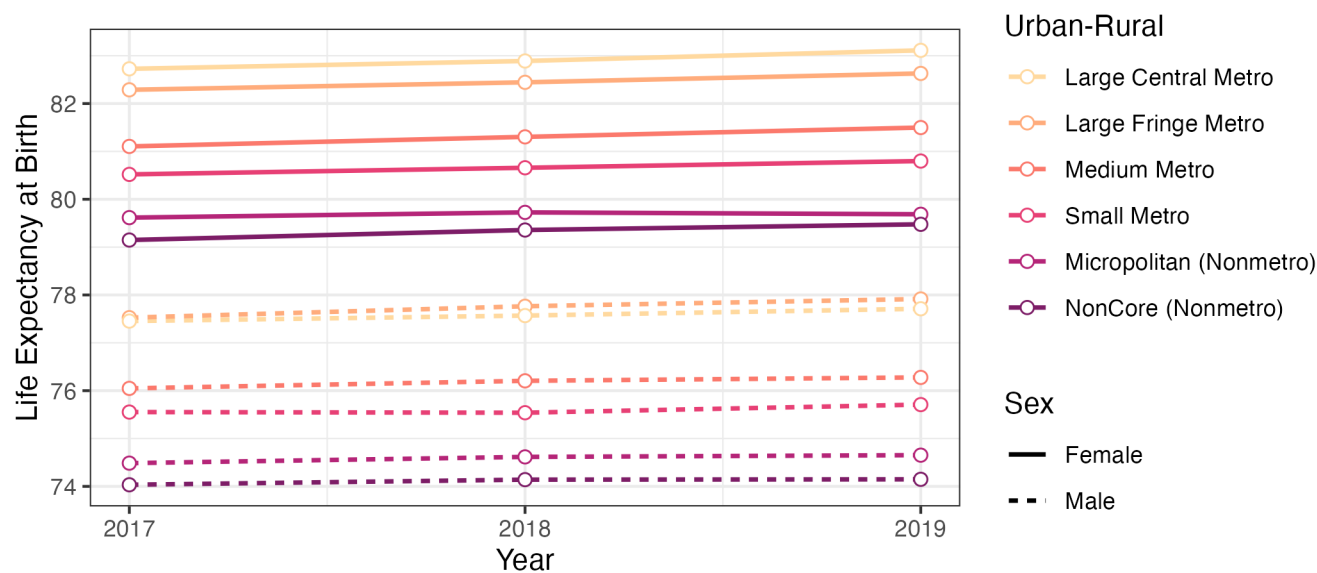
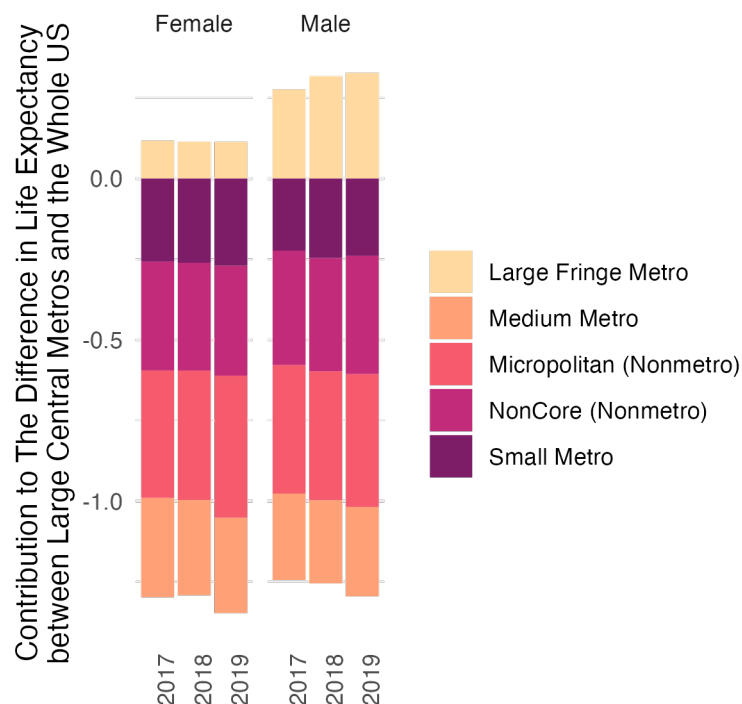
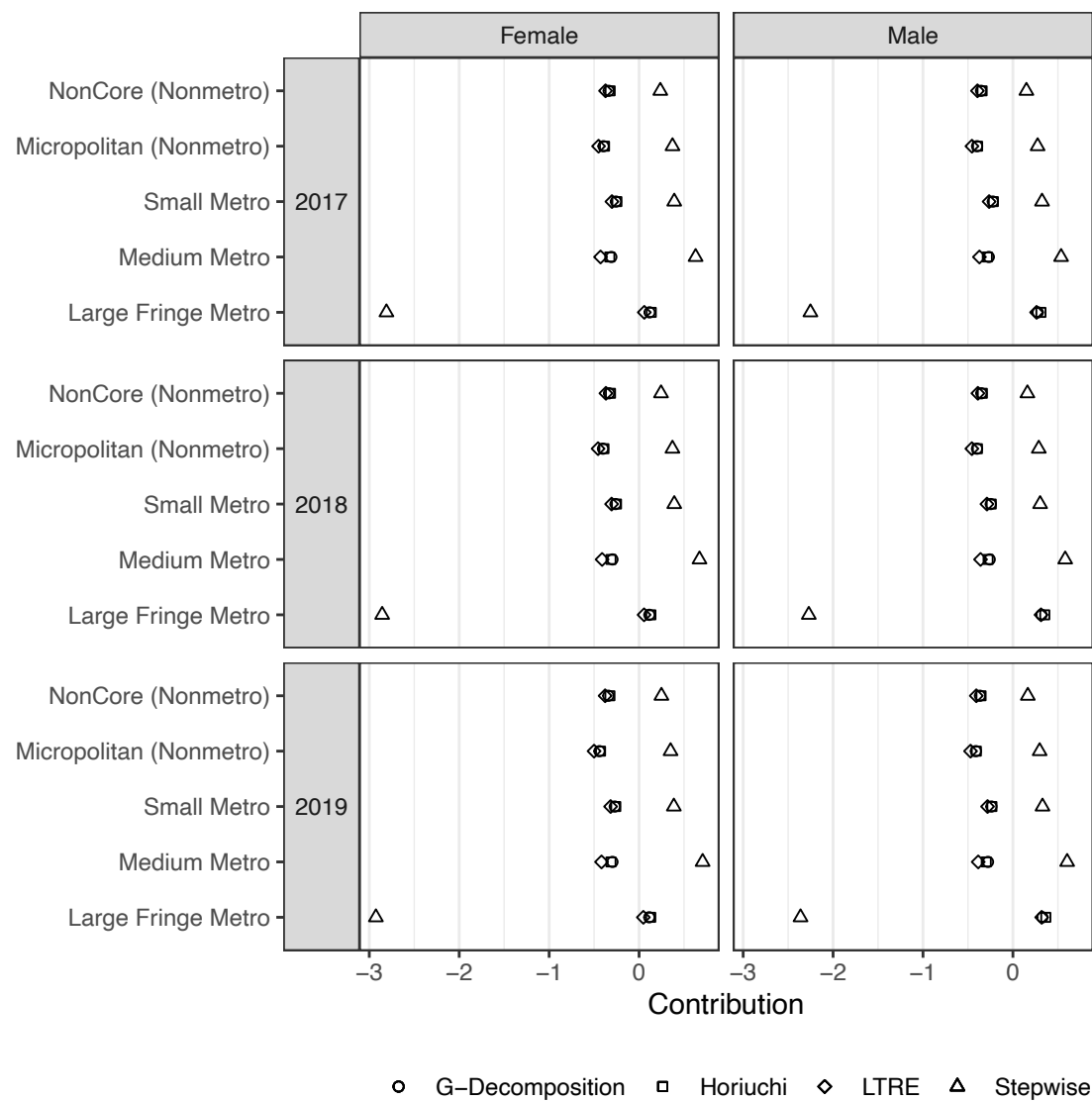


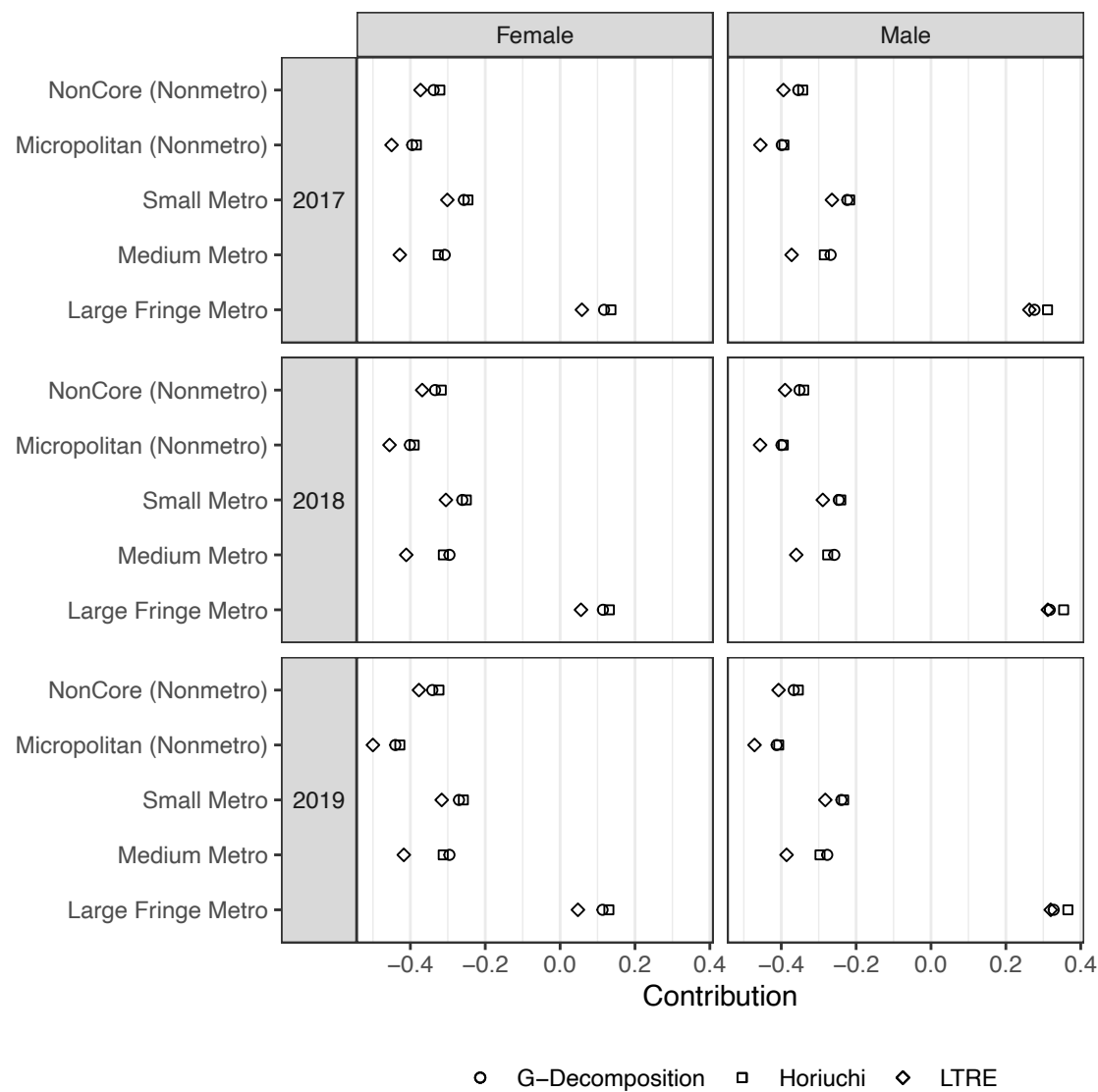
Figure 2: Decomposing the Contribution of Non-Large Central Metro Counties to National Life Expectancy by Urban-Rural Categories.



**Figure 3:** Comparing Decomposition Results from the G-Decomposition with Those Obtained with Other General Decomposition Methods: Horiuchi, LTRE, and Step-Wise.

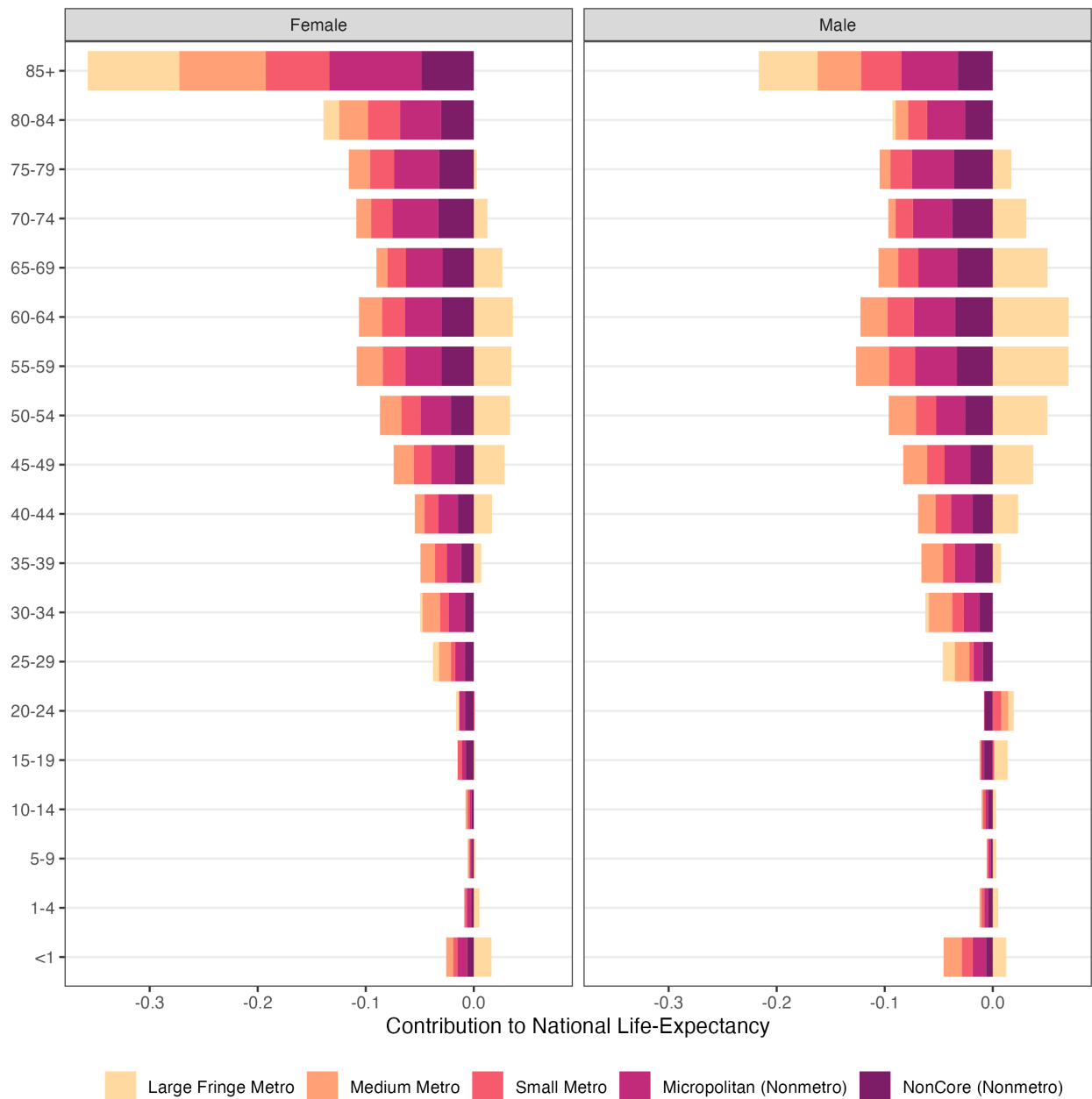


**Figure 4:** Comparing Decomposition Results from the G-Decomposition with Those Obtained with the Horiuchi and LTRE General Decomposition Methods.



**Figure 5:** Decomposition of Contributions to National Life Expectancy by Metro Type and Age (2019)

Using the G-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).

