Survey Estimates of Wartime Mortality*

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August 16, 2025

Abstract

Many scholarly literatures require mortality rates from conflict zones, but accurate information is usually among the earliest casualties of war. While political scientists typically obtain mortality data from the news media or others, much progress has been made in demography, epidemiology, and public health conducting original surveys about the survival of siblings, friends, or others known to respondents. Unfortunately, the formal properties of estimators based on these surveys have not been established, the intuitions offered for them (and consequent data analysis strategies) are conflicting, and the statistical consequences of the political incentives of respondents in conflict zones remain unexamined. In this paper, we demonstrate the advantages of joining ongoing efforts in these other fields with insights from political science, including especially political methodology, international relations, and comparative politics. We offer the first formal proofs of the statistical properties of all existing estimators, along with simulation and empirical illustrations, to craft simple intuitions to guide best practices. We also build practical data analytic approaches, based on modern robust statistical methods, for when some respondents are suspected of intentionally biasing answers for political, military, or other strategic purposes. We offer practical advice for producing more complete and accurate mortality inferences for scholarship in our discipline and beyond.

*For helpful comments and advice we thank Dennis Feehan, Abie Flaxman, Kristian Gleditsch, Jason Lyall, Bruno Masquelier, Christoph Mikulaschek, Mike Spagat, Tyler VanderWeele, Carly Wayne, a reviewer for IQSS' RapidPeer service, and our fabulous collaborators on a related project, John Bair, Karam Dana, Abie Flaxman, and Abdullah Rahmanyar. The current version of this paper, its Supplementary Appendix, and an R package (TrimSib) that implements all the methods described herein are available at GaryKing.org/sibs.

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1 Introduction

Mortality estimation during wartime is academically important, militarily consequential, publicly debated, and among the most difficult, dangerous, uncertain, and politically contested scholarly challenges in the academy. Estimates for the same military conflicts from different sources vary widely and spark frequent controversy (Spagat et al., 2009). For example, estimates of civilian deaths in the Iraq War range from 100,000 to more than six times that number (Burnham et al., 2006), with similar large discrepancies in other recent conflicts (e.g., Watson, 2005). Mortality estimation is complicated by uncertain reporting practices, limited access to conflict zones, the difficulty of doing original research, military combatants with a stake in research conclusions, and politicized incentives of some sources (Spagat, 2024; Radford et al., 2023; Checchi and Roberts, 2008).

Political scientists have been among the major users of wartime mortality statistics. Especially in international relations and comparative politics, they use this data for defining war and militarized interstate disputes (see correlatesofwar.org, Lacina and Gleditsch 2005), understanding the strategy and causes of political violence (Harff, 2003; Valentino, Huth, and Balch-Lindsay, 2004; Valentino, 2014; Kalyvas, 2006; Downes and Cochran, 2010; Stein, 2015; Herrera and Kydd, 2024; Besley and Reynal-Querol, 2014), measuring the impact of conflict on civilians (Haas, 1969; Ghobarah, Huth, and Russett, 2003; Lupu and Peisakhin, 2017; Friedman, 2019), and assessing how conflicts affect domestic public opinion and electoral outcomes (Gartner, 2008; Koch and Nicholson, 2016; Kriner and Shen, 2014; Johns and Davies, 2019; Juan et al., 2024; Berman, Clarke, and Majed, 2024; Shaver and Shapiro, 2021; Wayne and Zhukov, 2022; Kreft and Agerberg, 2024; Loewen and Rubenson, 2021; Fetzer et al., 2024; Hintson and Vaishnav, 2023).

Unfortunately, although scholars appreciate that accurate "measurement. . . of conflict related deaths requires collaboration between disciplines" (Ferrario, Mahgoub, and Warsame, 2025), political scientists do not usually collaborate on primary data collection with scholars in demography, epidemiology, and public health and thus "rarely collect data on violence themselves" (Weidmann, 2015). Instead, with rare exceptions (e.g., Van der Windt and Humphreys, 2016), they mostly rely on second hand sources like media and government, which have well known measurement problems (Davenport and Ball, 2002; Lacina and Gleditsch, 2005; Raleigh, Kishi, and Linke, 2023; Weidmann, 2016; Eck, 2012). We seek to change this situation by bringing a political science perspective to original data collection in these literatures, building on the strengths of each, and enabling us all to learn more and progress faster. We begin with the methods in these other fields and add, from political science, political and strategic knowledge developed in international relations and comparative politics, and the design and evaluation of statistical methods, from political methodology.

Mortality rates could in principle be calculated via civil registration and vital statistics (CRVS) systems for recording deaths certified by medical personnel. Unfortunately, CRVS systems are highly incomplete, with less than 40% of deaths registered globally (Mikkelsen et al., 2015) and, when they exist, are almost always abandoned altogether at the onset of military conflict (Murray et al., 2002). Even if government officials issue mortality statistics during wartime, their unavoidable conflicts of interest as parties to the conflict often lead to controversy (Mills and Burkle, 2009). Highly uncertain alternatives include automated or hand coding of fatalities found in news stories or existing compilations (such as Gleditsch et al. 2002, Iraq Body Count Project 2003, acleddata.com, or ucdp.uu.se), multiple system estimation based on incomplete hospital and official records (e.g., Jamaluddine et al., 2025), and extrapolation based on existing demographic surveillance systems (e.g., Huynh, Chin, and Spiegel, 2024).

We focus here on a more direct survey-based approach increasingly popular in demography, epidemiology, public health, and medicine. The idea is to collect information about the mortality of a well-defined group known to the respondent, such as their siblings (Gakidou and King, 2006), parents (Brass and Hill, 1973), spouses (Malaker, 1986), sisters (Graham, Brass, and Snow, 1989), coworkers, household residents, or other networked individuals (Feehan, Mahy, and Salganik, 2017; Feehan and Salganikb, 2024). Analysts ask randomly selected survey respondents how many members of the chosen group were alive at the beginning of some period (perhaps for a certain cohort such as by sex and age) and how many are presently alive. We use sibling groups as a running example for expository purposes because it enables us to put off until the end of our paper a discussion of the measurement error-induced bias caused by eliciting information about larger and potentially non-disjoint groups.

Unfortunately, although multiple estimators have been proposed for this data over at least four decades, formal statistical properties have not been established for any one. The literature has instead relied on qualitative intuitions to drive empirical applications but, because "little has been proven" about mortality estimators' formal statistical properties, the choice of analytical methods is "very challenging," and the conflicting intuitions proposed for constructing estimators regularly leads to substantial "confusion" and disagreement (Feehan and Borges, 2021, p.1526).

In this paper, we offer the first formal proofs of the statistical properties for each estimator proposed in this literature, following standard practice in political methodology (and statistics more generally). These properties enable us to identify the precise sources of bias and uncertainty, to resolve existing methodological controversies and confusions, to evaluate proposed empirical strategies, and to construct simple, easy-to-understand — and provably accurate — qualitative intuitions that applied researchers and methodologists can build on to improve best practices.

Even with these results, much remains to be done in this highly uncertain area. We take one step forward on the remaining agenda and address a common unaddressed worry about intentional data contamination arising from respondents' strategic motivations. The concern is that survey respondents may inflate or deflate reports of their siblings' mortality to intentionally bias researchers' conclusions or for their own political, financial, military, or psychological reasons (Radford et al., 2023; Checchi and Roberts, 2008; Noor et al., 2012). We do not solve this problem but we use insights developed in international relations and comparative politics to craft novel data analytic strategies for understanding and potentially detecting and correcting it. To do this, we build on the "robust statistics" literature (Huber, 1981) to develop a diagnostic procedure to explicitly model strategic misreporting, decompose the effects of contamination, and adjust mortality estimates accordingly. This methodology is compatible with, and applicable to, recent innovations in survey research, including mobile phone-based surveys conducted during crises, which has become increasingly common (e.g., Kalleitner, Schiestl, and Heiler, 2022; Conroy-Krutz, 2025; Curtice, 2021; Pierskalla and Hollenbach, 2013).

In Section 2, we formally define the quantity of interest (separate from any measure), an essential step for formal statistical evaluation. Section 3 then clarifies the data-generating process underlying the sibship-survival method. Section 4 presents formal definitions of existing proposals for mortality estimators, their formal statistical properties, and (accurate) qualitative intuitions. Building on this foundation, Section 5 discusses how to approach mortality estimation where researchers have suspicions of politically motivated insincere survey responses. We then generalize our results in Section 6 to cover demographically and methodologically important technical issues, such as cluster-based or stratified sampling, cause-specific (or excess) mortality, bias-variance trade offs in reference group choices, person-year refinements, cohort estimation, and other issues. Section 7 concludes, with the appendices containing detailed mathematical proofs.

2 Quantity of Interest

In this section, we define the average *mortality rate* at time 2 of all those within a chosen cohort (such as 50-65 year old women in Ukraine) living at time 1. A *sibship* is the set of all children born to the same mother (although for our purposes we can also use the term to refer to any other well-defined, set of disjoint groups of individuals that meets the same assumptions given below, such as parents, children, coworkers, etc.) and a *sibsize* as the number of individuals in a given sibship.

Consider a population of individuals i ($i = 1, \ldots, N$) partitioned into sibships j ($j = 1, \ldots, F$) (where as a mnemonic device F can be thought of as "Family" size). Within sibship j, denote B_j as the number in this cohort alive at time 1 (or "births" into the cohort), and D_j and S_j as the number of deaths and survivors between times 1 and 2, so that $B_j = D_j + S_j$. Finally, let $M_j = D_j/B_j \in [0, 1]$ be the mortality rate of sibship j.

Finally, we define the quantity of interest as the average population mortality rate at time 2. Let d_i denote an indicator variable for whether individual i died between times 1 and 2. Then, the quantity of interest can be expressed in two equivalent ways

$$q = \frac{\sum_{i=1}^{N} d_i}{N} = \frac{\sum_{j=1}^{F} D_j}{\sum_{j=1}^{F} B_j} \tag{1}$$

representing *individual*-level (with index i) and *sibship*-level (with index j) expressions, respectively. The sibship-level expression can also be written as the mean over sibships of mortality weighted by sibsize: $q = \sum_{j=1}^{F} B_j M_j / \sum_{j=1}^{F} B_j$ or, in the special case where all sibsizes are the same, a simple mean: $q = \frac{1}{F}\sum_{j=1}^{F} M_j$.

We discuss generalizations to account for duration exposure among other issues in Section 6, opting here for expository simplicity, without loss of generality.

3 Data Generation Process

In this section, we introduce sample-level notation, introduce the data generation process produced by survivor sampling, and discuss sampling with and without replacement and the messy issues of real world surveys.

3.1 Sample Notation

We reuse the indexes from our population-level notation (in Section 2) in the sample for individual i ($i = 1, \ldots, n$) and sibship j ($j = 1, \ldots, J$). This simplifies the notation (but implies, for example, that $i = 4$ in the population does not necessarily refer to the same individual as $i = 4$ in the sample). These indices range up to maximum values for individuals of n (in the sample) and N (in the population), and for sibships of J (in the sample) and F (in the population). We also define B_i, D_i, and S_i as the number of births, deaths, and survivors, respectively, of the sibship j to which i belongs. Each of these values are identical across all individuals within the same sibship.[1]

3.2 Survivor Sampling

The simplest method of selecting respondents in surveys outside of the sibling survival context is "simple random sampling," where each individual is selected from a uniform

[1] Although we do not use this notation beyond this sentence, if $D_{j(i)}$ is the number of deaths reported by individual i within each sibship j, then $D_{j(i)} = D_{j(i')}$ for all i and i'.

distribution with $1/N$ probability. Simple random sampling can be used in mortality studies only when it is possible to sample at time 1 and follow a cohort until time 2 to see who survives, thus enabling unbiased mortality estimation via simple averaging over individuals. Unfortunately, this approach is typically infeasible when sampling at time 2 in conflict zones because we have no way to sample from all individuals who were alive at time 1 and, even if we could, asking individuals at time 2 whether they are alive is not a good plan.

A *survivor sampling* strategy, as widely used in sibling survival studies, solves both problems, but it requires statistical adjustments to produce estimators with known statistical properties. We define this strategy formally as follows:

Definition 1 (Survivor Sampling)**.** *Randomly select respondent i via a uniform distribution (with probability $1/N^*$) from the set of $N^* < N$ population members who survive until time 2 and elicit information about their sibship's mortality. Each sibship then has probability of selection $S_j/N^* \propto S_j$.*

The main difference between simple random sampling and survivor sampling is that, instead of being chosen following a random uniform distribution, respondents are selected in proportion to their sibsize. This means that people from large sibships are over-represented in the sample, and sibships with no survivors are never sampled. Mortality estimators that ignore this sampling strategy can be severely biased downward, as they over-represent the experience of larger surviving sibships.

3.3 Sampling with or without Replacement

We draw a sample of individuals of size n by repeating the survivor sampling strategy. The probability of sampling the same sibship twice, and thus having a dataset with repetitive information, is impossible under sampling without replacement and extraordinarily unlikely in realistic sized populations via sampling with replacement.[2] As such, we choose to evaluate statistical properties based on sampling with or without replacement based on mathematical convenience, without any practical implication. (Indeed, a diagnostic of a

[2]The expected number of unique sibships drawn under sampling with replacement is $N\left[1-\left(\frac{N-1}{N}\right)^n\right]$, which is rarely as small as $n-1$ in realistic sibling survival applications.

problem with sampling is if a sample contains a noticeable number of individuals from the same sibship.)

3.4 Real World Problems

Actual implementation of surveys always differ from chosen theoretical sampling strategies, including those above. All modern surveys are affected by the difficulty or impossibility of complete population enumeration, item and unit nonresponse, measurement error in survey responses, privacy and confidentiality problems, and many others. Conducting surveys in conflict zones only exacerbates these issues and adds others, such as nonignorable nonresponse perhaps due to survivors being less willing to take surveys in high mortality areas. Our approach, following most modern statistical modeling analyses, abstracts these issues away and tries to choose applications where biases induced by deviations from the theoretical plan are likely to be smaller than reported uncertainty estimates or effect sizes. Of course, researchers must always remain alert to the additional uncertainties induced by unanalyzed issues, and especially vigilant when implementing surveys in difficult locations impacted by war, famine, and other issues that make sibling survival research important in the first place, a subject to which we return in Section 5.

4 Estimators

We now define the three primary sibling survival estimators (in Section 4.1), briefly state their formal statistical properties (in Section 4.2, with detailed proofs given in the appendix), and then spend most of the time giving simple and easy-to-understand intuitions for these results (in Section 4.3).

4.1 Definitions

We focus here on the four existing mortality rate estimators, which we refer to as the naive ($\hat{q}$), subtraction ($\dot{q}$), weighted subtraction ($\ddot{q}$; Trussell and Rodriguez 1990), and G-K ($\tilde{q}$; Gakidou and King 2006) estimators. Although all continue to be debated in the methodological literature, applications usually use either the G-K estimator (e.g., Hagopian et al., 2013; Iraq Family Health Survey Study Group, 2008; Li et al., 2016; Bundervoet, 2009; Obermeyer, Murray, and Gakidou, 2008; GBD 2019 Demographics Collaborators, 2020) or the subtraction estimator (Moultrie et al., 2013; Croft, Allen, and Zachary, 2023; Hanley, Hagen, and Shiferaw, 1996). We define all but one of the estimators in two ways, paralleling the expressions for the quantity of interest in Equation 1 based on individuals and sibships. In each case, the second expression is only approximately equal to the first because of the remote possibility of random sampling in a large population yielding two survivors from the same sibship (see Section 3.3).

First is the naive estimator, which is a direct implementation of the expression for the quantity of interest in Equation 1 in the population applied to the sample:

Definition 2 (Naive Estimator)**.** *The naive mortality estimator $\hat{q}$ is simply the number of deaths at time 2 divided by the number of births at time 1.*

$$\hat{q} = \frac{\sum_{i=1}^{n} D_i}{\sum_{i=1}^{n} B_i} \approx \frac{\sum_{j=1}^{J} D_j}{\sum_{j=1}^{J} B_j}.$$

If the entire population were available in the sample, or we could use sample random sampling rather than survivor sampling, the naive estimator would have attractive statistical properties.

Second is the subtraction estimator. This is an analog of the naive estimator, but it subtracts the number of respondents themselves from the denominator on the grounds that respondents, who are always alive, should not be counted:

Definition 3 (Subtraction Estimator)**.** *The subtraction estimator $\dot{q}$ is defined by subtracting the number of respondents from the denominator of the naive estimator $\hat{q}$:*

$$\dot{q} = \frac{\sum_{i=1}^{n} D_i}{\sum_{i=1}^{n} (B_i - 1)} \approx \frac{\sum_{j=1}^{J} D_j}{\sum_{j=1}^{J} (B_j - 1)}.$$

Third is the weighted subtraction estimator which builds on the subtraction estimator with survivor weights.

Definition 4 (Weighted Subtraction Estimator (Trussell and Rodriguez, 1990))**.** *The weighted subtraction estimator $\ddot{q}$ is the subtraction estimator ($\dot{q}$) with survivor weights modifying* *the numerator and denominator:*

$$\ddot{q} = \frac{\sum_{j=1}^{J} S_j D_j}{\sum_{j=1}^{J} S_j (B_j - 1)}.$$

(This estimator is too complicated at the individual level and so is only expressed at the sibship level.) Unable to prove that the subtraction estimator has attractive statistical properties, Trussell and Rodriguez (1990) introduced this related approach, which is equivalent to the subtraction estimator under an assumption they introduced called "unrestricted random sampling," where all siblings becomes respondents within each randomly selected sibship. Of course, since all siblings in the same sibship would report identical information, actually interviewing them all is wasteful. Instead, the same assumption is implemented with a single interview per sibship by switching from the subtraction to the weighted subtraction estimator.

Finally, we define the G-K mortality estimator. We account for deaths in families with no survivors by imagining a different (and normally infeasible) sampling scheme. The idea is to sample individuals at time 2 from the population alive at time 1. We sample until we find n who are alive at time 2, a subsample equivalent to that drawn via survivor sampling (Definition 1). Then, we define a parameter ξ as the expected sum of the sibsizes of the remaining (deceased) respondents who are from sibships with no survivors.[3] Given an estimate of ξ, the G-K estimator is:

Definition 5 (G-K Estimator (Gakidou and King, 2006))**.** *The G-K estimator is a weighted average of mortality rates, conditional on an estimate $\hat{\xi}$ added to the numerator and demoninator. Denote weights at the individual-level as $W_i = B_i/S_i$ and sibship-level as $W_j = B_j/S_j$. Then,*

$$\tilde{q} = \frac{\sum_{i=1}^{n} W_i M_i + \hat{\xi}}{\sum_{i=1}^{n} W_i + \hat{\xi}} \approx \frac{\sum_{j=1}^{J} W_j M_j + \hat{\xi}}{\sum_{j=1}^{J} W_j + \hat{\xi}}.$$

[3]The parameter ξ is a population quantity. To simplify its interpretation, we can compute it from the parameter γ, *the number of deaths in the population in sibships with zero survivors*, which we compute as $\gamma = \sum_{k'} \gamma_{k'}$ from $\gamma_{k'}$, the number of deaths in the population in sibships of size k' with zero survivors, where k' is an index over all sibsizes that have at least one family with zero survivors. Then, we calculate ξ by making γ proportional to the sample size under the survivor sampling procedure: $\xi = \frac{J}{\sum_{j=1}^{F} I(M_j < 1)} \frac{\sum_{k'} k' \cdot \gamma_{k'}}{\sum_{k'} k'}$. Similarly, γ can be obtained by considering another quantity $\eta_{k'} \in [0, 1]$, the proportion of families with zero survivor and with sibsize k'. Then γ is redefined as $\gamma = \sum_{k'} k' \eta_{k'}$ and ξ is defined accordingly.

To estimate $\hat{\xi}$, Gakidou and King (2006) proposes that we first obtain the quantity $y = \log(\sum_{j \in S_j = s} D_j/S_j)$ for $s = 1, \ldots, 7$, and then regress y on s using the following model: $\mathbb{E}[y \mid s] = \beta_0 + \beta_1 s + \beta_2 s^2$. Finally, by the expected value of log-normal model, we extrapolate back to where $s = 0$ and compute $\hat{\xi} = \exp\left(\beta_0 + \text{Var}(\beta_0)/2\right)$.

4.2 Formal Properties

Although many sources of possible bias in sibling survival estimators have been discussed, proofs of formal statistical properties are mostly absent from the literature. We provide these proofs here, with details in the appendixes. As it turns out, all biases are due solely to *missing data*, because the time 2 sample includes no direct information about sibships with zero survivors, and *selection*, because sibships with larger numbers of survivors are overrepresented due to survivor sampling.

First, the naive estimator (Definition 2) seems straightforward because it is the formula used for the quantity of interest (Equation 1) applied to the sample, which merely divides total births by total deaths. It is, however, biased because the survivor sampling data generation process used to collect data at time 2 is ignored and thus induces selection bias. It also ignores sibships with zero survivors. We give this result formally here:

Theorem 1 (Biasedness of the Naive Estimator)**.** *The naive mortality estimator, $\hat{q}$, is biased:* $\mathbb{E}(\hat{q}) < q$.

Proof: see Appendix A.

Second, the subtraction estimator (Definition 3), which also doesn't correct for missing data or selection problems, is biased as well for the same (missing data and selection) reasons. Subtracting a constant from the denominator corrects for neither:

Theorem 2 (Biasedness of the Subtraction Estimator)**.** *The subtraction mortality estimator, $\dot{q}$, is biased:* $\mathbb{E}(\dot{q}) \neq q$.

Proof: see the first part of Appendix B.

The first hint that the subtraction estimator is biased comes from its originating idea, that all information comes from the respondent's siblings rather than the respondent. This claim is false: The fact that we can even find n living respondents to do a survey reveals that the mortality rate is no larger than $q \leq (N-n)/N$, which is informative and so affects bias claims (even if it of little practical use, given that mortality rates even in conflict zones are usually much lower).

More generally, whether subtracting n from the denominator produces attractive statistical properties has been debated based intuitively, without a (complete and correct) mathematical proof, for decades. The resulting confusion was implicit in the early development of the sibship survival method (e.g., Hill and Trussell, 1977), was later made explicit (e.g., Graham, Brass, and Snow 1989; see also Trussell and Rodriguez (1990)), and continues (and continues to be acknowledged) in the modern era (Feehan and Borges, 2021; Masquelier, 2013).

Unfortunately, the subtraction estimator is biased in general, with or without the "unrestricted random sampling assumption," or, put differently, the weighted subtraction estimator is also biased. Trussell and Rodriguez (1990) tried to avoid the problem by adding an (unrealistic) assumption, that the probability of death is constant across all individuals, but both estimators are still biased with or without this assumption. To be more specific, addressing selection bias by including weights (via a logic similar to G-K) is a good idea, but unfortunately the weighted subtraction weights are wrong, and so this estimator is biased in general:

Theorem 3 (Biasedness of the Weighted Subtraction Estimator)**.** *The weighted subtraction mortality estimator, $\ddot{q}$, is biased (with or without a constant-probability-of-death assumption):* $\mathbb{E}(\ddot{q}) \neq q$.

Proof: see the second part of Appendix B.

The bias in the $\hat{q}$, $\dot{q}$, and $\ddot{q}$ estimators should be sufficient motivation to warrant building an approach that directly takes into account the data generation process so that we can incorporate adjustments to deal with both selection and missingness. We thus now consider the G-K estimator, which is a weighted average of components of the naive estimator (to adjust for selection bias) and an extra term (to help adjust for missing death data). Formally, we prove that the G-K estimator is asymptotically unbiased:

Theorem 4 (Asymptotic Unbiasedness of the G-K Estimator)**.** *Given an asymptotically unbiased estimator of ξ, the G-K estimator is asymptotically unbiased:* $\lim_{n\to\infty} \mathbb{E}(\tilde{q}) = q$.

Proof: see Appendix C. We also confirm through Monte Carlo simulations in Appendix D that this asymptotic result also holds in finite samples.[4]

For inference, we also need the variance of the G-K estimator to compute proper standard errors or confidence intervals. We do this via a formal Taylor Series approximation because the estimator is a ratio of random variables:

Theorem 5 (Variance of the G-K Estimator)**.** *With ξ known, the variance of the G-K estimator is approximated by:*

$$\text{Var}(\tilde{q}) \approx \frac{\text{Var}(X)}{\mu_Y^2} - 2\frac{\mu_X}{\mu_Y^3}\text{Cov}(X,Y) + \frac{\mu_X^2 \text{Var}(Y)}{\mu_Y^4}$$

where $X = \sum_{j=1}^{J} W_j M_j + \hat{\xi}$ and $Y = \sum_{j=1}^{J} W_j + \hat{\xi}$. μ_X and μ_Y represent the mean of X and Y, respectively.

Proof: see Appendix E. Simulations in Appendix D also confirm that this result holds in finite samples.[5]

4.3 Intuitions

We develop intuition by first comparing the naive and G-K estimators and then by comparing the subtraction estimator and G-K. Although Section 4.2 proves that the naive and subtraction estimators give biased results, understanding the intuition behind each is helpful in understanding G-K and potential future approaches.

4.3.1 Comparing the Naive and G-K Estimators

We compare estimators by introducing a tool in Figure 1 to make it easier to understand and correct for selection biases. We begin with a population (left panel) composed of two *types* of sibships, both with sibsizes of $B = 3$, one where only 1 of 3 siblings survive

[4]This is the first formal proof of a well-defined statistical property for the G-K estimator. Gakidou and King (2006) provides evidence of asymptotic unbiasedness via verbal argument, and unbiasedness via Monte Carlo simulations; Feehan, Mahy, and Salganik (2017) shows that G-K with $\hat{\xi}$ set to 0 is what they call "essentially unbiased" for the unusual special case where ξ is known to be zero in the population and then suggest trying to approximate the actual quantity of interest (Equation 1) informally via sensitivity tests (see also Croft, Allen, and Zachary 2023, p.56). In contrast, the naive, subtraction estimator, and weighted subtraction estimators are both biased and asymptotically biased.

[5]Although not often of direct use because of the large biases in the point estimators, we also give formal expressions for the variances of the naive and subtraction estimators: $\text{Var}(\hat{q}) = J\text{Var}(D_j)/(\sum_{j=1}^{J} B_j)^2$, and $\text{Var}(\dot{q}) = J\text{Var}(D_j)/\{\sum_{j=1}^{J}(B_j - 1)\}^2$, which is straightforward to compute because B_j is fixed.

between times 1 and 2 (the red frowny face, $S = 1$) and the other where all 3 survive (the yellow smiley face, $S = 3$). By assumption, this population has equal numbers of the two sibship types and so the true mortality rate is $1/3$, which can be calculated as the total number deaths divided by the total number of births ($2/6$) or equivalently the average of the two separate mortality rates $((1/2)(2/3) + (1/2)0)$. These calculations, which also appear at the bottom of the first column, are of course identical to the naive estimator applied to the population.

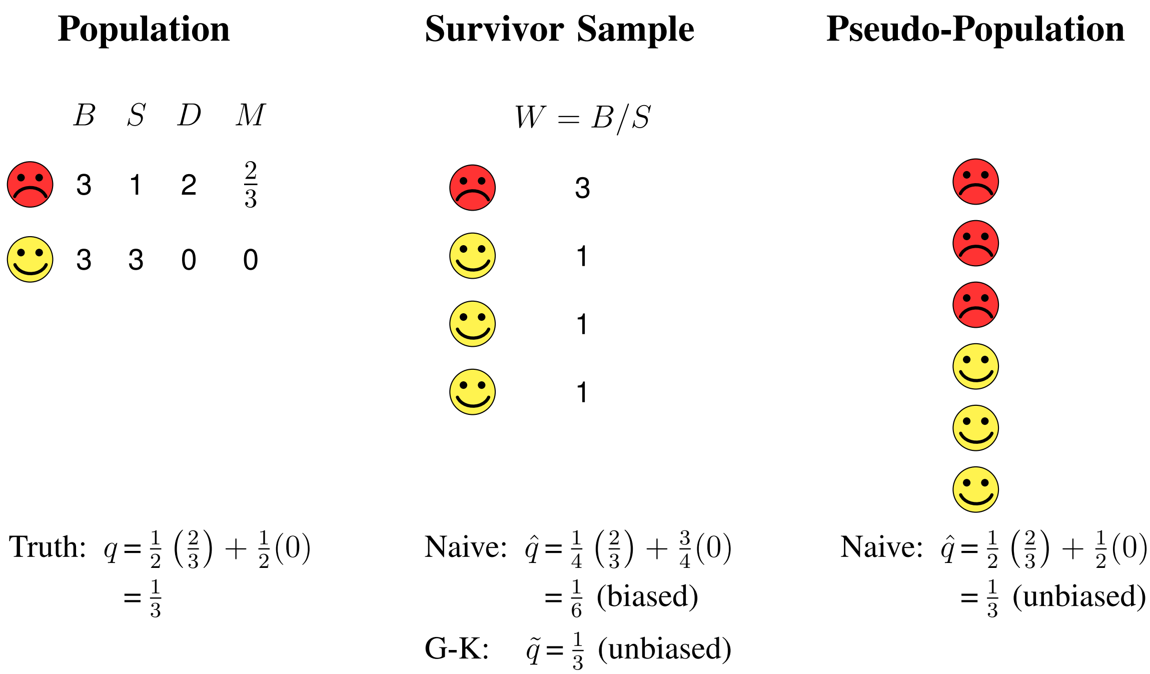

Figure 1: Intuition: Faces refer to two types of sibship mortality experiences: those with (1) zero mortality (as yellow smiles) and (2) two-thirds mortality (as red frowns). The two types are represented equally in the population (left panel), with yellow smiles over-represented because of survivor sampling (middle panel, constructed from S in the left panel), and equally again in the pseudo-population (right panel, constructed from G-K weights W in the middle panel). G-K applied to the survivor sample and naive applied to the pseudo-population produce identical and unbiased estimates. (For clarity, we omit normalizations that keep the number of observations fixed.)

As simple random samples from the population are infeasible in conflict zones, we illustrate survivor sampling in middle panel, which includes a different distribution of the same types of sibships that survive from the population — one high mortality (red frowny face) sibship and three low mortality (yellow smiley faces) sibships (the number of each sibship type in the middle panel is determined by the S column in the left panel, omitting, for simplicity, the normalization that keeps the number of observations the same). The sibship types are the same as in the population but, because of the proportions of each changed, survivor sampling biases the naive estimator towards survivors (with mortality now 1/6 rather than 1/3; see the bottom of the middle panel). Fortunately, the biases are corrected by the G-K estimator's weights.

We also include an easier way to visualize the G-K weights by constructing a pseudo-population (in the right panel of Figure 1) with the number of sibships of each type determined by weights in the survivor sample (in the middle panel). This leads to three high and three low mortality sibships in the pseudo-population. Because the weights are incorporated, the naive estimator applied to the pseudo-population gives the same (correct 1/3) answer as the G-K estimator applied to the survivor sample.

4.3.2 Comparing the Subtraction and G-K Estimators

The subtraction estimator seems intuitive because the guaranteed survival of respondents means they contain almost no information. Yet, this estimator is biased (see Theorem 2). For example, the subtraction estimator applied to the survivor sample in Figure 1 is incorrect (1/4, rather than the truth of 1/3; the pseudo-population does not help either, as the estimate is 1/2).

Yet, the subtraction estimator does come with an important intuition, even though subtracting from the denominator does not fix the problem. Its key intuition is that the selection process, which guarantees that respondents are always alive, must be incorporated into the estimator. This logic has been restated in many articles over at least four decades; for example, "It is particularly important to ensure that…respondents do not include themselves among the [siblings] reported as this would inflate the denominator and thus deflate the true …mortality ratio." (Graham, 1989). The logic does indeed makes sense, but what has been missed for so long is that the biases induced by selecting a survivor to interview affects information about *both* the respondent — who indeed is always alive — *and* the remaining siblings — who have higher mortality on average than the entire original sibship (which included one more survivor, the respondent). Even if subtracting n from the denominator were enough to fix the first problem, it ignores the second, leaving substantial bias. Indeed, any selection on an outcome variable can bias estimates.

For example, consider a population of sibships, each of which has sibsize two of which only one survives (i.e., the mortality rate is 1/2 for every sibship). All respondents at time 2 are by definition alive, but all siblings of respondents are deceased, and yet the mortality rate is obviously not 100%. The same holds for larger sibships as well: removing one sibling (the respondent) known to be alive leaves a set of siblings with higher mortality than their whole sibship. As a statistical principle, selection on mortality induces bias in estimates of mortality for both the respondent and the non-respondents, and so both must be corrected. To avoid this bias, we can either not select at all (by demographic surveillance, which is infeasible in war zones) or select survivors as respondents and correct for both the respondents and nonrespondents.

The G-K estimator makes both corrections, which we can build up to in four steps:[6]

1. Suppose all sibsizes B_j are the same over j and we take a simple random sample of sibships at time 1. Then we can estimate mortality without selection bias by merely averaging over sibships: $\text{mean}(M_j)$.

2. Now allow B_j to vary and sample proportionally to it (i.e., equivalent to randomly sampling individuals) at time 1, we can avoid bias by weighting the mean by sibsize, B_j: $\text{wmean}(M_j, B_j)$ (which is equivalent to the quantity of interest expression in Equation 1 applied to the population).

3. If we apply survivor sampling (i.e., Definition 1, which samples proportional to S_j) at time 2, we can avoid selection bias by multiplying the B_j weights by $1/S_j$: $\text{wmean}(M_j, B_j/S_j)$.

4. Finally, to take into account the fact that sibships with zero survivors are not represented in the sample, weighting is insufficient, and so we must estimate ξ separately, which leads to using the full G-K estimator (Definition 5).

[6]We simplify notation below by defining the mean as $\text{mean}(a_j) = \sum_{j=1}^{J} a_j/J$ and the weighted mean as $\text{wmean}(a_j, w_j) = \sum_{j=1}^{J} w_j a_j / \sum_{j=1}^{J} w_j$.

5 Adversarial Respondents and Data Contamination

Until now, we have followed the literature by assuming that all respondents give sincere, cooperative survey responses, generally following the Gricean maxims of ordinary conversation, producing no systematic measurement error (Schwarz, 1999). In practice, however, conducting surveys in war zones likely produce many types of respondent-driven measurement error, where the reported values of variables (such as B_j and S_j) differ from the true values. Consider three situations: (1) the respondent is unaware of the true values; (2) the respondent is aware of the true values, and would like to help the researcher, but is afraid to reveal the truth to the researcher for political or other reasons; and (3) the respondent chooses answers for the purpose of biasing the researcher's conclusions in the direction of their own political preferences.

Researchers try (or should try) to deal with (1) by carefully choosing questions or referent groups (siblings, parents, children, coworkers, etc.) in ways that the respondent is more likely to be aware of in the culture being surveyed. Although (2) has not been addressed in this literature, political methodologists and others have developed methods for eliciting information about sensitive subjects adapting techniques such as randomized response, list experiments, and other privacy-protected approaches (Rosenfeld, Imai, and Shapiro, 2016; Evans et al., 2024).

We focus in this section on (3), in particular the precise statistical problems that occur when a small percentage of respondents are "adversarial," in that they intentionally misrepresent information for the purpose of biasing the researcher's conclusions in a particular direction. We discuss the political incentives that may lead to this behavior in Section 5.1, optimal adversarial responses in Section 5.2, diagnostics in Section 5.3, and empirical illustrations from real research that apply these methods in Section 5.4.

5.1 Political Motivations

Scholars in demography, epidemiology, public health, and medicine have made significant contributions to estimating mortality rates in settings without comprehensive vital statistics. Notable advancements include the use of verbal autopsies (interviewing family members to ascertain causes of death) (Fottrell and Byass, 2010; King and Lu, 2008; King, Lu, and Shibuya, 2010), the deployment of mobile phone surveys (e.g., Kalleitner, Schiestl, and Heiler, 2022; Conroy-Krutz, 2025; Curtice, 2021; Pierskalla and Hollenbach, 2013), and the establishment of high quality, cross national surveys such as the Demographic and Health Surveys (DHS) and the Multiple Indicator Cluster Surveys (MICS).

However, much of this progress has occurred without proposals to address the consequences of respondents with *political* incentives to influence research conclusions, even when discussing the issue explicitly (Guha-Sapir and Checchi, 2018). While demographers and public health scholars have examined the accuracy of survey-based mortality estimation, they often focus on inaccuracies due to institutional capacity limitations (e.g., Seidler et al., 2025) or recall bias (Obermeyer, Rajaratnam, et al., 2010), but have not yet examined the strategic incentives of political actors to misrepresent information (Gibilisco and Steinberg, 2023), which implicitly assumes its absence. Yet, as Mills and Burkle (2009) explain, "[t]he collection of health-status information is political by nature. Collecting data in a conflict setting is no different" (Mills and Burkle, 2009).

Political science scholarship identifies at least four reasons why survey respondents might strategically misrepresent wartime mortality. First, political actors may possess political incentives to misrepresent their fighting capacities. Mortality rates during warfare are critical indicators of a political entity's strengths. Fearon (1995) demonstrates that rational actors have incentives to misrepresent private information such as resolve and capabilities, a point that can extend to survey respondents, who might misreport mortality to conceal their true fighting capacities. While identifying the direct evidence is challenging, the unreliability of surveys in war zones illustrates these incentives. For an extreme instance, a U.S. counterinsurgency officer remarked to *The Washington Post* that in Afghanistan, "[e]very data point was altered" and "[s]urveys were totally unreliable" (Whitlock, 2019).

Second, following Kalyvas (2006)'s work on the logic of violence during civil war, respondents may misreport mortality experiences due to fear of reprisal or targeting by controlling political actors. Violence against civilians is often used as a tool to punish non-compliance. Civilians, therefore, have incentives to tailor their reported mortality experiences to avoid punishment from the dominant political actor. Such "preference falsification" (Kuran, 1997) is frequently observed in surveys conducted in war-torn zones (e.g., Lyall, Blair, and Imai, 2013).

Third, respondents are rational actors (Popkin, 1979) and may manipulate reported mortality experiences to pursue material benefits. For example, civilians in areas controlled by a rebel group might provide responses they perceive as favorable to that group, particularly if they believe their answers could affect their access to future aid, security, or resources (Lyall, Blair, and Imai, 2013).

In addition to the three rational mechanisms, there exists a fourth mechanism that stems from political psychology known as "competitive victimhood." Civilian groups or factions may compete to demonstrate that their community has suffered more extensively than opposing groups, a phenomenon frequently documented in post-conflict reconstruction phases (Noor et al., 2012).

5.2 Optimal Adversarial Responses

Even when the political mechanisms driving misrepresentations of mortality are clear, identifying which specific individuals misreport, and to what extent, is empirically challenging. And, of course, assuming the absence of any measurement error when it is present can significantly bias mortality estimates. We thus now develop diagnostics for contexts where such politically motivated data contamination is suspected, building on the robust statistics literature (Huber, 1981).

To begin, we formalize strategic political behavior (detailed in from Section 5.1) by showing what an adversarial respondent would do to maximally influence research results in the direction consistent with their preferences — first intuitively and then mathematically. Surprisingly, this optimal impact is highly asymmetric, in that it is far easier to bias the researcher's estimate upward than downward.

5.2.1 Intuition

Consider a survey question with possible responses $a_j \in \{1, 2, \ldots, 10\}$, for each respondent j (but without loss of generality). Suppose a researcher aims to estimate a population quantity via a weighted average of a_j with weight w_j over n respondents, wmean(a_j, w_j) (using notation from Section 4.3). Suppose also that the survey includes one respondent who chooses an answer insincerely for the purpose of causing the researcher to overestimate the population quantity by increasing the value of the weighted average. How could this adversarial respondent best accomplish their (disruptive) goal? In this case, they would answer $a_j = 10$; in addition, if the respondent could influence w_j, they would want it to be as large as possible, so that their one response counts for more.

Because we estimate ξ separately, for intuition we consider the G-K estimator with $\xi = 0$, which is also a weighted average, wmean(M_j, W_j), but with an unusual feature that the variable and the weight are determinstically related: $W_j = B_j/S_j = 1/(1 - M_j)$. One consequence is that the largest an adversarial respondent can make M_j is $(B_j - 1)/B_j$, since the respondent is always alive. This is consequential since if $B_j = 2$, the maximum mortality that could be reported in the respondent's sibship is 0.5, whereas if the respondent reports $B_j = 10$, then the maximum mortality could be 0.9. Thus, to maximally increase the value of the G-K estimator (still assuming $\xi = 0$), an adversarial respondent would choose the largest value of B_j that the survey allowed along with the highest mortality rate possible, which can be accomplished by setting $S_j = 1$ (indicating that all the respondents' siblings have died). The important consequence is that this choice would increase the variable and the weight as well. For example, if $B_j = 10$, then this one response would have the influence of a remarkable $W_j = 10/1 = 10$ others.

Now suppose the adversarial respondent were on the other side of the military conflict with the opposite political incentives and thus wanted the researcher to report a lower mortality estimate. In this case, they would choose $M_j = 0$, but, because of the deterministic relationship between the variable and the weight, this response would only have a relatively small weight of $W_j = 1$. That is, because the two are deterministically related, the adversarial respondent has no way to increase their influence after they choose the mortality rate. This response would indeed bias the weighted average downward, but it would have a much smaller impact than an adversarial respondent who wanted to increase the researcher's mortality estimate.

5.2.2 Formal Definitions

We now introduce a new metric of robustness, which we call *maximum influence* (built on the concept of the "influence function" in the robust statistics literature; See Supplementary Appendix A1). Intuitively, maximum influence measures the maximum possible absolute impact of a given fraction of contaminated observations constructed by adversarial respondents on the overall estimate. We denote two types of maximum influence as the maximum *increase* and maximum *decrease*.

Formally, let the data generation process for mortality rates without contamination at time 2 be denoted by $M_j \sim F^S$, and the process with contamination by $M_j \sim F^\delta$, where F^δ is a contaminated distribution such that a proportion $\delta \in [0, 1]$ is contaminated. We first define the *influence of contamination* as follows.

Definition 6 (Influence of Contamination)**.** *The influence of contamination (IC) of a statistic T with the probability of contamination δ is*

$$IC(T, \delta) = T(F^\delta) - T(F^S),$$

where $\delta \in [0, 1]$.

Definition 6 says that the influence of contamination is the difference between test statistics with or without data contamination.[7]

In our application, we consider a case where politically motivated respondents set their mortality to be $x \in [0, 1)$ to inflate or deflate the estimated population-level mortality. That is, M_j follows a contaminated distribution F^δ, where $M_j = x$ with probability δ. Thus, we denote the influence of contamination of the G-K estimator to be a function of both δ and x: $IC(\tilde{q}, \delta, x)$. The influence of contamination of the G-K estimator has the following property:

[7]Readers familiar with the robust statistics literature may notice that IC resembles the influence function (see Supplementary Appendix A1). However, our focus is not on the marginal influence of contamination, but rather on the overall influence, which accounts for both the degree (x) and the proportion (δ) of contamination.

Theorem 6 (Influence of Contamination as an Increasing Function)**.** *$IC(\tilde{q}, \delta, x)$ is an increasing function in x.*

Proof: see Appendix F.

Theorem 6 implies that politically motivated respondents can inflate or deflate the mortality estimates optimally by reporting the highest or lowest possible mortality, regardless of other respondents' reports. Therefore, in order to inflate or deflate mortality estimates, politically motivated respondents seeking to have the maximum influence in the direction they choose will set their mortality either $(B-1)/B$ or 0, where $B = \max(B_j)$. This prompts us to consider the maximum influence *increase* (MI^+) and *decrease* (MI^-), which we formally express as follows:

Definition 7 (Maximum Influence of the G-K Estimator)**.** *The maximum influence increase (MI^+) and decrease (MI^-) of the G-K estimator is*

$$MI^+(\tilde{q}, \delta, x) = IC\left(\tilde{q}, \delta, \frac{B-1}{B}\right) \quad \textit{and} \quad MI^-(\tilde{q}, \delta, x) = IC\left(\tilde{q}, \delta, 0\right),$$

where $\delta \in [0, 1]$.

The maximum influence increase refers to the greatest possible increase in G-K mortality estimates that δ proportion of politically motivated respondents can induce, while the maximum influence decrease refers to the greatest possible reduction. As a corollary to Theorem 6, $MI^+(\tilde{q}, \delta, x)$ and $MI^-(\tilde{q}, \delta, x)$ have the following property, which aligns with the intuition from the previous section that it is easier to bias the estimate upward than downward:

Corollary 1 (Difference between the Maximum Influence Increase and Decrease)**.** *Let $d(B)$ be the difference in absolute values of $MI^+(\tilde{q}, \delta, x)$ and $MI^-(\tilde{q}, \delta, x)$:*

$$d(B) = |MI^+(\tilde{q}, \delta, x)| - |MI^-(\tilde{q}, \delta, x)|.$$

Then, $d(B)$ is an increasing function in B.

Proof: see Appendix G.

Corollary 1 states that, for a sufficiently large $B = \max(B_j)$, the maximum possible increase in the mortality estimate exceeds the maximum possible decrease.

So far, we have focused on M_j to analyze the influence of contaminated observations. However, for sibling survival estimators, it is more practical to see the influence of contamination as a function of weighted mortality. This is because all four mortality estimators are functions (sums) of the J weighted mortalities, and thus the test statistics $T(\cdot)$ are also functions of these J observations. For example, the naive estimator can be expressed as $\hat{q} \approx \sum_{j=1}^{J}(B_j/\sum_{j=1}^{J} B_j)M_j$, a sum of weighted mortality with the normalized sibsizes as weights. We can also express the subtraction estimator as $\dot{q} \approx \sum_{j=1}^{J}\{B_j/\sum_{j=1}^{J}(B_j - 1)\}M_j$. While these weights do not sum to one, the subtraction estimator is still a sum of weighted mortalities. Finally, the G-K estimator (without ξ, which is estimated separately) is expressed as $\tilde{q} \approx \sum_{j=1}^{J} Z_j M_j$ where $Z_j = W_j/(\sum_{j=1}^{J} W_j)$ and $W_j = 1/(1 - M_j)$.

The focus on weighted mortalities is particularly important in the case of the G-K estimator because contaminated observations with the same M_j can have varying influence on the test statistic. As explained in the previous section, contaminated observations with large B_j values can have a greater impact than those with small B_j values. Therefore, it is more reasonable to view the G-K estimator as a function (or summation) of $Z_j M_j$ and to perform diagnostics based on $Z_j M_j$, rather than focusing solely on M_j, in order to identify observations that can distort the estimates.

While Theorem 6 and Corollary 1 see the influence of contamination as a function of mortalities, we can easily tailor these to our context. Since ξ is estimated separately, consider the G-K estimator without ξ and reexpress the G-K estimator as $\tilde{q} \approx \sum_{j=1}^{J} Z_j M_j = \sum_{j=1}^{J} Y_j$ where $Z_j = W_j/(\sum_{j=1}^{J} W_j)$ and $W_j = 1/(1 - M_j)$. Also let $y = x/(1 - x)$ where $x \in [0, 1)$ and $y \in [0, \infty)$. Then, as a corollary to Theorem 6, we observe that the influence of contamination is increasing in y_j:

Corollary 2 (Influence of Contamination as an Increasing Function in Weighted Mortalities)**.** $IC(\tilde{q}, \delta, y)$ *is an increasing function in* y.

Proof: see Appendix H.

Similarly, as a corollary to Corollary 1, we observe that, for a sufficiently large $B = \max(B_j)$, the maximum possible increase in the mortality estimate exceeds the maximum possible decrease, when we see the influence of contamination as a function of weighted mortalities.

Corollary 3 (Difference between the Maximum Influence Increase and Decrease, with Weighted Mortalities)**.** *Let $d(B)$ be the difference in absolute values of $MI^{+}(\tilde{q}, \delta, y)$ and $MI^{-}(\tilde{q}, \delta, y)$:*

$$d(B) = |MI^{+}(\tilde{q}, \delta, y)| - |MI^{-}(\tilde{q}, \delta, y)|.$$

Then, $d(B)$ is an increasing function in B.

Proof: similar to Appendix G and thus omitted.

5.3 A Diagnostic

Corollaries 2 and 3 suggest the possibility of identifying potentially contaminated observations via weighted mortalities, which we now implement in a diagnostic procedure for detecting adversarial observations. Of course, definitively identifying contaminated observations is impossible without external information. (E.g., a report of $(B_j, D_j) = (20, 19)$ may look suspicious, but it could also reflect a genuine mortality experience.) Thus, we offer diagnostic techniques that may hint at adversarial responses under certain assumptions or when combined with external information. Probative external information may include the strategic incentives of a target survey population (as per Section 5.1), discussions in open ended questions, randomized experiments via privatized data collection, or direct observation on the ground.

The hypothesis behind the methods introduced here is that adversarial responses are more likely to be drawn from a distribution that looks different from the bulk of the data with ordinary, sincere responses. We reveal these potentially adversarial respondents by sequentially trimming off suspect observations in pairs, predicting the trimmed observations by using the untrimmed training data, and investigating the mean absolute prediction errors, as we now describe.

The top panels of Figure 2 illustrate our procedure. The vertical axis is weighted mortality under G-K ($Z_j M_j$) and the horizontal axis is the percent of observations trimmed. The gray dots in the top left panel show sibship-level weighted mortality from untrimmed sibships, with a quadratic line that back predicts to the out-of-sample test set (in blue at the left). The orange dots have unexpectedly high weighted mortality, and so may represent potentially contaminated observations.

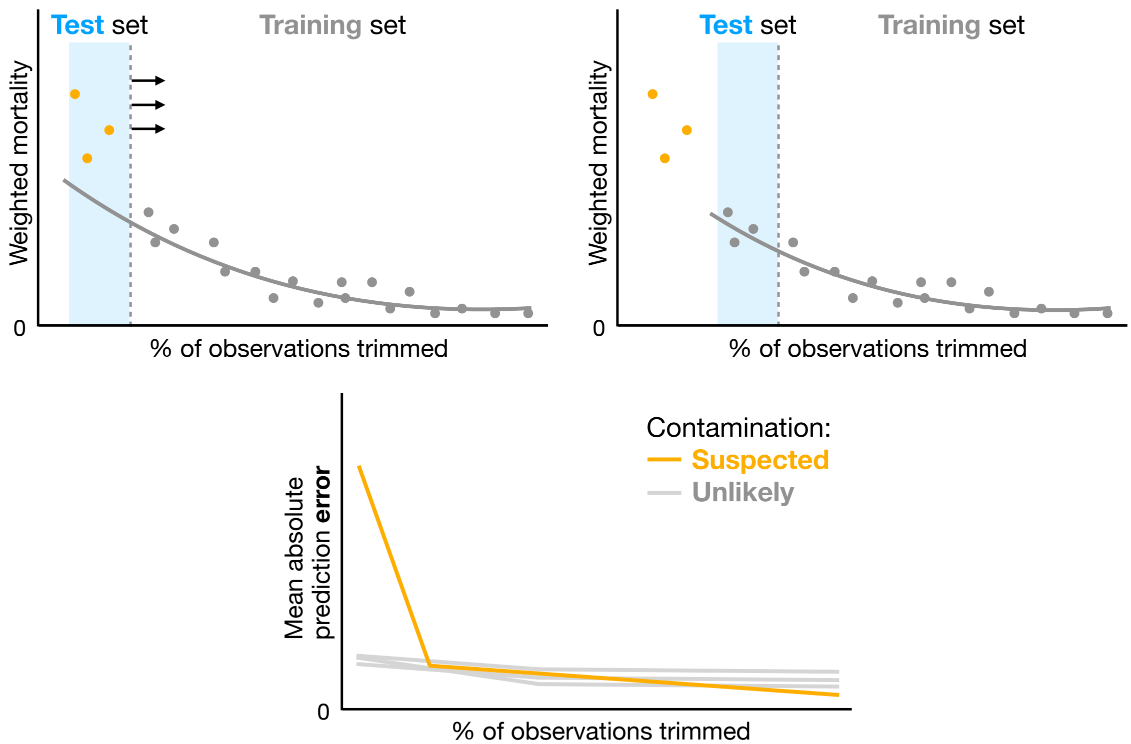

Figure 2: Trimmed prediction method: We predict trimmed observations and calculate the mean absolute prediction errors in each region. Data contamination induces a relationship between the mean absolute prediction errors and the proportion of trimmed observations (the bottom panel, orange line), which is different from regions with uncontaminated data.

We then move the forecast window to the right, as illustrated in the top right figure. Here, the blue test set area has moved to the right, and we are predicting anew from a quadratic fit to the weighted mortality points to the right of the vertical dashed line. We keep the out-of-sample test set of constant size (or width in the figure), and thus leave the three observations out of the analysis. In the top right figure, the observations in the test set seem to fit the extrapolated line well, suggesting that contamination may be unlikely. As the vertical dashed line continues to move to the right, we compute the mean absolute prediction error, which is summarized in the bottom panel. We suggest conducting this procedure at the regional or other relevant subgroup levels to allow for comparison across groups.

From these curves, we identify sets of potentially contaminated observations. Since the data generating process for contaminated observations differs from that of the remaining data, and since adversaries may attempt to report either the maximum or minimum possible mortality rates (see Theorem 6), we expect to observe high mean absolute prediction errors when a small proportion of observations are trimmed, followed by a substantial decline in prediction errors as the proportion of trimmed observations increases (illustrated by the orange line in the bottom panel of Figure 2).

5.4 Empirical Analyses

We now replicate two prominent studies in order to apply our proposed methodology to mortality survey data in war zones in Iraq (Hagopian et al., 2013) and Tigray, Ethiopia (McGowan et al., 2025). The Iraq dataset is derived from a nationally representative, cluster-sampled household survey conducted between May and July 2011. Mortality estimation during the Iraq War remains one of the most contentious areas in wartime mortality research. Studies have produced a wide spectrum of estimates, with correspondingly broad uncertainty intervals. For instance, Burnham et al. (2006) estimates approximately 655,000 excess deaths attributable to the conflict by June 2006, which is as much as six times higher than estimates from other sources such as Iraq Body Count Project (2003), depending on the definition of mortality, its estimators, and possibly adversarial respondents.

The Tigray dataset is based on an online, retrospective survey. The 2020–2022 war in Tigray, Ethiopia, similarly presents challenges in accurately determining civilian casualties. The estimated total number of deaths in this conflict ranges from 162,000 to 378,000 (Plaut, 2023). The Tigray war is also reported to have involved severe ethnic targeting and widespread human rights abuses, especially in the Western regions (Devi, 2021). Areas often changed hands or were inaccessible to independent observers, which can create opportunities for parties to manipulate data. A study of the media reports by the European Institute of Peace identifies that there existed "significant levels of disinformation, misinformation, and biased reporting" (Tofa, Kifle, and Kinkoh, 2022).

Figure 3 presents the main empirical results. The left and right panels display the calculated mean absolute prediction errors for each cluster (Iraq) and region (Tigray), re-

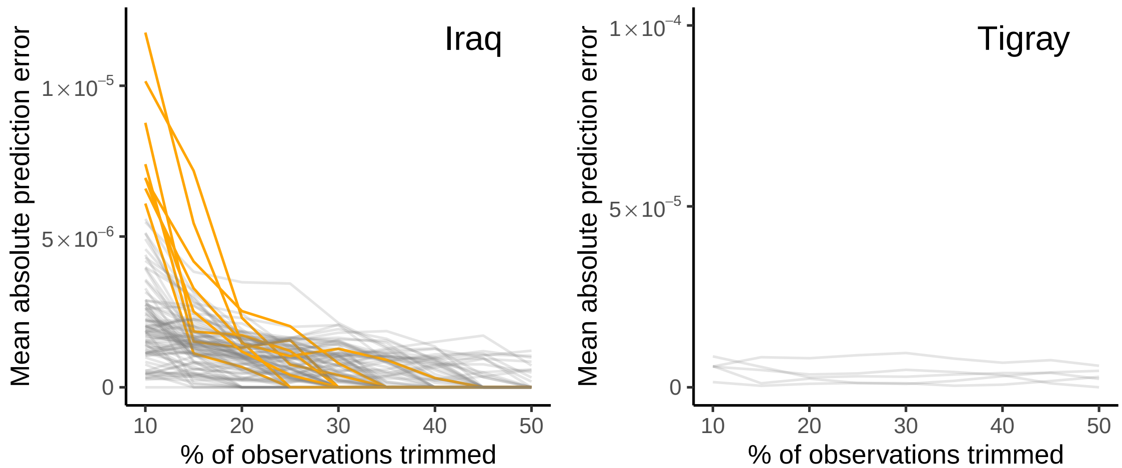

Figure 3: Mortality estimation in Iraq and Tigray, Ethiopia: The left and right panels present the mean absolute prediction errors at the cluster level (Iraq) and regional level (Tigray), respectively, with orange lines highlighting suspiciously different relationships.

spectively. Although specific cluster locations in Iraq are not identifiable in the publicly available data to which we have access, our analysis reveals that certain clusters with markedly different curves (depicted in orange) from others (gray). These results suggest that data contamination is suspected in several clusters in Iraq, and that trimming a fraction of observations to make the shapes of these curves more similar to others should be considered.

6 Generalizations

As discussed in Section 1, for expository reasons, we have until now abstracted from several demographic and methodological issues. We now generalize our approach to deal with these issues in five ways.

First, epidemiologists and public health scholars are often interested in age-sex or time-based cohorts, among others. We thus generalize the G-K estimator by redefining B_j as the number of persons in a desired cohort, such as 20–26 year old females siblings living in Uganda on 1/1/2015, and similarly for S_j and the other quantities.

Second, because rounding population figures to integer numbers of people can bias results, demographers fix this via person-years of exposure (Preston, Heuveline, and Guillot, 2001) . Following this logic, we can generalize the G-K estimator redefining S_j in Definition 5 as the number of person-years of exposure of respondents' siblings (Croft, Allen, and Zachary, 2023) and redefining $W_j = B_j/S_j$ accordingly. This logic is important for more fine grained analyses, such as mortality by cause or time, and especially in the presence of fertility variation, interactions between age, sibsize, and recall error, and different data analytic approaches, etc. (Masquelier, 2013).

Third, people in war zones often have knowledge of mortality well beyond those of their siblings, including about their parents, spouses, household members, coworkers, friends, acquaintances, neighbors, or, combining all of these, networked individuals. If we could collect accurate mortality counts in all these categories for each respondent, the G-K estimator applied to the entire group would have lower variance. However, we have until now made two implicit assumptions that are much more likely to be violated for groups other than siblings. In one, the groups defined by j (such as sibships) must be disjoint. Although in theory this is always possible, in practice different respondents assigned to the same group may perceive themselves as having different reference sets, which would invalidate all the methods discussed. Developing methods to accommodate non-disjoint groups without inducing bias or incorrect uncertainty estimates would be a valuable future research direction.

In the other, the potential extra information in different groups may induce measurement error, which could well be larger for larger groups. We know from Section 5 that measurement error in group size, which likely increases with the size of the group, makes any adversarial responding even more damaging. But, even without adversarial responses, error in larger groups can occur due to respondent errors in understanding or representing the definition of the group (like who their "neighbors" or "coworkers" are), which produces measurement error in B_j and S_j. These issues imply that choosing a reference group involves an important bias-variance trade off, which would be would be an important topic to formalize in future research.

To see this, consider a case where the reported values B_j, D_j, and S_j consist of the true values B_j^*, D_j^*, and S_j^* as well as measurement errors B_j^e, D_j^e, and S_j^e, so that $B_j = B_j^* + B_j^e$, and analogously for the other quantities. We can easily show that, without measurement error, the approximate variance of the generalized G-K estimator reduces as the number of individuals in the reference group increases:

$$\begin{aligned}\text{Var}(\tilde{q}) &\approx \frac{\text{Var}(X)}{\mu_Y^2} - 2\frac{\mu_X}{\mu_Y^3}\text{Cov}(X,Y) + \frac{\mu_X^2\text{Var}(Y)}{\mu_Y^4} \\ &= \frac{1}{J}\left\{\frac{\text{Var}(W_jM_j)}{(\mathbb{E}[W_j]+\hat{\xi}')^2} - 2\frac{(\mathbb{E}[W_jM_j]+\hat{\xi}')}{(\mathbb{E}[W_j]+\hat{\xi}')^3}\text{Cov}(W_j, W_jM_j) + \frac{(\mathbb{E}[W_jM_j]+\hat{\xi}')^2\text{Var}(W_j)}{(\mathbb{E}[W_j]+\hat{\xi}')^4}\right\}\end{aligned}$$

where $\hat{\xi}' = \hat{\xi}/J$ (see Theorem 5). However, the likely larger measurement errors in survey responses from larger reference groups means sampling probabilities cannot be properly estimated, and thus would likely produce substantial bias in mortality estimates (see Appendix C). In particular, the G-K estimator's nonlinearity means that measurement error will not be averaged away and so must be corrected with a method that would need to be developed. Until then, best practice should probably be to stick with reference groups likely to be well known to the respondent, in the specific context in which the survey is being conducted. An important topic for future research is to develop methods for correcting the bias due to measurement error so that we can can take advantage of the additional information in larger reference groups.

Fourth, sampling designs, such as stratified or cluster sampling, can be incorporated in the G-K estimator by applying survey weights at the appropriate level of aggregation. This can easily be done by redefining W_j in Definition 5 as a product of the individual-level and cohort-level probabilities of sampling. Such weights are analogous to those used in the adult mortality estimator employed by the DHS for more specific purposes (Croft, Allen, and Zachary, 2023; Feehan and Borges, 2021). We also recommend that, whenever clusters are available, researchers recognize this not merely as a problem to be fixed but as extra information that might be useful for estimation. An easy first step would be to estimate mortality separately within each of these separate areas.

Finally, throughout we have estimated total mortality, but often interest is in cause-specific mortality, such as whether deaths can be attributed to the war or would have occurred even if the war had not occurred. This sounds like a clear distinction, but classifying any individual death, especially by non-medical professionals, can be highly error prone (Pison et al., 2018). Except in circumstances where it is possible to elicit this information accurately by survey, or methods are developed to correct these measurement errors, researchers may prefer instead to estimate excess mortality by extrapolating mortality from pre-war statistics, if available, and subtracting these from survey based estimates of total mortality.

7 Concluding Remarks

This paper attempts to unify the political, strategic and methodological perspectives of political science with the detailed knowledge and context of mortality data in demography, public health, and medicine. Our main point is that the two sets of scholars will make faster progress by building on each other's work and working together going forward.

In the process, we provide proof for the first time the formal statistical properties of all existing estimators. We also show how adversarial reporting — long discussed qualitatively in the literature — may contaminate quantitative estimates due to their political incentives. We then develop diagnostic techniques for detecting and correcting for this insidious, but potentially widespread, type of measurement error.

Our approach provides a principled basis for future applications of sibling survival and other related types of survey research in difficult-to-study conflict zones. As a companion to this paper, we offer open-source software to implement our proposed methodology. Promising directions for further work to explore include collecting more systematic data on the behavioral incentives of misreporting, empirically validating trimming thresholds across different survey modes and conflict environments, and extending our robust framework to other demographic measures vulnerable to strategic manipulation.

Appendix A Proof that the Naive Estimator is Biased

In this appendix, we prove Theorem 1.

Proof. We begin by rewriting the quantity of interest from Equation 1:

$$q = \frac{\sum_{j=1}^{F} D_j}{\sum_{j=1}^{F} B_j}$$

$$= \sum_{j=1}^{F} \frac{B_j}{\sum_{j=1}^{F} B_j} \frac{D_j}{B_j}$$

$$= \sum_{j=1}^{F} \frac{B_j}{\sum_{j=1}^{F} B_j} M_j$$

$$= \sum_{j=1}^{F} \frac{B_j}{\sum_{j=1}^{F} B_j} I(M_j < 1) M_j + \sum_{j=1}^{F} \frac{B_j}{\sum_{j=1}^{F} B_j} I(M_j = 1) M_j$$

$$= \sum_{j=1}^{F} V_j I(M_j < 1) M_j + \sum_{j=1}^{F} V_j I(M_j = 1) M_j$$

where $V_j = B_j / \sum_{j=1}^{F} B_j$. This decomposition makes it intuitive that the naive estimator is biased. While q is based on weighted mortality experiences from families with and without survivors, the naive estimator only takes a look at families with at least one survivor.[8] It also upweights families with more survivors (see Figure 1). We formalize this intuition below.

Let i^S be the set of indices of individuals who are in the survivor population, i^J be the set of indices of individuals who are sampled from the survivor population, and i^j be the set of indices of individuals who are from family j. Also, denote $S = \sum_{j=1}^{F} S_j$, which is the number of survivors.

Using the individual-level notation, we now rewrite $\hat{q}$ as follows.

$$\hat{q} = \frac{\sum_{i \in i^J} D_i}{\sum_{i \in i^J} B_i} = \frac{\sum_{i \in i^J} B_i \cdot \frac{D_i}{B_i}}{\sum_{i \in i^J} B_i} = \frac{\sum_{i \in i^J} B_i M_i}{\sum_{i \in i^J} B_i} = \sum_{i \in i^J} \frac{B_i}{\sum_{i \in i^J} B_i} M_i = \sum_{i \in i^J} V_i^J M_i$$

where $V_i^J = B_i / \sum_{i \in i^J} B_i$. Thus, $\hat{q}$ is the weighted sample average of M_i. Since the sampling procedure from the survivor population is random, the weighted sample average is an unbiased estimator of the weighted survivor population average:

$$\mathbb{E}[\hat{q}] = \sum_{i \in i^S} V_i^S M_i = \sum_{j=1}^{F} \sum_{i \in i^j} V_i^S M_i.$$

where $V_i^S = B_i / \sum_{i \in i^S} B_i$.

Additionally, for $\forall i \in i^j$, we have $B_i = B_j$ and $M_i = M_j$. Also, since we have a total

[8] The notion that q is decomposed as families with or without survivors is in keeping with the existing literature. For example, see Feehan and Borges (2021).

of S_j survivors whose sibsize is B_j,

$$\sum_{i \in i^S} B_j = \sum_{j=1}^{F} S_j B_j.$$

Therefore, the weight V_i^S for $i \in i^j$ is re-expressed as:

$$V_i^S = \frac{B_i}{\sum_{i \in i^S} B_i} = \frac{B_j}{\sum_{j=1}^{F} S_j B_j}.$$

Thus,

$$\begin{aligned}
\mathbb{E}[\hat{q}] &= \sum_{j=1}^{F} \sum_{i \in i^j} V_i^S M_j \\
&= \sum_{j=1}^{F} \sum_{i \in i^j} \frac{B_j}{\sum_{j=1}^{F} S_j B_j} M_j \\
&= \sum_{j=1}^{F} S_j \frac{B_j}{\sum_{j=1}^{F} S_j B_j} M_j \\
&= \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j B_j} \frac{B_j}{\sum_{j=1}^{F} B_j} M_j \\
&= \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j B_j} V_j M_j \\
&= \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j B_j} V_j I(M_j < 1) M_j + \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j B_j} V_j I(M_j = 1) M_j.
\end{aligned}$$

Hence, for the naive estimator to be unbiased, the following condition must be satisfied:

$$\frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j B_j} = 1 \qquad \forall j \in \{1, \cdots, F\}.$$

However, this is clearly violated for families without survivors since $S_j = 0$ for such families. Therefore, the naive estimator is biased: $\mathbb{E}[\hat{q}] < q$. The unbiasedness only holds when $\gamma = 0$ and S_j is a constant across all observations, which does not happen in practice. ■

Appendix B Proof that the Subtraction and Weighted Subtraction Estimators are Biased

In this appendix, we prove Theorems 2 and 3. First, for the subtraction estimator:

Proof. We express the expectation of the subtraction estimator, $\dot{q}$, as:

$$\begin{aligned}\mathbb{E}[\dot{q}] &= \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j(B_j - 1)} \frac{B_j}{\sum_{j=1}^{F} B_j} M_j \\ &= \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j(B_j - 1)} V_j I(M_j < 1) M_j + \sum_{j=1}^{F} \frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j(B_j - 1)} V_j I(M_j = 1) M_j\end{aligned}$$

Therefore, for the subtraction estimator to be unbiased,

$$\frac{S_j \sum_{j=1}^{F} B_j}{\sum_{j=1}^{F} S_j(B_j - 1)} = 1 \qquad \forall j \in \{1, \cdots, F\}.$$

Yet this is violated when $S_j = 0$ (even asymptotically). Thus, the subtraction estimator is in general biased: $\mathbb{E}[\dot{q}] \neq q$. It is also asymptotically biased. ■

Second, the weighted subtraction estimator $\ddot{q}$ is also biased, which we can see because the Trussell and Rodriguez (1990) proof implements their constant-probability of death via the binomial assumption of sibship-level death counts D_j, takes the expectation of the numerator and denominator at the sibship level before summing up across sibships, and claims that the estimator is unbiased if every sibship has the same expected mortality. This claim is false because the expectation of a ratio is not equal to the ratio of two expectations. Trussell and Rodriguez (1990) try to sidestep this issue by claiming that "since the focus here is on mortality, which appears only in the numerator, and not family size, then the denominator can be treated as fixed, in which case the estimator is unbiased" (Trussell and Rodriguez, 1990). Yet their "unrestricted random sampling" assumption, which is equivalent to switching from the subtraction estimator to the weighted subtraction estimator, means that this claim is also false: while the denominator of the subtraction estimator is fixed (see Definition 3), the weighted subtraction estimator has S_j in the denominator, which is random. Therefore, their proof is not justifiable and their $\ddot{q}$ estimator is biased.

We can also show that the estimator is not asymptotically unbiased by rewriting $\ddot{q}$ as:

$$\begin{aligned}\ddot{q} &\approx \frac{\sum_{j=1}^{J} S_j D_j}{\sum_{j=1}^{J} S_j(B_j - 1)} \\ &= \frac{\sum_{j=1}^{J} D_j/S_j + \sum_{j=1}^{J}(D_j S_j - D_j/S_j)}{\sum_{j=1}^{J} B_j/S_j + \sum_{j=1}^{J} \{S_j(B_j - 1) - B_j/S_j\}}\end{aligned}$$

$$= \frac{\sum_{j=1}^{J} W_j M_j + \sum_{j=1}^{J}(D_j S_j - D_j/S_j)}{\sum_{j=1}^{J} W_j + \sum_{j=1}^{J} \{S_j(B_j - 1) - B_j/S_j\}}.$$

Comparing this new form to the G-K estimator, for example, we can see that, for $\ddot{q}$ to be asymptotically unbiased, it must follow that

$$\sum_{j=1}^{J}(D_j S_j - D_j/S_j) = \sum_{j=1}^{J} \{S_j(B_j - 1) - B_j/S_j\} = \hat{\xi},$$

which is false except in an unusual special case. In some situations, these terms will reduce the bias, compared to the subtraction estimator, such as when Cor$(B_j, M_j) = 0$, but bias (and asymptotic bias) will increase in other circumstances.

Thus the subtraction and weighted estimators are biased (and asymptotically biased).

Appendix C Proof that the G-K Estimator is Asymptotically Unbiased

In this appendix, we prove Theorem 4.

Proof. By substitution, we express the G-K estimator $\tilde{q}$ as

$$\tilde{q} \approx \frac{\sum_{j=1}^{J} W_j M_j + \hat{\xi}}{\sum_{j=1}^{J} W_j + \hat{\xi}} = \frac{\sum_{j=1}^{J} \frac{D_j}{S_j} + \hat{\xi}}{\sum_{j=1}^{J} \frac{B_j}{S_j} + \hat{\xi}}.$$

Let J' be the sum of J and the number of sibships with zero survivors that would have been observed if it were possible. We can think of J' as the number of sibships in this pseudo-sample.

Then, rewrite the numerator and denominator with scaling up to the pseudo-sample:

$$\begin{aligned}
\tilde{q} &= \frac{(\sum_{j=1}^{J'} S_j)\Big(\sum_{j=1}^{J} \frac{D_j}{S_j} + \hat{\xi}\Big)}{(\sum_{j=1}^{J'} S_j)\Big(\sum_{j=1}^{J} \frac{B_j}{S_j} + \hat{\xi}\Big)} \\
&= \frac{\sum_{j=1}^{J} \frac{D_j}{(S_j/\sum_{j=1}^{J'} S_j)} + \frac{\hat{\xi}}{(1/\sum_{j=1}^{J'} S_j)}}{\sum_{j=1}^{J} \frac{B_j}{(S_j/\sum_{j=1}^{J'} S_j)} + \frac{\hat{\xi}}{(1/\sum_{j=1}^{J'} S_j)}} \\
&= \frac{\sum_{j=1}^{J'} \frac{D_j}{(S_j/\sum_{j=1}^{J'} S_j)} I(M_j \neq 1) + \sum_{j=1}^{J'} \frac{D_j}{(1/\sum_{j=1}^{J'} S_j)} I(M_j = 1)}{\sum_{j=1}^{J'} \frac{B_j}{(S_j/\sum_{j=1}^{J'} S_j)} I(M_j \neq 1) + \sum_{j=1}^{J'} \frac{D_j}{(1/\sum_{j=1}^{J'} S_j)} I(M_j = 1)}.
\end{aligned}$$

Because the probability of sampling sibship j with S_j survivors at time 2 is proportional to $S_j/\sum_{j=1}^{J'} S_j$, the quantity $\sum_{j=1}^{J'} \frac{D_j}{(S_j/\sum_{j=1}^{J'} S_j)} I(M_j \neq 1)$ is an inverse probability-weighted (IPW) sum. This IPW sum is an asymptotically unbiased estimator of the population mean of D_j excluding sibships with zero survivors. Formally,

$$\lim_{J' \to \infty} \sum_{j=1}^{J'} \frac{D_j}{(S_j/\sum_{j=1}^{J'} S_j)} I(M_j \neq 1) = \mu_D - \sum_{j=1}^{J'} \frac{D_j}{(1/\sum_{j=1}^{J'} S_j)} I(M_j = 1)$$

where μ_D is the population mean of D_j.

Therefore, the numerator asymptotically becomes

$$\lim_{J' \to \infty} \sum_{j=1}^{J} \frac{D_j}{(S_j/\sum_{j=1}^{J'} S_j)} + \frac{\hat{\xi}}{(1/\sum_{j=1}^{J'} S_j)} = \mu_D.$$

Similarly, for the denominator,

$$\lim_{J' \to \infty} \sum_{j=1}^{J} \frac{B_j}{(S_j/\sum_{j=1}^{J'} S_j)} + \frac{\hat{\xi}}{(1/\sum_{j=1}^{J'} S_j)} = \overline{B}$$

where $\overline{B} = \frac{1}{J}\sum_{j=1}^{J} B_j$. Thus, since $J \to \infty$ is equivalent to $J' \to \infty$,

$$\lim_{J \to \infty} \mathbb{E}[\tilde{q}] = \mathbb{E}\Big[\frac{\mu_D}{\overline{B}}\Big] = q$$

which proves that $\tilde{q}$ is asymptotically unbiased under the stated assumption. ■

Appendix D Finite-sample Properties

To examine finite-sample properties, we create population-level datasets of sibling mortality experiences as follows. First, we draw $B \sim$ Pois(5) and set $B_j = \max(1, \min(B, 20))$ so that $B_j \in \{1, \cdots 20\}$. To induce specified correlation between B_j and M_j, we model logit$(M_j) = \beta_0 + \beta_1 z(B_j)$, where $z(B_j)$ is the standardized sibsize and $\beta_1 = -0.2, 0, 0.2$ correspond to negative, no, and positive correlation cases, respectively. We calibrate β_0 so that $\mathbb{E}[M_j] = 0.05$. We then draw $D_j \sim$ Binomial(B_j, M_j).

We generate $N = 400,000$ observations for each of the three correlation scenarios. For each scenario, we sample $J = 1,000$ survivors $C = 1,000,000$ times. For each of the C samples, we apply all three estimators and G-K's analytically derived variance from

Theorem 5, and then summarize these across all C samples the empirical mean of the estimates, the mean of the analytic variances, and the empirical variance of the estimates.

We find that the G-K estimator is approximately unbiased, with the absolute bias less than 0.0072 percentage points (in the positive correlation case; the absolute biases are 0.00024 and 0.00087 percentage points for the zero and negative correlation cases, respectively). Additionally, the absolute differences between the G-K empirical and analytically derived variances are all less than 1×10^{-7}. We also find that the absolute bias of the subtraction estimator is as high as 0.45 percentage points (in the positive correlation case; even in the zero correlation case, the bias is 0.0092 percentage points, which is approximately 38 times greater than the bias of the G-K estimator), while that of the naive estimator is up to 1.1 percentage points (all negative biases for the naive estimator).

Appendix E Derivation of the Variance of the G-K Estimator

In this appendix, we derive the G-K estimator's variance given in Theorem 5.

Proof. For notational simplicity, let $X = \sum_{j=1}^{J} W_j M_j + \hat{\xi}$ and $Y = \sum_{j=1}^{J} W_j + \hat{\xi}$. Then, the G-K estimator is written as $f(X,Y) = X/Y$.

Let μ_X and μ_Y denote the means of X and Y, respectively. Also let f'_X and f'_Y denote the partial derivative of $f(X,Y)$ with respect to X and Y, respectively. Notice that

$$f'_X(x,y) = \frac{1}{y} \quad \text{and} \quad f'_Y(x,y) = \frac{-x}{y^2}.$$

Thus, the variance of $f(X,Y)$ is approximated by

$$\begin{aligned}
\text{Var}(\tilde{q}) &\approx f'_X(\mu_X,\mu_Y)^2\text{Var}(X) + 2f'_X(\mu_X,\mu_Y)f'_Y(\mu_X,\mu_Y)\text{Cov}(X,Y) + f'_Y(\mu_X,\mu_Y)^2\text{Var}(Y) \\
&= \frac{\text{Var}(X)}{\mu_Y^2} - 2\frac{\mu_X}{\mu_Y^3}\text{Cov}(X,Y) + \frac{\mu_X^2\text{Var}(Y)}{\mu_Y^4}
\end{aligned}$$

where

$$\begin{aligned}
\mu_X &= J\mathbb{E}[W_j M_j] + \hat{\xi} \\
\mu_Y &= J\mathbb{E}[W_j] + \hat{\xi}
\end{aligned}$$

$$\text{Var}(X) = J\text{Var}(W_j M_j)$$
$$\text{Var}(Y) = J\text{Var}(W_j)$$
$$\text{Cov}(X, Y) = J\text{Cov}(W_j, W_j M_j).$$

■

Appendix F Influence of Contamination as an Increasing Function in Mortality

In this section, we prove Theorem 6.

Proof. Let $\mathcal{C}$ be a set of contaminated sibship-level mortality reports. Also, let $T(\cdot)$ be the G-K estimator as a function of a distribution of mortality reports. Then,

$$T(F^\delta) = \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + \sum_{j:M_j \in \mathcal{C}} \frac{x}{1-x} + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + \sum_{j:M_j \in \mathcal{C}} \frac{1}{1-x} + \hat{\xi}} = \frac{g(x)}{h(x)}$$
$$T(F^S) = \frac{\sum_j \frac{M_j}{1-M_j} + \hat{\xi}}{\sum_j \frac{1}{1-M_j} + \hat{\xi}}$$
$$IC(\tilde{q}, \delta, x) = T(F^\delta) - T(F^S) = \frac{g(x)}{h(x)} - T(F^S).$$

Now, denote $f(x) = IC(\tilde{q}, \delta, x)$. Also let $J_C \in \mathbb{N}$ be the number of sibships with contaminated data. Then,

$$g(x) = \sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + J_C \frac{x}{1-x} + \hat{\xi}$$
$$h(x) = \sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + J_C \frac{1}{1-x} + \hat{\xi}$$
$$\therefore g'(x) = h'(x) = \frac{J_C}{(1-x)^2}$$
$$\therefore f'(x) = \frac{g'(x)h(x) - g(x)h'(x)}{h^2(x)} = \left\{ \frac{J_C}{(1-x)h(x)} \right\}^2 > 0.$$

Therefore, $IC(\tilde{q}, \delta, x)$ is an increasing function in x. ■

Appendix G Comparison of the Maximum Influence Increase and Decrease

In this section, we prove Corollary 1.

Proof. By definition,

$$MI^{+} = IC\left(\tilde{q}, \delta, \frac{B-1}{B}\right) = \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + J_C(B-1) + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + J_C B + \hat{\xi}} - T(F^S)$$

$$MI^{-} = IC(\tilde{q}, \delta, 0) = \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + 0 + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + J_C \cdot 1 + \hat{\xi}} - T(F^S)$$

Then, since $MI^{+} \geq 0$ and $MI^{-} \leq 0$,

$$\begin{aligned} d(B) &= |MI^{+}| - |MI^{-}| \\ &= MI^{+} + MI^{-} \\ &= \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + J_C(B-1) + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + J_C B + \hat{\xi}} + \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + J_C + \hat{\xi}} - 2T(F^S) \\ &= \frac{q(B)}{r(B)} + \frac{\sum_{j:M_j \notin \mathcal{C}} \frac{M_j}{1-M_j} + \hat{\xi}}{\sum_{j:M_j \notin \mathcal{C}} \frac{1}{1-M_j} + J_C + \hat{\xi}} - 2T(F^S). \end{aligned}$$

Therefore,

$$d'(B) = \frac{q'(B)r(B) - q(B)r'(B)}{r^2(B)} = \frac{J_C\left\{r(B) - q(B)\right\}}{r^2(B)} = \left\{\frac{J_C}{r(B)}\right\}^2 > 0$$

and it follows that $d(B)$ is an increasing function in B. ■

Appendix H Influence of Contamination as an Increasing Function in Weighted Mortality

In this section, we prove Corollary 2.

Proof. Let $\tilde{q} \approx \sum_{j=1}^{J} Z_j M_j$ and $f(x) = IC(\tilde{q}, \delta, x)$. By Theorem 6, we have $f'(x) > 0$.

By definition, $y = \frac{x}{1-x}$ where $x \in (0, 1)$. We first reexpress $f(x)$ as

$$f(x) = f\left(\frac{y}{1+y}\right) = g(y).$$

Then,

$$\frac{\partial g(y)}{\partial y} = f'(x)\frac{\partial x}{\partial y}.$$

Also,

$$\frac{\partial x}{\partial y} = \frac{\partial}{\partial y}\left(\frac{y}{1+y}\right) = \frac{1+y-y}{(1+y)^2} = \frac{1}{(1+y)^2} > 0.$$

Thus, $\frac{\partial g(y)}{\partial y} > 0$ and $IC(\tilde{q}, \delta, y)$ is an increasing function in y. ■

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