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Mortality Crises as Experienced by their Survivors:
Computational Approaches to the Study of Bereavement

By
Mallika Amruta Snyder

A dissertation submitted in partial satisfaction of the
requirements for the degree of
Doctor of Philosophy
in
Demography
in the
Graduate Division
of the
University of California, Berkeley

Committee in charge:

Professor Kenneth Wachter, Co-Chair
Professor Joshua Goldstein, Co-Chair
Professor Ayesha Mahmud
Professor Dennis Feehan

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Mortality Crises as Experienced by their Survivors:
Computational Approaches to the Study of Bereavement

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Abstract

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by

Mallika Amruta Snyder

Doctor of Philosophy in Demography

University of California, Berkeley

Professor Kenneth Wachter, Co-Chair

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Although the study of mortality is central to demography, comparatively little is known about its lived experience: how population-level mortality translates to individual experiences of loss within families and communities. Given the significance of bereavement for the health and socioeconomic outcomes of survivors, better understanding the impacts of mortality crises on family networks is crucial for predicting their longer-term consequences. The data required to study kin loss, however, is seldom available, leading many demographers to rely on computational approaches such as microsimulation to estimate the impact of these events.

This dissertation presents microsimulation-based approaches to examining the impact of a mortality crisis, in this case COVID-19, on kin networks in the short and long term. The first study presents estimates of monthly excess kin loss by age and type of kin relation in 31 countries during the period of March 2020 to June 2021. These estimates demonstrate a generational pattern of kin loss reflecting COVID-19 age-specific excess mortality risk, and highlight the significant effect of excess mortality on family bereavement. The second study extends this estimation approach to 120 countries over the 2020-2021 period, documenting high rates of excess kin loss in many low-and-middle-income countries higher than or comparable to those observed in high-income countries. It also considers the extent to which differences in country estimates were shaped by both excess mortality and pre-existing kinship structure. The third study projects how “kinship memory”, the estimated share of national populations related to victims of COVID-19 excess mortality, may change over the next century in 120 countries around the world, and considers what this may mean for how this crisis is remembered in the future. These three studies combined highlight the significant burden of COVID-19 excess mortality in terms of bereavement experienced by surviving family members, and demonstrate the importance of computational approaches in helping better understand the experiences of populations for which limited data exists.

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Author Contributions for Chapters 2 and 4

Since Chapters 2 and 4 contain co-authored work, author contributions are listed here, in line with practices in many academic journals.

For Chapter 2: Mallika Snyder, Diego Alburez-Gutierrez, and Emilio Zagheni designed research; Mallika Snyder and Diego Alburez-Gutierrez performed research; Iván Williams contributed new reagents/analytic tools; Mallika Snyder analyzed data; and Mallika Snyder, Diego Alburez-Gutierrez, Iván Williams, and Emilio Zagheni wrote the paper.

For Chapter 4: Mallika Snyder, Diego Alburez-Gutierrez, Emilio Zagheni, and Ashton Verdery designed research; Mallika Snyder performed research; Mallika Snyder analyzed data; and Mallika Snyder wrote the paper, in consultation with Diego Alburez-Gutierrez, Emilio Zagheni, and Ashton Verdery.

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Chapter 1

Introduction

Measuring the Lived Experience of Mortality

For centuries, demographers have sought to develop and improve upon methods of measuring the population processes at work around them. Censuses and household surveys have seen significant changes to enumeration and sampling strategies, advanced statistical methods have been employed to measure and forecast vital rates in cases where data is absent or incomplete, and mathematical models have been used to fill in gaps in measurement approaches and understand the relationships between the components of demographic change. These, and many other developments in the field, have helped to provide a rich foundation for current efforts to understand mortality, fertility, and migration in a world that has recently seen a dramatic mortality shock in the form of the COVID-19 pandemic, but in which information on the extent of this shock is scarcely available, except through statistical models, for the vast majority of countries around the world.

What is more difficult to study, using existing approaches, is what these population processes mean and have meant in the past for those living through them—how changes in vital rates and population size are felt at the individual level. When emigration increases, how many neighbors does a person see pack up and leave the country? When fertility increases, how many more children are attending a child’s school? And during a mortality crisis, how many people in an individual’s social network will die as a result? The scale of this impact, and when and how it is experienced in an individual’s life, will determine how they respond to and perceive this change. The effects of any change are likely to be unequally distributed—some groups may see hardly any impact, while others may be severely affected—but, on aggregate, this may shape how countries and societies react to demographic events, now and in the future.

A particularly salient and challenging aspect of this issue is the impact of a mortality crisis

on family networks. The consequences of losing a relative can be devastating to a person’s mental and physical health, family relationships, and socioeconomic conditions. And yet comparatively little is known about how changes in mortality translate into individual experiences of loss. Aside from countries with population registers, where deaths can be linked to family members, or household surveys covering certain sub-populations, mortality data is not available at the family level. Without this information, it is difficult to put into context what a mortality crisis means for those who survive it, and how it may shape them in the future. At a policy level, accounting for both victims of a mortality crisis and its impacted survivors may alter cost-benefit calculations for mortality reduction efforts, and further emphasize their importance. It may also help governments and communities identify the scale and distribution of loss experienced, and to mobilize and direct support towards individuals who have lost a loved one. Such considerations have proved important in the context of the COVID-19 pandemic, which, in its mortality impacts, has had catastrophic implications for the health, social support systems, and subsequent well-being of many people around the world.

This need to account for bereaved survivors, combined with a lack of readily available data on these populations, has led over the years to multiple conceptual and technical advances in approaches to estimating kin loss and its impacts. Early research on this subject included Le Bras’s macrosimulation-based estimates of ages of death for ancestors (parents, grandparents, and great-grandparents), with discussion of how this might impact inheritances in France and Venezuela (Le Bras, 1973), and Uhlenberg’s conceptual model to consider how changing demographic conditions might influence the availability of relatives, and the timing of the experience of their loss (Uhlenberg, 1980). Since then, there have been numerous studies of how kinship resources may change for older adults (Wachter, 1997; Verdery & Margolis, 2017), for women caring for both elderly and young dependents (Menken, 1985), and for the elderly of Thailand (Wachter et al., 2002) and young children of Zimbabwe (Zagheni, 2011) in response to the HIV/AIDS epidemic. From a technical perspective, this has included the development of new indicators to measure kin loss, such as a simple and intuitive “bereavement multiplier”, highlighting the number of individuals who would mourn a single COVID-19 victim (Verdery et al., 2020), as well innovations to study the impacts of crises in populations with uncertain and limited data on vital rates (Zagheni, 2011), and to consider the impact on estimates of factors such as within-family mortality correlations (Wachter et al., 2002). The papers in this dissertation seek to build on these and other studies in this rich tradition of research.

In doing so, I rely on demographic microsimulation, one of the most popular tools for estimating kin network dynamics associated with demographic change. In the next section, I discuss the history of the development of this technique, and its applications to studies like those contained in this dissertation. ¹

¹The next two sections are indebted to work by Emilio Zagheni on the history of demographic microsimulation (Zagheni, 2015) and insights from Kenneth Wachter.

A Short History of Demographic Microsimulation

Many “macro” population-level demographic processes can be summarized in relatively straightforward models or equations, often based on their underlying biological processes; the Lotka-Euler renewal equation provides such an example. The individual-level “micro” outcomes that determine these population processes and estimates, however, are more challenging to model in the absence of empirical data, and substantial micro-level heterogeneity can be obscured by population aggregates. In this context, demographic microsimulation offers a valuable way of generating synthetic microdata, by the creation of a population of stochastically generated fictional individuals whose life course events and family networks approximate in aggregate the macro-level population processes of the population they are meant to represent. In doing so, microsimulation can address several issues related to modeling population heterogeneity: allowing for some individuals or population sub-groups to experience different vital rates than others, capturing the effects of random variability in kin network sizes, and better accounting for non-linearities in population dynamics, such as partnership formation in two-sex populations. These and other advantages of microsimulation will be discussed in the following sections.

The concept of demographic microsimulation has been considered since at least the 1950s (Orcutt, 1957), and methods for generating this data have developed in step with improvements in computational power over the following decades. SOCSIM, one of the earliest and most popular demographic microsimulators today, exemplifies these improvements in computational power and methods: originally written in FORTRAN (Hammel et al., 1976) and now in C (Mason, 2016), with an R package under development (Theile & Alburez-Gutierrez, 2022); and having been enriched by the addition of numerous additional features, such as a fertility multiplier, designed to better capture population heterogeneity. Originally developed at Trinity College, Cambridge, and UC Berkeley in the 1970s by Peter Laslett, Eugene Hammel and Kenneth Wachter to understand the role of demographic factors in the formation of multigenerational household structures in premodern England (Wachter et al., 1978), SOCSIM has since been used in numerous studies of kin networks and availability of kinship resources. This has included research on kinship resources for the elderly in the United States (Wachter, 1997; Verdery & Margolis, 2017); for the elderly in Thailand (Wachter et al., 2002, 2003) and orphans in Zimbabwe (Zagheni, 2011) in the context of the HIV/AIDS epidemic; and for individuals of various ages experiencing the loss of a relative to COVID-19 (Verdery et al., 2020; Snyder et al., 2022).

Since empirical data on kin networks is often unavailable or incomplete, SOCSIM has proved particularly valuable in generating this data, including in examining the characteristics of populations unrepresented in historical data (Hammel & Wachter, 1996). The question of how to address limited availability of another type of data—vital rates needed by the simulations as input—was also a central issue in SOCSIM’s development, and remains so today: balancing a need to reflect real-world populations accurately by incorporating as many significant features as possible, while considering that rates for specific sub-populations may not be available (Wachter & Hammel, 1986). Nevertheless, in its ability to present, through

its stochastic output and features accounting for population heterogeneity, an understanding of how chosen rates and assumptions factor into dynamic models of kinship (Wachter, 1987), SOCSIM has helped to capture important aspects of kinship networks for which alternative data sources may not be available.

This dissertation focuses on SOCSIM, but it is important to note the development of alternate microsimulation programs that have proved useful in other studies. This includes CAMSIM, developed in the 1970s and 1980s after SOCSIM by Peter Laslett, James Smith and Jim Oeppen, as a modified version of SOCSIM. While SOCSIM is a closed-population simulator, in that individuals only enter the simulation through birth, and only exit it through death, CAMSIM is an open-population simulation, in which individuals can be randomly generated in response to marriage market matching (Zhao, 2006). MOMSIM, another program developed by Steven Ruggles, separately simulates family groups based on a single female ancestor, before combining them to form a population (Ruggles, 1987). Other microsimulation approaches have been used to examine constraints on childbearing in terms of family caregiving responsibilities (Menken, 1985) and identifying the most recent common ancestor of modern humans (Rohde et al., 2004). Also relevant in this context are agent-based computational models, which, like microsimulation, involve individual heterogeneous agents acting based on pre-specified rules; an example is the “Wedding Ring” model (Billari et al., 2007), which provides a realistic distribution of marriage by age based on simple rules of partner availability and the share of individuals already married.

After discussing the history of the method, it is worth describing briefly what a simulation in SOCSIM, the tool used in this dissertation, entails (Zagheni, 2015; Mason, 2016). SOCSIM requires an initial population file with kin relationships between individuals, which in some cases can be obtained by sampling from a household survey (Wachter et al., 2002) or census (Verdery & Margolis, 2017). In other cases, however, when a linked initial population is not available, SOCSIM itself can be used to obtain a starting population, by running the simulation for a long period of time prior to its “official” start to obtain a stable population with kinship links (Wachter et al., 1978). This can be accomplished by using a single block of the monthly rates that SOCSIM requires, in addition to an unlinked starting population (Alburez-Gutierrez, Mason, & Zagheni, 2021; Snyder et al., 2022). These rates, which can vary by pre-specified population subgroups, must include fertility and mortality rates; many versions include marriage rates as well. In the absence of marital-specific fertility rates, some recent research, including the papers in this dissertation, has chosen to model partner matching in terms of making the match occur at the time of the birth of the mother’s first child, the timing of which is based on age-specific fertility rates, and the choice of male partner based on a target distribution of age differences between partners (Alburez-Gutierrez, Mason, & Zagheni, 2021; Snyder et al., 2022). Despite its limitations, this approach has proved valuable in contexts where data on marriage-specific fertility may not be available.

Based on these rates and their demographic characteristics, the individuals in SOCSIM simulations are scheduled to experience certain events (childbirth, marriage, divorce, death) based on stochastically generated piecewise exponential waiting times and a competing risk model. The timing of these events is recorded for each individual, along with pointers that

can connect kin (for example, a child’s parents are recorded, as is a mother’s last-born child). This can be used to construct demographic histories for these individuals, along with a population genealogy that can be then examined to study micro-level processes such as family formation and kin loss over time. Such output is used in each of the papers presented in this dissertation.

Why Use Demographic Microsimulation?

It is important to note at this point that demographic microsimulation is not the only tool that can be used to study kinship processes. At the same time as SOCSIM was being developed, Leo Goodman, Nathan Keyfitz, and Thomas Pullum published their influential work on estimating kin using formal demographic methods (Goodman et al., 1974). The Goodman-Keyfitz-Pullum (GKP) equation approach uses multiple integration of fertility rates and survival probabilities to calculate the probability that a particular woman has a living female biological relative. Originally intended for stable single-sex populations, it has been applied to non-stable settings (Alburez-Gutierrez, 2022), and can be augmented to yield tabulations of kin of both sexes, although it is commonly used only in single-sex settings. Following this tradition, Hal Caswell’s matrix approach to kinship measurement has emerged recently as a complement to the original multiple integration approach, allowing for non-stable dynamics and linear projection-matrix-based tabulations of male and female kin counts (Caswell, 2019; Caswell & Song, 2021; Caswell, 2022).

Like demographic microsimulation, formal approaches have the advantage of requiring relatively few inputs, typically only mortality and fertility rates; since programs like SOCSIM also require a number of parameters such as the mean age difference between spouses that normally have default values but may need to be specified for a given population, formal approaches may in some cases be less demanding in terms of inputs. They are also well-suited to generating simple summary quantities, such as the number of living relatives or the probability of living kin, that can be used to compare the experiences of individuals living in varied demographic regimes. A major challenge with demographic microsimulation is the computational resources, including time spent calibrating a model, required to ensure that simulation output is realistic and effectively captures the population under study. While recent developments, such as the R package version of SOCSIM (Theile & Alburez-Gutierrez, 2022), may reduce some of these barriers to use, formal models of kinship may more readily generate summary quantities, without many of these computational challenges, and within a framework that may permit some mathematical decomposition of processes underlying kin availability (Williams & Alburez-Gutierrez, 2021; Keyfitz & Caswell, 2005). Despite these advantages, formal approaches, whether based on matrices or multiple integration, also involve significant drawbacks.

Lateral Kin

One of the most notable challenges in this regard relates to lateral kin, such as sisters. Direct progenitors and descendants can be easily identified, in the GKP approach, using some version of the generating equation: granddaughters are the daughters of a woman's daughters, for example, and can be calculated with the help of an additional integral. Lateral kin are more complicated, however, since not only is it necessary to consider separately lateral kin born before or after a reference individual (e.g. older and younger sisters), but the expected number of these relatives for a particular individual depends on the distribution of family sizes in a population, information that is not always readily available. This can be obscured by the average family size: for example, two populations, one with one girl per family and the other with half of families having two girls and half having none, will both have one as the average number of daughters. However, in the first population, the average number of sisters for a girl will be zero, while in the second population, this number will be one.

Goodman, Keyfitz, and Pullum acknowledge this issue in an addendum to their original article (Goodman et al., 1975), considering the extent to which the expected number of sisters can be adjusted by knowledge of its variance. The mathematical solution used, however, to assume a Poisson distribution of family sizes where the mean is equal to the variance, does not necessarily resemble real population distributions of family sizes. In Caswell's matrix approach, there is no attempt in current formulations to account for the variance of family sizes in lateral kin. Such heterogeneity is challenging to account for in matrix formulations without significant increases in dimensionality to account for all possible family sizes and the use of rates for specific sub-populations that may not be available. A further complication arises when considering that fertility levels are to some extent heritable, further adding to the dimensions required to address this issue with matrix methods.

With these challenges in mind, SOCSIM contains multiple features that, by accounting for heterogeneity of fertility, are better able to capture variance in the distribution of lateral kin. The first is a fertility multiplier, which assigns each woman a random number by which her monthly hazard of giving birth is proportionally adjusted over her entire life (Mason, 2016); the distribution of these multipliers mimics empirical data on family sizes. Depending on the settings chosen, these multipliers can be partly heritable by a woman's daughters. The second relevant feature in this respect is the potential to vary fertility rates by parity; in situations where data is available, this provides an opportunity to better capture fertility heterogeneity. Finally, SOCSIM also allows for vital rates to vary by population sub-group. Based on the availability of data, the studies in this dissertation include a non-heritable fertility multiplier, allowing them to account, at least partially, for variance in the distribution of family sizes.

Affinal Kin

Affinal kin, such as spouses or cousins, also present another significant issue for formal approaches. Both the original GKP formulation and Caswell’s matrix approach focus only on biological kin; extending these models to consider spouses would require a large increase in dimensionality to account for different combinations of partner ages. In this context, it may be worth noting that two-sex kinship models for biological kin are already relatively challenging for formal methods; given the mathematical complexity of accounting for a two-sex population, Goodman, Keyfitz, and Pullum propose applying simple multipliers to female-only estimates (Goodman et al., 1974), an approach that is not able to replicate the dynamics of real-world two sex populations. Similarly, while Caswell (2022) proposes a linear projection matrix-based approach incorporating separate male and fertility and survival matrices, this approach will not capture non-linear characteristics of two-sex population dynamics.

Although microsimulation may not still be able to fully account for non-linear dynamics, it is able to capture with relative ease some important features, such as the formation of partnerships between individuals based on expected age differences between spouses. Critical to SOCSIM’s success in this area is its closed-population structure, which ensures that after a partner is selected for a given individual, the partner also has a kin network of their own that will facilitate a realistic distribution of affinal kin for the individual in question. Also valuable is the flexibility of approaches with which it can assign a spouse to this individual, either through marriage rates at various ages (Zagheni, 2011; Verdery & Margolis, 2017) or, as in the papers in this dissertation, through assigning a partner at the time of the birth of a woman’s first child (Alburez-Gutierrez, Mason, & Zagheni, 2021; Snyder et al., 2022). Depending on specifications selected, SOCSIM will also aim to match a target distribution of age differences between spouses. These features and their implications for the interpretation of affinal kin counts are discussed further in subsequent chapters of this dissertation.

Stochastic Variability

A final important aspect of kinship dynamics to consider in this regard is stochastic variability; as a result of random chance, some kin networks may end up much larger or smaller than others. This is especially noticeable in small populations, but remains an issue even in larger ones when considering specific sub-populations based on an age-sex combination. The GKP equations are deterministic (Goodman et al., 1974); similarly, a stochastic extension to Caswell’s matrix approach has not yet been implemented (Caswell & Song, 2021), although previous work by Pollard on matrix variances and higher moments for stochastic population models would be relevant in this context (Pollard, 1966). However, failing to consider the impact of this random variability may produce significant statistical error, as discussed by Wachter in an examination of issues in relying on stable population theory to generate counts of sisters (Wachter, 1980). Understanding sources of this random variability and its extent

is thus critical to estimating kinship networks and their dynamics.

As a stochastic simulator, SOCSIM is especially well-positioned to address this issue. Simply replicating simulation runs can provide a measure of simulation uncertainty (although this will not capture uncertainty related to the inputs themselves). It is also possible to more carefully account for variability in inputs, through techniques such as Bayesian melding (Poole & Raftery, 2000), applied in Zagheni (2011) to calibrating SOCSIM microsimulations with uncertain vital rates. Although more research is needed into optimal approaches to microsimulation calibration, SOCSIM can represent a particularly effective and parsimonious approach to capturing the random variability in population dynamics necessary for estimating kin counts.

Mortality Crises as Experienced by their Survivors

It is now clear from the preceding sections that demographic microsimulation can provide a valuable means of quantifying individual-level experiences of demographic change, including kin loss associated with mortality crises. Before turning to three examples of such estimates in the next three chapters of this dissertation, it is important to take a moment to consider in more detail what these measures of kin loss are likely to mean for individuals reflected in these statistics.

As death is a fundamental demographic process, so too is bereavement and the loss of kin; nevertheless, its effects on affected individuals may be profound. Losing a relative may result not only in severe, often long-lasting (Raker et al., 2020), psychological and physical distress, but also in a loss of social and economic resources and support. Many studies have focused on spousal loss (Stroebe et al., 2007; Elwert & Christakis, 2008a,b), but others have considered the impacts of the loss of a child (Li et al., 2003; Qin & Mortensen, 2003; Doku et al., 2020), sibling (Fletcher et al., 2013), parent (Bergman et al., 2017), or grandparent (Stokes et al., 2019), some considering the impacts of various types of losses in comparison (Patterson et al., 2020). What emerges from this diverse range of studies is an elevated risk of mortality for bereaved individuals (Elwert & Christakis, 2008a,b), along with increases in depressive symptoms and depression (Tseng et al., 2017; Wang et al., 2021), risk of dementia (Liu et al., 2021; Umberson et al., 2020), and other illness (Stroebe et al., 2007). This is combined with potential negative impacts on educational attainment (Patterson et al., 2020), family relationships (Kim et al., 2021), and other socioeconomic outcomes (Fletcher et al., 2013). Concerns about support for bereaved individuals are especially salient in light of a mortality crisis, where social support systems may be further disrupted, further compounding the effects of kin loss. This has been illustrated in the context of the HIV/AIDS epidemic in Africa (Zagheni, 2011), where diminished availability of extended family members for HIV/AIDS orphans has involved increased reliance on grandparents and adolescents and led to the establishment of more child-headed households (Foster, 2000; Foster et al., 1996).

The COVID-19 pandemic, which, especially in early mortality waves, saw significant disruptions to mourning rituals such as funerals and resulted in large-scale losses, illustrates clearly the potential extent of such impacts. Research has shown that bereavement due to COVID-19, which in the traumatic circumstances often associated with it epitomizes a “bad death” (Carr et al., 2020), is linked to rates of prolonged grief disorder comparable to that experienced in response to an unnatural death (Eisma et al., 2021, 2020). The risk of self-reported depression and loneliness is also higher for those bereaved during the COVID-19 pandemic than during the pre-pandemic period (Wang, Smith-Greenaway, et al., 2022). In accelerating existing risks of age-specific mortality, COVID-19 has increased the likelihood that younger individuals will experience the loss of older relatives, such as grandparents and parents, and that older individuals may experience the loss of a sibling or spouse (Snyder et al., 2022; Verdery et al., 2020). The loss of a parent or spouse has well-documented negative effects on well-being, and has, accordingly, received considerable attention in light of COVID-19 (Kidman et al., 2021; Hillis et al., 2021; Wang, Smith-Greenaway, et al., 2022). However, the losses of siblings for older individuals and grandparents for younger individuals are also likely to have significant effects: sibling relationships have been shown to be an important mitigating factor for loneliness in adulthood (Stocker et al., 2020). Similarly, grandparents, especially grandmothers, provide critical social support and nurturing for children (Hayslip Jr. & Fruhauf, 2019; Sear & Mace, 2008; Song & Mare, 2019), and their loss is a risk factor for adolescent experiences of depression and exposure to maternal depression (Livings et al., 2022). Each individual kin death is likely to be experienced differently, based on the characteristics of the individual involved, but it is clear that these losses will shape those bereaved for years to come.

Such concerns are key to interpreting and placing in context the estimates of COVID-19-associated kin loss contained in this dissertation. For each point increase in population-wide rates of kin loss above expected levels, a significant number of individuals who might not have been bereaved at this time are now experiencing its effects. This experience is further exacerbated by the isolation, losses of social support, and other challenges associated with this mortality crisis. It is critical to remember these individuals, and their deceased relatives, in considering the impact of the pandemic on populations around the world.

The rest of this dissertation proceeds as follows. In the second chapter, I present published estimates of excess kin loss associated with COVID-19 excess mortality (Snyder et al., 2022), coauthored with Diego Alburez-Gutierrez (Max Planck Institute for Demographic Research), Iván Williams (University of Buenos Aires), and Emilio Zagheni (MPIDR). In a set of SOC-SIM demographic microsimulations for 31 countries that had varied experiences of COVID-19 excess mortality, we estimate monthly rates of excess kin loss for individuals who survived the period from March 2020 to June 2021. The estimates presented highlight the dramatic effects of COVID-19 excess mortality on family networks, with some countries seeing over a doubling of rates of kin loss for certain demographic groups in high mortality periods, and document a generational pattern of kin loss, where younger individuals were most at risk of losing a grandparent, while older individuals were most at risk of losing a sibling. This study’s focus on rates of kin loss experienced by survivors of various ages complements other approaches designed to estimate numbers of kin lost as a result of the pandemic (Verdery et

al., 2020; Hillis et al., 2021). The demographic microsimulation approaches laid out in this section provide a foundation for the subsequent chapters of this dissertation.

In the third chapter, I examine more closely the demographic factors that have shaped the estimates of kin loss presented in Snyder et al. (2022) and other studies. Despite the significant toll of COVID-19 excess mortality in low-and-middle-income countries (LMICs), estimates of associated kin loss have been limited so far in these contexts to orphanhood and losses of caregiving grandparents experienced by children (Hillis et al., 2021). As seen in high-income countries, however, multiple age groups are vulnerable to different types of kin loss as a result of COVID-19 excess mortality (Snyder et al., 2022). Moreover, individuals with larger kin networks in higher-fertility LMICs may have been more vulnerable to certain types of kin loss. In this chapter, I employ a set of demographic microsimulations in SOCSIM to estimate kin loss across 120 countries, and develop a kinship structure standardization approach to better understand the relative contributions of excess mortality and kinship structure to these estimates. This provides greater insight into differences in country experiences of COVID-19, as well as the way in which kinship structure mediates the relationship between mortality change and kin loss.

Finally, the fourth chapter, co-authored with Diego Alburez-Gutierrez (MPIDR), Emilio Zagheni (MPIDR), and Ashton Verdery (Penn State), takes a long-term view of the impacts of a mortality crisis on kinship networks, considering what the survival of relatives bereaved by COVID-19 suggests about how the pandemic may be remembered in the coming decades. Building on recent studies that have formalized the concept of demographic memory, the share of a population who were living and aware of an event when it occurred (Denton & Spencer, 2021), or related to a victim of a mortality crisis (Alburez-Gutierrez, 2022), this chapter uses demographic microsimulation for 120 countries to project the share of the population related to a victim of COVID-19 excess mortality over the next century. It also considers how this measure, termed “kinship memory”, is likely to change over the coming century, and how demographic factors such as the population growth rate and kin network sizes shape these estimates. As questions remain as to how this pandemic, which has represented a significant excess mortality shock in many countries, may influence subsequent policy and attitudes in the coming decades, estimating the population share of this group with significant lived experience of COVID-19 mortality is important for better understanding this issue. The results of this chapter document the importance of the age structure of a mortality crisis in shaping which bereaved relatives will be alive to remember it, and highlight an as-yet unstudied aspect of the pandemic’s impact on kin networks around the world.

Chapter 2

Estimates from 31 countries show the significant impact of COVID-19 excess mortality on the incidence of family bereavement¹

As excess mortality associated with the COVID-19 pandemic is better estimated and understood (Goldstein & Lee, 2020; Németh et al., 2021), less is known about how this is reflected in kin loss by survivors of the pandemic. The scale of pandemic-associated bereavement is significant. Each US COVID-19 death leaves nine close kin bereaved (Verdery et al., 2020), including 0.078 children aged 0 to 17 y experiencing parental bereavement (Kidman et al., 2021), and the pandemic has resulted in over 1 million new orphans under age 18 y globally as of May 2021 (Hillis et al., 2021). This will have important population health and welfare implications given the known negative consequences of kin loss, including declines in physical and mental health and the loss of social and economic support (Raker et al., 2020; Patterson et al., 2020; Wang et al., 2021). What remains to be better understood, however, is how these increases in population-wide bereavement shape individual-level risks of losing relatives—by how much does the incidence of kin loss increase in periods of high excess mortality, and which demographic groups are likely to be affected? Answering this question is key for better understanding the lived experience of pandemic excess mortality for those who survive it.

In this study, we complement estimates of numbers of bereaved individuals associated with COVID-19 mortality by extending a set of existing demographic microsimulations (Alburez-Gutierrez, Mason, & Zagheni, 2021) to consider how pandemic-associated excess mortality affected the number of individuals experiencing losses in their close family networks, across

¹This chapter was previously published as: Snyder, M., Alburez-Gutierrez, D., Williams, I., and Zagheni, E. (2022, June). Estimates from 31 countries show the significant impact of COVID-19 excess mortality on the incidence of family bereavement. *Proceedings of the National Academy of Sciences*, 119 (26), e2202686119.

31 countries, each month between March 2020 and June 2021. Our estimates, which demonstrate a generational pattern of kin loss, show consistent increases across countries in the numbers of younger individuals losing a grandparent, and of older individuals losing a sibling. Moreover, our results highlight the role of heterogeneity in excess mortality and population and kinship structure in shaping levels of family bereavement.²

2.1 Results

To estimate our outcome measure, termed “excess bereavement,” we consider individuals who survive to at least July 2021. Some of these individuals experienced the loss of a certain type of biological relative between March 2020 and June 2021, but would not have in the absence of COVID-19 mortality. Our approach focuses on the average additional losses associated with a COVID-19 excess mortality scenario over those associated with a scenario in which only seasonally adjusted mortality in line with previous years had occurred (a counterfactual baseline scenario). We divide the number who lost kin in each month by the total population of survivors (irrespective of their kin availability) and use it to calculate the absolute difference in the number of individuals who experience loss per 100,000 in a given month and age group ($EB_{x,t}$) across the two scenarios. In the case of lower mortality than expected, $EB_{x,t}$ may be negative. This measure, which is comparable across different countries and types of kin, is expressed in Eq. (2.1), where N is the number of individuals of either sex in age group x (as of February 2020) who survive to July 2021, with subscripts b , for bereaved, denoting the number who lose kin in a particular month t between March 2020 and June 2021, and 0 denoting the counterfactual case,

$$EB_{x,t} = \left(\frac{N_{b,x,t}}{N_x} - \frac{N_{b,x,t,0}}{N_{x,0}} \right) \times 100,000 \quad (2.1)$$

In Fig. 2.1, we plot values of $EB_{x,t}$ for a set of countries with varied mortality experiences associated with COVID-19. As expected, the concentration of COVID-19 excess mortality among older individuals is reflected in accompanying increases in numbers of younger individuals aged 15 to 44 y losing a grandparent, and in numbers of older individuals aged 65 y and above losing a sibling. We report results aggregated across sexes, as values of $EB_{x,t}$ do not differ significantly by sex. Country-specific trends in COVID-19 mortality, such as mortality “waves,” are mirrored in trends in excess bereavement. Notable in Fig. 2.1 are short periods of negative excess bereavement following spikes in excess mortality. This suggests that these spikes may have reflected an acceleration of kin mortality, with deaths occurring sooner than otherwise expected.

²We thank Carl Mason, Kenneth Wachter, Tim Riffe, Ugofilippo Basellini, and two anonymous reviewers, as well as participants in the CenSoc Working Group, the Wittgenstein Centre Conference 2020, the Population Association of America Annual Meeting 2021, and the International Population Conference 2021. We gratefully acknowledge support from NIH Training Grant (2T32HD007275). The content is solely the responsibility of the authors and does not necessarily represent the official views of NIH.

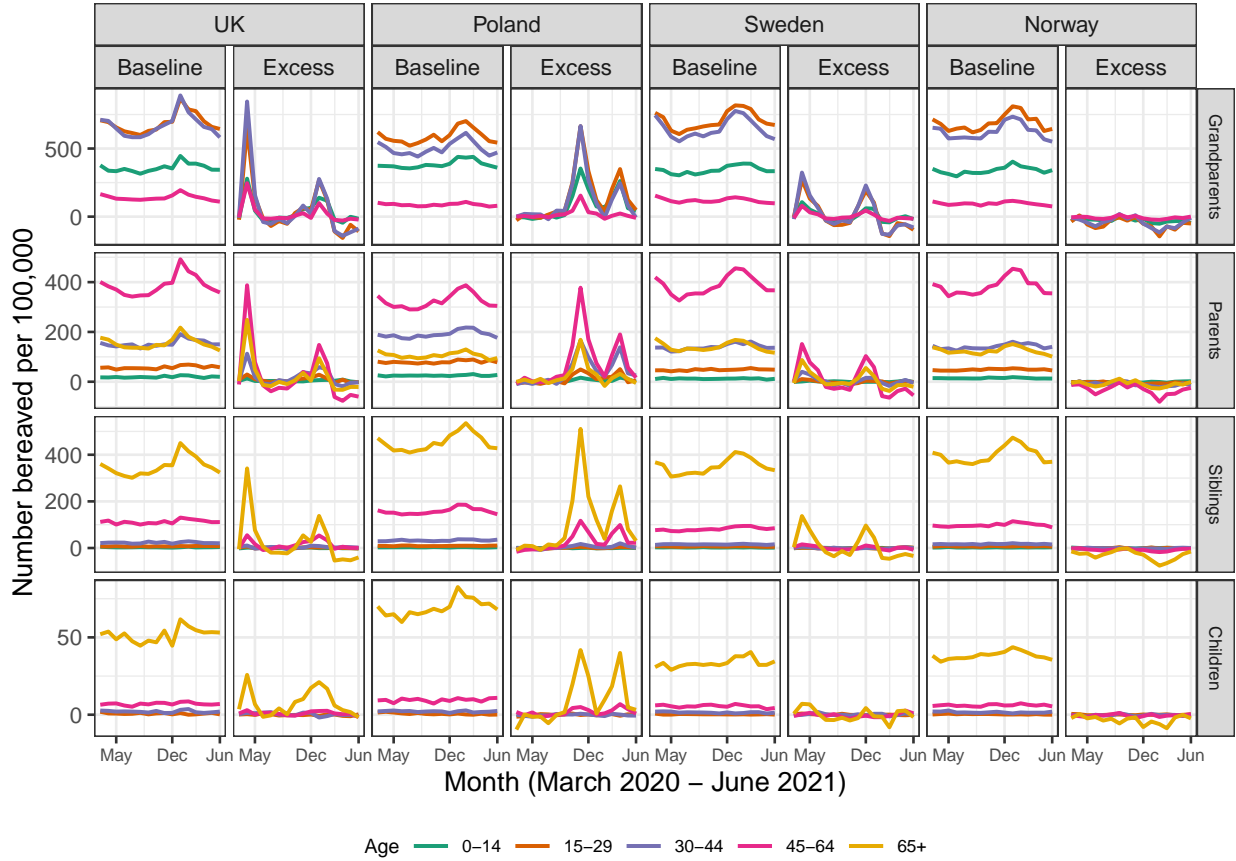


Figure 2.1: Estimates of monthly excess bereavement ($EB_{x,t}$) and counterfactual bereavement, in multiple countries, by age of the bereaved individual and type of biological kin. Note the different scales on the y axis across panels. Results are shown where more than 1% of the group had a living relative of the type considered in February 2020.

Comparing Sweden, which saw high excess mortality early in the pandemic, and Norway, which saw lower mortality than might have been expected, reveals the role of excess mortality in shaping experiences of countries with otherwise very similar age-sex and kinship structures. Sweden saw significant increases in kin loss during the period, while Norway saw very low or negative changes in the number of individuals experiencing bereavement. The similarity in counterfactual rates of loss across not only Sweden and Norway but all countries considered in Fig. 2.1 further indicates the importance of excess mortality even when considering countries with more varied demographic structures.

Kin loss would have been high for some groups even in the absence of COVID-19 mortality. For example, 711 (SEM of 19 across 100 paired simulations) per 100,000 UK individuals aged 30 to 44 y would have experienced the loss of a grandparent in March 2020 under a baseline scenario. However, very high excess mortality associated with the pandemic resulted in kin loss more than double the baseline levels. For example, by April 2020, over 845 (SEM 31) per 100,000 more individuals in this same group lost a grandparent, 1.2 times higher than the

expected baseline of 703 (SEM 21) per 100,000. A comparably large increase in bereavement for older individuals was also observed, with 511 (SEM 15) per 100,000 or 1.15 times more individuals in Poland aged 65+ y losing a sibling in November 2020 than the expected 443 (SEM 8) per 100,000. The scale of loss associated with the pandemic is brought out even more clearly in Fig. 2.2, which multiplies $EB_{x,t}$ values from Fig. 2.1 by country populations in 2020 to highlight the large total number of individuals as of July 2021 who may have lost relatives as a result of COVID-19 excess mortality.

2.2 Discussion

With estimates showing, in some cases, a doubling of kin loss risks over expected levels, our results help put into context the staggering toll of excess mortality and bereavement associated with COVID-19 and highlight which groups are most likely to be affected. They also highlight the importance of excess mortality in shaping country experiences: The countries in our sample would have had similar population-adjusted projections of kin loss in the absence of COVID-19, but they diverged considerably based on COVID-19 excess mortality.

This similarity of counterfactual kin loss reflects other similarities between countries in our sample, which are high-income countries for which excess mortality data are readily available. We might see different impacts of similar levels of excess mortality for younger populations with more-varied kinship structures, such as in countries in the Global South. Excess bereavement is not simply a rescaled value of excess mortality. It results from complex interactions between fertility and survival functions over time. Further work is needed to understand how excess mortality and demographic structure shape country-level excess bereavement.

We present a lower-bound estimate, as the pandemic continues to take its toll. Furthermore, the quantities we estimate are averages at the country level; levels of excess bereavement are likely to be considerably higher in hard-hit subnational populations, and among individuals with larger or high-risk families. Our estimates do not account for within-country heterogeneity or clustering of excess mortality within groups or families. However, as with other large-scale public health crises, COVID-19 excess mortality tends to be clustered within population subgroups (Vahabi et al., 2021). This means that those who experience the death of a member of their extended family are more likely to face additional loss in their kin network. Future work to assess the extent of clustering of bereavement would be important to inform policies supporting vulnerable individuals.

Our study underlines recent calls for more support to be given to individuals bereaved from COVID-19 (Verdery et al., 2020; Hillis et al., 2021), whether from their communities or governments. This is particularly urgent if, as recent evidence suggests, grief from COVID-19-associated bereavement is especially detrimental for survivors (Eisma et al., 2020). Our results also identify groups who may lose significant members of their support network as a result of pandemic mortality, such as older individuals who lose a sibling. These losses will

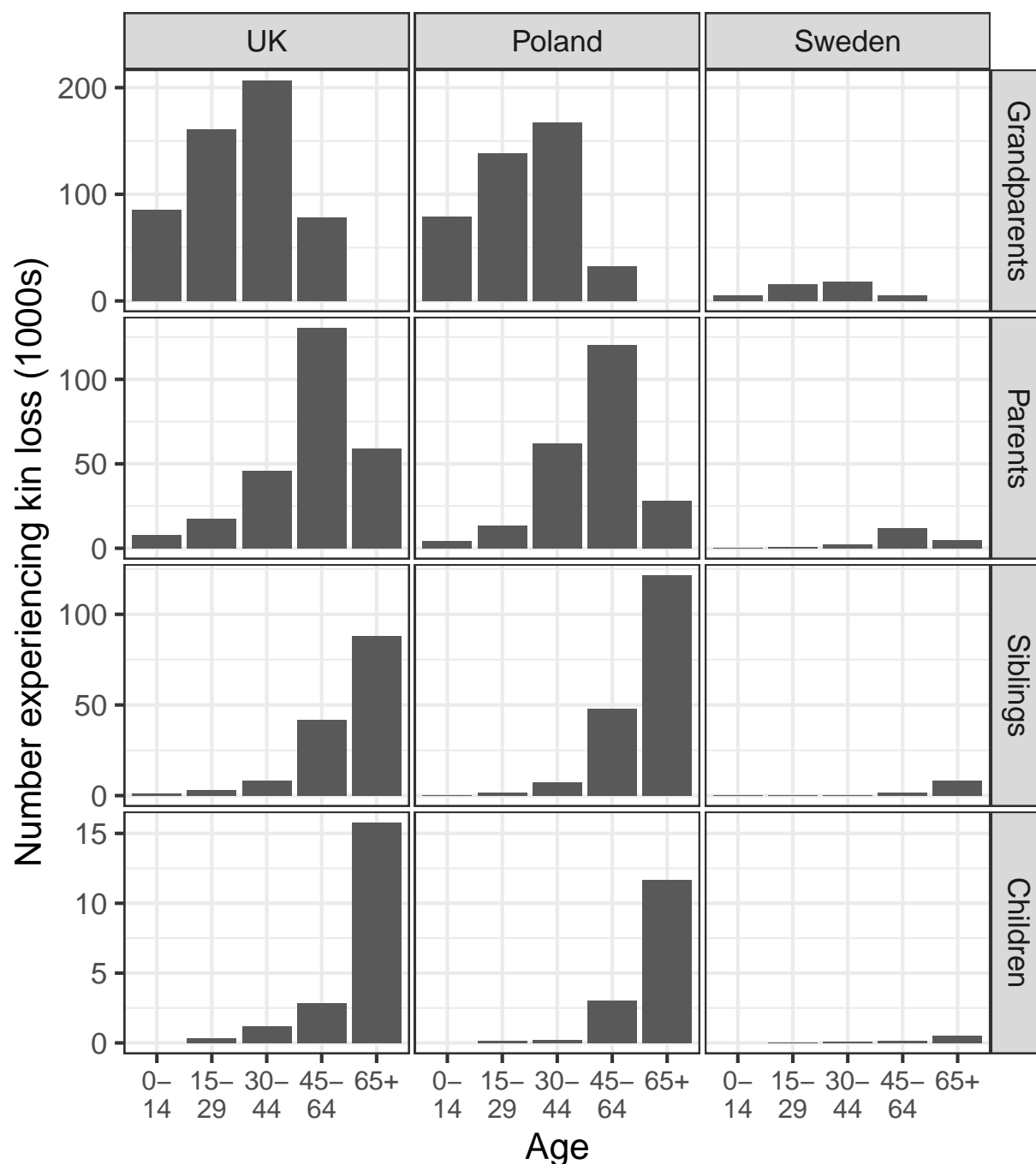


Figure 2.2: Number of additional survivors (in thousands) who lost a given relative type. The figure multiplies EB_x values from Fig. 2.1 by 2020 population estimates from the 2019 Revision of the United Nations World Population Prospects to find the total number of surviving individuals bereaved as a result of COVID-19 excess mortality, as of July 2021; EB_x values are bounded at zero to reflect deaths associated with the pandemic. Note the different scales across panels. Results are shown where more than 1% of the group had a living relative of the type considered in February 2020.

reverberate in kin networks for generations to come. More research is needed on the impacts of excess bereavement on survivors, not just in the context of COVID-19, but for mortality crises, past and present, around the world.

2.3 Materials and Methods

Our analysis uses SOCSIM, a stochastic microsimulation platform that generates population-level genealogies using vital demographic rates as input (Hammel et al., 1976; Wachter, 1997; Verdery et al., 2020). Our simulations use, as input, vital rates for the 1950–2035 period from the 2019 Revision of the United Nations World Population Prospects (medium scenario). To identify the effects of COVID-19 mortality on kinship structures, we run 200 microsimulations for each country, half representing a COVID-19 mortality case and the other half representing a counterfactual scenario without excess mortality, with adjustments made using the Human Mortality Database’s Short-term Mortality Fluctuations dataset (Németh et al., 2021).³

Some caveats should be noted. We assume zero international migration, and do not include marriage rates; the latter means we consider only biological kin (see SI Appendix for more details). We also assume demographic stability before 1950 in our simulations: This is a necessary assumption, since reliable historical demographic data are not available for all countries studied. In SI Appendix, we apply formal demographic methods to historical Swedish data and show that the pre-1950 demographic stability assumption is unlikely to significantly affect the number of expected kin after 2015 for the types of kin considered in this paper.

As an additional robustness check, we compared our estimates of COVID-19–associated parental bereavement experienced by children to those in other published estimates (Hillis et al., 2021; Kidman et al., 2021), and found similarities in magnitude, despite differences in the age groups considered and methods employed.

2.4 Supplementary Information Appendix: Extended Methods

2.4.1 Adjusting Simulation Inputs for Excess Mortality

In order to obtain simulation inputs, we first convert UNWPP 5-year mortality rates into monthly values assuming uniform mortality across the interval, except for the period from

³Dataset and replication files have been deposited in Open Science Framework (https://osf.io/jn2h9/?view_only=ce87de3c2310424da30bb3a520c4f0ce).

March 2020-June 2021. For this period, we employ weekly age and sex-disaggregated mortality data from the Human Mortality Database’s Short-term Mortality Fluctuations dataset (STMF), to adjust the monthly rates in line with two possible mortality scenarios: a COVID-19 case using rates from the 2020-2021 period, and a counterfactual case using an average of the 2016-2019 monthly rates.

Since SOCSIM employs monthly vital rates, we first convert HMD STMF weekly data to monthly data by dividing each week’s total by 7 and assigning each day thus generated to a month according to the ISO8601 standard, which is used by almost all of the countries in the STMF. We use this method to generate monthly exposures (from the STMF data) and death totals for 2016-2021. An average of 2016-2019 values forms our baseline of “expected” 2020-2021 mortality, and we use this to also calculate an annual average expected mortality rate by averaging across all monthly mortality rates. We then use this as the denominator of the ratio used in calculating the adjustment factors used in the two scenarios: in the COVID-19 case, the numerator is 2020-2021 monthly mortality rates, and in the counterfactual case, the numerator is the baseline 2016-2019 rate. Since the original rates to be adjusted are annual averages which do not account for seasonality, this approach allows for us to consider by how much mortality would have been expected to change in the months from March 2020-June 2021 in the absence of COVID-19 excess mortality, and by how much it increased above annual expected values during the period as a result of COVID-19 excess mortality.

2.4.2 Additional Details on Fertility, Marriage, and Kinship in Our SOCSIM Microsimulations

Our approach follows closely that used by Alburez-Gutierrez et al. (2021) (Alburez-Gutierrez, Mason, & Zagheni, 2021), which adopts a SOCSIM setup without marriage rates in which births are based on female fertility, with male partners selected at the time of childbirth from all unpartnered living males in the population. This selection is based on minimizing differences between the observed and the pre-specified target distribution of the difference in ages between partners. This ensures a reasonable age distribution for fathers in our simulations. There is potential for bias associated with not capturing the full range of age differences possible in cases such as childbirth outside of marriage or remarriage; however, we consider such potential bias to be likely relatively small, at least when attempting to achieve a reasonable approximation of kinship networks for the purposes of our study and in the countries considered. Fertility heterogeneity is accounted for with the use of a beta-distributed random fertility multiplier assigned to each female in the population; this allows for greater variability in the number of siblings present than might otherwise be observed (Mason, 2016). As mentioned in the main text, we do not account for other sources of heterogeneity, such as frailty, given data limitations. This may lead to a more homogeneous distribution of excess bereavement experienced across the population than might occur in the case of mortality clustering, or when considering other possible sources of heterogeneity (Ruggles, 1993). These potential sources of bias should be noted when interpreting these

results.

In the absence of marriage rates, the kin identified are biologically related to each other. Our definition of siblings, for example, includes half-siblings who share one biological parent, but does not include step-siblings without biological ties. In our simulations, half-siblings can result from childbirth in couples where one partner was previously widowed and re-entered the queue to form a partnership. As we do not explicitly model union dissolution via divorce, and the models are calibrated to match female fertility rates, our simulation outputs would include all siblings (half or full) who share the same mother, but may underestimate half-siblings who share the same father, leading to conservative estimates of number of half-siblings. Grandparents refer only to the biological mother and father of an individual’s biological parents. Since studies on family networks typically focus on households, rather than kin networks independent of co-residence, ascertaining the share of sibships and other kin relations explored in the countries studied that are biological is challenging. However, in terms of household configurations, which may represent particularly salient kinship ties for the individuals involved, biological sibships involving full and half sibling relationships account for the vast majority of sibling compositions, with only around 1 percent of children in the United States in 2009 living only with one or more non-biological step-siblings (Manning et al., 2014). This suggests that our approach should account for a considerable fraction of close kin networks for the individuals studied.

2.4.3 Sample of Countries Considered

After running the simulations, as a robustness check we use simulation outputs to calculate excess mortality for the period by age group and compare this to equivalent estimates based on the STMF. In line with our input mortality adjustment factors, we calculate excess mortality as the average ratio across simulations of COVID-19 to counterfactual 65+ age-specific mortality rates for the March 2020-June 2021 period. There is a high correlation between input and output (simulated) excess mortality rates of .98 across the 31 countries considered, and there is at most a 3 percent difference between input and output estimates, despite differences in simulation sizes (simulated country populations range from around 12,000 to 120,000 in the middle of the period considered, with simulation size proportional, with some adjustments, to country population size) and in the exposures used in calculating both types of rates. This suggests that our simulations suitably account for excess mortality related to the pandemic in these countries. The sample of countries for which we provide estimates in the replication files are: Austria, Belgium, Bulgaria, Chile, Croatia, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Israel, Latvia, Lithuania, Luxembourg, Netherlands, New Zealand, Norway, Poland, Portugal, Republic of Korea, Slovakia, Slovenia, Spain, Sweden, Switzerland, the United Kingdom (obtained by combining mortality data from England and Wales, Scotland, and Northern Ireland), and the United States of America.

2.4.4 Investigating the pre-1950 Demographic Stability Assumption

In this section, we consider the implications of assuming demographic stability before 1950. In particular, we examine the degree to which extrapolating the particular demographic characteristics of the 1950-1954 period into the past (including the baby boom) can bias the initial kinship structures for the countries we study.

One way to consider the impact of assuming demographic stability prior to 1950 on living kin is to think in terms of a particular kin relation, especially in terms of ancestors who experienced vital rates prior to the ego's birth. In the case of mothers, the probability that an ego aged a in year y , from cohort $c = y - a$, had a living mother $M_1^y(a)$, can be approximated based on Keyfitz & Caswell (2005) with:

$$M_1^y(a) \approx p^{[c-k_c]}(k_c, a), \quad (2.2)$$

where $p^{[c-k_c]}(k_c, a)$ is the mother's probability of surviving a years from age k_{y-a} (the mean age of childbearing when ego was born), given cohort mortality risk for a person born in $[c - k_c]$.

Let us consider an ego born before 1950 who survives to subsequent years. This ego could be aged $a = 30$ in $y = 1960$, $c = 1930$, living 20 years prior to 1950 and 10 after. Formula 2.2 can be factorized with the year 1950 as pivot:

$$M_1^{1960}(30) \approx p^{[1930-k_{1930}]}(k_{1930}, 20) * p^{[1930-k_{1930}]}(k_{1930} + 20, 10) \quad (2.3)$$

If rates (mortality and fertility) are assumed constant before 1950 (and female population structure by age too, which is relevant to the mean k), we should have a slightly different probability $M_1^{1960*}(30)$, given that all the rates before 1950 now are related to that last observed year:

$$M_1^{1960*}(30) \approx p^{1950}(k_{1950}, 20) * p^{[1930-k_{1950}]}(k_{1950} + 20, 10) \quad (2.4)$$

We can identify two main effects that drive the difference between $M_1^{1960*}(30)$ and $M_1^{1960}(30)$, given a direction of change for each one. Let us assume constant aging and a mortality decline. Before 1950 mothers would experience 1950 period rates instead of cohort ones, increasing mother's survival during ego's life. The second main effect goes in the opposite direction, given that the relation of maternal ages is $k_{1930} < k_{1950}$, survival chances decrease because of age (risk period starting in age k_{1950} instead of k_{1930}) and a cohort effect (mortality schedule from $[1930 - k_{1950}]$ cohort instead $[1930 - k_{1930}]$). The net result will depend on the

curvature of l_x , its change with time, and the slope of k with time, not directly estimable without observed data or a parametric assumption on components. A similar approach can be made for older ancestors. For direct descendants both factors would also include cohort fertility rates.

This last case applies when ego is born before 1950 and is alive after. If she is born in 1950 or later, $y_1 \geq 1950$, then this effect on living mothers would disappear. It also disappears for grandmothers if ego is born on $y_2 \geq 1950 + k_{1950}$, and for great-grandmothers if ego is born in $y_3 \geq 1950 + k_{1950} + k_{1950+k_{1950}}$, and so on. Of course, if ego is born after 1950, all living descendants would not be affected by the change. In general terms, the bias in constant rates before 1950 in living ancestors older than mothers (when $i > 1$), will disappear for M_i if ego is born at $y_{i+1} \geq y_i - k_{y_i - k_{1950}}$ ⁴. In a stable population context, when there is a sudden change in rates (here in 1950), changing the regime itself, this series could be useful to ensure that ancestors until i degree belong to the new and latest regime.

We carried out separate analyses to understand the effect of assuming demographic stability before 1950 for a specific population. For a numeric example we applied kin estimation for an ego aged 30 (an age where it is not unlikely to have a surviving grandmother in low mortality countries, and also a living child (Alburez-Gutierrez, Mason, & Zagheni, 2021)) using vital rates from Sweden and locating ego in successive years from 1950 to 2015.

We ran two sets of analyses: ‘historical’ analyses used the estimated historical rates for the 1751-1950 period and ‘stable’ analyses assumed that the 1950 demographic rates applied throughout the 1751-1950 period. Age-specific mortality rates (starting from 1751) come from the Human Mortality Database and fertility rates (starting from 1891) come from the Human Fertility Database. In all cases, we assumed demographic stability for fertility in the 1751-1891 period. We combined these data with official demographic projections of fertility and mortality provided by Statistics Sweden. Sweden is the ideal case for this analysis given its long time series of high quality demographic rates. Crucially, Sweden also experienced a moderate increase in fertility after WWII (Van Bavel & Reher, 2013). As such, the Swedish case would allow us to explore whether our stability assumption extrapolates the conditions of the post-WWII baby-boom into the past.

The results suggest that there is a general convergence in all the relatives types included in the study. The fact that older ancestors had later converged is consistent with the mentioned series y_i . In general terms the differences are null for all type of kin in year 2015 (last year of evaluation), when in 1950 we could see bigger differences, like 50% in cousins 9% in older sisters, -50% in grand-mothers and -80% in grand-daughters ($[\frac{\text{historical}}{\text{stable}} - 1] * 100$). In conclusion, at least in the Swedish case, no significant bias is expected in kin counts after 2015 because of assuming fixed rates before 1950.

⁴The assumption of a concentrated fertility schedule around k is necessary.

2.4.5 Validating our Simulations with Formal Methods

To ensure that the simulated populations capture the kinship structure implied by the input demographic rates, we estimate a set of independent matrix kinship models with the same input data. We use an implementation of matrix kinship models (Caswell, 2019) extended for populations with time-variant demographic rates, as implemented in the *DemoKin* R package (<https://github.com/IvanWilli/DemoKin>), to show that the estimates are consistent with the simulated kinship structures.

We report a comparison of estimates for living kin for a women in Sweden in July 2020 (the first wave of excess mortality), based on both microsimulation and formal methods. While the kin relations presented in the main text are for male and female kin, here we present only female kin in a single-sex population model so as to achieve comparability with the formal approach we present. The results suggest that there is considerable similarity between methods in terms of the results obtained, providing an important robustness check for our microsimulation-based results.

Kin counts are generally similar across the two methods. There are no significant differences for mothers, except for individuals aged 65+, for whom SOCSIM estimates .07 living mothers and the GKP approach estimates .02 mothers in both the COVID-19 and counterfactual scenarios. In general, for a given method, population-level kin counts are fairly similar across the two scenarios, reflecting the relative brevity of the mortality shock considered as well as the large number of individuals included in the simulations. Differences in the number of living grandmothers are all under 0.15, with the largest discrepancies in the 30-44 age interval, followed by the 15-29 age interval. This is likely associated with the increased rarity of having a living grandmother at older ages, leading to more statistical variability in the SOCSIM estimates (although even older individuals might be so unlikely to have a living grandmother as to make estimates of kin availability and associated differences relatively small). The expected number of daughters is higher in GKP-based estimates for most age groups by about 0.1 to 0.18. Consistent with our expectations, we tend to find the largest discrepancies for the relative types that are less common overall. Our simulations have a limited size (for example, across simulation runs, there were around 6,300 women aged 30-44 in Sweden who survived the COVID-19 mortality period from March 2020 to June 2021) and, as a result, there is bound to be more uncertainty around the prevalence of relatively rare kin ties.

2.4.6 Comparison to Other Published Estimates

As an additional robustness check, we compared our results to those from Hillis et al. (2021)'s modeled estimates of parental bereavement for children in which Hillis et al. (2021)'s estimates were calculated using excess mortality, and from Kidman et al. (2021)'s estimates for the United States. In general, our estimates are slightly lower, reflecting the lower age

group endpoint (14 versus 17); most parentally bereaved children would likely be in the older portion of the age group. Hillis et al.'s estimate of 8,495 parentally bereaved children aged 0-17 in England and Wales alone by the end of April 2021 resembles our estimate of 7,567 children aged 0-14 for the United Kingdom as a whole for the same period, despite differences in the groups considered (Hillis et al., 2021). Similarly, we estimate 2,298 orphans aged 0-14 in France, compared to the Hillis et al. (2021) estimate of 4,064 orphans aged 0-17. Some countries show greater variability: our results for Spain are higher than those estimated by Hillis et al. (2021) (3,905 orphans aged 0-14 versus 2,309 aged 0-17), likely reflecting differences in modeling strategies used. Existing published estimates for the United States vary considerably: Kidman et al. (2021) estimate 43,000 orphans aged 0-17 up to the end of January 2021 using excess mortality (Kidman et al., 2021), while Hillis et al. (2021) estimate 104,884 for the same group up to the end of April 2021. Our results, when calculated up to the end of January 2021 (to match the time period Kidman et al. (2021) considered) are close to those of Kidman et al. (2021): We estimate a value of 36,716, which, given the shorter age interval of 0-14, is slightly lower, as we expected.

2.5 Addendum by Mallika Snyder, May 2023

Since this paper was published, some of my further research has highlighted a few minor issues with the input rates used for the simulations in this paper. To the best of my knowledge, no issues identified should have a noticeable effect on the results reported. I assume full responsibility for these errors, and discuss their implications here for any readers who may be interested in replicating the results of this paper.

First, in the calculation of the adjusted input mortality rates for the March 2020—June 2021 period, there was an incorrectly specified age interval n of 5 instead of 4 for the mortality rates for the 1-4 year age interval, meaning that the monthly child mortality estimates for this period are scaled upwards by an additional factor of around 20%. This calculation was applied across all countries, as well as across the observed COVID-19 and counterfactual simulations, so it is unlikely to have a significant effect on cross-country comparisons or estimates of excess bereavement, which are derived from a comparison between COVID-19 and counterfactual simulations.

Second, the use of mortality and fertility rates from the United Nations World Population Prospects 2019 revision was incorrectly based on the assumption that the 5-year intervals presented are from January to December, rather than July to June. This is likely to have the greatest effect on estimates of excess bereavement for March to June 2020, since these calculations used rates that were intended to only apply from July 2020 onwards. Considering that most countries in this sample would have been projected to see declining mortality and fertility between 2015-2020 and 2020-2025, this could lead to slightly underestimated mortality and fertility. This error applied across all countries, as well as across the observed COVID-19 and counterfactual simulations, so it is unlikely to have a significant effect on estimates of excess bereavement, or cross-country comparisons.

Finally, the code for input age-specific fertility rates mistakenly assumed that rates as written were inclusive of the upper end of the age intervals. However, based on SOCSIM documentation (Mason, 2016), the rates as written would have ran as 15-18 inclusive, with other fertility rates shifted downwards by one year, so that the rates for ages 20-24 were applied to ages 19-23, and so on. Given that SOCSIM additionally adjusts for birth intervals based on input fertility rates, this is unlikely to significantly affect fertility in simulation output, with some births still expected to occur to women aged 49, despite the input rates as written ending before the start of age 49. Like with the previously identified issues, this error applied across all countries, as well as across the observed COVID-19 and counterfactual simulations.

These issues do not apply to chapters 2 and 3, which used input rates based on the UNWPP 2022 revision, which contains single-year January—December lifetables and age-specific fertility rates.

Chapter 3

The Demographic Determinants of Cross-Country Variation in COVID-19-related Kin Loss

3.1 Introduction

The dramatic mortality toll of the COVID-19 pandemic has led to large increases in kin loss around the world (Verdery et al., 2020; Hillis et al., 2022; Snyder et al., 2022), with significant negative health consequences for many of those bereaved (Eisma et al., 2021; Wang, Paulson, et al., 2022). Little is still known, however, about how the pandemic may have increased exposure to kin loss in low-and-middle-income countries, some of which have seen the highest levels of excess mortality in the world (The Economist & Solstad, 2022; Msemburi et al., 2023). Most estimates of COVID-19-associated kin loss have focused on high-income countries, with the exception of estimates of orphanhood and caregiver loss among young children (Hillis et al., 2021; Unwin et al., 2022; Hillis et al., 2022). By developing a set of comprehensive microsimulation-based estimates of COVID-19-related excess kin loss in 120 countries, this paper attempts to help address this significant gap in our understanding of the pandemic’s impact on families around the world.

In addition to presenting these estimates, this paper also seeks to better understand the relative contributions of two key demographic factors that may shape cross-country rates of excess kin loss: excess mortality and pre-existing kinship structure. While it would be expected that higher-excess-mortality countries would see higher rates of excess kin loss, it has not yet been considered to what extent these cross-country differences could be influenced by pre-existing kinship structure. A country’s history of mortality and fertility shape the likelihood that a person alive today might have a living relative, with mortality having a larger impact on the availability of ancestors, such as parents and grandparents, and fertility

tending to shape the availability of relatives like siblings, cousins, and aunts (Sembiring, 1978; Keyfitz & Caswell, 2005). Simply comparing cross-country estimates from varied contexts may fail to fully capture the impact of kinship structure in shaping the vulnerability of a population to kin loss. With this in mind, I develop in this paper an approach to understanding the contributions of these two factors, drawing on the demographic technique of direct standardization by considering the effects on kin loss derived from substituting an alternative counterfactual “standardized” kinship structure. This flexible approach, which could be applied to other mortality crises, provides insight into the relative impacts of historical demographic conditions (in the form of kinship structure) and present-day mortality (in the form of excess mortality) for the countries studied in this paper.

The dual objectives of this paper thus aim to help advance our understanding of the impact of COVID-19 on family networks. Hard-hit low-and-middle income countries (LMICs) may have had very different experiences of loss than hard-hit high-income countries (HICs), with some evidence suggesting a flatter age pattern of excess mortality, with elevated mortality risks even at younger ages (Demombynes et al., 2022); higher fertility leading to larger kin networks and potentially greater exposure to loss; and higher pre-existing mortality leading to the reduced availability of ancestors, and reduced exposure to their loss. Without country estimates for a wide range of countries, and a model to estimate the potential impacts of demographic factors, it is difficult to know how LMICs might have been affected by this mortality crisis. As noted by Keyfitz and Caswell (2005), formal demographic specifications of kin availability, the complement of kin loss, reveal that these estimates depend on birth and death rates, but do not indicate the way in which a change in inputs affects outputs (Keyfitz & Caswell, 2005). While previous work using formal demographic methods has attempted to develop model-based intuition for the relationship between mortality change and kin loss (Williams & Alburez-Gutierrez, 2021; Keyfitz & Caswell, 2005), this type of analysis has not been attempted in a two-sex non-stable population for other kin relationships, likely as a result of mathematical complexity. The mortality shocks considered have also been permanent, rather than temporary, limiting the applicability of this approach. Microsimulation, by which a two-sex non-stable population may be more easily modeled, and in which kin relationships may be identified more readily, offers a possible alternative: with known inputs and outputs, and the potential to generate outputs for a wide range of settings, these estimates can serve as a valuable testing ground for modeling the effects of demographic processes.

In this paper, I extend the microsimulation setup used in Snyder et al. (2022) to 120 countries in the 2020-2021 period. In doing so, I rely for input data on annual lifetables from the 2022 revision of the United Nations World Population Prospects (United Nations, Department of Economic and Social Affairs, Population Division, 2022), which account for estimated excess mortality during this period, based partly on estimates from the World Health Organization (WHO) (Msemburi et al., 2023). Despite the limitations of relying on model-based estimates rather than raw data, the availability of these estimates for all countries facilitates international comparison in a case where data is otherwise unavailable. My results highlight the significant burden of excess kin loss experienced by surviving individuals in many LMICs, and the importance of kinship structure in shaping country experiences.

3.2 Measuring Kinship Networks and their Characteristics

To be at risk of experiencing kin loss, an individual must have living kin in the first place. Recognition of the importance of having available kin has led to numerous studies of kinship resources. These studies have sought to measure the size of networks and rates of kin availability, or its complement, kinlessness.

3.2.1 Insights from Formal Demography

Information contained in life table and fertility schedules can be used to estimate expected population change, as in the Euler-Lotka equation, and, by extension, changes in sub-populations with a kin relationship to a particular individual. Numerous mathematical and formal demographers have employed this information to estimate kinship resources, including Lotka's estimates of orphanhood (Lotka, 1931) and Brass's estimates of child survival for mothers (Brass, 1953). The most well-known mathematical treatment of this approach, the Goodman-Keyfitz-Pullum kinship equations (Goodman et al., 1974), provide a framework for quantifying kin availability using the multiple integration of vital rates. These equations are presented in terms of female kin in a stable population, but can be applied to others. This approach has been generalized to non-stable settings in an examination of trends in women's experience of child death over the life course (Alburez-Gutierrez, Kolk, & Zagheni, 2021).

As Keyfitz and Caswell note (Keyfitz & Caswell, 2005), the use of mortality and fertility rates as inputs into equations that provide kin counts and probabilities as output should seem to readily provide an indication of the impact of demographic change on kin availability; however, in practice, it is difficult to discern, from merely looking at the equations, the impact that a change in an input rate might have. One method of assessing the relative importance of these rates is to compare permutations of fertility and mortality rates. While the authors do not apply this approach to all kin types, their results imply that mortality rates may be especially important in shaping availability of ancestors, while fertility rates are more important in terms of the availability of cousins, a finding previously confirmed through statistical simulations (Sembiring, 1978).

Mathematical decomposition of these equations may also provide insight into this relationship. Of particular interest for this paper is an approximation presented by Keyfitz and Caswell of the impact of a uniform change in mortality on $M_1(a)$, the likelihood that a woman of a certain age a has a living mother. When the mortality increase k is uniform over age, $M_1(a)$, which can be written as follows,

$$M_1(a) = \int_{\alpha}^{\beta} \frac{l(x+a)}{l(x)} e^{-rx} l(x) m(x) dx$$

can be written in terms of an approximation using the mean age of childbearing κ . With this approximation, $M_1(a)$ is primarily determined by the fraction $\frac{l(\kappa+a)}{l(\kappa)}$, which declines in the ratio e^{-ka} . Thus, the change in the probability that a woman has a living mother can be written as follows, when k is small enough that $e^{-ka} \approx (1 - ka)$,

$$\Delta M_1(a) = -kaM_1(a) \tag{3.1}$$

Equation (3.1), which can also be applied to other types of female ancestors, demonstrates that for the conditions described, the change in kin availability, i.e. kin loss, that results from a mortality increase, is proportional to the mortality increase itself and the original availability of that kin relation. This can be thought of as the product of excess mortality and kinship structure, with a serving as a proportionality term. Although the conditions under which this equality will hold are restrictive, equation (3.1) highlights the importance of excess mortality and kinship structure in determining age-specific rates of kin loss. I will similarly focus on these key explanatory variables in the subsequent analysis.

3.2.2 An Alternative Approach: Demographic Microsimulation

Despite the potential for use of these mathematical approaches in non-stable settings, these calculations become more mathematically challenging when considering kin relationships other than the mother-child relationship, and when assuming time-varying rates; they have also not yet been applied to a two-sex population. A recent matrix-based approach proposed by Caswell (Caswell, 2019), and further extended to cover time-varying rates and provide linear two-sex kin tabulations (Caswell & Song, 2021; Caswell, 2022), has been used to overcome some of these limitations by providing greater insight into the age distribution of kin. Multiple challenges remain with both approaches, however, including their inability to reflect stochasticity and random variability in kin counts, which may succeed in reproducing population averages but may not fully account for variance.

Demographic microsimulation, a popular approach for estimating kinship resources, presents an alternative to mathematical techniques that addresses some of their challenges, while relying on other assumptions of its own. One of the most widely used platforms, the stochastic demographic microsimulator SOCSIM (Hammel et al., 1976), has undergone numerous revisions since its origins at UC Berkeley in the 1970s. These additions have included features such as a heterogeneous fertility multiplier, an important inclusion for addressing concerns about homogeneity from other kinship modeling techniques (Ruggles, 1993). Like mathematical kinship models, SOCSIM requires age-structured mortality and fertility rates; however, instead of generating averages and distributions, SOCSIM generates a population of individuals and their accompanying genealogies. This approach thus provides an efficient and flexible means for identifying the extended kin networks of individuals, including for identified sub-populations using the groups feature. SOCSIM has been used for numerous studies of kinship resources, including for the elderly of the United States (Wachter, 1997; Verdery

& Margolis, 2017), as well as the elderly of Thailand (Wachter et al., 2002) and orphans in Zimbabwe (Zagheni, 2011) in the context of the HIV/AIDS epidemic.

An added advantage of demographic microsimulation is that it captures not only kin availability, but the age structure of a kinship network: the distribution of kin of various ages for an individual of a particular age. Some formal demographic models, such as the Goodman-Keyfitz-Pullum equations, do not provide information on the age distribution of available kin, an issue addressed in Caswell’s matrix approach. Quantifying the age structure of kinship networks is important for understanding the potential for inter-generational interaction, and the nature of the associated kinship resources. In the context of this paper, it is also crucial for predicting their vulnerability to an age-specific mortality shock. Some intuition as to the nature of these age structures is provided by a country’s demographic characteristics; for example, the mean age at childbearing can be used to estimate the relative ages of grandparents. However, the interaction of various demographic factors, as discussed above, warrants a more systematic examination of the impact of different mortality and fertility patterns on kinship networks and their characteristics at the cross-country level. The next section describes the microsimulation setup used in this paper to examine these issues.

3.3 Microsimulation Setup

The microsimulation approach used in this paper draws upon a set of SOCSIM simulations that have been used to study kin loss associated with COVID-19 excess mortality (Snyder et al., 2022), and which were built on a simulation setup first developed to study kinship-based caregiving requirements for individuals “sandwiched” between young and aging dependents (Alburez-Gutierrez, Mason, & Zagheni, 2021). The simulations use as inputs the annual blocks of vital rates from the 2022 revision of the United Nations World Population Prospects (UNWPP), using the medium fertility scenario, and with rates converted to the monthly format that SOCSIM requires by assuming constant mortality over the year. The effect of excess mortality is identified by averaging over 20 simulations per country to account for simulation stochasticity, in which half of the simulations represent an “observed” baseline case, where 2020 and 2021 excess mortality occurred (represented by the UNWPP estimates for 2020 and 2021, which are based partly on the WHO estimates) and the other half represent an “expected” counterfactual case where COVID-19 excess mortality did not take place (obtained from the expected linear trend in mortality rates, based on the 2015-2019 UNWPP estimates). Important to note in this context is that all estimates and rates considered are age-specific; while some countries may have seen higher crude estimates of kin loss or excess mortality due to their population structure, this is not discussed in this paper.

3.3.1 Estimating Excess Mortality

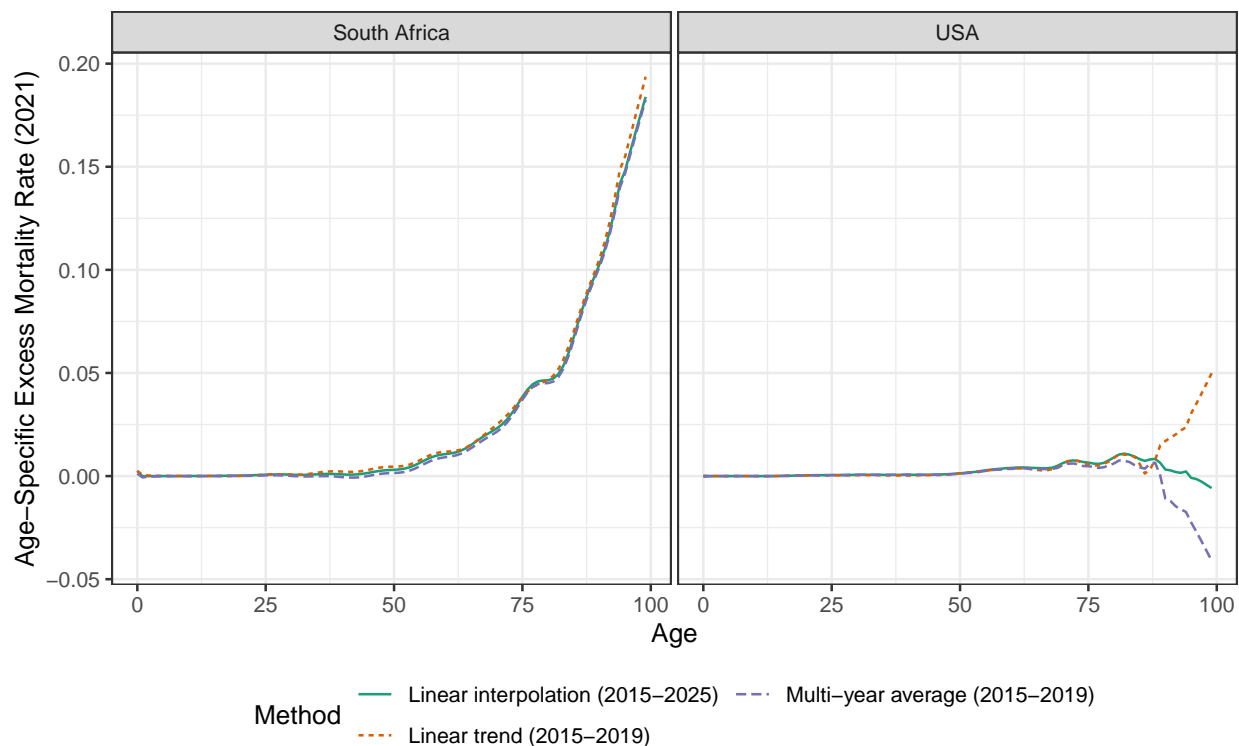
Excess mortality is considered the “gold standard” in measuring the impact of a mortality crisis (Beaney et al., 2020), given its potential to capture direct effects of crisis mortality as well as indirect impacts on health systems and other causes of death. However, the approaches used to calculate a baseline for excess mortality vary considerably (Németh et al., 2021), ranging from multi-year averages (Beaney et al., 2020), linear trends (Karlinsky & Kobak, 2021), and more elaborate statistical models (Basellini et al., 2021; Verbeeck et al., 2021). Such estimates are highly sensitive to the choice of baseline (Nepomuceno et al., 2022), which in turn is based on considerations such as whether to account for seasonality, secular trends in mortality associated with population structure, and the effects of single-year mortality shocks. While SOCSIM rates are applied in single-month blocks, the lifetables used here are for an entire year, obscuring any seasonal variation; although it could be possible to account for seasonal variation in some countries, the lack of high-frequency mortality data in many countries makes such an adjustment challenging. Accordingly, the excess mortality baselines considered will not adjust for seasonality, instead focusing on estimating expected changes in annual lifetable age-specific mortality rates, which are then used to calculate the monthly mortality probabilities used by SOCSIM.

In this context, the multi-year linear trend has emerged as a popular choice for its simplicity and potential for capturing the effects of changes in population structure and other factors (Karlinsky & Kobak, 2021); multi-year averages may fail to capture the effect of these trends. Linear interpolation, another common technique, poses certain challenges in the context of the UNWPP lifetables, since the forecasted length of the impact of COVID-19 excess mortality varies by country characteristics. However, since the latest year by which country mortality conditions are expected to return to normal is 2025, it is possible to interpolate rates between 2019 and 2025. Although this length of time may be unnecessary for some lower-mortality countries, the alternative of interpolating too few years in countries where an excess mortality shock is still likely to continue into 2022 or 2023 is likely to result in more significant bias.

A comparison of 2021 excess mortality estimates derived from these various methods is presented for two sample countries, South Africa and the United States, in Figure 3.1. Unlike subsequent excess mortality estimates used in this paper, these are calculated directly from UNWPP lifetables, not from simulation output; as in later analysis, however, they are calculated from predicted m_x values, not their logarithmic values. As can be seen, the differences between methods are minimal until around age 90, after which in the United States the estimated linear trend is significantly lower than the multi-year average, resulting in much higher estimates of excess mortality when using the linear trend as baseline. On the other hand, South Africa saw less variation across measures for all age groups, suggesting that the linear trend may not be statistically significant in that case.

Given the uncertainty around projected trajectories of pandemic mortality, and the necessity of accounting for cases where the multi-year average may significantly under or over-estimate

Figure 3.1: Age-specific UNWPP male excess mortality rates for 2021, South Africa and the United States of America



excess mortality, I use the 2015-2019 linear trend as a baseline in this paper. Important to note in this context is that, since the UNWPP lifetables did not use the WHO excess mortality estimates for all countries, rankings of countries in terms of excess mortality will not replicate the WHO estimates, and will likely vary from other models such as those from the Institute for Health Metrics and Evaluation (IHME) (Wang, Paulson, et al., 2022) or *The Economist* (The Economist & Solstad, 2022). Moreover, many of these models tend to report either crude excess mortality rates or excess deaths, which reflect both the age-specific excess mortality rates that are given here, as well as population age-sex structure.

The challenges of calculating excess mortality for all countries have been well-documented: Acosta (2022), in a discussion of the WHO estimates, notes that only 37 percent of countries had complete all-cause mortality data for 2020 and 2021, and 43 percent lacked any data at all. Moreover, these estimates did not adjust for averted or displaced mortality, instead quantifying all changes in mortality during the period (Acosta, 2022). This lack of input data reflect the fact that limited civil and vital registration systems in many LMICs mean that the majority of deaths, and a large fraction of births, go unrecorded, an issue referred to as the “scandal of invisibility” (Setel et al., 2007; Mikkelsen et al., 2015). Although this paper attempts to use some of the best available data to address this issue, the lack of high-quality input data for many countries means that these modeled estimates will likely fail to

fully capture the impact of the pandemic on their populations. With this necessary caveat in mind, I turn to other aspects of the simulation setup that are relevant to how SOCSIM constructs populations and kinship networks.

3.3.2 Simulation Specifications and the Formation of Kinship Networks

In recognition of the challenges of obtaining historical census data for many countries, the simulations use as a starting population a stable population structure derived from the application of rates from the UNWPP 1950 rates for 200 years prior to the start of the simulations in 1950, in line with recent work using a similar stable starting structure (Snyder et al., 2022). As discussed previously, these estimates will not fully account for heterogeneity across individuals and groups, especially clustering of age-specific COVID-19 mortality within vulnerable families and population subgroups. Nor do they account for migration, as a result of data and modeling limitations; however, fertility and mortality of migrants is accounted for in UNWPP lifetables, making this unlikely to significantly bias the estimates involved.

Attention must be paid to the potential impact that this lack of within-family mortality clustering may have on simulation output.¹ If high levels of mortality clustering are expected, then comparatively few families would account for the majority of excess deaths, meaning that population-wide rates of excess loss would be much lower than estimated without within-family correlations. This could result from either similar health behaviors, such as being vaccinated against COVID-19; similar levels of frailty between family members, with some families much more susceptible to dying of the disease than others; or the fact that, in the case of a contagious disease and co-resident household members, one relative catching the disease may make it more likely that others will. Research so far has suggested that, although the household secondary attack rate for COVID-19 has increased with more transmissible variants (up to around 40% for Omicron), vaccination may have an important preventive effect (Madewell et al., 2022); this implies that the likelihood of other relatives catching the disease from an infected relative may be more limited in countries with high vaccination rates. However, the high levels of clustering of COVID-19 mortality within vulnerable subpopulations, such as Black and Hispanic individuals in the United States (Aburto et al., 2022), suggest that there may be important differences in health behavior and frailty across families. Thus, it is likely that these estimates may overestimate population-level rates of excess kin loss within countries with high levels of mortality clustering. Further analysis, potentially with family-specific frailty multipliers, along with mortality correlations of the type used in previous research on HIV/AIDS (Wachter et al., 2002), would be needed to better understand the impact that this issue may have on these estimates.

Simulation initial population sizes are calibrated, following Alburez-Gutierrez et al. (2021),

¹This discussion is indebted to helpful insights from Ronald Lee.

based on population growth rates and a target population in order to prevent simulations from reaching sizes that may lead the program to stall. Since the simulations only run up to 2025, however, the initial population sizes are larger than those used in Alburez-Gutierrez et al. (2021); using the largest simulated population size possible is important for reducing uncertainty in simulation output. In 2020, simulated mid-year population sizes range from around 30,000 to 100,000.

Given potentially higher uncertainty around modeled vital rates in very small countries, I consider in this paper a sample of 120 countries based on those with mid-year populations larger than or equal to 5 million in 2020 as per UNWPP estimates.² Given revisions to the WHO estimates of excess mortality for Germany and Sweden (Van Noorden, 2022), I do not discuss these countries in the main text, although their estimates are included in multi-country figures and regional aggregates.

Special attention must be paid to the way in which this microsimulation approach assigns individuals to one another to form “spousal” partnerships. While SOCSIM offers multiple means of carrying out this process (Mason, 2016), this paper does not use marriage rates, as in previous studies with this microsimulation setup (Alburez-Gutierrez, Mason, & Zagheni, 2021; Snyder et al., 2022). Instead, the simulations assign a male partner from all living unpartnered males in the population to an unpartnered woman at the time of the birth of her first child. In line with SOCSIM’s one-queue system, the choice of this male partner seeks to reduce as much as possible the gap between the realized distribution of age differences between partners and a pre-set “target” distribution of age differences (Mason, 2016). The SOCSIM default, used here as in previous research (Alburez-Gutierrez, Mason, & Zagheni, 2021), is a mean of 2 and a standard deviation of 3 years difference in ages between females and their male partners. Analysis of simulation output from the simulations in this paper finds that the realized distribution of age differences between partners accrued by the end of the simulation in 2025 closely mirrors the target distribution, with almost perfect overlap.

The uniform application of this distribution to all countries in the simulation is a simplification that may affect the eventual results. Average age differences between partners can vary considerably between countries and sub-national groups, ranging from close to nine years in some African countries to around 2 years in North America (Ausubel et al., 2022). However,

²The full list of countries included is: Afghanistan, Algeria, Angola, Argentina, Australia, Austria, Azerbaijan, Bangladesh, Belarus, Belgium, Benin, Bolivia, Brazil, Bulgaria, Burkina Faso, Burundi, Cambodia, Cameroon, Canada, Central African Republic, Chad, Chile, China, China (Hong Kong SAR), Colombia, Congo, Costa Rica, Côte d’Ivoire, Cuba, Czech Republic, Democratic Republic of the Congo, Denmark, Dominican Republic, Ecuador, Egypt, El Salvador, Ethiopia, Finland, France, Germany, Ghana, Greece, Guatemala, Guinea, Haiti, Honduras, Hungary, India, Indonesia, Iran, Iraq, Israel, Italy, Japan, Jordan, Kazakhstan, Kenya, Kyrgyzstan, Laos, Lebanon, Liberia, Libya, Madagascar, Malawi, Malaysia, Mali, Mexico, Morocco, Mozambique, Myanmar, Nepal, Netherlands, New Zealand, Nicaragua, Niger, Nigeria, Norway, Pakistan, Papua New Guinea, Paraguay, Peru, Philippines, Poland, Portugal, Republic of Korea, Romania, Russia, Rwanda, Saudi Arabia, Senegal, Serbia, Sierra Leone, Singapore, Slovakia, Somalia, South Africa, South Sudan, Spain, Sri Lanka, State of Palestine, Sudan, Sweden, Switzerland, Syrian Arab Republic, Tajikistan, Thailand, Togo, Tunisia, Turkey, Uganda, United Kingdom, Ukraine, United Arab Emirates, United Republic of Tanzania, USA, Uzbekistan, Vietnam, Yemen, Zambia, and Zimbabwe.

limited data availability for this measure, and issues with modeling large mean age differences in SOCSIM, which would require many individuals to remain unpartnered (Mason, 2016), make it challenging to replicate these conditions effectively. Instead, this paper applies the SOCSIM default to all countries, with the understanding that this may bias downward the ages of male partners, which may also lead to higher availability of fathers, grandfathers, and husbands.

The extent to which this may affect male kin availability is explored in Figure 3.2, which considers the impact of using target mean differences in ages that more closely reflect empirical values (less data is available on standard deviations, so the SOCSIM default of 3 years is used throughout). This comparison is performed for South Africa, using an alternative mean difference of 3.8 years, and India, using a difference of 5.6 years; these values are close to those suggested by recent data (Ausubel et al., 2022). These empirical values represent an almost two or three-fold increase in the mean age difference over the SOCSIM default, suggesting that they are likely to capture a substantial portion of the impact of a change in this parameter.

Figure 3.2: Comparison of male kin availability for female reference individuals in December 2019 based on empirical and default spousal age differences, India and South Africa

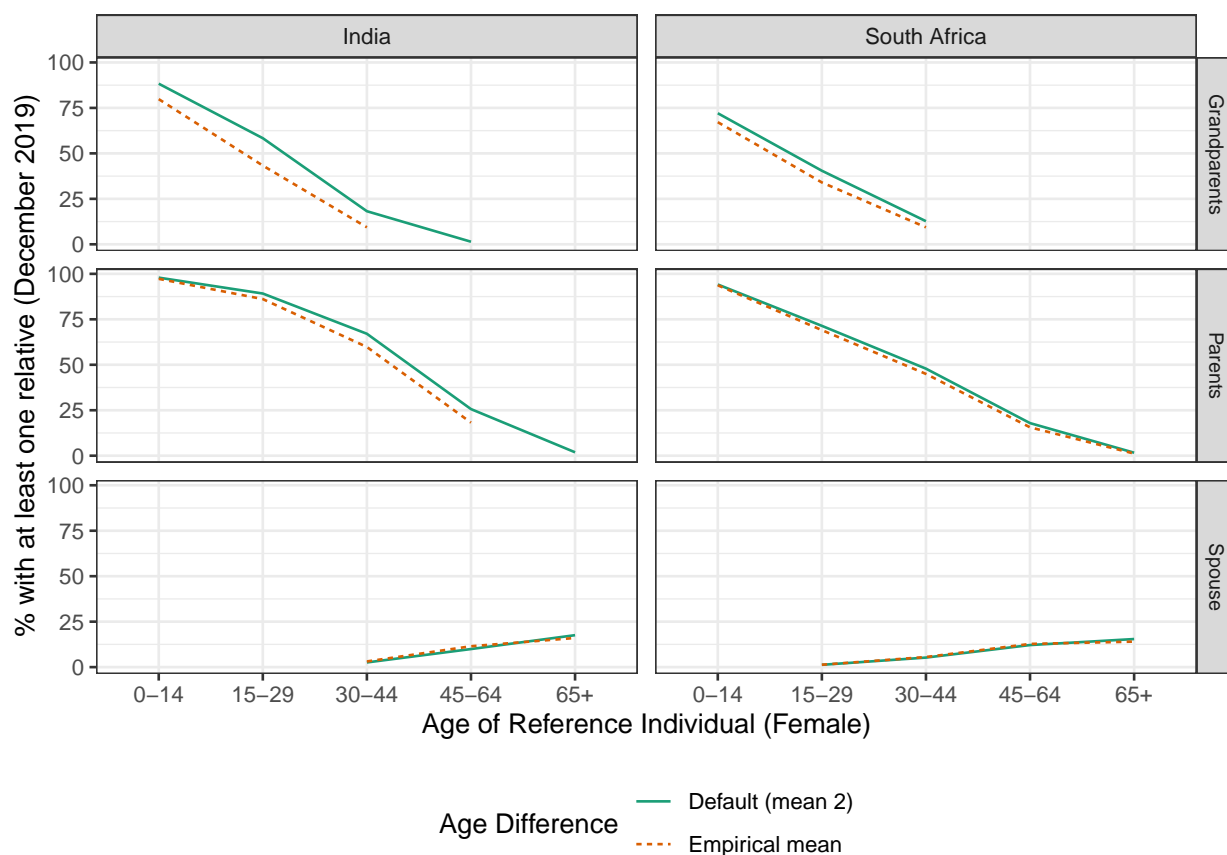


Figure 3.2 shows that, for female survivors of the pandemic excess mortality period, there is relatively little difference in the share of individuals with a surviving male grandparent, parent, or spouse in December 2019, regardless of the mean partner age difference chosen; these results also hold for male pandemic survivors. In the panels for India, which show estimates based on an empirical mean that is almost three times as large as the default value, the only noticeable difference is for the availability of grandfathers (at most a 15 percentage point difference, seen for the 15-29 age group), and to a lesser extent fathers. While an even larger empirical mean, as would be warranted for countries such as Nigeria, might lead to lower male kin availability, these results suggest that this is unlikely to have a large impact on results for most kin relationships studied.

A related issue important to explore in this context is that, since marriages in these simulations are based entirely on the birth of a first child, the distribution of age differences between partners also has a direct impact on the age distribution of male fertility. Less data is typically available for the study of male fertility, but, in some countries, its distribution is very different from female fertility. In Senegal, for example, the mean age at fatherhood is 14 years higher than the mean age at childbearing, while in France, the difference is only three years (Schoumaker, 2019).

Since partnership in this context is based on the first birth, it is instructive to compare the male age at first birth from simulation output to empirical quantities. In the United States, the male mean age at first birth, according to the 2006-2010 National Survey of Family Growth, was 25 years for men aged 15-44 (Martinez et al., 2012); in simulation output, it is around 26 years for the period. In Norway, the male mean age at first birth for all births has increased from around 28 years in 1961 to 32 years in 2020, a trend that is mirrored in simulation output showing these estimates at 27 and 30 years (Statistics Norway, 2022). While the gap between simulation output and empirical values is likely to be larger in countries with a higher mean difference in age between partners, this relative similarity in these two cases suggests these simulations are likely to capture to a reasonable extent the age distribution of male fertility.

This model of union formation based on female fertility is advantageous in that the simulations do not require data on marriage rates or marital versus non-marital fertility; such data would be challenging to obtain for such a wide range of countries. Interpreting these results, however, requires some attention to the potential challenges associated with this approach. Since spouses in these simulations are assigned only through female fertility, the simulations do not include childless unions or explicitly model divorce. A related issue is that the birth of children born after a first child will be based on age-specific fertility rates, which may affect realized parity distributions. With this in mind, this paper will present estimates for spouses, but with the important caveat that this does not include the full range of possible unions. In some countries, the share of childless unions can be relatively high, requiring caution in interpreting these estimates.

This model of union formation and dissolution also has implications for how kin are defined in this paper (Snyder et al., 2022). Lateral kin here are biologically related, with grandparents

consisting only of the parents of a child’s parents, and siblings consisting of individuals who share at least one biological parent. In the absence of a model of divorce, half-sibships can be formed by children being born to a second union emerging after the death of a previous partner. For the most part, accounting for biological sibships is likely to capture the vast majority of sibships, especially in terms of individuals who are likely to be co-resident with each other. This is brought out in research showing that, in 2009, only 1 percent of US children were living in households where the only co-resident siblings were one or more non-biological step-siblings (Manning et al., 2014). These estimates will not, however, account for all forms of kinship that may be important to an individual, as they do not consider wider reckonings of kin ties, which are important in some countries, polygamy, or other forms of kin support such as adoption or fostering.

After a population genealogy has been generated in SOCSIM, the next step of the analysis is to select individuals of interest, who in this case are those who survive until the start of 2022, modeled in this paper as the end of COVID-19 excess mortality. After this selection, it is possible to identify their kin networks and measure loss experienced in these networks during the period of excess mortality. This next section discusses excess bereavement, the measure of loss used in this paper.

3.4 Measuring Kin Loss: Excess Bereavement

The key measure of kin loss considered in this paper, excess bereavement (Snyder et al., 2022), represents the absolute difference in the population-level rate per 100,000 of losing a relative for an individual in a particular age group, regardless of their kin availability, where the difference is calculated between an observed scenario with COVID-19 excess mortality and a baseline scenario with mortality expected in the absence of COVID-19 (Equation (3.2)). An advantage of this measure is that, since it accounts for kin availability by age, it is comparable across countries, age groups, and types of kin relation. It also closely resembles the measures of kin loss that can be derived from the Goodman-Keyfitz-Pullum kinship equations; excess maternal bereavement for a woman aged a is equivalent to $\Delta M_1(a)$ presented previously in (3.1). This allows for intuitive comparisons between the two approaches, even if direct comparisons are more challenging without accounting for the assumptions required by either method. Excess bereavement can be summarized in the following equation, where N_x refers to the number of individuals surviving to at least January 2022 in age group x , the subscript b indicates individuals who lose a relative in time period t , and the subscript 0 denotes the counterfactual case:

$$\text{Excess bereavement} = \left(\frac{N_{b,x,t}}{N_x} - \frac{N_{b,0,x,t}}{N_{0,x}} \right) \times 100,000 \quad (3.2)$$

Considering just the subset of surviving individuals with at least one living relative of a

particular type in December 2019 prior to the beginning of COVID-19 excess mortality in these simulations, $N_{w,x}$, the previous equation can be written as:

$$\text{Excess bereavement} = \left(\frac{N_{b,x,t}}{N_{w,x}} \frac{N_{w,x}}{N_x} - \frac{N_{b,0,x,t}}{N_{w,0,x}} \frac{N_{w,0,x}}{N_{0,x}} \right) \times 100,000 \quad (3.3)$$

Since kin availability prior to the start of the period of excess mortality should be very similar across observed and counterfactual scenarios, and the composition of survivors should be relatively similar, given the significant size of the surviving population, $\frac{N_{w,x}}{N_x}$ and $\frac{N_{w,0,x}}{N_{0,x}}$ can be considered as equivalent.³ The equation can now be written as follows:

$$\text{Excess bereavement} = \left(\frac{N_{b,x,t}}{N_{w,x}} - \frac{N_{b,0,x,t}}{N_{w,0,x}} \right) \frac{N_{w,x}}{N_x} \times 100,000 \quad (3.4)$$

The first term represents the excess rate of kin loss for those with a living relative prior to the start of excess mortality, while the second represents kin availability, or the share of individuals who had a living relative of the type considered in the first place. A re-examination of Equation 3.1 from Keyfitz and Caswell highlights that $\Delta M_1(a)$ also is proportional to these two factors, since the rate of excess kin loss for those with kin is equivalent to the excess mortality rates experienced by these relatives. However, while the Keyfitz and Caswell equation is based on a set of specific assumptions and a single-sex population, the approach presented in Equation (3.4) is applicable to a two-sex, non-stable population and to different types of kin. This mathematical decomposition of the factors shaping excess bereavement is the basis for the analysis in the following sections.

3.4.1 Key Dimensions of Excess Bereavement: Age, Sex, and Kin Relationship

The first objective of this paper is to calculate estimates of kin loss for individuals of different ages and sexes around the world. With this goal in mind, I present in Figure 3.3 regional averages of excess bereavement for the 120 countries included in the paper, with UNWPP 2019 mid-year populations as weights.⁴ I use the United Nations regional definitions, except

³Subsequent analysis based on a Student's t-test on microsimulation output to compare the means of kin availability in the two scenarios finds no statistically significant difference between them, suggesting that this assumption holds.

⁴Representing simulation uncertainty is a concern in this study, since the width of the confidence interval derived from simulations is inversely proportional to their size. Given that the size of these simulations is directly related to country growth rates, this may result in higher uncertainty for higher-growth LMICs. Consistent with previous work using this simulation setup (Snyder et al., 2022), I thus do not report confidence intervals, while recognizing the importance of developing alternative approaches to measuring uncertainty in this context.

for the Americas, where I combine data from the Latin America and Caribbean and Northern America regions into a single region. Consistent with previous research, across all regions, older individuals were particularly at risk of losing a sibling, while younger individuals were most at risk of losing a grandparent (Snyder et al., 2022). In general, excess rates of spousal or child loss were significantly lower than grandparental or sibling loss. The large difference in magnitude between rates of sibling and spousal loss at older ages likely relate to the limitations of this paper’s treatment of marriage formation. Interestingly, although there is substantial variation in age patterns and levels of kin loss across types of kin, there is relatively limited variation across regions, with only a few regional differences of note at this stage: higher sibling loss for the Americas, and lower grandparental loss for Africa.⁵

An important point to consider is that magnitude of these rates does not necessarily reflect the severity of the consequences of experiencing such a loss, which may be partly related to its impact on the number of kin available to provide support, as well as the amount of time that an individual might have been expected to share with a relative in the absence of excess mortality. Neither of these factors are captured in the definition of excess bereavement, although an extension of these methods, with insight from the relevant sociological and psychological literature, could provide an indication of what these estimates may mean in terms of impacts on social support systems and the wellbeing of survivors. For example, the loss of a parent may have significant implications for a young child, including elevated mortality risk (Rostila & Saarela, 2011), reduced educational attainment (Patterson et al., 2020), and increased risk of later-life cognitive impairment (Liu et al., 2021), especially considering the many years that they might have been otherwise expected to be able to have their parent in their life. This is reflected in the existing literature on estimating the impact of COVID-19 mortality on family networks, which has tended to focus on the deaths of parents and other caregivers as experienced by young children (Kidman et al., 2021; Hillis et al., 2021, 2022), even though excess risks to children aged 0-14 of experiencing the loss of parent are lower than the risks of parental loss for older individuals.

As in previous work (Snyder et al., 2022), age groups of reference individuals considered in Figure 3.3 are more disaggregated at younger ages, reflecting the age distribution of COVID-19 excess mortality. However, for certain kin relationships, such as siblings, spouses, and children, risks of excess kin loss increase sharply with age, and represent a significant vulnerability in terms of social support available to older pandemic survivors. With this in mind, Figure 3.4 presents a more granular age grouping for these kin relationships, with the 65 and over age group divided into groups for 65-79 and 80 and older. For some kin relationships such as siblings and to a lesser extent spouses, there appears to be a slightly lower rate of excess kin loss for individuals aged 80 and above, compared to those aged 65-79. However, this is not seen for children, where excess rates of kin loss increase continuously with age. This suggests that there may be some interaction in this case between kin availability and excess mortality, where individuals aged 80 and above would be less likely to have a living sibling in December 2019.

⁵Oceania in this paper only includes three countries, Australia, Papua New Guinea, and New Zealand, so its estimates are likely to be subject to considerable uncertainty.

CHAPTER 3. DEMOGRAPHIC DETERMINANTS OF CROSS-COUNTRY VARIATION

Figure 3.3: Excess bereavement (per 100,000 surviving individuals) by region and kin relation, 2020-2021

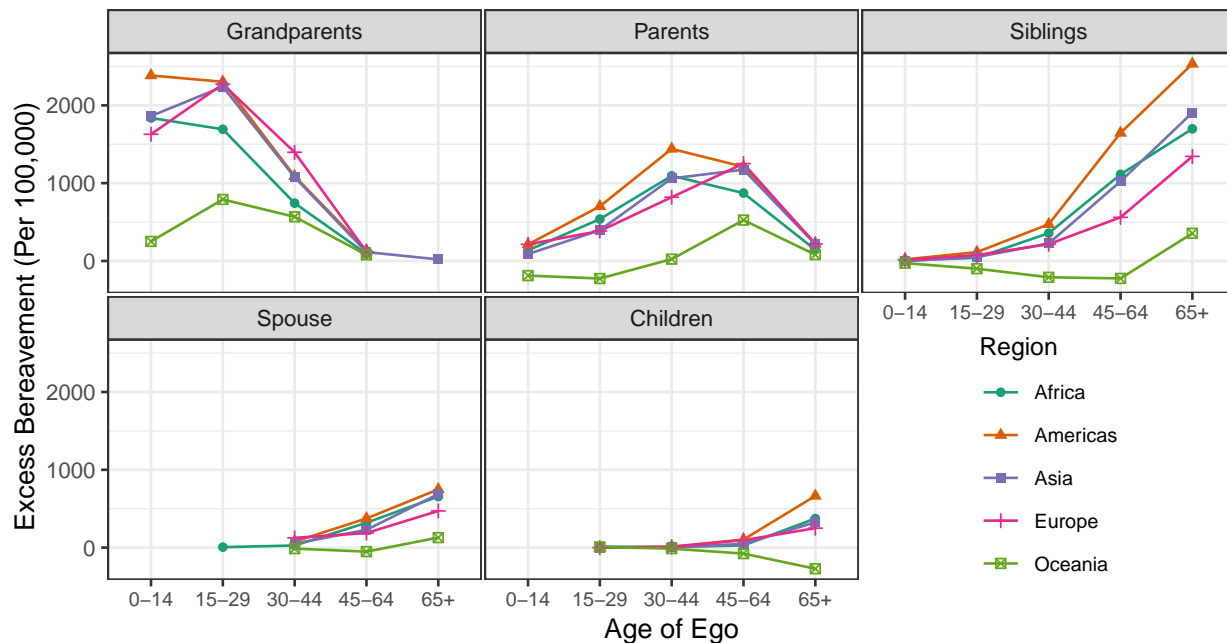
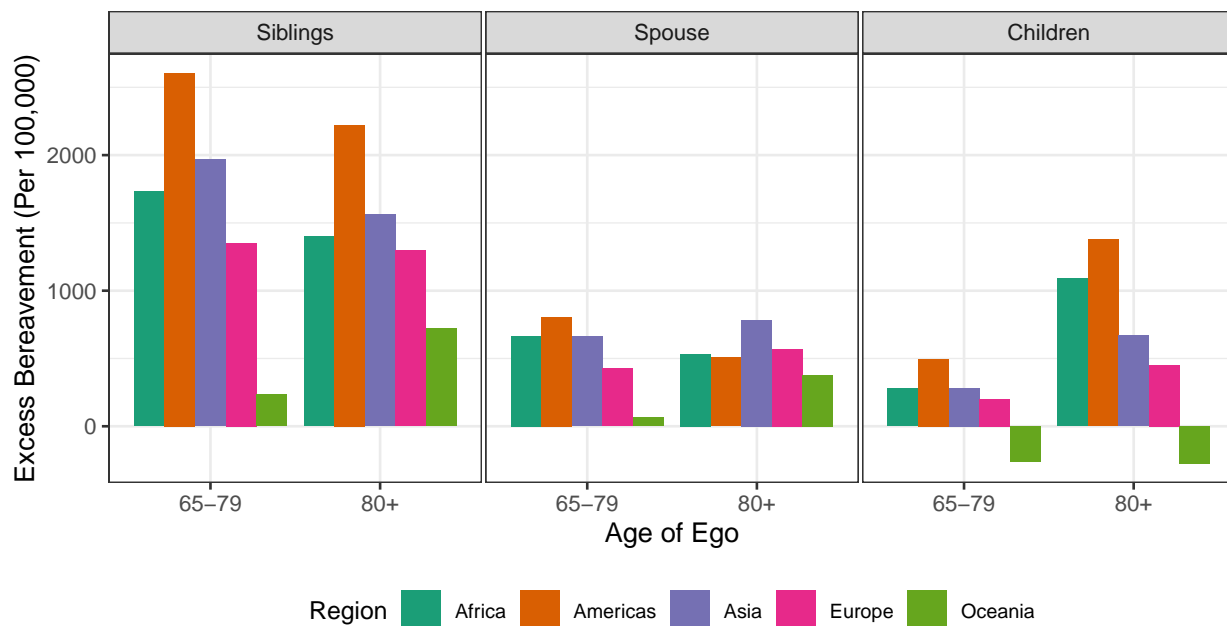
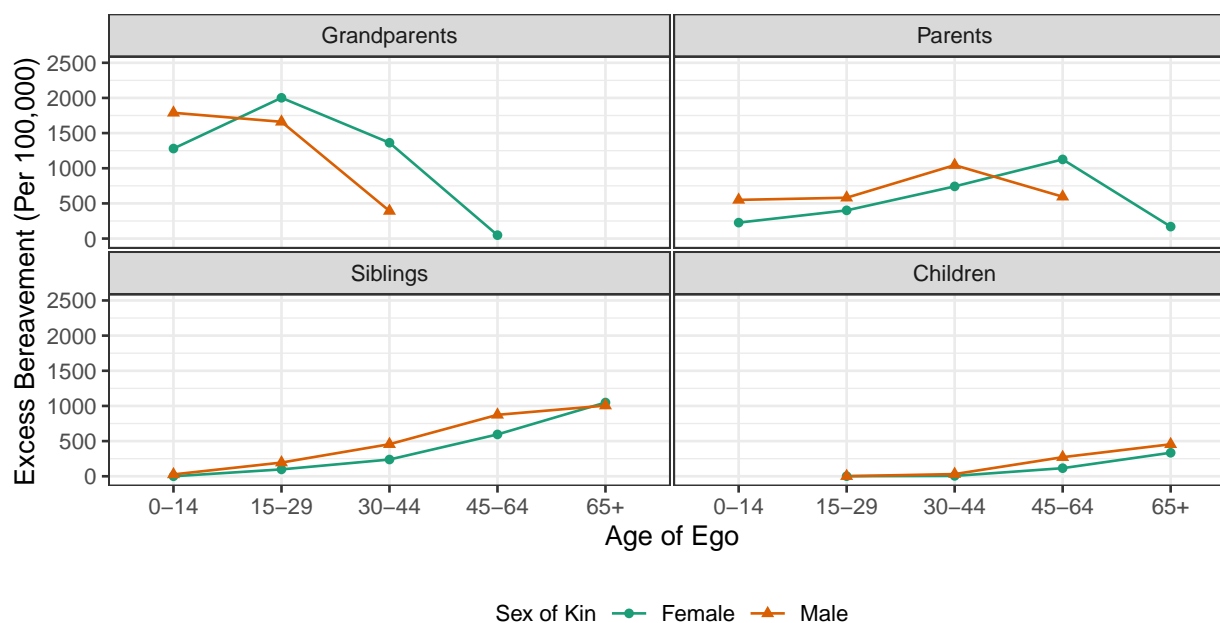


Figure 3.4: Excess bereavement (per 100,000 surviving individuals) by region for selected older age groups and types of kin, 2020-2021



Another important dimension to consider in this regard is the sex of an individual’s relative. While COVID-19 excess mortality risk increases markedly with age (Goldstein & Lee, 2020), males have also tended to see higher mortality risk (Nielsen et al., 2021). This in turn is likely to shape the sex distribution of the population of survivors and, to a greater extent, the sex distribution of kin lost. This is brought out in Figure 3.5, which presents rates of excess kin loss for female reference individuals by the sex of the relative lost (I do not present estimates by sex of the reference individual, as these show much less variation, or estimates for spouses, which in this model would only be male). These estimates are presented for Russia, which has one of the largest gaps in life expectancy by sex in the world (Oksuzyan et al., 2014), and might accordingly have been expected to see significant differences in excess mortality as well. As can be seen in Figure 3.5, the sex of the relative in question can have a noticeable effect on estimates of kin loss by age. For example, sibling loss of brothers is higher than that for sisters at most ages, as is the loss of sons in comparison to that of daughters. For ancestors, loss for female relatives (mothers and grandmothers) peaks at an older age group than does loss for male relatives, likely reflecting higher male excess mortality at younger ages. While subsequent results will be presented aggregated across sexes, this dimension of variation should be considered when identifying groups that may have become increasingly vulnerable to kin loss as a result of differential excess mortality by sex.

Figure 3.5: Excess bereavement (per 100,000 surviving female individuals) for Russia by sex of kin, 2020-2021



This definition of excess bereavement focuses on the experience of the loss of one or more relatives; however, it is also possible to redefine this measure in terms of the number of relatives lost. While the former is more comparable across kin relationships, given that some biological kin relationships are constrained to a certain number (such as four grandparents)

while others such as siblings are not, the latter captures more clearly the effects of fertility on family sizes, especially as relates to the number of siblings and children. However, in this paper, the two measures are almost perfectly correlated. This is partly a result of the kin relationships studied, some of which are biologically constrained in terms of their number, as well as the magnitude of the mortality shock. The similarity between these estimates likely also relates to simulation setup: although COVID-19 excess mortality has represented a significant increase in mortality conditions in many countries, the absence of a model of correlated within-family mortality in these simulations makes it less likely that a single individual might experience the loss of multiple relatives of a particular type. Accordingly, subsequent analysis focuses on excess bereavement.

3.4.2 Excess and Baseline Estimates

So far, the estimates presented have focused on excess kin loss over baseline levels that might have been expected in the absence of COVID-19 excess mortality. However, it is important to consider how this varied from baseline levels, including across countries with different levels of baseline bereavement determined by their demographic histories. In Figure 3.6, I map for all countries estimates of baseline bereavement, as well as the relative increase in kin loss above baseline levels, defined as the ratio of excess to baseline bereavement, that these excess bereavement estimates would imply. Instead of showing these estimates for all ages and types of kin, however, I focus instead on age groups that previous estimates for Figure 3.3 would suggest to be especially hard-hit in terms of rates of excess kin loss. This focus on the hardest-hit groups is important for distinguishing relative changes potentially driven by stochasticity and small population sizes from those likely driven by excess mortality. Although the hardest-hit group may vary slightly between regions, the general age-specific patterns hold; in these estimates, I will focus on grandparental loss for individuals aged 15-29; parental loss for individuals aged 30-44; and sibling, spousal, and child loss for individuals aged 65 and above.

The right-hand panels of Figure 3.6 contextualize the levels of excess bereavement seen in Figure 3.3, showing that, not only are these estimates relatively large in absolute terms, they highlight significant increases above baseline levels expected in the absence of COVID-19 excess mortality. This figure also captures significant within-region and cross-regional heterogeneity not captured in the population-weighted estimates in Figure 3.3, with countries such as Peru, Bolivia, Russia, India, and South Africa seeing high levels of excess kin loss. On the other hand, there is fairly little variation in these relative levels across types of kin, except for slightly lower values of relative change for grandparents. Limited variation along this dimension reflects the fact that, in focusing on the hardest-hit age groups, these estimates are based on the loss of individuals at greatest risk of dying due to COVID-19 excess mortality. Given some expected distribution of baseline loss, the relative excess increase in loss implied by a corresponding increase in excess mortality is likely to be fairly similar across different types of kin.

As can be seen in the left-hand panels of Figure 3.6, however, the denominator of this measure of relative change—baseline bereavement—also varied significantly across countries. Unlike in previous research on high-income countries (Snyder et al., 2022), the countries in this paper had markedly demographic histories prior to COVID-19 mortality, which could influence both expected and excess levels of kin loss. For example, many African countries were expected to have lower levels of grandparental loss for individuals aged 15-29, even in the absence of COVID-19, along with higher levels of parental loss for those aged 30-44 and child loss for those aged 65 and above. The levels of expected loss and extent of variation also differ based on the type of kin considered, with levels of grandparental and sibling loss being much higher than levels for other types of kin, and greater variability being observed for sibling loss in country estimates. This variation is shaped both by differences in age-specific excess mortality as well as the demographic histories of these countries, which may affect kinship structures. The extent to which these factors contribute to estimates of excess bereavement is explored in the next section.

3.5 Understanding the Demographic Determinants of Cross-Country Variation

3.5.1 Demographic History and Excess Mortality

We know from Equation (3.4) that the excess rate of kin loss depends on both the rate of kin loss for those with a living relative at the start of the period, as well as the availability of those relatives. The first of those factors is closely related to excess mortality—for individuals who survived the period of excess mortality and had a living relative prior to its start, the key factor determining whether they might experience the death of that relative was the excess mortality regime to which that relative was subject. This is borne out in analysis of average correlations between excess mortality and excess kin loss for those with a living relative in December 2019, especially for kin relationships with a sufficient spread of age groups in the data: 0.9 for siblings in 2020-2021 across all countries (for both sexes of kin and reference individuals combined), around 0.74 for parents, and 0.69 for children. Lower average correlations for spouses and grandparents of 0.45 likely reflect, in the case of spouses, previously discussed limitations of the marriage matching approach used in this paper, and in the case of grandparents, limited spread of age groups for kin and reference individuals. Although these are not perfect correlations, likely reflecting uncertainty associated with output in a stochastic simulator, the fact that many are fairly high suggests that excess mortality rates are a significant determinant of rates of excess kin loss for those with kin.

This high correlation between excess mortality and excess kin loss for those with kin suggests that, by matching the average age of individual’s relatives to an age-specific excess mortality rate, the effect of excess mortality on excess kin loss can be identified, especially for types of kin with sufficient spread of age groups in the data. As can be seen in the first two panels

of Figure 3.7, which plots for all countries the logarithmic transformations of kin excess mortality against excess bereavement for parental loss (ages 30-44) and sibling loss (ages 65 and over), the relationship shows a positive correlation: as the excess mortality experienced by relatives increases, so too does the likelihood that an individual might lose a relative.

However, this is not a perfect correlation, suggesting that the analysis has yet to account for kinship structure, defined in this context as kin availability. From formal methods and previous simulation-based studies (Keyfitz & Caswell, 2005; Sembiring, 1978), it is known that the availability of ancestors closely relates to mortality conditions, while fertility is related to the availability of siblings (Sembiring, 1978). Thus, I examine the effects of two proxy measures for demographic history: period life expectancy at age 15, which is likely to reflect mortality conditions for ancestors, and which is measured in year 2019 according to UNWPP data⁶; and the total fertility rate for 1950, which is likely to reflect the historical fertility conditions that might shape availability of siblings for individuals aged 65 and above. As can be seen from these panels, there is little clear relationship between these factors and excess bereavement, although there appears to be a slight positive correlation between the TFR in 1950 and sibling loss which may be driven by regional clustering of both measures; and what appears to be a very slight negative correlation between excess bereavement and life expectancy at age 15 in 2019. This suggests that the effects of kinship structure are likely to be much more slight, in comparison to the effects of excess mortality. It also suggests that, in order to examine the effects of kinship structure and demographic history, another approach may be required.

3.5.2 Standardizing Kinship Structure

I turn at this point to an approach commonly used by demographers to compare populations with variation in both rates and population structures: standardization. Instead of population age structure, however, the focus here is on differences in kinship structure as measured in terms of kin availability by age. Although there may yet be considerable within-region heterogeneity between countries, some regions of the world have had historically higher fertility or mortality than others, which in turn may have shaped their kin availability. This is brought out in Figure 3.8, which plots kin availability by age across regions, with regional estimates obtained as a weighted average with UNWPP 2019 mid-year populations as weights. In these estimates, Africa and Europe both emerge as outliers: Europe for low levels of sibling and child availability; Africa for low levels of parental and grandparental availability, and high levels of sibling, spousal, and child availability. These differences reflect important aspects of the demographic histories of these regions. Africa has higher fertility than many other regions, implying increased availability of spouses (since spousal matching depends in these simulations on fertility rates), children, and siblings (especially at younger ages, where mortality is unlikely to play as large a role). However, it also has had historically higher

⁶The preferable choice would be cohort life expectancy at age 15 for the cohort of 1950, but this is not yet available.

mortality in the period considered, meaning that fewer older individuals would have a parent or grandparent still alive. The reverse can be said for Europe, which has had historically low mortality and fertility in the period considered. Although which region has the highest value of kin availability depends on the age considered (for example, sibling availability at age 65 and above is highest for the Americas), these estimates show that kinship structure is likely vary significantly between regions, and that these differences are likely to serve as a useful proxy for a region’s demographic history.

These regional estimates of kin availability can be thought of as regional “standard” kinship structures. Since excess bereavement can be mathematically decomposed into its two components, by substituting a standardized kinship structure for empirically observed kin availability, directly standardized rates of excess bereavement can be calculated. In Figure 3.9, I examine to what extent changing the kinship structure of a given country to the maximum level of kinship availability across regional standards might have on excess bereavement estimates for the hardest-hit age groups. Plotted in each panel is the absolute and relative change in the ratio of excess to baseline bereavement that occurs after changing kinship standards (see the right-hand panels of Figure 3.6 for the original ratios), with the height of the bars determined by the number of countries that saw this level of change and the fill of the bars determined by the regions of the countries involved. This measure aims to capture how much a given change in kinship standard might affect country estimates of excess bereavement in relation to baseline levels.

What do we learn from Figure 3.9? First, that a change in kin availability can have a relatively large impact on estimates of kin loss for a particular country, both in absolute and relative terms. In absolute terms, it can imply an increase of up to around 10 percentage points above baseline levels (for example, if a hypothetical country had an initial relative difference between excess and baseline levels of 20% that increased to 30%, i.e. from 120 to 130 percent of baseline levels). In relative terms, this can imply high percentage changes, often in the 20-50% range, above the previous ratio of excess to baseline loss (these estimates were bounded at 100 to account for some countries with especially high estimates, which are likely to relate to small denominators). At the same time, however, the distribution of country estimates show that, for almost a third to a fourth of countries in any given graph (and even more in some cases), the estimated change is close to zero. This reflects the similarities between regional estimates of kin availability for certain ages, as well as the fact that some of these countries will have kin availability close to the regional standard, even if they are associated with a different region.

Examining which regions would see the greatest shifts highlights the extent of differences between regional kinship standards. For example, an increase in grandparental and parental availability to European levels would have resulted in large increases in excess bereavement in African countries, reflecting the large discrepancies between these two regions in terms of ancestor availability. Meanwhile, Europe would have seen the largest gains in sibling, spousal, and child loss in response to increasing kin availability in line with the American standard for siblings or the African standards for children and spouses. These changes can be observed in both absolute and relative terms, highlighting the extent to which a relatively extreme change

in kin availability—to the maximum value possible across regions—might affect estimates of excess loss. That some regions see such noticeable shifts in response to changes in kin availability reveals the extent to which a simple cross-country comparison might fail to capture the severity of their experiences of COVID-19 excess mortality. For example, if African countries had had the ancestor availability of European countries, their estimates of excess bereavement for parents and grandparents would have been significantly higher. This suggests that rates of ancestor loss for those with these types of kin were especially high for African countries, highlighting the significant effects that COVID-19 excess mortality had on kin networks in these countries.

While these calculations are strictly counterfactual—kinship availability is a product of prior mortality and fertility, so a different kinship structure implies a very different population altogether—they present a means of understanding, in an intuitive fashion, the extent to which variation in excess bereavement across countries stemmed from pre-existing demographic conditions. As seen in Figure 3.9, changing standards did in many cases result in changes in estimated excess kin loss. However, in others, there was little variation even after adjusting for kin availability, suggesting that this is highly dependent on the kin relationship and country considered. This suggests that, of the two factors, excess mortality (or kin loss for those with kin) is a much more important determinant of cross-country variation than kinship structure. This is not surprising, given the significant excess mortality seen in many countries, as well as the fact that this relatively restrictive definition of kinship structure (percentage with a living relative) does not capture fully differences in the size of kinship networks, which are likely to vary more dramatically between countries. Incorporating the size of kinship networks, or the number of kin available at the start of the excess mortality period, into a future alternate definition of excess loss may help to capture these differences more effectively.

3.6 Conclusion

Two main findings emerge from these results. The first is that many LMICs saw high rates of excess kin loss, in many cases higher than or comparable to rates seen in high-income countries. Moreover, the generational patterns of loss resembled to a great extent those seen in high-income countries, with some slight variation based on the age structure of excess mortality. This reflects the available evidence and models on the pattern of age-specific COVID-19 excess mortality, which suggest accelerating mortality risk with age (Goldstein & Lee, 2020), despite some evidence of variation in the slope of age-specific excess mortality across countries (Demombynes et al., 2022). As further evidence emerges as to the impact of COVID-19 on kin mortality through sources such as household surveys of excess mortality, it will be increasingly possible to validate these synthetic estimates against empirical data, as well as against other modeled estimates that may be developed. The high rates of excess kin loss observed in these estimates, however, serve as an important reminder of the pandemic’s dramatic toll on kin networks around the world, and complement existing estimates that

have primarily focused on high-income countries.

The second is that, based on their pre-existing kinship structures, which in turn had been shaped by prior demographic history, countries were more or less vulnerable to COVID-19 excess kin loss as a result of the excess mortality that they experienced. Whether individuals lost a relative was shaped, in part, on whether they had a relative to lose in the first place. Although country excess mortality remained a major determinant of excess kin loss, kinship structure played an important role in mediating its effects.

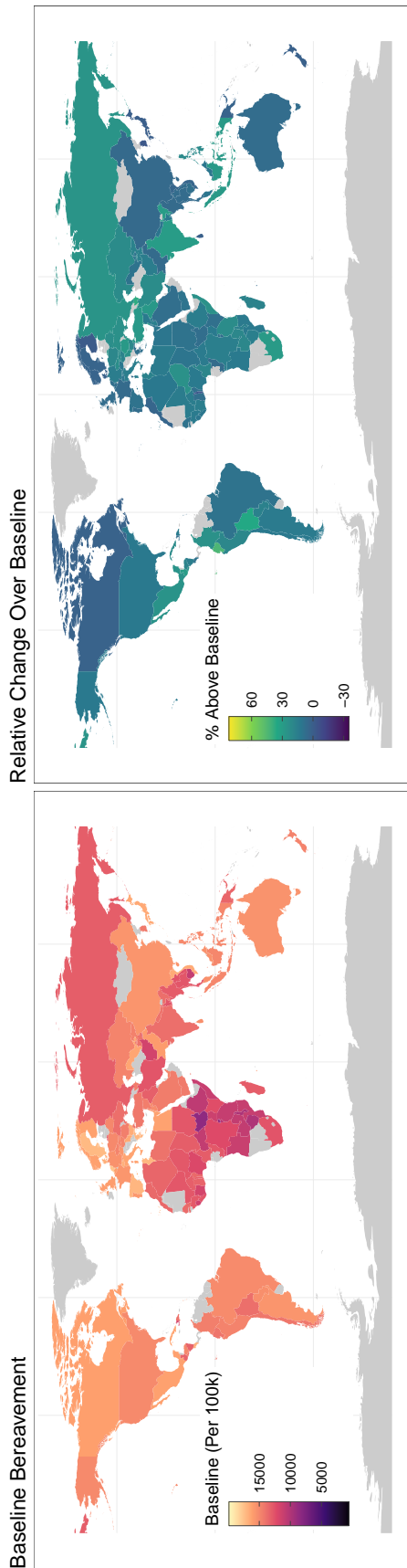
This study has many limitations. Aside from the microsimulation simplifications and assumptions discussed previously, it is important to note that, while these estimates provide insight into the quantitative effects of crisis mortality on kinship networks, they reveal less about the qualitative aspects of these effects, and what these losses might mean to survivors around the world. Kinship may be reckoned differently, and rates of interaction and contact may vary across countries. This approach, which focuses on biological kin, does not account for these important differences. Further work will be needed to consider how cultural definitions of kinship influence subsequent estimates of the pandemic's impact on families and communities.

The standardization approach presented is also less likely to be effective when comparing populations that saw very different age-specific patterns of mortality. While this does not pose significant challenges in the COVID-19 case, this could prove more difficult when comparing the effects of mortality crises with very different levels of mortality or age structures, since standardized output might vary too greatly to be easily compared.

Nevertheless, the flexible framework provided by this approach, which provides a complement to methods from formal demography, presents promise in estimating excess kin loss and understanding the reasons for variation in the experiences of different populations. Despite COVID-19's comparative recency, far less is known about the impact of crises such as the 1918 influenza pandemic on kinship networks, and how this might have varied around the world. Similarly, only limited evidence on COVID-19 related kin loss exists for subnational populations. This paper presents a broadly applicable method for examining the impact of these and other mortality crises, and understanding the demographic determinants of their effects on kinship networks in populations for which data may not otherwise be available.

Figure 3.6: Baseline bereavement and relative change over baseline levels from 2020-2021 in all countries

(a) Grandparents of survivors aged 15-29



(b) Parents of survivors aged 30-44

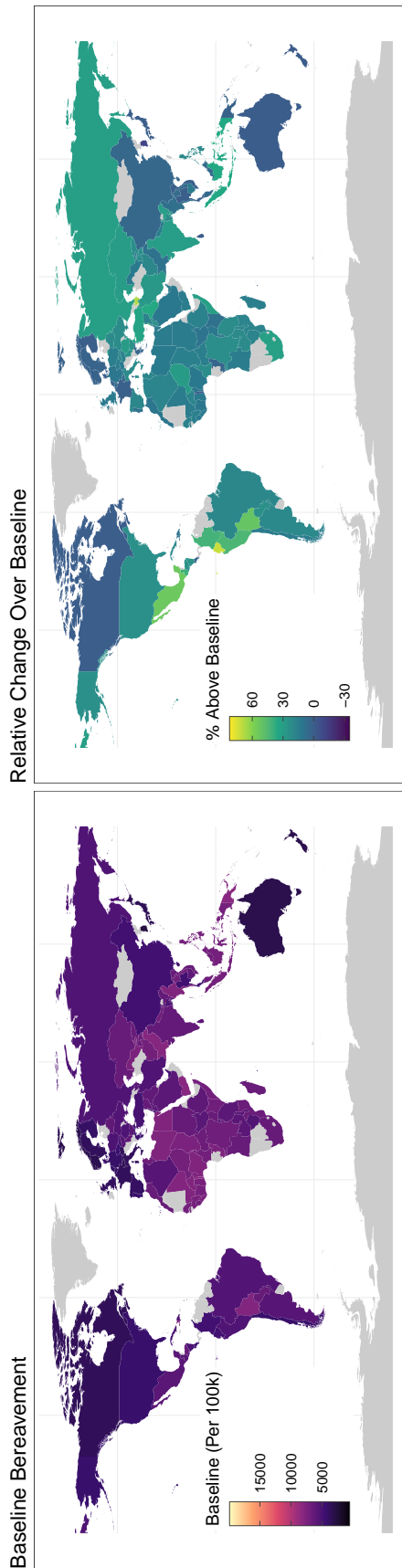
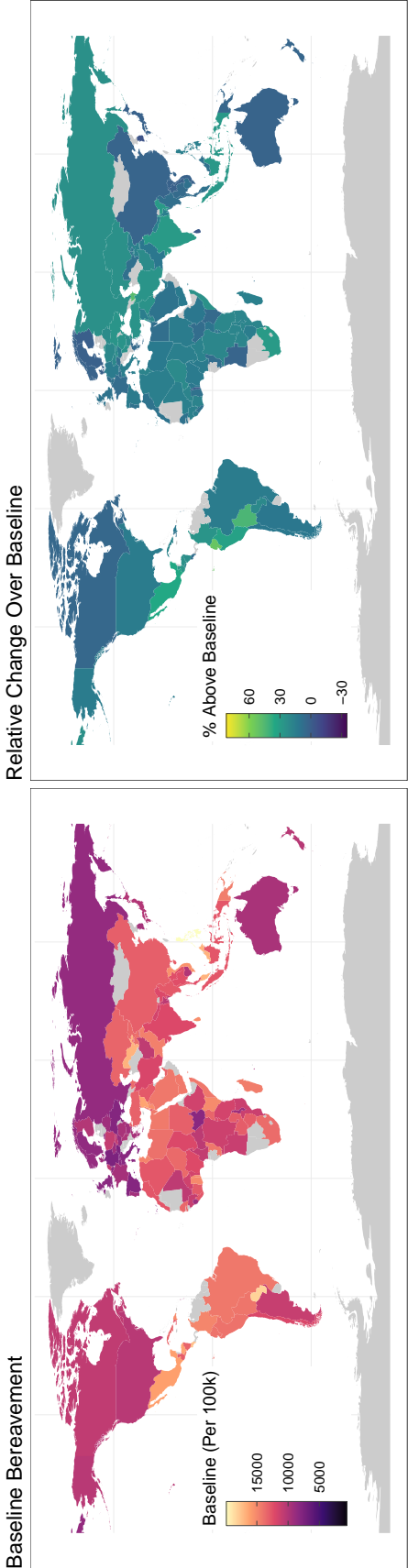


Figure 3.6: Baseline bereavement and relative change over baseline levels, 2020-2021, all countries (continued)

(c) Siblings of survivors aged 65 and over



(d) Spouses of survivors aged 65 and over

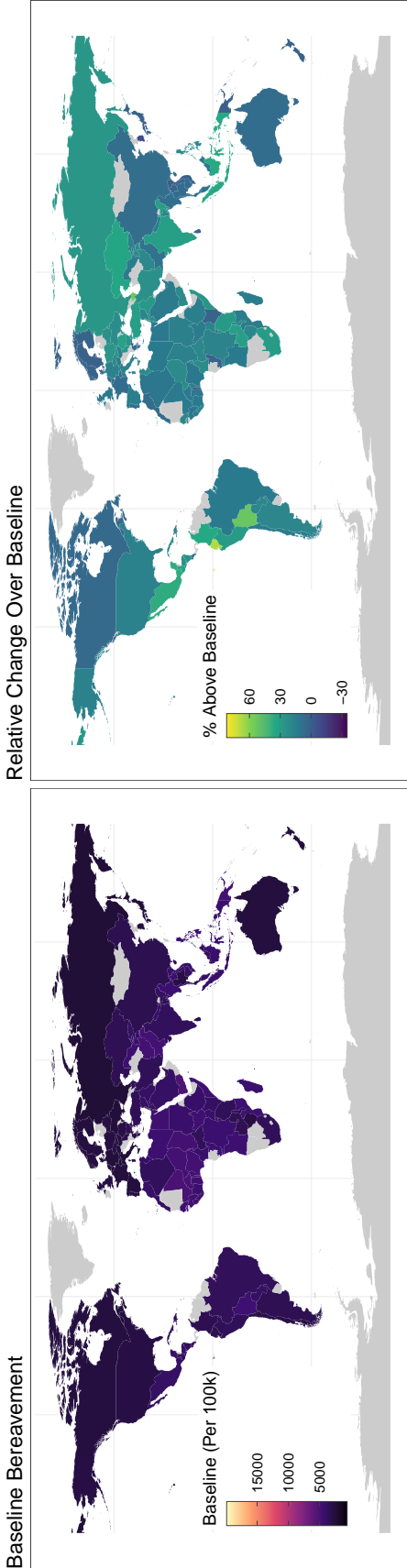


Figure 3.6: Baseline bereavement and relative change over baseline levels, 2020-2021, all countries (continued)

(e) Children of survivors aged 65 and over

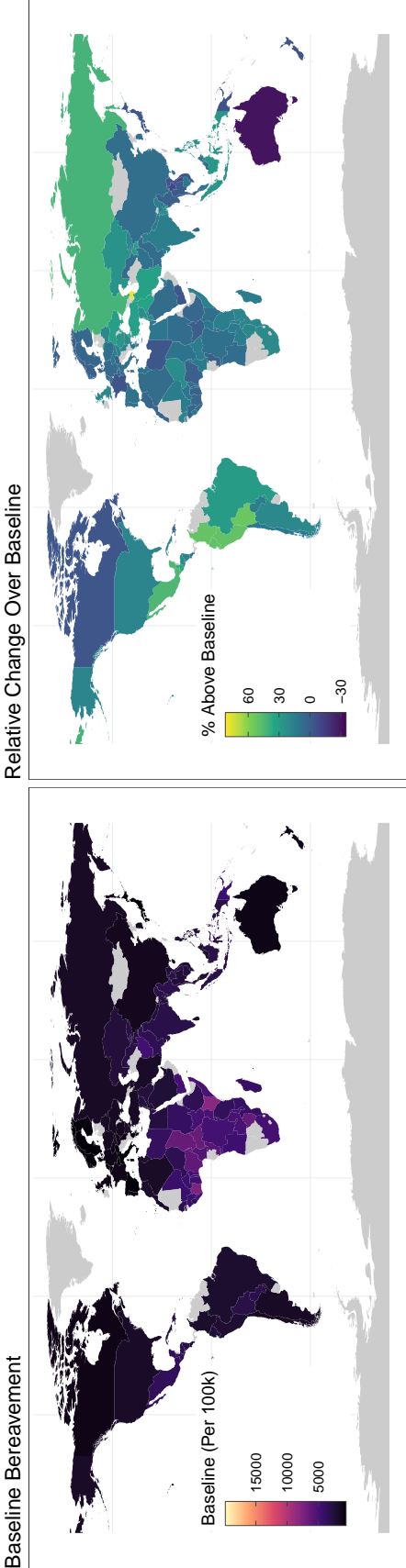


Figure 3.7: Comparisons between parental and sibling excess bereavement estimates and selected demographic factors in all countries

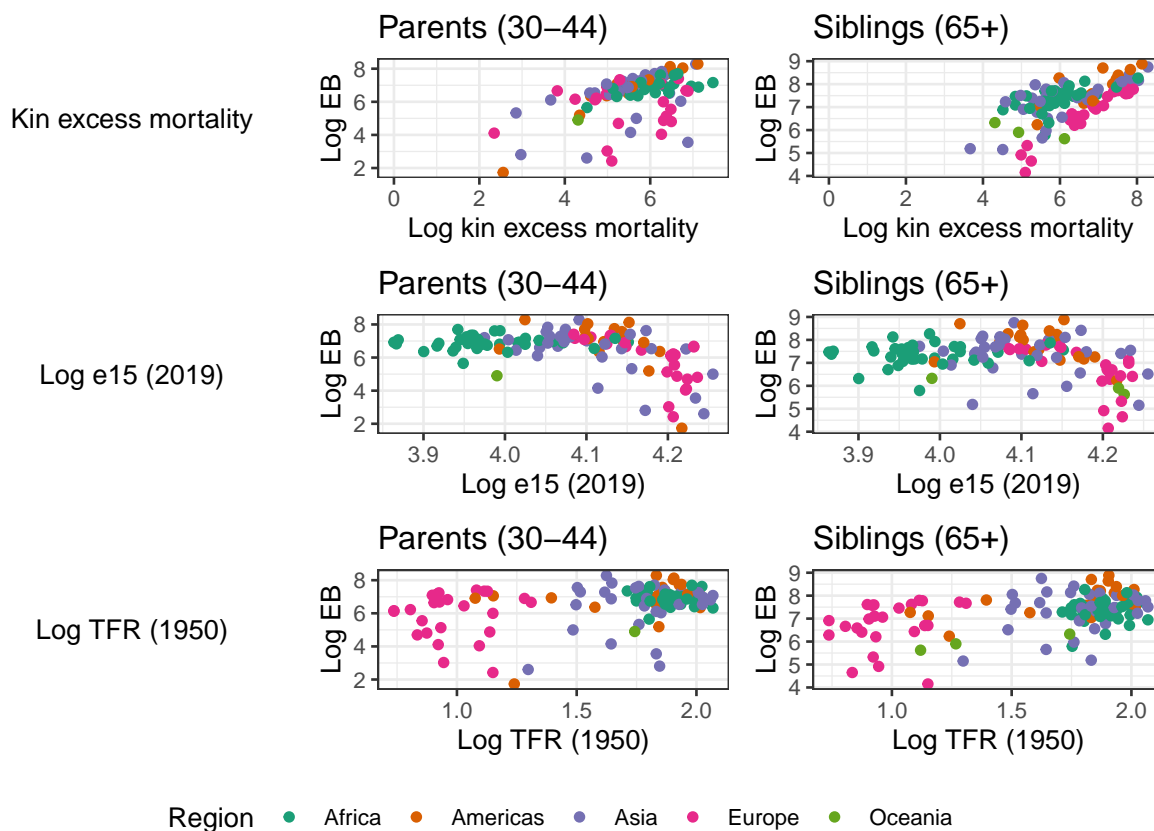


Figure 3.8: Kin availability in December 2019 by age, country, and kin relation for surviving individuals

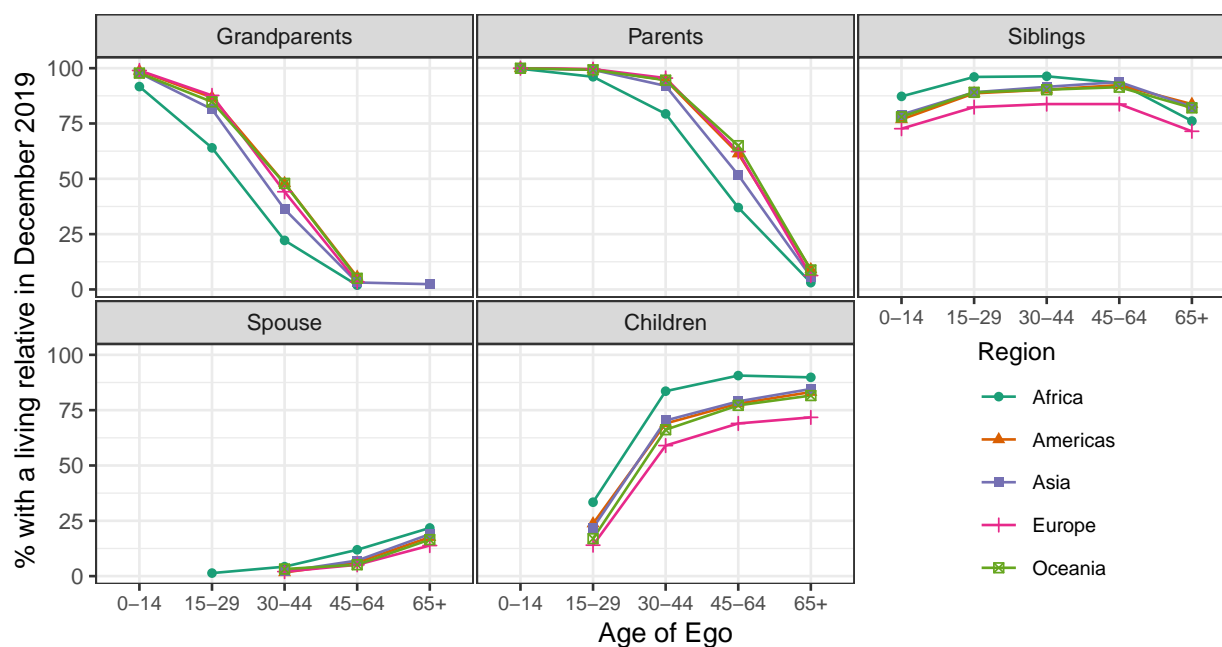


Figure 3.9: Additional absolute and relative change over baseline levels after applying kinship standard, 2020-2021, all countries

(a) Grandparents of survivors aged 15-29

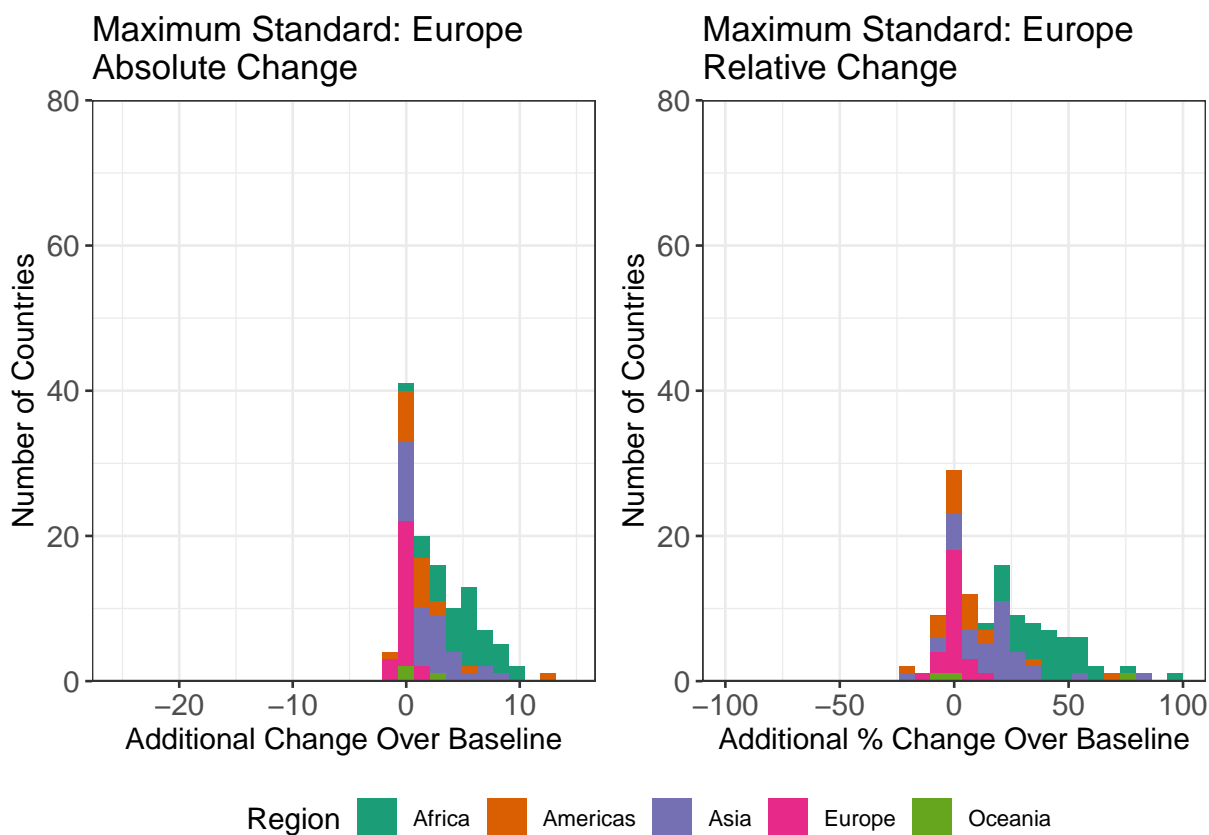


Figure 3.9: Additional absolute and relative change over baseline levels after applying kinship standard, 2020-2021, all countries (continued)

(b) Parents of survivors aged 30-44

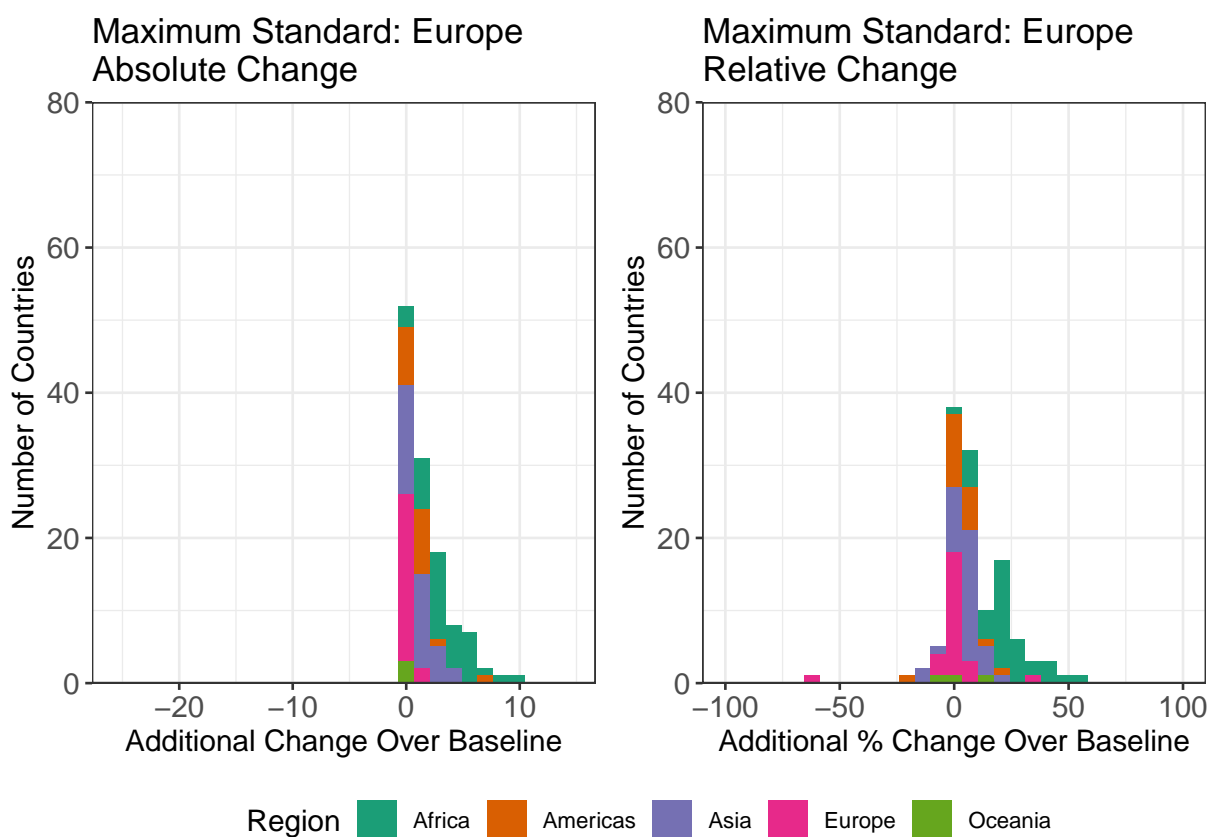


Figure 3.9: Additional absolute and relative change over baseline levels after applying kinship standard, 2020-2021, all countries (continued)

(c) Siblings of survivors aged 65 and over

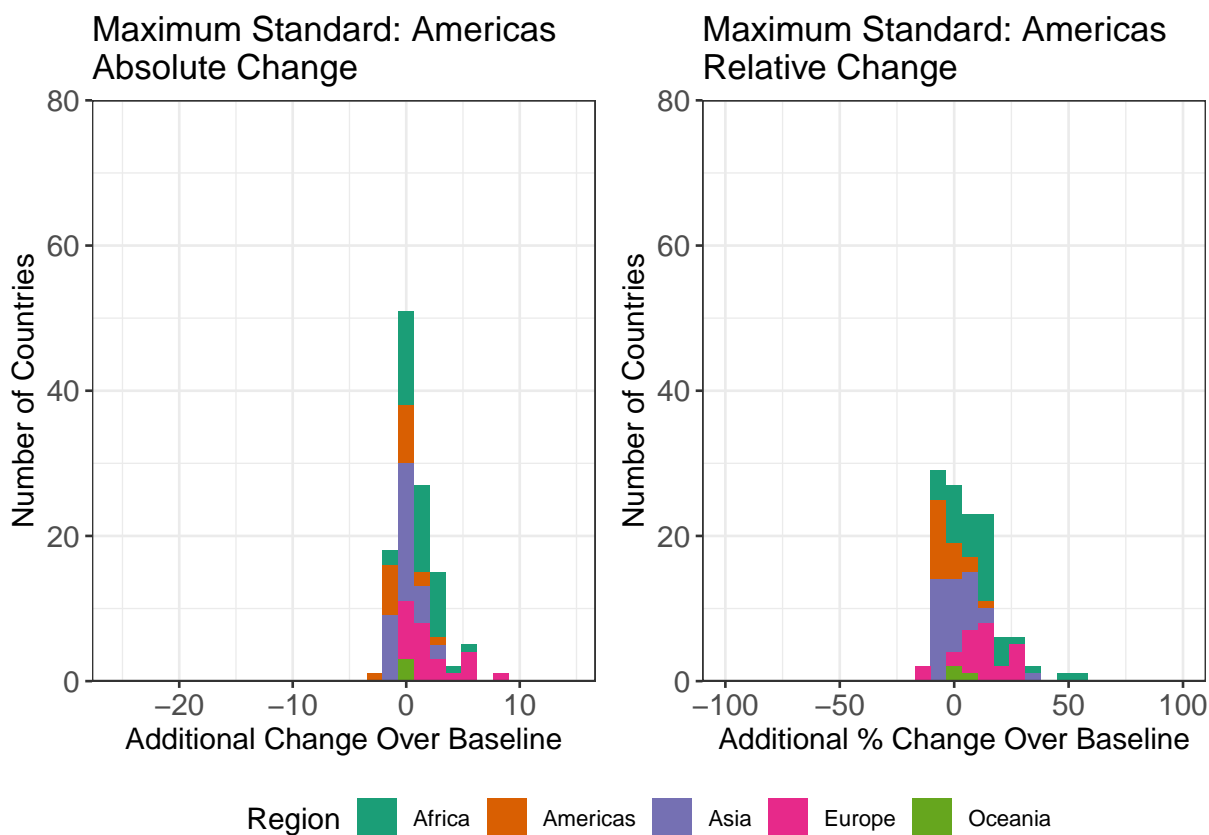


Figure 3.9: Additional absolute and relative change over baseline levels after applying kinship standard, 2020-2021, all countries (continued)

(d) Spouses of survivors aged 65 and over

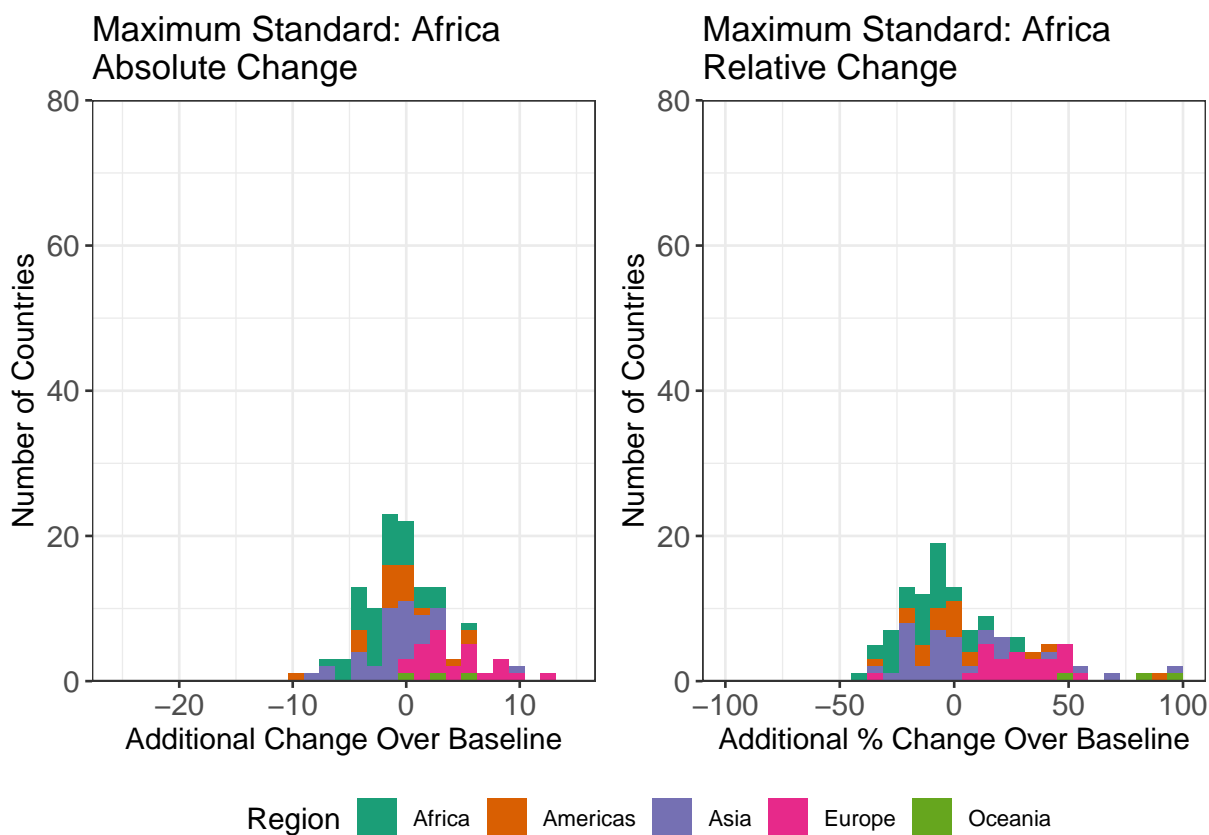
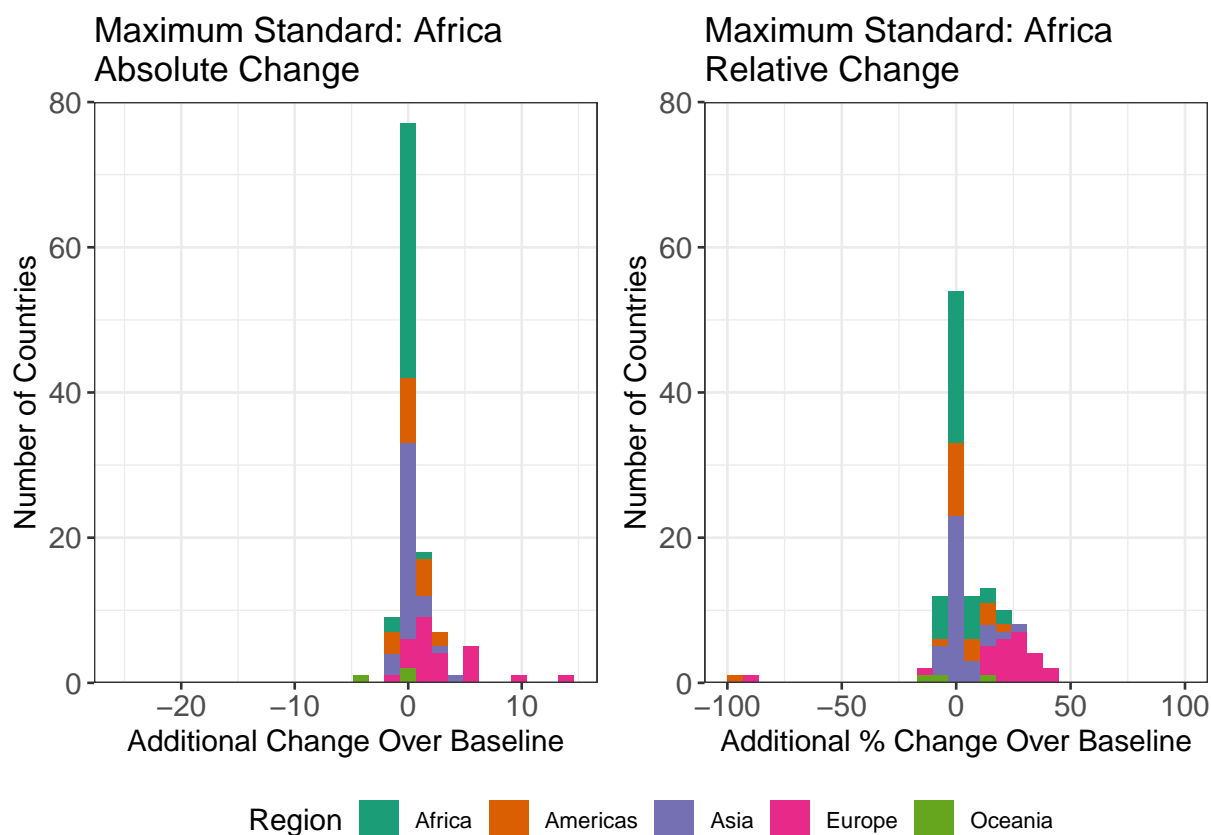


Figure 3.9: Additional absolute and relative change over baseline levels after applying kinship standard, 2020-2021, all countries (continued)

(e) Children of survivors aged 65 and over



Chapter 4

Who Will Remember COVID-19? Kinship Memory after a Global Pandemic¹

4.1 Introduction

Three years after the start of the COVID-19 pandemic, the population who lived through the early years of this crisis, and thus has direct lived experience of their impact on population mortality and well-being, is as large as it ever will be. This is a simple result of demographic processes—the size of the population of “rememberers”, individuals who live through an event, can only decrease with time (Denton & Spencer, 2021). In most countries, this will imply a shrinking share of the population who witnessed the pandemic, a measure recently conceptualized by Denton and Spencer (2021) as “demographic memory” of an event. What implications might this decline in demographic memory hold for how COVID-19 is remembered, and how these memories affect policy and popular responses to future crises? In this paper, we examine whether demographic memory operating through kinship networks, which we term “kinship memory”, may help to stave off this decline in overall demographic memory through the continued survival of individuals who lost a relative to pandemic excess mortality. This type of memory is likely to be especially salient for those who contribute to it, given that it represents a connection to a relative whose death may have been associated with uniquely traumatic circumstances and negative consequences for surviving kin (Eisma et al., 2021). As a result, better understanding the extent of kinship memory and the demographic forces shaping changes in its magnitude over time is a vital part of understanding the role that memories of COVID-19 may play in the experiences of bereaved relatives, the overall population, and governments of countries around the world.

¹This chapter has been co-authored with Diego Alburez-Gutierrez (MPIDR), Emilio Zagheni (MPIDR), and Ashton Verdery (Penn State).

Why demographic and kinship memory matter can be perhaps best understood through considering the case of the 1918 influenza pandemic. At the start of the COVID-19 pandemic, renewed attention was focused on past mortality crises, including the 1918 influenza pandemic, widely considered to have been largely absent from the public memory for almost a century (Erll, 2020a; Youde, 2017). In a book titled *America's Forgotten Pandemic: The Influenza of 1918*, Crosby (2003) writes: “*The important and almost incomprehensible fact about Spanish influenza is that it killed millions upon millions of people in a year or less. Nothing else—no infection, no war, no famine—has ever killed so many in as short a period. And yet it has never inspired awe, not in 1918 and not since...*”[p.311] (Crosby, 2003) The same passage goes on to highlight how despite early calls for greater investment in public health research and institutions, the extent of health policy change in the wake of the 1918 influenza pandemic was limited and involved little additional mobilization of funds.

Despite this lack of media or public attention to the 1918 influenza pandemic, it nevertheless had a noticeable impact on individuals’ lives, whether through death or bereavement, or changes in life circumstances or plans. This is brought out in personal correspondence and reminiscences (Crosby, 2003), which have been the subject of recent efforts to memorialize the 1918 pandemic (Centers for Disease Control and Prevention, 2018). Research has highlighted its long-term negative effects on social trust in individuals who lived through the pandemic and their descendants (Aassve et al., 2021), as well on later-life health and mortality of young children (Myrskylä et al., 2013), including those *in utero* at the time of the pandemic (Almond, 2006). And yet on a Gallup.com poll, cited in Denton and Spencer (2021), which was conducted in 1999 asking individuals to rank what they felt were the most important events of the twentieth century, the 1918 influenza pandemic did not appear in the initial lists generated from participants, or on the final list of 18 events sent to the wider sample (Newport et al., 1999).

The way in which one of the deadliest mortality crises in global history, whose effects are seen clearly in a time series of historical period life expectancy (Noymer & Garenne, 2000), still found itself virtually forgotten in public discourse, highlights the fragility of memory, even of highly consequential events. It also suggests that there are many types of memory of a crisis, some more public-focused, such as historical (Badie et al., 2011) or collective memory (Erll, 2020b; Roediger & De Soto, 2016), and others more personal, such as the memory of a deceased relative or one’s own fortunate escape from a potentially fatal disease. Furthermore, it suggests that the extent of one type of memory may not necessarily predict the extent of another nor their trajectories over time, nor how memory may translate into policy action.

This example would seem to imply that the COVID-19 pandemic should be forgotten just as quickly: after all, estimates of its global excess mortality toll are considerably lower than some of the estimates of the number who died due to the 1918 influenza pandemic, which some have argued should be close to 50 to 100 million (Johnson & Mueller, 2002). However, the age structure of excess mortality for the two pandemics is very different, which may have important implications for bereavement. Crosby (2003) raises the question of whether the 1918 influenza pandemic was scarcely remembered in the public consciousness because

very few famous people died of it, as very individuals of prominence were likely to be young enough to be at the greatest risk of mortality (Crosby, 2003). From our perspective of kinship memory, the age pattern of 1918 influenza mortality would suggest that those bereaved would be primarily parents and young children, with very few grandchildren. For COVID-19, the age pattern of bereavement is much older (Snyder et al., 2022), meaning more bereaved grandchildren, although fewer bereaved parents. Although the children and grandchildren of COVID-19 victims may be older than those bereaved by the 1918 influenza pandemic, the presence of so many bereaved grandchildren suggests a longer period of kinship memory. The way in which this may affect our estimates in the case of COVID-19 is discussed at length in this paper.

There are also other reasons to think that processes related to memory of COVID-19 may be different from those in the case of the 1918 influenza pandemic. One source of potential difference is how these diseases outbreaks may be perceived, stemming partly from their epidemiological context. Part of this relates to the idea of epidemiological transition (Omran, 2005), with the 1918 influenza pandemic occurring at a time when infectious disease outbreaks, though decreasing in frequency, were still relatively common, and COVID-19 emerging around a century later, when much of the world would have thought of large-scale infectious disease mortality as a largely historical concern. On a related note, unlike the 1918 pandemic influenza strain, which has not yet caused another outbreak of similar significance, COVID-19 is an endemic health threat that continues to cause deaths around the world; while many countries did see bounce-backs in terms of life expectancy losses early in the pandemic, others had not by 2021, making it likely that some countries will take longer to recover (Schöley et al., 2022).

Not only were the epidemiological contexts of these two events very different, so too were their impacts on daily life, and the extent to which such impacts would have been reflected in media reports and public discourse at the time. Memory of an event need not only stem from its mortality toll: disruptions to daily life could also play a significant role in shaping whether memories are retained. The 1918 influenza pandemic occurred during World War I, at a time when concerns about public morale led to widespread censorship in countries at war, with many local authorities refusing to publish data on the death toll, and newspapers providing information on public health measures, but little information on the mortality impacts of the disease (Martini et al., 2019). Even as some local authorities enacted moderately successful public health measures, and individuals reduced their rates of contact with others (Bootsma & Ferguson, 2007), restricted information may have prevented the public from understanding the true salience of the events through which they were living. While similar political considerations may have played a role in some countries with regard to COVID-19, data, though sometimes limited, was much more freely available in many countries (Németh et al., 2021; Riffe et al., 2021), and the disruptions to daily life, such as shelter-in-place measures, more apparent in contrast to the relatively “normal” conditions prior to the pandemic’s emergence.

This difference in availability of information also highlights a key difference in the potential for memorialization of these two crises. In contrast to the limited flow of information possible

during the 1918 influenza pandemic, COVID-19 is the “the first worldwide digitally witnessed pandemic”, with potential for digital media to play a valuable role in memorialization, even as public memorials have yet to be built in many countries (Ofri, 2022). Due to the ease of global digital connectivity, this can enable local memorialization efforts to resonate with global audiences (Adam, 2023), and for individuals to identify closely with global, rather than merely national, events in connection with the pandemic (Öner et al., 2023). This may in turn shape how COVID-19 is memorialized and remembered.

On the other hand, however, there is evidence to suggest that, in the words of one media commentary, “the pandemic seems slated to fade from our collective memory” (Barkan, 2023). Country pandemic control policies are now relatively stable, leading sources that previously tracked changes in stringency to no longer report this data for most of the world (Oxford COVID-19 Government Response Tracker (OxCGRT) Team, 2022). Many countries have now significantly reduced or ceased efforts to mitigate the spread of infection, despite ongoing mortality. This focus on a “new normal”, combined with limited public memorialization, suggests that the early crisis phase of the pandemic in 2020-2021 may yet find itself largely forgotten. In this context, the presence in the population of a group of people who are least likely to forget its impact may serve as a valuable repository of memory that may otherwise be limited in terms of government-led memorializing or policy response. Understanding the relative size of this group over time may thus provide context, in line with what Denton and Spencer suggest in their study of demographic memory (Denton & Spencer, 2021), for public and societal views of this and future pandemics.

What do we know of those bereaved by the COVID-19 pandemic, and how this experience may have shaped them? Losing a relative can have negative impacts on health (Raker et al., 2020; Stroebe et al., 2007), longevity (Elwert & Christakis, 2008a,b), and socioeconomic conditions (Fletcher et al., 2013; Patterson et al., 2020), and research suggests that these effects were exacerbated by the traumatic conditions of COVID-19 (Wang, Smith-Greenaway, et al., 2022; Eisma et al., 2021, 2020). As might be expected, the voices of those bereaved have sometimes played a significant role in media coverage of this crisis, with United Kingdom news reports early in the pandemic quoting surviving relatives’ calls for adherence to government infection control policies (Sowden et al., 2021). How the experience of loss may have more systematically impacted surviving kin’s attitudes and behaviors with respect to the pandemic remains to be seen. One early study in the United States highlighted significant increases in the odds of vaccine refusal for individuals who had not experienced a COVID-19 death in their families, suggesting the importance of personal proximity to COVID-19 mortality (Khubchandani et al., 2021). Another study, however, found inconsistent effects, some negative, on support for pandemic control policies (Janning et al., 2021). This suggests that this group, as might be expected, is likely fairly heterogeneous in its views; and even greater heterogeneity is likely to exist in other countries, for whom more even limited evidence on this issue exists. Nevertheless, the severe negative impacts of COVID-19 bereavement that many experienced suggest that memory of the pandemic is likely to remain especially salient for this group.

In this paper, we use demographic microsimulation to predict the extent and trajectory of

kinship memory in 120 countries around the world from 2025 to 2100. Our findings show that the continued survival of a large proportion of grandchildren will contribute to greater stability of kinship memory, with around 1 percent of the 2100 population of most regions related to a victim. However, the extent of this stability is limited by the relatively older age structure of COVID-19 excess mortality, which shapes the predicted ages of bereaved kin and the extent of their projected survival. Our results complement previous research on these topics that has been conducted on either hypothetical populations amenable to stable population modeling (Denton & Spencer, 2021) or in a single sub-population exposed to an event (Alburez-Gutierrez, 2022). In doing so, our work highlights the role of demographic structure of both the group of bereaved relatives and the overall population in shaping memory of a crisis.

The rest of the paper proceeds as follows. We discuss literature and formal models related to the concept of demographic memory in the next section, ‘Demographic and Kinship Memory’, before presenting estimates in the section titled, ‘Projecting Kinship Memory of COVID-19 using Demographic Microsimulation’. We discuss our findings and conclusions in the Conclusion.

4.2 Demographic and Kinship Memory

4.2.1 Background

The idea that a population consists of groups of individuals with variation in lived experience based on their place in historical time dates back to Ryder’s theory of cohort effects and demographic metabolism, which examines how distinct generations replace each other and contribute to social change (Ryder, 1965; Lutz, 2013). One of the factors that defines a cohort is the events that it experiences: Ryder writes that the “dramatic impact” of “traumatic events such as war and revolution” may transform a cohort into “an entelechy with an explicit mission, a virtual community of thought and action”. Such commonalities in attitudes and behaviors are by no means expected to be universal, especially in the face of other historical processes. Nevertheless, Ryder’s theory establishes a clear link between the lived experiences of a demographic group and its behaviors and attitudes.

Recent research has sought to quantify the size of these cohorts with particular lived experiences relative to the size of the population as a whole under the concept of demographic memory (Denton & Spencer, 2021). Denton and Spencer (2021) model the survival of a stable population of “rememberers” alive and aware of an event when it occurred. Their model distinguishes between local and universal events, based on how widespread their geographical relevance might be, and considers how the population of witnesses or rememberers might vary as a result of the age at which a witness might be expected to remember an event. A key insight is that, while the growth rate of a population shapes the initial size

of a population of rememberers, it does not have any effect on their number after the event occurs—demographic memory here is conceptualized in terms of a gradual replacement of a cohort of rememberers by non-rememberers, with accounting for the possibility that immigration by other rememberers may slow this decline.

Having lived through and been aware of an event when it occurred reflects one kind of memory, while having a personal connection to the event in question represents another. In a study of kinship networks of genocide victims in Guatemala, Alburez-Gutierrez (2022) introduces and examines a kinship-based approach to demographic memory as the share of a population related to a genocide victim. Although the population of kin alive at the time of an individual’s will only decrease in subsequent years, the addition of new members in future generations or by marriage, in line with the process of demographic subsidy (Caswell, 2019), contributes to continued growth and stability in the population related to a victim (Alburez-Gutierrez, 2022). While Denton and Spencer (2021)’s population of rememberers can only grow through in-migration of individuals familiar with an event, demographic subsidy ensures that the temporal duration of demographic memory based on kinship will be considerably longer. In this paper, we use the term “kinship memory” to refer more specifically to the demographic memory that operates through kinship networks, and apply measures of kinship memory similar to those used by Alburez-Gutierrez (2022).

4.2.2 Measuring Kinship Memory

There are multiple ways to conceptualize kinship memory; in this paper, we follow closely the population share approach used in previous research by focusing on the measure KM_t , the proportion of the overall country population related to a victim of a mortality crisis in year t (Denton & Spencer, 2021; Alburez-Gutierrez, 2022). An individual’s death leaves a large number of survivors bereaved, from close relatives, to more distant relatives, to friends and acquaintances, with potentially different consequences based on the degree of closeness between the survivor and the deceased. This analysis focuses only on close relatives, but it should be understood that this is but a small fraction of the network of individuals who may find themselves affected by the death of someone that they knew in connection with a mortality crisis.

In our definition of kinship memory, the numerator, consisting of the number of relatives of the deceased alive in a particular year t , accounts for two types of relatives: $K_{w,t}$, kin who were born before or during the mortality crisis and thus can be thought to have “witnessed” their relative’s death, and $K_{s,t}$, kin who were born after the crisis and who can be thought of as “subsidizing” an individual’s kin network and contributing to its continued growth after the individual’s death (Caswell, 2019). Many kin relationships for which we consider kinship memory will not incorporate this second term; since we focus primarily on close kin relationships in our paper, only estimates for grandchildren will include $K_{s,t}$, and so account for the possibility of individuals being added to the population after the mortality crisis. The numerator consisting of bereaved kin of a given type can be written as follows:

$$\text{Bereaved Kin}_{t,\text{kin}} = K_{w,t} + K_{s,t} \quad (4.1)$$

Consistent with the population share approach, our denominator consists of all individuals alive in the population in a given year P_t , including bereaved relatives. For a given kin relationship, kinship memory can thus be expressed as in the following equation:

$$KM_{t,\text{kin}} = \frac{K_{w,t} + K_{s,t}}{P_t} \quad (4.2)$$

This equation highlights some of the factors that may shape kinship memory of a crisis. As a fraction, KM_t depends on the relative magnitudes of the numbers of kin and the population size, as well as the rates at which they change over time. $K_{w,t}$ can only decrease, while both P_t and $K_{s,t}$ may increase, decrease, or remain unchanged, based on age-specific mortality and fertility rates. While individuals in $K_{s,t}$ will be born during this period, and thus will experience younger-age demographic rates, the overall population P_t will have an age-sex structure determined by the country's demographic history, with vital rates assigned accordingly. This shapes the way in which these two populations will change over the subsequent time period, and how these changes may compare: while $K_{s,t}$ will be much smaller than P_t , it may be much younger, which may affect its eventual relative size and growth with respect to the overall population.

By allowing for the population of individuals related to a victim of a mortality crisis to grow over time, $K_{s,t}$ contributes to the temporal stability of kinship memory. An example of such stability is highlighted in Alburez-Gutierrez (2022), where the population related to a genocide victim remained stable over several decades, as grandchildren and other more distant relatives were added to kin networks (Alburez-Gutierrez, 2022). An important caveat is that the type of memory associated with these more distant kin relationships may be different and potentially less salient than those for closer relationships, such as children or siblings; the impact of kin loss can vary depending on the type of kin relationship (Patterson et al., 2020), and memory is likely to do so as well. This is likely to be especially true for individuals in this subsidy term, who never met the relative who was lost to the mortality crisis: their memory of that relative is likely to be very different from that of those whose lives overlapped in some way with their deceased relative.

Different though this memory may be, it is likely that the absence of a relative, even one an individual never knew, could have significant implications for their lives. This is certainly the case for grandchildren, the kin subsidy population considered in this paper. Research has emphasized the importance of grandparents in providing caregiving support to their grandchildren, with a special emphasis on the positive impact of grandmothers, especially maternal grandmothers, on child survival, a phenomenon known as the "grandmother effect". (Sear & Mace, 2008; Hayslip Jr. & Fruhauf, 2019; Hawkes, 2004). While there is little research about the effects of not having a grandparent, these significant positive effects associated with having a relative of this kind suggest that such an absence could be detrimental. Related

insights can be found in the literature on bereavement: while the emotional implications of such an absence, as opposed to a loss, are likely to be different, the socioeconomic impacts may be somewhat similar. In this context, a study by Patterson et al. (2020) found that, for White grandchildren in the United States, a grandparent’s death may be associated with slight increases in educational attainment, a finding that is hypothesized to relate to inheritance and the transfer of resources. However, this is not the case for all racial groups, with no beneficial association for Black grandchildren. There is also a negative association between experiencing a grandmother’s death and educational attainment (Patterson et al., 2020). This set of findings suggests that these absences could have potential negative effects on the well-being of the grandchildren included in the $K_{s,t}$ term in this paper, which could in turn lead these absences to be more noticed and remembered.

Availability of other relatives is likely to play a role in how this absence in the kinship network is perceived by those who are born after the loss has occurred. With mortality declines brought about by the Demographic Transition, the availability of grandparents has increased (Murphy, 2010; Uhlenberg, 2004, 1980), reflecting the importance of mortality rates in shaping the availability of ancestors (Sembiring, 1978). It is an open question as to whether, against this backdrop of an increasing likelihood of having multiple grandparents alive well into young adulthood or later, a crisis-related absence of a grandparent may seem more or less conspicuous. Will an absence seem less acute if there are other grandparents still alive, or will it seem more shocking to have lost a grandparent earlier than expected, especially to a traumatic mortality crisis? Further research will be needed to better understand how these factors may affect this population’s experiences of this un-witnessed, but potentially significant loss.

4.3 Projecting COVID-19-related Kinship Memory with Demographic Microsimulation

4.3.1 Microsimulation Setup

In order to estimate and project kinship memory of COVID-19, we employ demographic microsimulation using the SOCSIM platform. SOCSIM, a stochastic microsimulation platform originally developed at the University of California, Berkeley in the 1970s, is one of the most popular demographic tools for studying dynamics in kinship resources in a variety of contexts (Wachter, 1997; Wachter et al., 2003; Zagheni, 2011; Verdery & Margolis, 2017). Requiring monthly vital rates and an initial population, it generates synthetic population genealogies which can be used to carry out kin censuses of individuals of interest. In this paper, the kin census focuses on spouses and close lateral consanguineous kin: parents, siblings, children, and grandchildren. To account for stochasticity, these estimates are averaged across 25 simulation runs for each country and United Nations projected fertility scenario. The size of our sample of 120 countries is based on the list of countries with populations greater than

or equal to 5 million people in 2020, as per the United Nations World Population Prospects 2022 (UNWPP); this cutoff is based on potentially greater uncertainty of vital rates for very small populations.² Given the large number of countries studied in this paper, we use internationally comparable fertility and mortality rates derived from the UNWPP, and a stable starting population based on running the UNWPP rates for 1950 for 200 years prior to the start of the simulation, extending other work by the authors (Alburez-Gutierrez, Mason, & Zagheni, 2021; Snyder et al., 2022).

It is important to note the effects that this stable starting population may have on kin availability in our results. In order to be able to run simulations for all countries, a simplified starting population is needed, since census data prior to 1950, or data of any kind that includes kinship structures, which would be the preferred choices, are not available for most countries. Previous analysis on the effects of this stability assumption has highlighted that it does not bias kinship structures for cohorts born in or after 1970 (Alburez-Gutierrez, Mason, & Zagheni, 2021). Many of the individuals most at risk of COVID-19 excess mortality, however, are likely to have been born before 1970. In our simulations, this means that some these individuals may see higher sibling counts than might be otherwise expected, as a result of an extrapolation backwards in time of Baby Boom-era fertility rates. Some differences may also be expected in terms of the availability of their parents and grandparents, given lower mortality rates and a lower mean age at childbearing than might be expected in the early 1900s. However, this is unlikely to affect the availability of their children and grandchildren, who, for these older cohorts, are more likely to be alive than their siblings or parents at the time of our kin census in 2025.

In this paper, we identify these individuals of interest with the help of the groups feature in SOCSIM, where different groups of individuals can experience different vital rates. The individuals who die of COVID-19 excess mortality in our simulations form a second group, entry to which is determined by monthly age and sex-specific excess mortality rates. Meanwhile, individuals who do not enter this group experience mortality rates in line with what would have been expected in the absence of excess mortality. These group transition and expected mortality rates are derived from the UNWPP lifetables, which, in the 2022 revision, included an accounting for excess mortality in all countries; since excess mortality data is not available for most countries, many of these estimates relied on estimates from

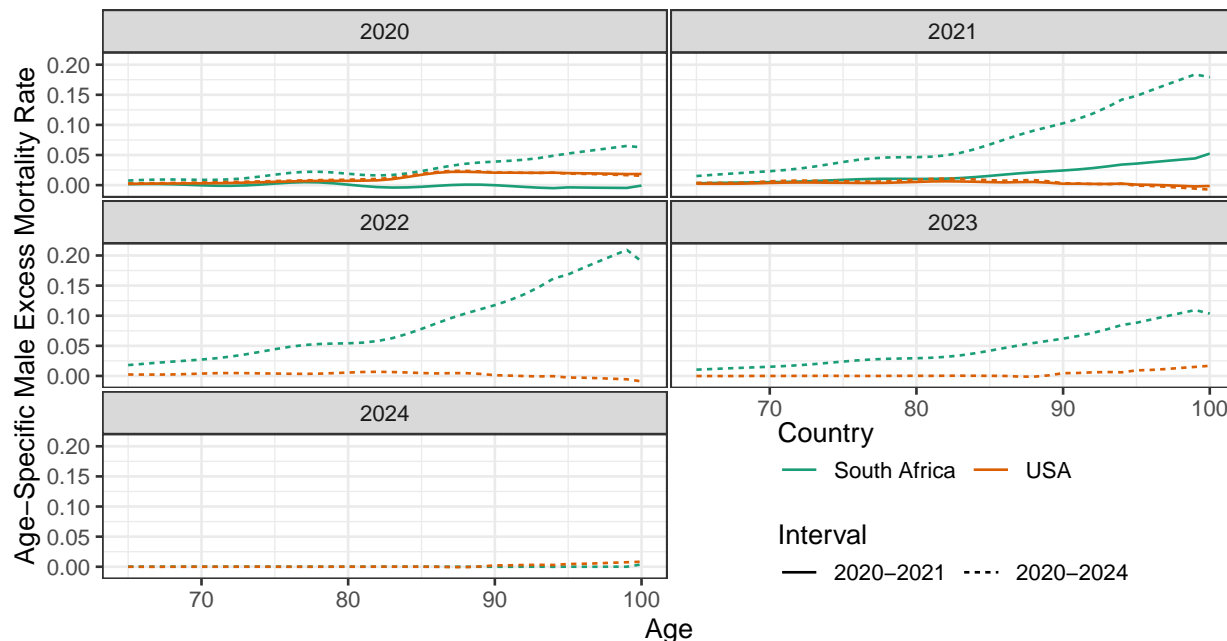
²The full list of countries is as follows: Afghanistan, Algeria, Angola, Argentina, Australia, Austria, Azerbaijan, Bangladesh, Belarus, Belgium, Benin, Bolivia, Brazil, Bulgaria, Burkina Faso, Burundi, Cambodia, Cameroon, Canada, Central African Republic, Chad, Chile, China, China (Hong Kong SAR), Colombia, Congo, Costa Rica, Côte d’Ivoire, Cuba, Czech Republic, Democratic Republic of the Congo, Denmark, Dominican Republic, Ecuador, Egypt, El Salvador, Ethiopia, Finland, France, Germany, Ghana, Greece, Guatemala, Guinea, Haiti, Honduras, Hungary, India, Indonesia, Iran, Iraq, Israel, Italy, Japan, Jordan, Kazakhstan, Kenya, Kyrgyzstan, Laos, Lebanon, Liberia, Libya, Madagascar, Malawi, Malaysia, Mali, Mexico, Morocco, Mozambique, Myanmar, Nepal, Netherlands, New Zealand, Nicaragua, Niger, Nigeria, Norway, Pakistan, Papua New Guinea, Paraguay, Peru, Philippines, Poland, Portugal, Republic of Korea, Romania, Russia, Rwanda, Saudi Arabia, Senegal, Serbia, Sierra Leone, Singapore, Slovakia, Somalia, South Africa, South Sudan, Spain, Sri Lanka, State of Palestine, Sudan, Sweden, Switzerland, Syrian Arab Republic, Tajikistan, Thailand, Togo, Tunisia, Turkey, Uganda, United Kingdom, Ukraine, United Arab Emirates, United Republic of Tanzania, USA, Uzbekistan, Vietnam, Yemen, Zambia, and Zimbabwe.

the World Health Organization (Msemburi et al., 2023). While challenges with these modeled estimates, which included revisions to estimates for Germany and Sweden, have been well-documented (Van Noorden, 2022; Acosta, 2022), they represent one of the few sources of internationally comparable data on excess mortality; similarly the UNWPP lifetables are one of the only sources likely to capture to some extent these effects on the mortality profiles of all countries. While COVID-19 case data is also available (Riffe et al., 2021), this is unlikely to capture the full impact of pandemic mortality (Beaney et al., 2020; Karlinsky & Kobak, 2021), due to differences in testing rates, health systems impacts of the pandemic, and death classification approaches between countries. These considerations motivate our use of COVID-19 excess mortality estimates, even if such an approach may not, given data limitations, fully capture the effect of the pandemic on mortality in all countries.

Different baselines and approaches can be used to calculate excess mortality, with the choice of a baseline making a significant difference to estimates (Nepomuceno et al., 2022); other work by the authors has used different methods for this calculation, including a multi-year average (Snyder et al., 2022) and a multi-year linear trend (Chapter 2). Unlike the previously cited work, this paper focuses to a much greater extent on future projections of mortality, so it is important that our excess mortality baseline account for future trends as well. This consideration makes a linear interpolation from the pre-COVID-19 period to the post-COVID-19 period a suitable choice for this analysis; we then calculate the excess mortality rates that are used for group transition probabilities from the difference between the observed and expected rates. An important point is that, given differences in baselines and data used, our estimates of excess mortality are not likely to fully match up with other published estimates (Msemburi et al., 2023; The Economist & Solstad, 2022; Wang, Paulson, et al., 2022). However, they are likely to capture relative differences in magnitude between countries, and to identify countries that saw exceptionally high or low excess mortality.

Attention is needed as to how the time period of this interpolation is calculated for the UNWPP lifetables, since, depending on the vaccination coverage and mortality impacts on the country in question, COVID-19 excess mortality was either projected to end in 2022 or in a subsequent year, with excess mortality only ending in 2025 in particularly hard-hit and low-vaccine-coverage countries (United Nations, Department of Economic and Social Affairs, Population Division, 2022). While it is not possible, from the available documentation, to identify exactly which assumptions were used for which country, this suggests that, if a single interval should be chosen for all countries, it should be 2020-2024 rather than 2020-2021; in our implementation, we use the data series from 2015-2025 for this interpolation, in order to reduce the effect of historical mortality shocks. Our choice of 2020-2024 is motivated the fact that if we only interpolate the years 2020 and 2021 for countries where excess mortality was projected to end much later than 2022, we will overestimate expected mortality for these countries, and thus under-estimate excess mortality in 2020 and 2021, while completely omitting excess mortality in the 2022-2024 period. However, for countries where excess mortality was expected to end by around 2022, an interpolation to 2025 is unlikely to result in significant departures from excess mortality estimates for the 2020-2021 period. This is brought out in Figure 4.1, which examines male age-specific excess mortality rates for ages 65 and older, as calculated from UNWPP lifetable data as a difference between observed and

Figure 4.1: Comparison of excess mortality rates derived from different linear interpolation intervals, South Africa and the USA



expected m_x values. South Africa, which saw significant excess mortality in 2021 and had relatively low vaccination rates by mid-May 2022, would see much lower estimated excess mortality for 2020 and 2021 if we interpolated only the years 2020-2021. Meanwhile, the United States would see relatively minor differences, and comparatively very low excess mortality in 2022-2024, suggesting that adding a few years of “extra” excess mortality for countries where the pandemic had already likely ended, according to UNWPP assumptions, is unlikely to significantly bias our results.

The large sample of countries studied also necessitates other simplifications, which are important to consider in the interpretation of our results. One of these is the way in which spousal partnerships are formed; rather than being based on marriage rates by age, our implementation uses female age-specific fertility rates to determine the timing of partnerships, with a spousal relationship being created at the time of the birth of a woman’s first child. The male partner chosen in this case is selected from all living unpartnered males in the simulation, with the aim of minimizing the difference between the distribution of spousal age differences thus obtained in the overall population and a target distribution. In this case, we use the SOCSIM default of a mean age difference between spouses of 2 years, with a standard deviation of 3 years (Mason, 2016). While many countries, especially LMICs, see higher age differences between partners (Ausubel et al., 2022), lack of data and issues with simulated matching with large mean age differences (Mason, 2016) lead us to choose to use the SOCSIM default, as in previous work by authors (Snyder et al., 2022; Alburez-Gutierrez, Mason, & Zagheni, 2021). This may lead to individuals having higher numbers of living male

lateral kin (especially fathers and grandfathers) than might otherwise be expected; however, in related work by one of the authors (Chapter 2), the effects of this simplification are shown to be relatively slight, at least for countries with moderately high mean age differences between spouses, such as India (5.6 years) and South Africa (3.8 years). This simplification is also likely to have implications for the age distribution of fertility in terms of the male mean age at first birth; data on this measure is not available for many countries, making assessing this issue more challenging. However, Chapter 2 does show that this is unlikely to be a concern for lower-fertility countries such as the United States and Norway.

This simplified model of marriage and partnership has important implications for how kin relationships are interpreted in this paper, an issue that is also explored in Chapters 1 and 2. The most significant point to note in this regard is that spouses in these models are connected only through the birth of a first child, so the partnerships identified will include only those involving children. This is likely to be an issue in low-fertility countries, and estimates for spouses should be considered with particular caution in these contexts. Another issue is that kin identified are related to one another biologically; thus, our analysis includes half-siblings who share one biological parent, but not step-siblings. An individual's children refer only to their biological children, not any step-children that they may have through their spouse. While this is likely to capture many salient kin relationships, it is also likely to omit some relationships that may be important, especially in countries with limited kin availability, more extensive reckonings of kin networks, polygamy, or reliance on support systems such as fostering.

As in other research using a similar setup (Snyder et al., 2022; Alburez-Gutierrez, Mason, & Zagheni, 2021), these simulations do not account for international migration. This simplification is likely to affect population growth rates of high-migration countries, such as Canada, Australia, or the United Arab Emirates. While this is less likely to pose issues for studies focused on within-kin network changes like in Chapter 1 and 2, this is of some concern for this analysis, given that calculations include total population in the denominator. Analysis of the differences in annual population growth rates derived from our simulations show that they have a correlation of .92 with UNWPP population growth rates and .98 with UNWPP rates of natural change (note that the growth rates in simulation output were calculated based on mid-year population estimates, while UNWPP rates were calculated based on January population estimates). The higher correlation with rates of natural change would be expected, given that we do not account for migration. 42 countries see, on average, a 0.5 percent difference in population growth rates from UNWPP predictions in our simulations, and 7 countries see a greater than 1 percent difference. These differences suggest that this lack of migration may have an impact on our estimates for certain countries, an issue discussed at greater length in later sections of the paper.

After this discussion of the simulation setup and its potential limitations, we turn to the results of our simulations. Kinship memory as conceptualized in this paper is based on the relative sizes of the numerator, kin bereaved by a mortality crisis, and denominator, the total surviving population, over time. Discussing each component in turn is helpful for better understanding our estimates of kinship memory, which are presented in the final section.

4.3.2 Relative Size of the Bereaved Population

4.3.3 Initial Population Size

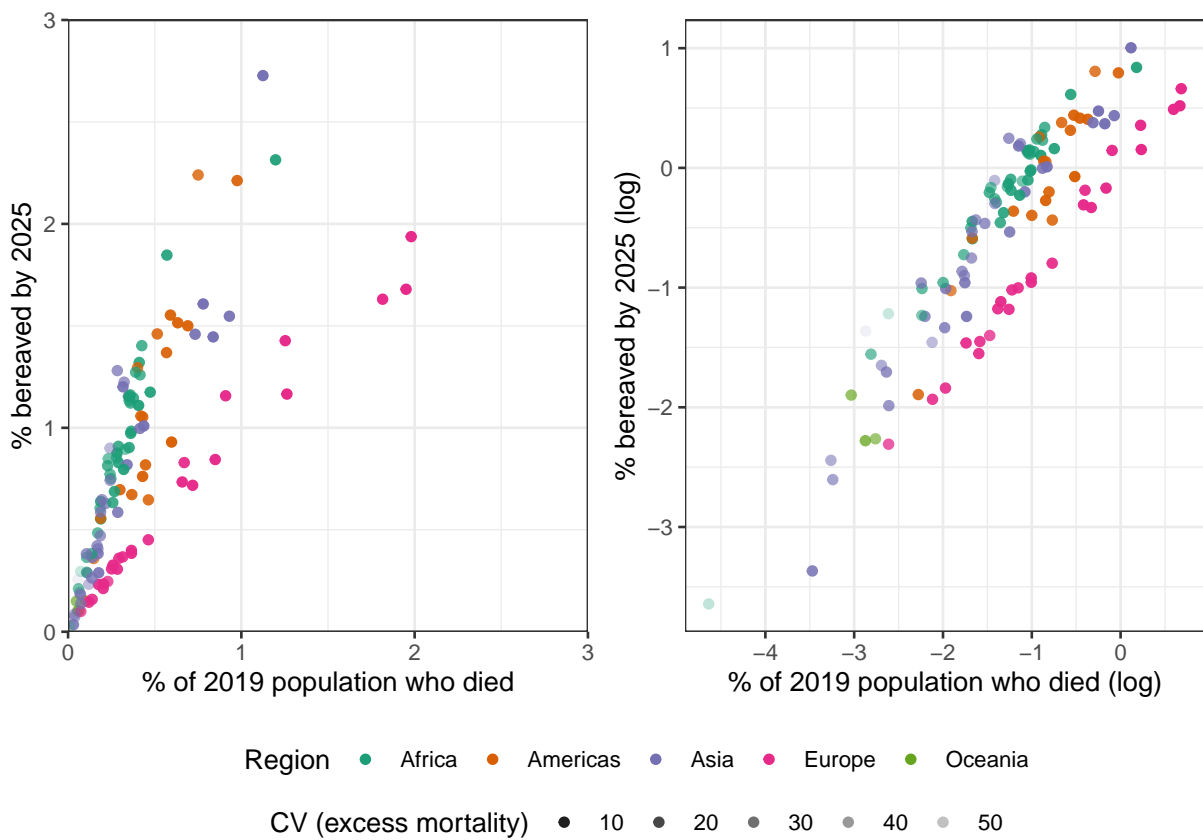
Given that most of the types of kin that we consider will not see more individuals added to the population after the crisis, the initial bereaved population $K_{w,t}$ also represents, in all types of kin except grandchildren, the peak size of the numerator of our kinship memory calculation. Thus, its relative size in comparison to the denominator (total population alive in a given year) is key to determining the peak of kinship memory, especially in the early years after a crisis where it might be expected that these losses, and memories of the crisis, might be especially salient for both the bereaved and the overall population.

As might be expected, the relative size of the initial bereaved population is directly related to the extent of excess mortality experienced. This is brought out in Figure 4.2, which plots for each country, based on simulation output for the UNWPP medium fertility scenario, the share of the bereaved population who were alive at the time of their relative's death during the crisis and are projected to be still alive in 2025, compared to the share of the 2019 mid-year population who died as a result of pandemic excess mortality. While subsequent estimates will look at different kin relationships separately, Figure 4.2 considers individuals who lost a relative of any type considered in the paper. This is plotted both on a regular (left panel) and a log scale (right panel) for all of the 120 countries included in the paper.

As previously discussed in Chapters 1 and 2, the sizes of country simulations are inversely related to the uncertainty associated with country estimates in these results. This implies that some country results may be more uncertain from a statistical perspective than others. This is captured by the shading on the points in Figure 4.2, which correspond to the coefficient of variation seen in estimates of crude excess mortality for each country, with higher coefficients of variation seeing lighter shading. This uncertainty partly explains differences between our crude excess mortality estimates and those from other sources, and also puts in context subsequent estimates that will be presented in the paper. Subsequent graphs will not report confidence intervals, given that, in this paper, these are related to simulation sizes and do not capture other aspects of uncertainty. However, the potential variation in uncertainty seen here, which will mean that high population-growth countries which require smaller simulations will thus see wider confidence intervals around estimates, should be taken into account when examining later estimates.

Figure 4.2 shows that not only does the expected direct relationship between excess mortality and the prevalence of associated bereavement hold for the countries studied, there appears to be a diverging trend between countries in Europe and in other regions, with European countries seeing a lower prevalence of bereavement in 2025 even with higher excess mortality. This is reflected on both regular and log scales, with the roughly parallel trends on the right log-scale panel suggesting a different relationship for Europe than for Asia, Africa, or the

Figure 4.2: Excess mortality (2020-2024) vs. the prevalence of bereavement (2025), UNWPP medium fertility scenario



Americas.³

The divergence in the relationship between excess mortality and bereavement reflects a second factor that determines the size of the bereaved population: kinship structure. A population with large kinship networks may see a large number of people bereaved, even with relatively few deaths, while a population with a large number of deaths but relatively small kin networks may still see fewer people bereaved than might be otherwise expected. Accounting for kinship structure, defined in this context as the number of relatives who will mourn a single death, thus helps us understand a key determinant of the prevalence of bereavement.

Based on a country’s prior mortality and fertility, and the age structure of excess mortality, an individual who dies of COVID-19 will have a certain number of surviving relatives. In the United States, this number was estimated as nine close kin in work by one of the authors (Verdery et al., 2020), in a study which first formulated this concept under the term “bereavement multiplier”. By calculating a version of these bereavement multipliers, using the types of kin studied in our paper, we can develop a rough approximation of how the kinship structure of those who die of COVID-19 excess mortality varies across countries, and what this could mean in terms of the numbers of individuals bereaved by the pandemic in each country. An important caveat is that, in the absence of a model of within-family mortality clustering, we would not expect that numbers of kin should vary dramatically between individuals who die of excess mortality, so our simulations are likely to underestimate variation between individuals.

In Figure 4.3, we present bereavement multipliers of the average number of kin alive at the time of an individual’s death of COVID-19 excess mortality, calculated under the UN-WPP medium fertility scenario for all countries in our simulations, with results for selected countries—the United States, Russia, Brazil, India, South Africa, and Italy—highlighted. In the first sub-figure, we present results aggregated across all types of kin, with other sub-figures showing estimates for parents, siblings, spouses, children, and grandchildren. These estimates show the average number of kin alive at the time of an individual’s death, not in 2025 (as will be reported in subsequent estimates). While this means that some of these individuals will not be alive in 2025, this is unlikely to significantly affect these estimates. Moreover, considering individuals still alive at the time of their relative’s death in this context helps provide a sense of its real-time impact, while accounting for the possibility that some countries would be expected to see a longer period of pandemic excess mortality than others.

This definition also enables comparison with the estimates in Verdery et al. (2020) for the United States. Our estimates are likely to vary somewhat from those in Verdery et al. (2020), given that this paper uses a different marriage matching model and different

³In this paper, Oceania is only represented by three countries, Australia, New Zealand, and Papua New Guinea. As a result, estimates for this region are likely to be less prominent in cross-country comparison in this paper, with regional aggregates subject to greater uncertainty.

rates; here, we see that the average number of bereaved kin of all types is slightly lower (7.7 for the overall population, compared to the Verdery et al. (2020) estimate of 8.91 for the combined White and Black population). Considering individual types of kin, we estimate twice as many parents (0.4 instead of 0.2), around the same number of siblings (2 versus 2.04), more spouses (0.7 instead of 0.46), around the same number of children (2.1 instead of 2.15), and fewer grandchildren (3.2 instead of 4.01). Part of this discrepancy likely relates to uncertainty in our estimates (there are very few parents still alive, for example). Simulation setup differences could also play a role, especially with regard to the excess mortality rates used: Verdery et al. (2020)'s input infection fatality rates were based on early-pandemic estimates from Wuhan, China, but subsequent months saw, at least in the United States, the mortality pattern shifting slightly towards younger ages (Elo et al., 2022). The slightly younger population of victims of COVID-19 excess mortality in this paper, in comparison with Verdery et al. (2020), would imply the availability of more parents, more spouses, and fewer grandchildren, consistent with what we observe here. Overall, these similarities with published estimates suggest that these numbers are likely to be of a reasonable order of magnitude for the other countries studied.

The multipliers presented in Figure 4.3 provide an intuitive way of understanding how a population's prior history of mortality and fertility shape its kinship networks in the context of COVID-19 (note the different scales between sub-figures, highlighting relative magnitudes of kin availability between types of kin). In general, with a few exceptions, lower-mortality high-income countries tend to see a higher number of parents and spouses, while higher-fertility low-and-middle-income countries tend to see larger numbers of siblings, children, and grandchildren. This is consistent with insights from formal demography suggesting that the availability of living ancestors is primarily related to mortality conditions, while fertility plays a larger role in the availability of kin such as siblings, aunts, and cousins (Keyfitz & Caswell, 2005; Sembring, 1978). These differences help explain why, even with comparatively lower crude excess mortality, many African countries saw such higher rates of bereavement in 2025, as per Figure 4.2. They also provides insight into how these estimates may change over time: since children and grandchildren are likely to be much younger than parents, siblings, or spouses, this suggests that we might expect a longer duration of kinship memory through these kin relationships for LMICs.

Another important factor to consider in this context is that the age structure of COVID-19 excess mortality may have varied across these populations. While COVID-19 excess mortality has shown an acceleration of mortality risks at older ages (Goldstein & Lee, 2020), data from a number of low-and-middle-income countries (LMICs) suggests that there may have been higher excess mortality at younger ages than might have been expected, leading to a flatter mortality risk-by-age curve (Demombynes et al., 2022). This is reflected in Figure 4.4, which shows the average age at death for individuals who die of COVID-19 excess mortality by country in our simulations. While these results are subject to considerable uncertainty, not least due to data quality issues in many LMICs that may affect estimates of excess mortality, they help explain some of the cross-country patterns observed in Figure 4.3, including some of the exceptions to the general patterns noted previously. For example, high-excess mortality Brazil saw a young mean age at death in our estimates, while low-excess mortality Australia

saw a very high mean age. This explains the low availability of spouses in our earlier estimates for Australia compared to other developed countries, and the high availability of parents in Brazil. These estimates are likely partly shaped by simulation uncertainty, but provide valuable context for understanding the cross-country estimates observed in Figure 4.3: older individuals would be expected to have fewer surviving parents, spouses, or siblings, but more children and grandchildren.

Post-Crisis Additions to the Bereaved Population

This multiplier framework also provides an intuitive way of understanding the size of $K_{s,t}$, the population of kin (grandchildren in this case) who will be born after their relative’s death. Figure 4.5, which plots for each country the average number of grandchildren born after an individual’s death from COVID-19 excess mortality, under the UNWPP medium fertility scenario, demonstrates that, for most countries, this population is likely to be much smaller than population of “witnesses” alive when the death occurred. Only in several sub-Saharan African countries is the average number of additional grandchildren born likely to exceed 2 (in Nigeria, shown in Figure 4.5, the number is 4.2). For most countries in Europe, the Americas, or Asia, the number is close to or under 1.

These cross-country and cross-regional differences likely relate to fertility rates, as well as the age structure of excess mortality. If mean ages at excess mortality were younger in sub-Saharan Africa than in Europe, as suggested by Figure 4.4, this would mean that children of COVID-19 excess mortality victims would be likely younger and more likely to not have completed their fertility at the time of their parent’s death. Overall, however, these estimates suggest that, for most regions, the initial bereaved population will play a much larger role in kinship memory of the crisis than kin born after their relative’s death has occurred.

4.3.4 Kin Survival and Population Growth: Changes in Kinship Memory over Time

As previously discussed, the age structure of COVID-19 excess mortality, and a population’s demographic history, shape the composition of the bereaved population. Similar factors shape its survival over time, which will help in determining how kinship memory of a crisis changes in the decades after it has occurred.

In Figure 4.6, we plot by region surviving kin as a share of the peak number of bereaved kin in each year from 2025 to 2100, using the UNWPP medium fertility scenario. Regional and global averages are calculated as a weighted average, with 2019 UNWPP populations as weights, of estimates from all countries that are included in our simulations, using regional definitions based on those from the United Nations, except for the Americas, which is presented as a single region combining the Latin America and Caribbean and Northern America

regions. Unlike the bereavement multiplier estimates, these results focus on the entire population of bereaved individuals, not the average number of bereaved kin for each death. Given the stochastic nature of our simulations, these populations may see the kin networks of some individuals better-represented than others, although kin networks, which include correlations between the fertility of mothers and daughters but not clustered within-family mortality, are likely to vary less between individuals than might be expected in empirical data.

Conversely, some bereaved relatives may have lost more than one relative, whether of the same or a different type—for example, someone may have lost a parent as well as a sibling, or have lost both parents. Our approach to this issue is to avoid duplication within kin relationships, but not across types of kin. This means that, if an individual lost two parents, they would only be recorded once in the population of individuals who lost a parent, but if they lost both a parent and a child, they would be recorded in both populations. This helps account for the fact that losing different types of relatives may have different impacts on individuals' support networks (Patterson et al., 2020). The estimates for all types of kin combined will provide the total un-duplicated population of bereaved kin, so these numbers are likely to be slightly smaller than the sum of the populations associated with each kin relationship.

For most of the kin relationships presented in Figure 4.6, the peak number of kin alive is reached in 2025 itself, since there is no subsidy population. The rapidity of declines in the survival of these types of kin is directly related to their age. By 2050, fewer than 25 percent of bereaved parents would be expected to be alive. Meanwhile, this share is reached by around 2060 for spouses and siblings, with some variation by region, and the mid-2070s for children.

The survival of grandchildren, however, is not expected to fall below 25 percent at any point during the period. This reflects their relatively young age, as well the fact that the peak number of grandchildren is expected to be reached only in the 2040s. Similarly, the measure for all kin combined (which is heavily dominated by the population of grandchildren, as seen in Figure 4.3) would see a peak around the mid 2030s in Africa and a peak of around 2025 in other regions, with a decline below 25 percent around 2080. As can be seen in Figure 4.6, there is generally much greater variation in kin survival between types of kin relationship than between regions. However, this particular difference suggests that the larger number of grandchildren being added to the African population of bereaved kin, as well as the younger age structure of excess mortality, may contribute to this slower decline in kin survival.

These different rates of survival for types of kin imply a changing composition of our numerator for kinship memory over time. Even at the time of a COVID-19 victim's death, many of their surviving relatives would be expected to be from younger generations, such as their children or grandchildren. However, by the end of the century, the population of bereaved kin would be almost entirely grandchildren, some of whom would have never met their deceased grandparent, with many kin from some of the closest kin relationships (such as parents, spouses, and children) having already died. As discussed previously, this could impact the salience that these deaths would have for those still alive, as well as their consequences for

those bereaved.

As the population of bereaved individuals changes over time, so too does the overall population. The rates of change of these two populations are likely to be different. While populations of bereaved kin will mostly decrease, and with particular rapidity as grandchildren reach older ages as well, the overall population can grow, decline, or remain constant. This is reflected in Figure 4.7, which plots regional differences in the time path of the annual growth rate of the population of all bereaved kin alive (including both witness and subsidy kin) against the population growth rate for the overall population, using the UNWPP medium fertility scenario. Given greater uncertainty around estimates for very small populations, the time path for each region ends in the year in which fewer than 25 percent of all bereaved kin, as compared to their peak population value, would be still alive.

Figure 4.7 highlights regional differences in both kin survival and population growth that are likely to affect the evolution of kinship memory over this period. While, as previously discussed, the population growth rates from our simulations are lower than UNWPP predictions, this relationship holds in additional calculations even if population growth rates are shifted upwards, given correlations between simulation growth rates and UNWPP rates. Most regions in Figure 4.7 would expect to see low, or negative, rates of population growth in this period. However, these rates are expected to decline to a much greater extent in Africa than in other regions, given their much higher starting point. This means that, even as the kin population declines at a similar rate as in other regions, this will be spread out over a period of much higher and much more slowly-declining growth. This can be contrasted with Europe, in which population growth rates are expected to decline and then rebound slightly due to a return to replacement-level fertility in line with UNWPP predictions. This difference in growth rate trajectories suggests that we may expect that population growth may play a greater role in the erosion of kinship memory in Africa than in other regions.

Since the choice of UNWPP fertility scenario would affect both population growth, as well as the rate of addition of grandchildren to the bereaved population, we test the impact of this choice in Figure 4.8, which plots the time path for Figure 4.7 for Africa by UNWPP fertility scenario; since Africa is expected to see higher growth than other regions, the choice of fertility scenario is likely to have the most significant implications for our results. From Figure 4.8 we see that the choice of fertility scenario has its greatest effect on the simulation population growth rate expected at the end of the century, with a higher growth rate in the high-fertility scenario above 0.5 percent. Meanwhile, this is expected to have comparably little effect on the growth rate of the population of bereaved kin, which would see a similar endpoint of almost negative 6 percent growth close to 2100 in any of the fertility scenarios. This reflects the fact that, for most relatives considered, the UNWPP fertility scenario only affects the population denominator of kinship memory, not the numerator of bereaved kin, since all kin of this type would have been born prior to the start of fertility rates assumed by the scenario in question. Only for grandchildren are projections of fertility rates likely to affect the numerator, and even in this case, the relatively older age profile of COVID-19 victims means that their children are likely to have been close to completing their fertility. This greater impact on the population growth rate, as compared to rates of kin survival, is

reflected in Figure 4.8.

4.3.5 Estimates of Kinship Memory

The previous sections have examined the components of kinship memory, as captured by Equation (4.2). We have seen that, for the most part, the share of the population related to a COVID-19 excess mortality victim is expected to be at its highest levels directly after the crisis has occurred, and that this level is a function both of excess mortality as well as pre-existing kinship networks. We also have seen that we would expect a much more rapid decline in populations of bereaved older kin, such as parents and siblings, with some level of kin subsidy from the birth of grandchildren that varies by region. How these rates of change interact with population growth rates—for example, many African countries would see both high levels of population growth and higher levels of kin subsidy—will shape the evolution of kinship memory over the next century.

These various factors are reflected in our estimates of kinship memory, which are discussed in this section. In Figure 4.9, we present our main results: global and regional estimates of kinship memory, by type of kin in Figure 4.9a and by region in Figure 4.9b, with both sets of estimates based on the UNWPP medium fertility scenario. This focus on the medium fertility scenario is motivated by the lack of variation in regional estimates based on UNWPP fertility scenarios seen in Figure 4.10, which plots trends in kinship memory for all types of kin combined by region and fertility scenario. While Figure 4.9a has different scales for each panel, to better display trends in each of these types of kinship memory, the relative sizes of these measures are captured in Figure 4.9b, which highlights the large share that grandchildren form of the bereaved population in all regions over this century, followed by children and to a lesser extent siblings, with parents and spouses forming very small shares of the bereaved population.

Before turning to a closer examination of cross-regional and cross-country magnitudes and trends, it is important to consider the extent to which these estimates might be affected by the lower population growth rates seen our simulations as compared to UNWPP estimates. In Figure 4.11, we plot both the absolute and relative differences between regional estimates of kinship memory based on simulation output versus after adjusting population denominators to have UNWPP growth rates (note that UNWPP growth rates are calculated as being from January to January, while the populations used in our estimates are calculated mid-year). Since we expect that higher population growth rates would result in lower kinship memory, these differences should be negative when our simulation-based estimates are used as the reference. As we see in Figure 4.11, these differences increase in relative magnitude over time, from around 10% in 2025 to around 30% in many regions by the end of the period; as might be expected, the difference is especially pronounced for Africa, which will have the highest growth rates over this period (Oceania’s estimates are very low, meaning that small differences in absolute magnitude could lead to large relative differences). Even though these relative differences increase over time, however, we see in the left panel that the absolute

magnitude of this difference peaks towards the middle of the period, with a peak of around 0.5 percentage points difference for Africa and the Americas. These results suggest that while our simulated growth rates may tend to overestimate kinship memory, these differences are likely to be relatively slight for much of the projection window, with the largest relative differences at a time when kinship memory is fairly low in all regions.

One of the key insights from Figure 4.9 is the relative similarity between regions in terms of the magnitude and trajectory of kinship memory. An exception is Oceania, which, in terms of the countries studied in this paper, saw mostly very low excess mortality and would be expected to have much lower kinship memory as a result. In other regions, by the end of the period the share of the population related to a victim of COVID-19 excess mortality would be estimated to be around 1 percent, from a peak in 2025 of around 4 percent. Some regions would see different rates of change in certain types of kinship memory than others—for example, Africa would see a much higher peak of the share of the population who are bereaved grandchildren, but also a more precipitous decline. This follows closely our estimates and predictions in the previous sections: while higher-fertility African countries would be expected to see larger populations of bereaved kin, even with lower crude excess mortality, faster population growth would be expected to erode more quickly the share that these bereaved relatives form in the overall population.

Examining these estimates at the country level, in a series of annual snapshots for the years 2025, 2050, 2075, and 2100 in Figure 4.12, reveals considerable cross-country heterogeneity not captured in population-weighted regional averages. For example, South Africa would be expected to see much higher levels of kinship memory than many other countries in Africa, with a starting point of 11.37 percent of the population in 2025, over six times the estimate for more-populous Nigeria (1.78 percent). Similarly, Russia would see much higher levels than other European countries, with its 6.16 percent in 2025 being over five times the level seen in France (1.18). While kinship memory is expected to decline significantly in all countries over the coming century, many of these countries with initially high levels will continue to see higher levels than other countries in the region even at the end of the period. However, this relationship may differ slightly between regions based on predicted population growth trajectories. This is brought out in Figure 4.13, which plots levels of kinship memory in 2025 against levels for 2100 in all countries: while there is a positive relationship between estimates for the beginning and end of the period, African countries would typically see lower levels of kinship memory than predicted by their initial levels, suggesting a more rapid erosion of kinship memory brought about by higher population growth.

Although some of our estimates have examined all types of kin together, it is important to note that there is likely to be considerable variability in how a relative's loss is remembered, based on the type of relative and the age of the surviving individual at the time of their relative's death. The age structure of kin who witnessed their relative's death and who are still alive in 2100 will be very different from the same age structure in 2025. This is brought out in Figure 4.14, which plots the temporal and age distribution of kinship memory based on the witness population. By 2100, almost the entire population of surviving kin will be individuals who were younger than 15 years of age at the time of their relative's death

from COVID-19 excess mortality, or were not yet born (not shown this graph, but seen in other estimates of the subsidy population of kin). This may in turn influence the salience that this memory has for them, much later on in their lives, and whether they are likely to remember it, or if they will be primarily relying for their memories on descriptions passed down to them from previous generations who were older at the time of the crisis. Previous studies of demographic and kinship memory have highlighted the potential impact of this age of awareness and the potential for decay of memory (Denton & Spencer, 2021; Alburez-Gutierrez, 2022). How these factors may affect memory of COVID-19 is an open question, and one that will need to be revisited in future decades, as the dynamics of memory, in a time of widespread digital coverage but limited public memorialization, become more apparent.

4.4 Conclusion

What do these results tell us? 1 percent of most regions of the world in 2100 is a small number in terms of population share, but large in terms of the number of individuals (around 100 million of an around 10 billion global population) it implies (United Nations, Department of Economic and Social Affairs, Population Division, 2022); it is also worth noting that kinship memory will be expected to be around above 2 or 3 percent for much of the century, dropping only to 1 percent around 2080. These numbers, though somewhat small, are nevertheless much larger than comparable estimates that might be derived from natural disasters, for example, which are estimated from some sources to have had a global death toll of fewer than 30,000 deaths in 2020 and 2021 combined (Ritchie et al., 2022). In comparison, the COVID-19 pandemic is estimated to have resulted in around 15 million excess deaths in the same period (Msemburi et al., 2023), with a correspondingly large number of individuals bereaved. It is worth noting in this context that these estimates do not take into account international migration, so the true impacts, when transnational kinship networks are taken into account, may be still higher. Although it remains unclear how, and whether, the views of these bereaved relatives have been shaped by the tragedy that they have experienced, and the extent to which their views may be represented in popular discourse or public policy, the size of this group suggests that this may be an important area for future research.

While we have focused primarily on bereaved relatives as a potential repository of memory, these estimates can also be used to identify the scale of individuals in need of support. A relatively modest share of a large population can imply a large number of individuals suffering the adverse consequences of losing a relative, or the consequences of never having had that relative in the first place. This issue is explored in this paper with regard to grandchildren, but may also have implications for other types of kin. These estimates thus complement other studies that have highlighted the burden of COVID-19 bereavement, and the need for greater government support for affected individuals (Verdery et al., 2020; Kidman et al., 2021; Hillis et al., 2022; Snyder et al., 2022).

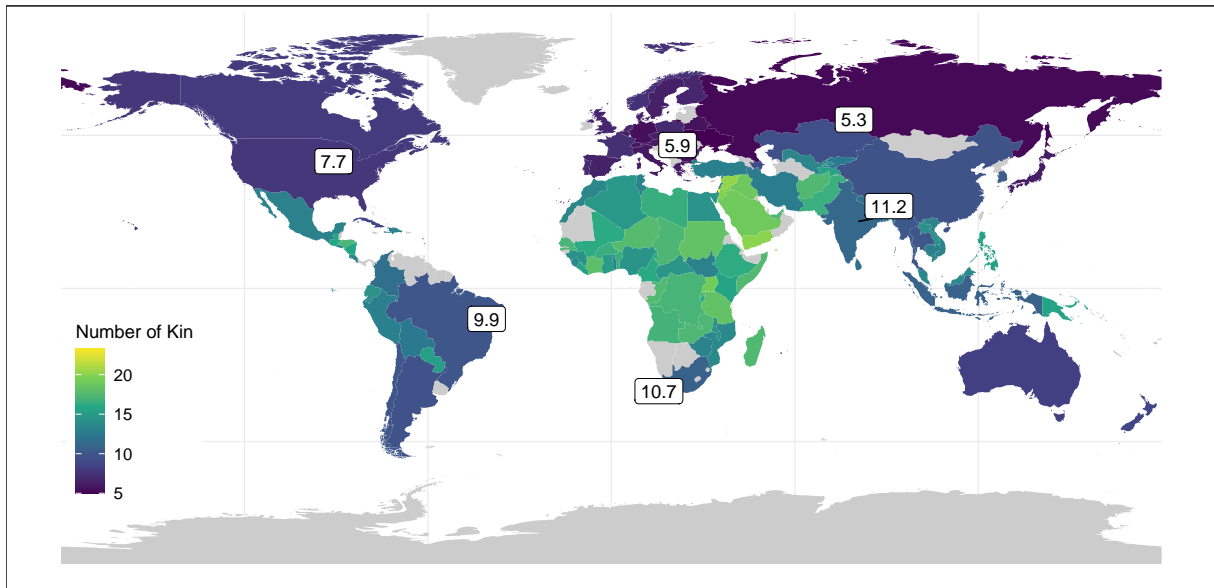
These estimates also highlight the importance of the demographic structure of a crisis in

shaping who is alive to remember it. In this context, the much greater temporal stability of kinship memory that Alburez-Gutierrez found for a genocide affected-population in Guatemala reflects the age structure of that crisis, with individuals of all ages suffering relatively similar levels of excess mortality, as well as the greater number of types of kin considered (Alburez-Gutierrez, 2022). This is not the case for COVID-19, for which kinship memory is expected to decline steadily over this next century. Nor would it likely have been the case for the 1918 influenza pandemic, in which the younger age of the victims might have implied both longer kinship memory based on surviving children and grandchildren, or a more rapid decline due to fewer numbers of children, and thus fewer grandchildren having been born. The composition of bereaved relatives determines in each of these cases the trajectory of kin survival as compared to population growth. How these differences in kin composition shape the overall valence of kinship memory—given that, as discussed previously, the impact of losing a relative may be different depending on the type of relative lost—is another important avenue for future research.

These many as-yet unanswered questions will have a bearing on the interpretation of these estimates. However, it is our hope that by presenting these estimates, and considering how they may shape memory of COVID-19 in the century to come, this paper may serve as an encouragement to future research to better understand the long reach that COVID-19 and other mortality crises may have on kin networks and support systems around the world.

Figure 4.3: Average number of kin bereaved by each death due to COVID-19 excess mortality, UNWPP medium fertility scenario

(a) All Bereaved Relatives



(b) Bereaved Parents

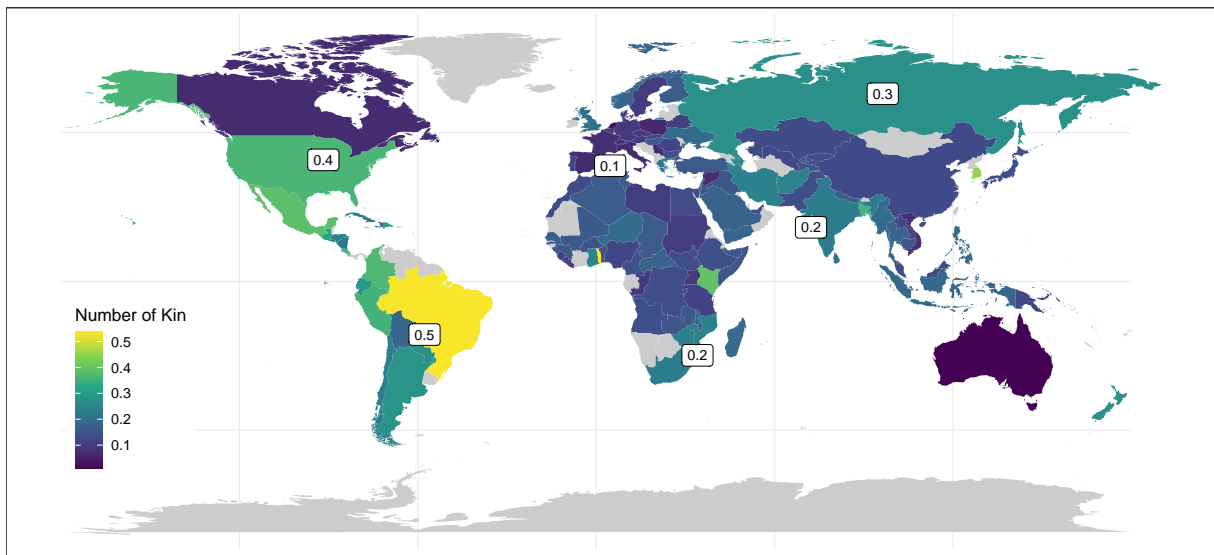
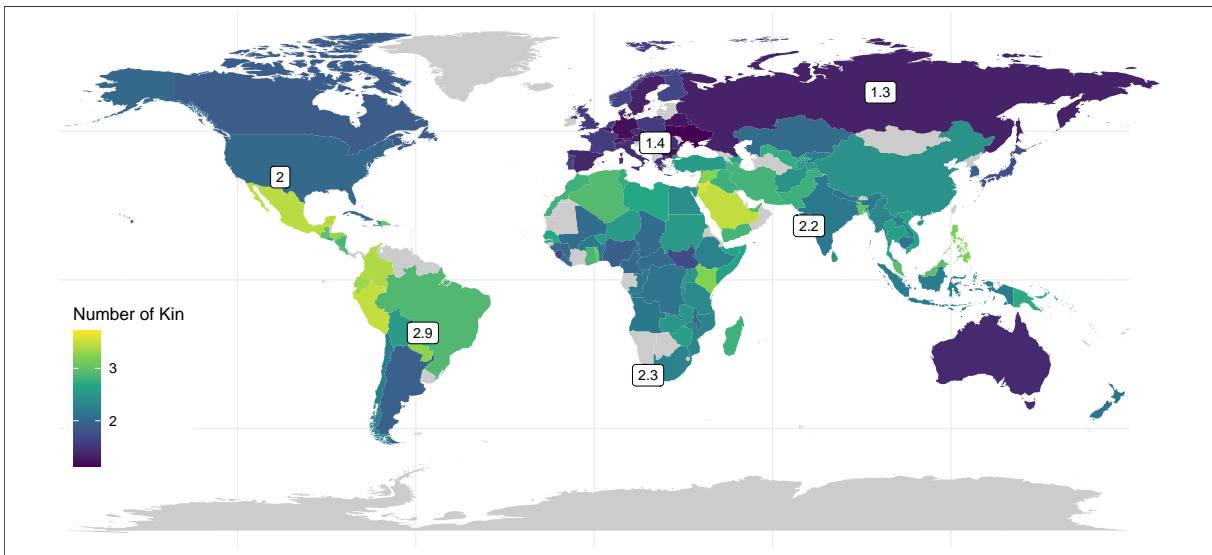


Figure 4.3: Average number of kin bereaved by each death due to COVID-19 excess mortality, UNWPP medium fertility scenario (continued)

(c) Bereaved Siblings



(d) Bereaved Spouses

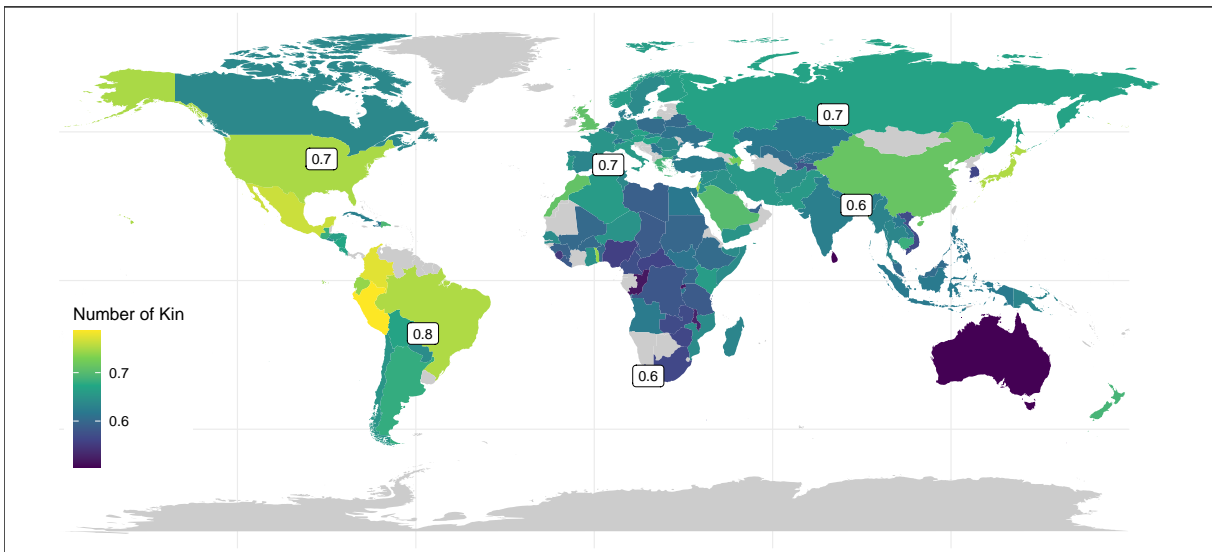
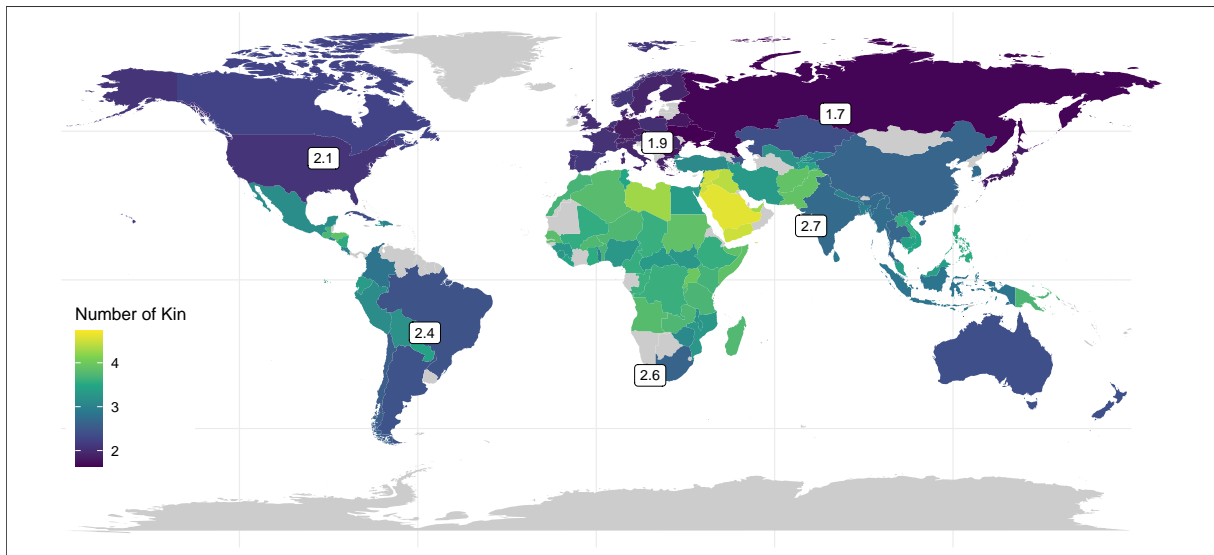


Figure 4.3: Average number of kin bereaved by each death due to COVID-19 excess mortality, UNWPP medium fertility scenario (continued)

(e) Bereaved Children



(f) Bereaved Grandchildren

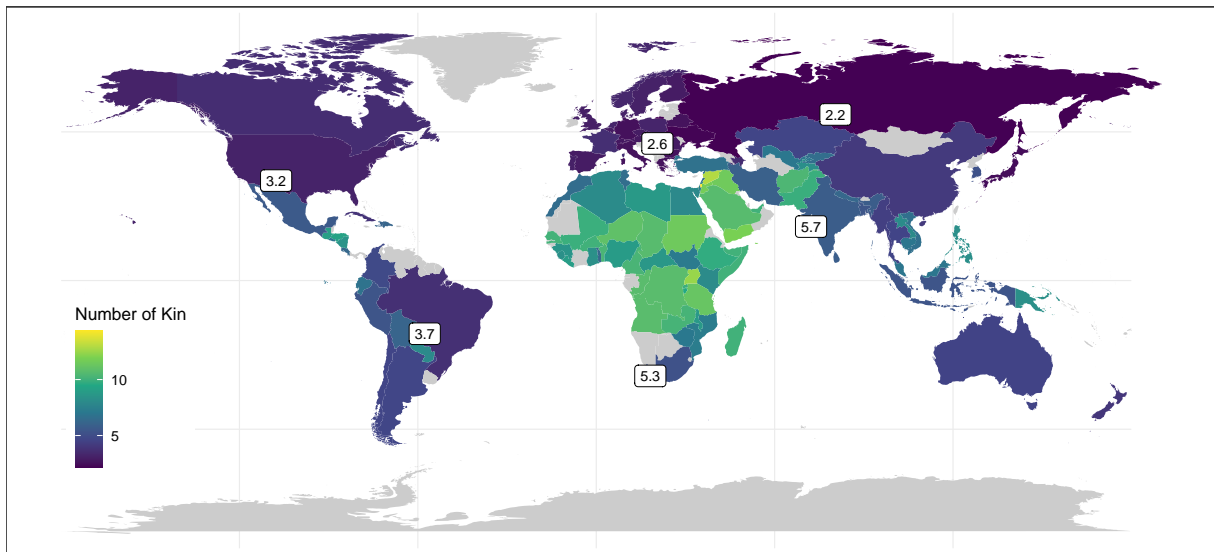


Figure 4.4: Mean age at death for COVID-19 excess mortality in simulation output, UNWPP medium fertility scenario

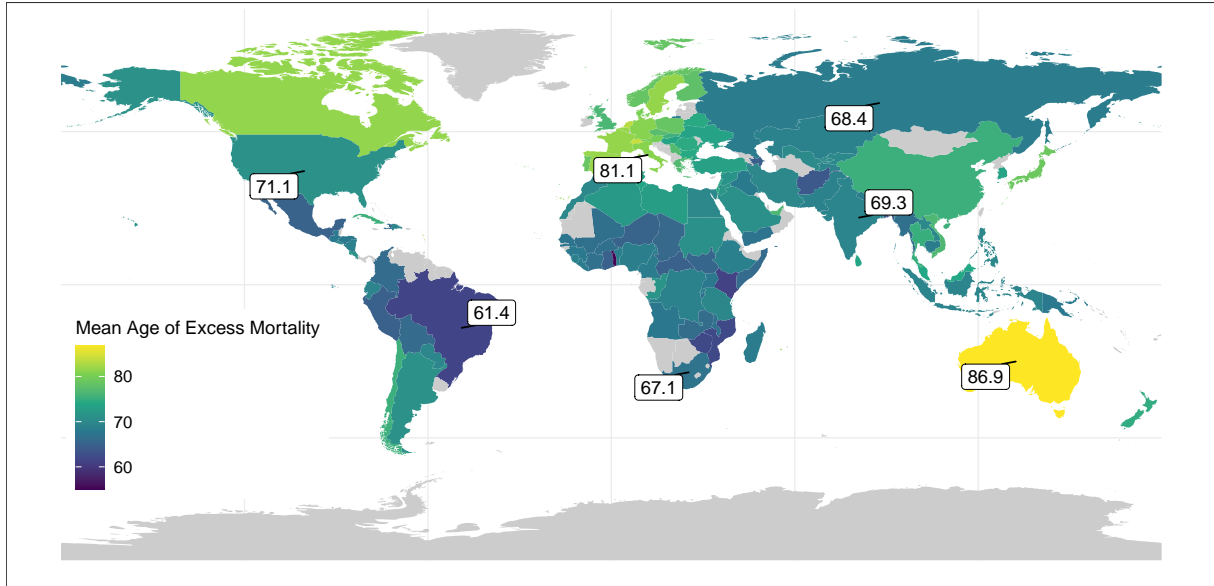


Figure 4.5: Average number of grandchildren born after an individual's death due to COVID-19 excess mortality, UNWPP medium fertility scenario

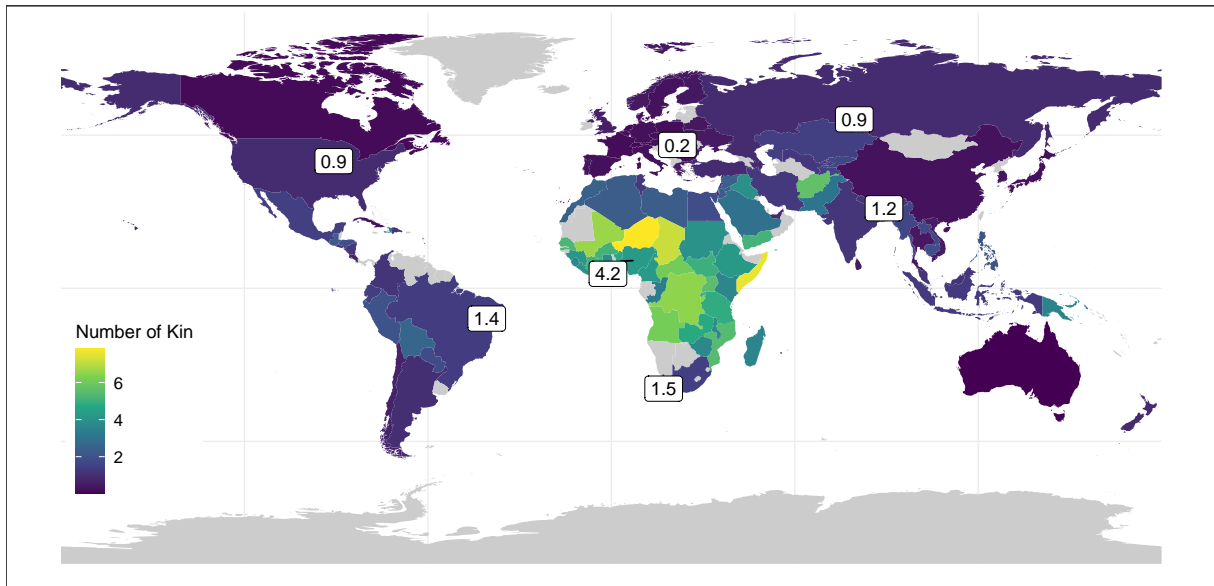


Figure 4.6: Surviving kin as a share of the peak number of kin, UNWPP medium fertility scenario

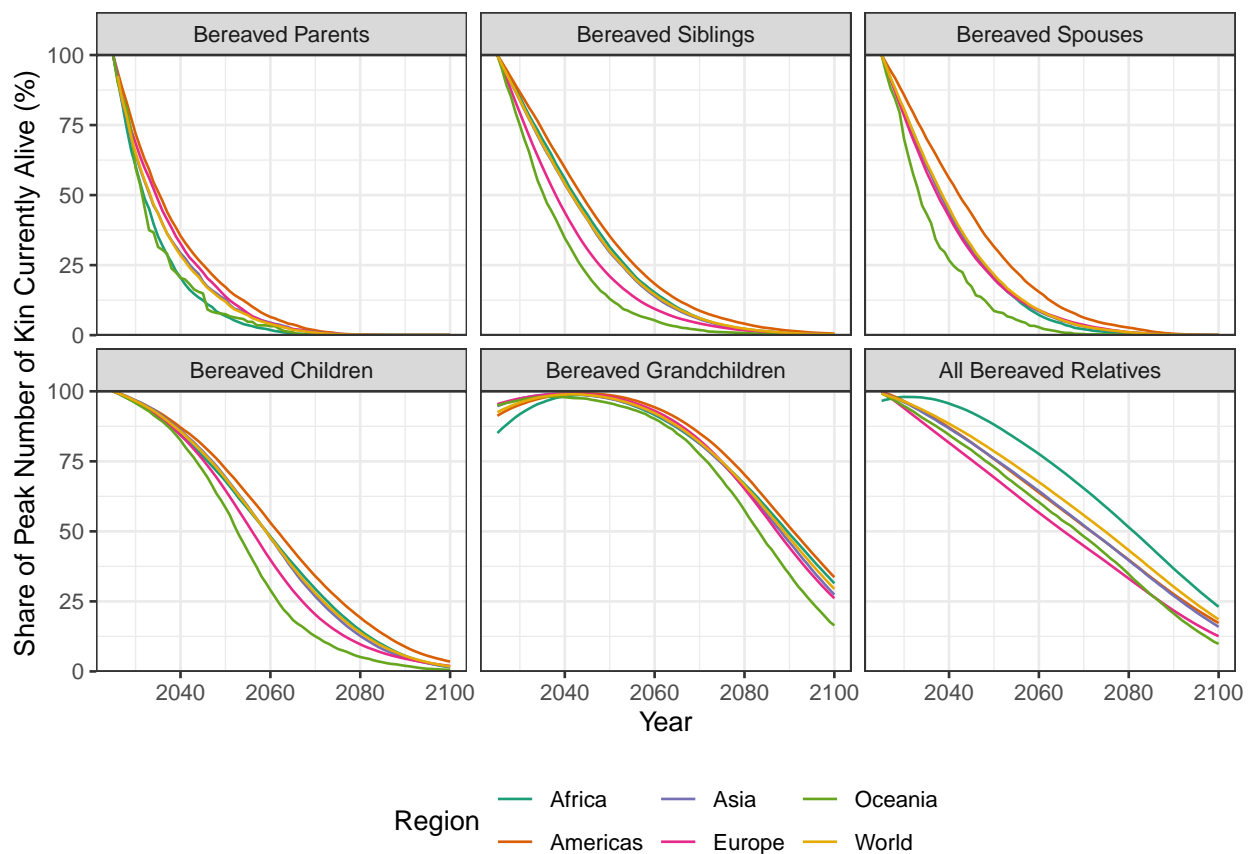


Figure 4.7: Comparison between the rate of change in the total bereaved population and the population growth rate, UNWPP medium fertility scenario

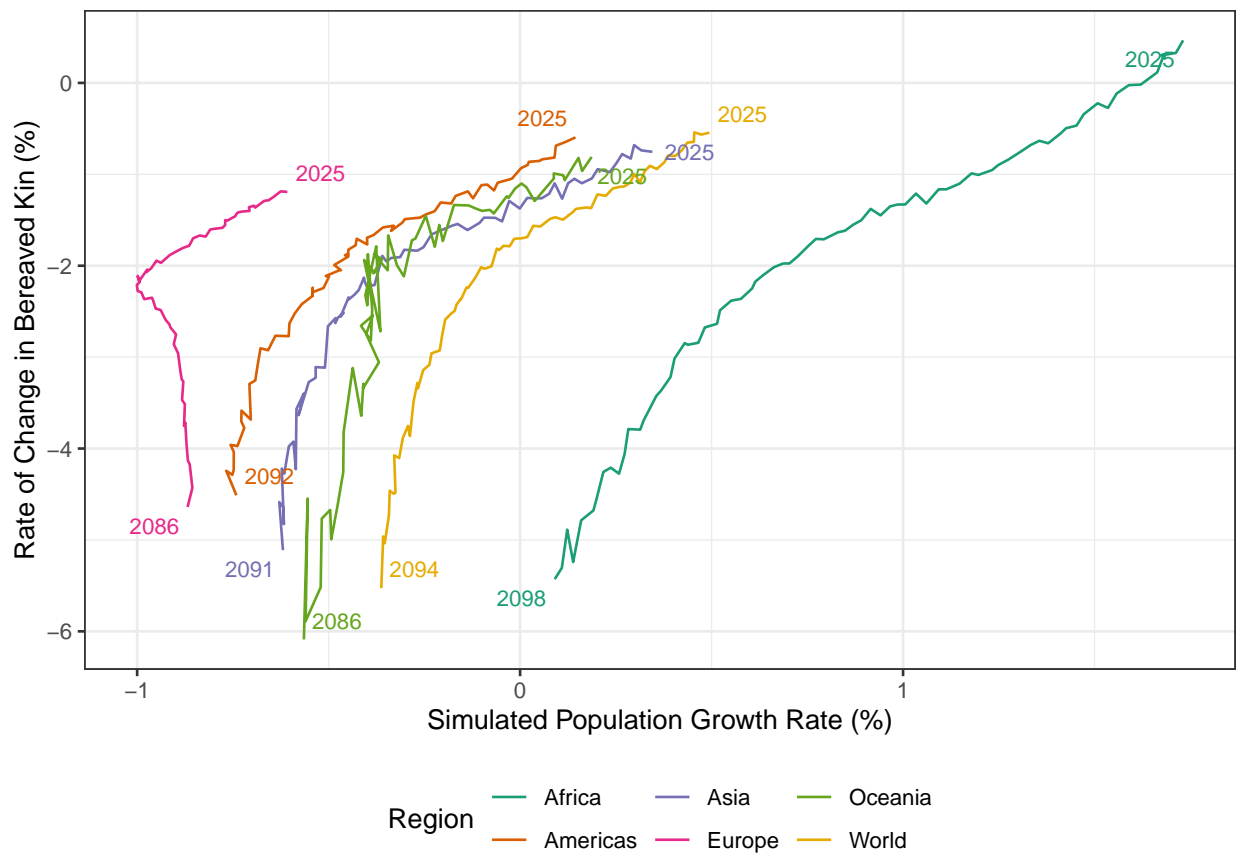


Figure 4.8: Comparison between the rate of change in the total bereaved population and population growth rate in Africa by UNWPP fertility scenario

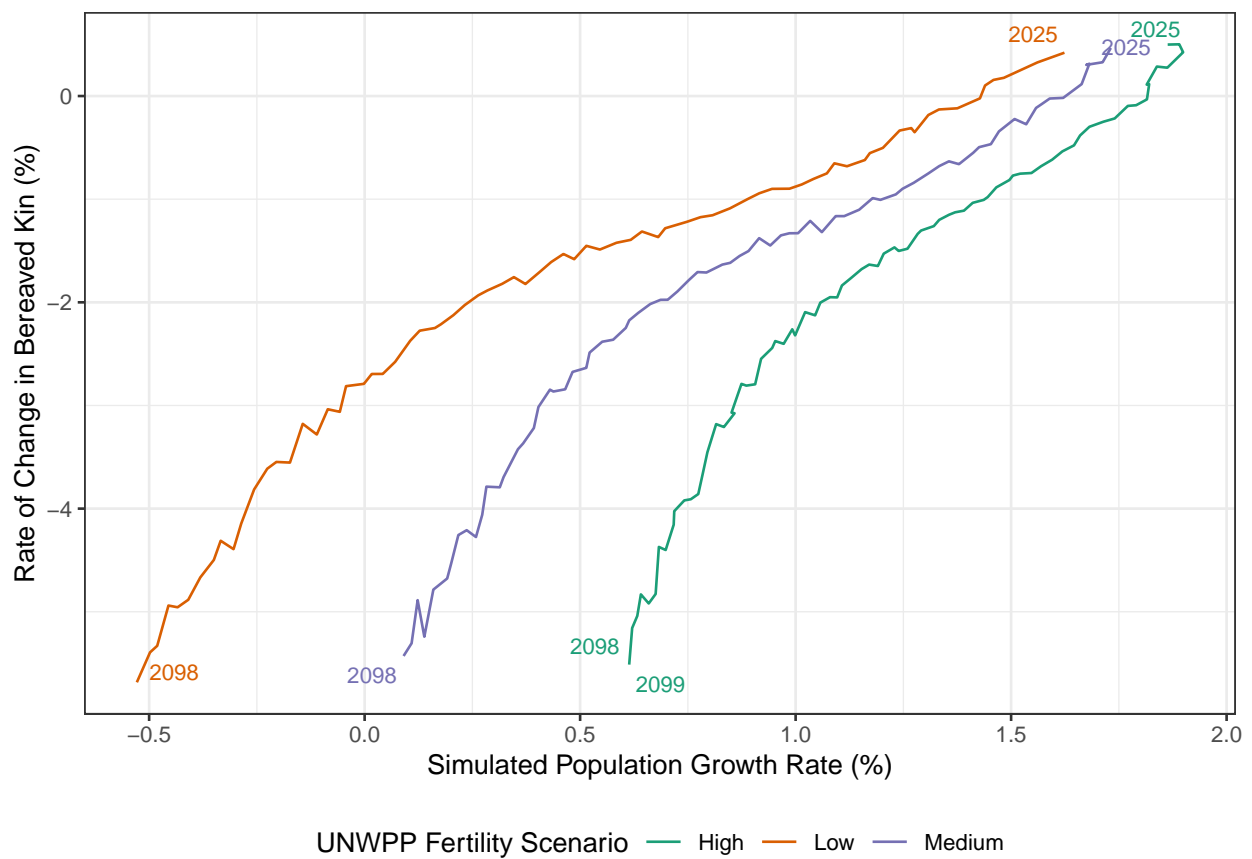


Figure 4.9: Kinship memory, UNWPP medium fertility scenario

(a) By type of kin

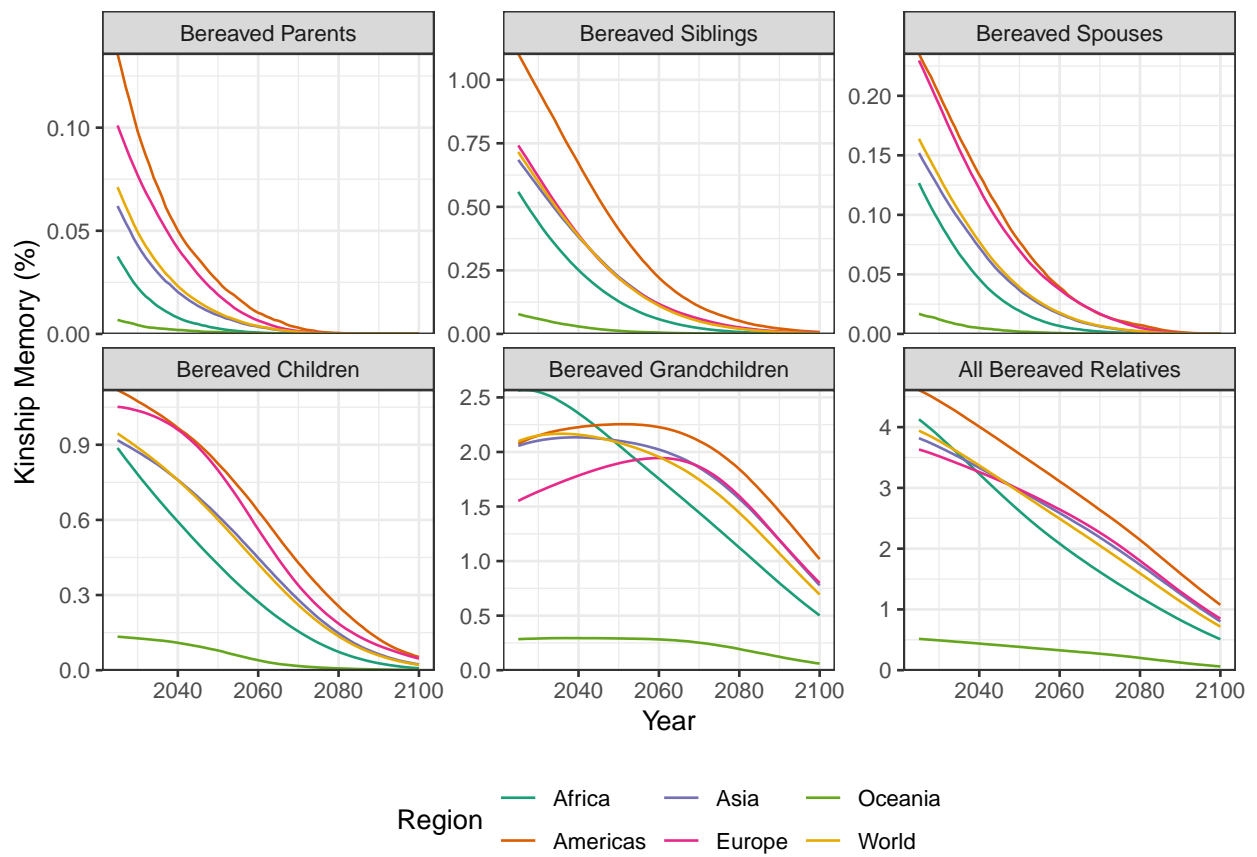


Figure 4.9: Kinship memory, UNWPP medium fertility scenario (continued)

(b) By region

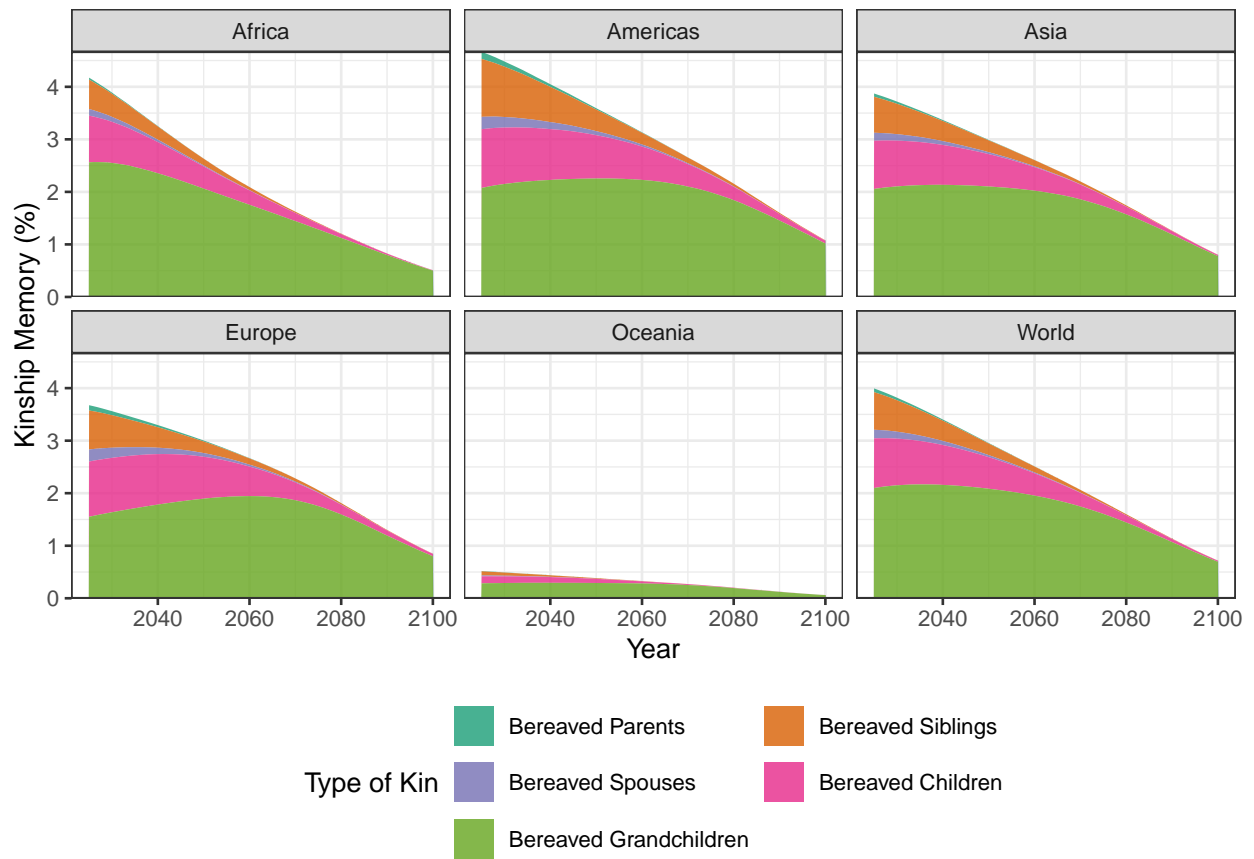


Figure 4.10: Kinship memory for all kin combined by UNWPP fertility scenario

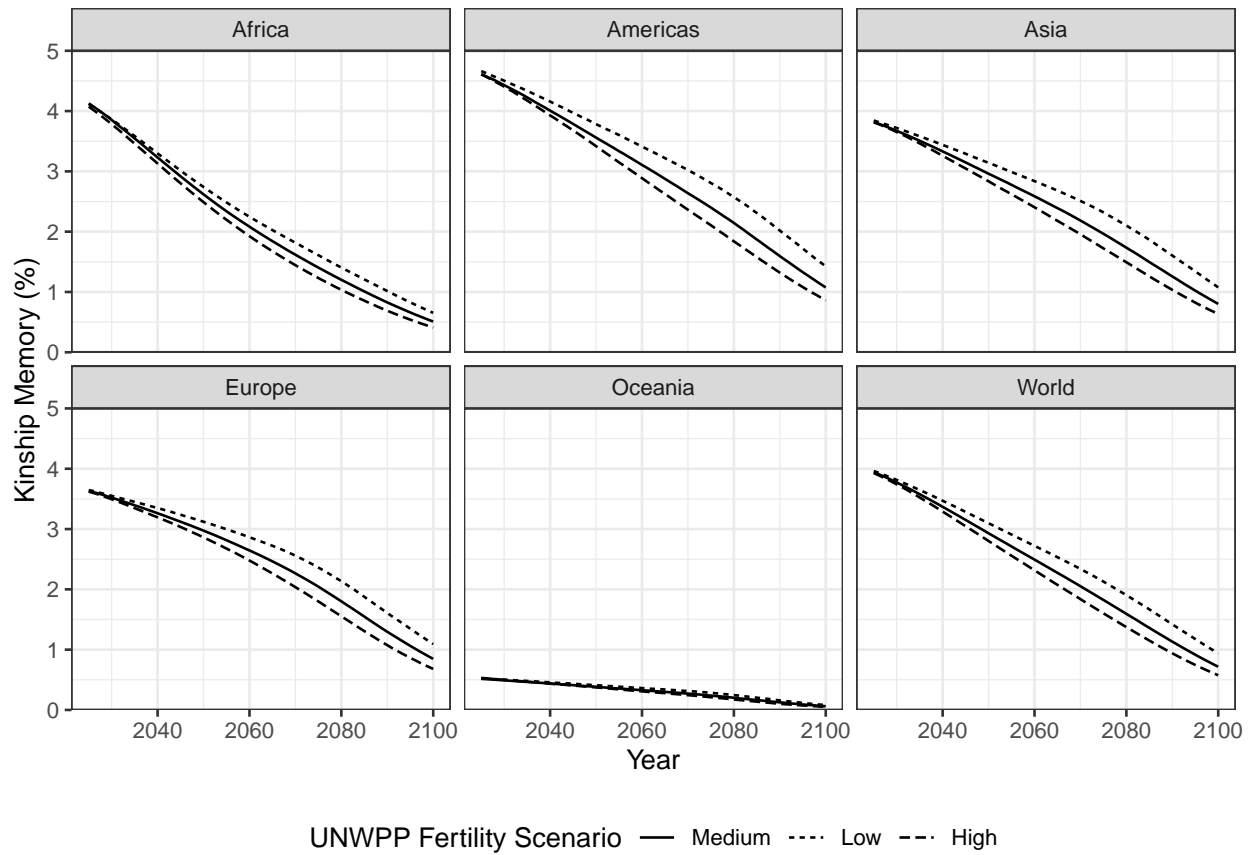


Figure 4.11: Absolute and relative differences in estimates of kinship memory for all types of kin combined between simulation output and estimates adjusted to reflect UNWPP population growth rates in the UNWPP medium fertility scenario

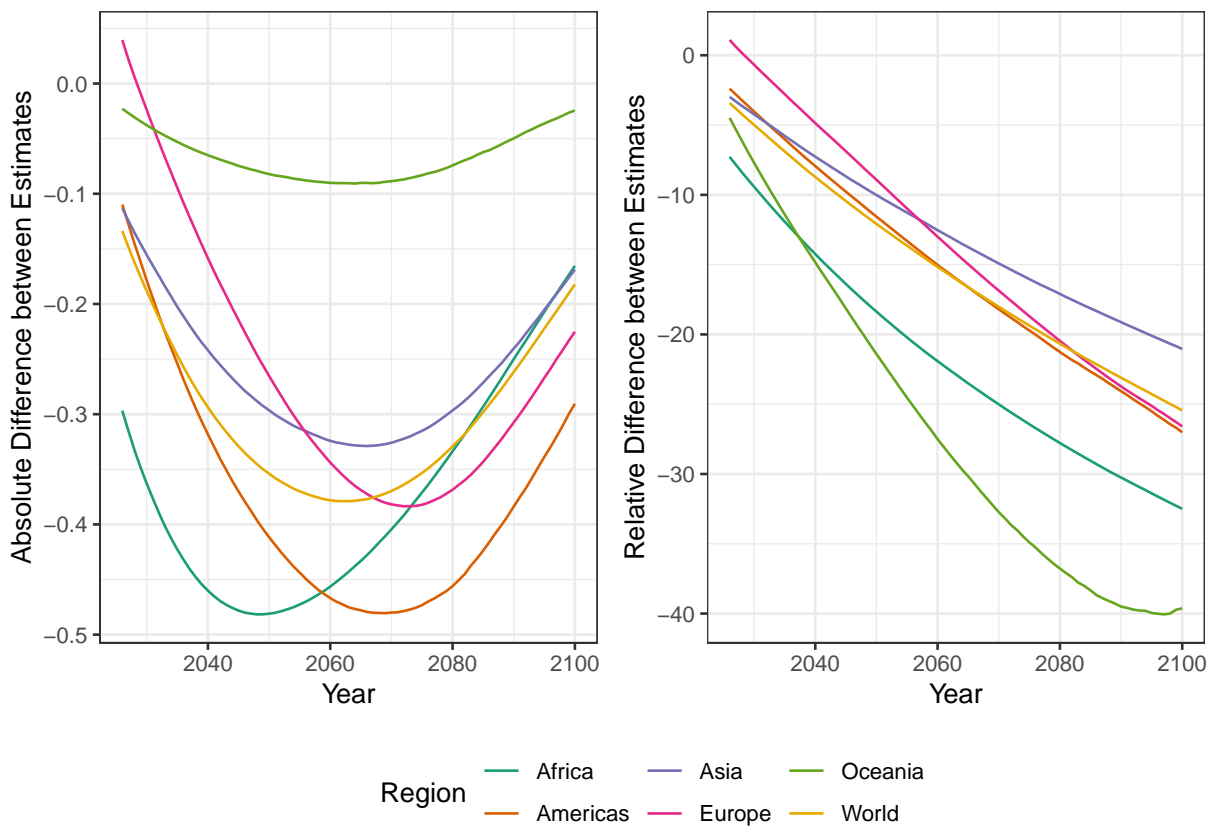


Figure 4.12: Kinship memory for all types of kin combined in selected years, UNWPP medium fertility scenario

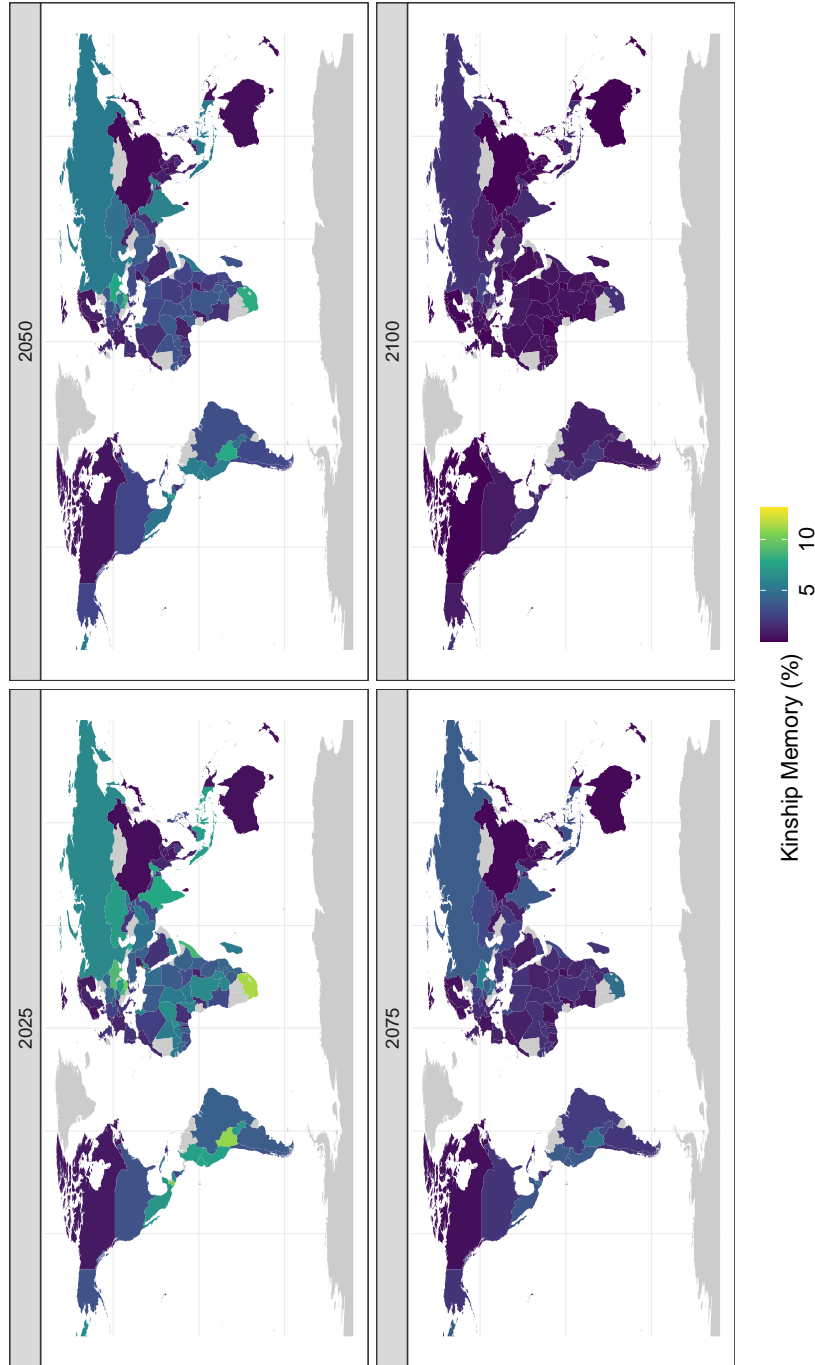


Figure 4.13: Kinship memory for all types of kin combined in 2025 vs. 2100, UNWPP medium fertility scenario

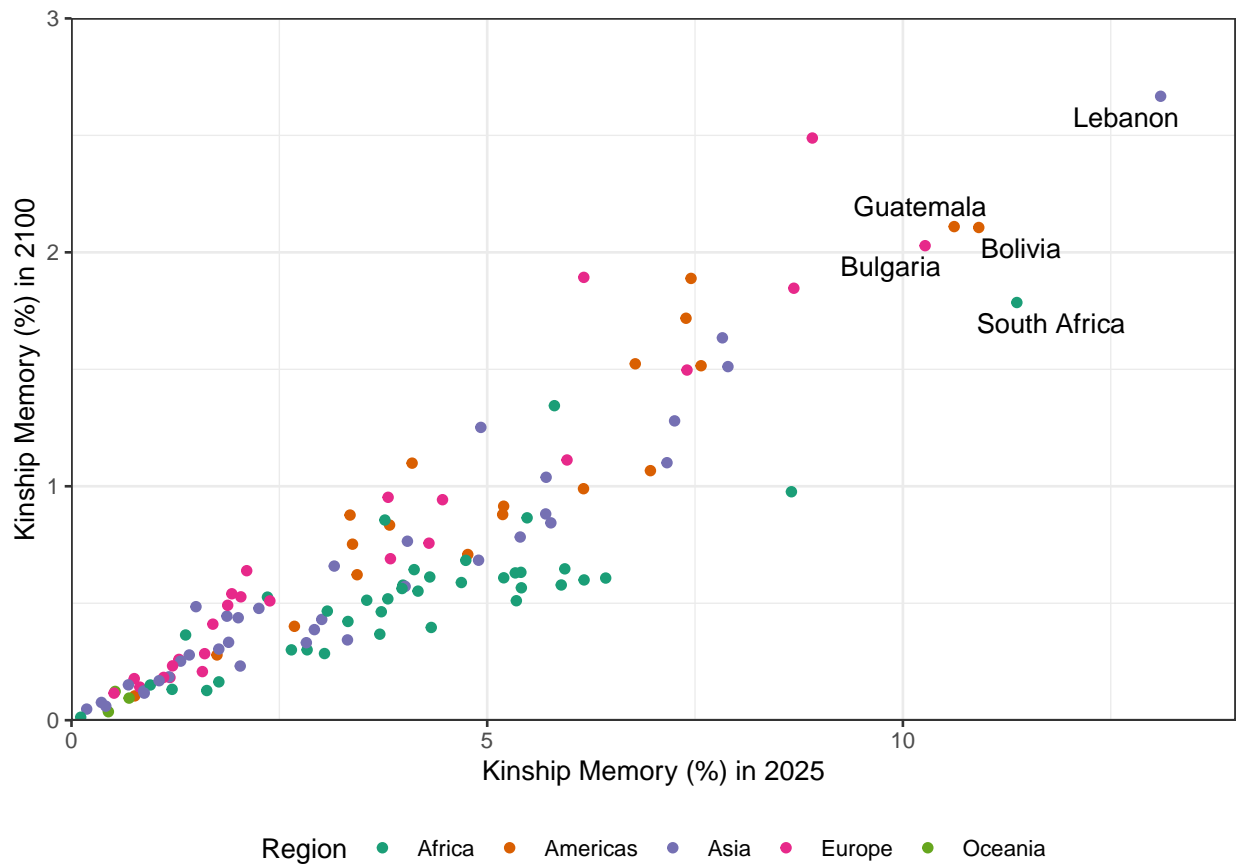
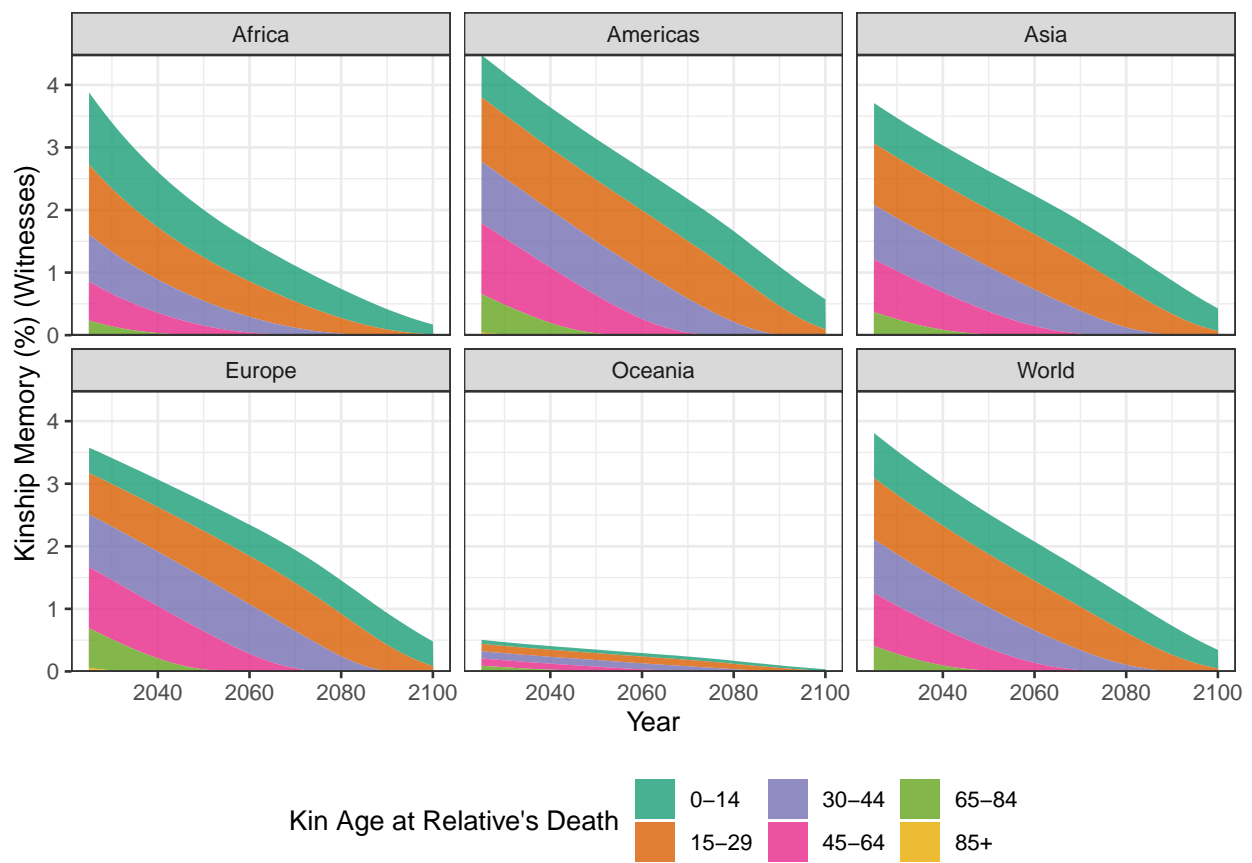


Figure 4.14: Kinship memory for all types of kin combined based on witnesses by age of kin at the time of their relative's death, UNWPP medium fertility scenario



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