Submission for 2024 EPC Annual Meeting

Leaving for life: Using online crowd-sourced genealogies to estimate the migrant mortality advantage for the United Kingdom and Ireland during the 18th and 19th centuries

Elena Maria Pojman,[1] Duke Mwedzi,[2] Orlando Olaya Bucaro,[3] Stephanie Zhang,[4] Michael Y. C. Chong,[5] Monica Alexander,[6] Diego Alburez-Gutierrez[7]

[1] Department of Sociology and Criminology, The Pennsylvania State University, empojman@psu.edu

[2] Department of Global Development, Cornell University, dem327@cornell.edu

[3] International Institute for Applied Systems Analysis, Wittgenstein Centre for Demography and Global Human Capital (IIASA, VID/OEAW, University of Vienna), olayabucaro@iiasa.ac.at

[4] Department of Sociology, University of California, Los Angeles, szhang19@g.ucla.edu

[5] Department of Statistical Sciences, University of Toronto, myc.chong@mail.utoronto.ca

[6] Departments of Statistical Sciences and Sociology, University of Toronto, monica.alexander@utoronto.ca

[7] Laboratory of Digital and Computational Demography, Max Planck Institute for Demographic Research, alburezgutierrez@demogr.mpg.de

Introduction

Across a range of different time periods and contexts, migrants are found to live longer than their counterparts in both the origin and destination countries. This effect has been found to be robust across a range of contexts (Abraído-Lanza et al., 1999; Aldridge et al., 2018; Swerdlow, 1991) despite possible statistical censoring issues such as the undercounting of return migrants (Pablos-Méndez, 1994). One hypothesized reason for the migrant mortality advantage is the healthy migrant effect, which argues that healthy individuals positively select into migration (Razum, 2008). If this is true, it is unclear the *extent* of migrants' mortality advantage over non-migrants, especially as migrant destinations may vary greatly from one another and from the origin country. Additionally, migrants' mortality outcomes may not be independent of family members' mortality outcomes, even among family members who did not migrate. Siblings are especially similar because of shared genetic and environmental factors. Yet, data limitations have typically limited researchers' ability to study how between-family effects may contribute to the migrant mortality advantage.

A common strategy in many migrant mortality studies is to compare migrants with non-migrants in the destination country. However, this strategy risks obscuring the relationship between migration and mortality, as it rests on the assumption that non-migrants in the destination serve as an appropriate comparison group. Instead, we use the online crowd-sourced genealogical dataset Familinx (Kaplanis et al., 2018) to study the migrant mortality advantage during a period of large emigration from the United Kingdom and Ireland from the mid-18th century until the early 21st century. The genealogical structure of the data permits comparison between migrants and non-migrants who are born in the same country, and even between siblings. We test whether this mortality advantage holds for this migration flow using mixed effects models which allow us to distinguish between the effects on mortality that stem from shared health advantages within families versus the direct effect of migration on mortality.

The current study is guided by the following questions: (1) What is the size of the migrant mortality advantage for migrants from the U.K. and Ireland between 1750-1910? (2) How does this mortality advantage vary across migrants' destination? Given the robustness of the migrant mortality advantage in other studies, we hypothesize that after accounting for family effects, migrants from the U.K. and Ireland live longer than those who do not migrate, though there will be variation by destination country.

The rest of the paper is structured as follows. We first review the literature on the healthy migrant hypothesis and discuss potential mechanisms driving the migrant mortality advantage. We discuss the historical context of our case study, i.e., emigration from the United Kingdom and Ireland during the 18th and 19th centuries. We next consider how the migrant mortality advantage may play out at the family level. Then, we describe our data and analytic strategy. We interpret the results from our models and conclude with a discussion of what these results imply for the literature on the migrant mortality advantage, as well as the use of crowd-sourced genealogical data in demographic research.

Background

Mechanisms driving the healthy migrant hypothesis

Studies consistently find a mortality advantage for immigrants in the destination country relative to the native-born population (Guillot et al., 2023; Mehta et al., 2016; Razum, 2008). This result has been explained using the *healthy migrant hypothesis* which suggests that the healthy individuals who already hold a mortality advantage are more likely to migrate (Abraído-Lanza et al., 1999; Feliciano, 2020). Studies of more recent migration flows have argued that this advantage is paradoxical, as migrants tend to be of lower socioeconomic status than individuals in the destination country (Abraído-Lanza et al., 1999; Bakhtiari, 2022). Measurement issues and other data limitations further complicate researchers' ability to understand this relationship. Return migrants may be negatively selected or undercounted in population statistics, leading to numerator-denominator bias and rendering them "statistically immortal" as their deaths are not recorded by the destination country (Pablos-Méndez, 1994; Puschmann et al., 2017). Additionally, observed demographic rates in either the origin or destination country may suffer from migration censorship, i.e., an overrepresentation of individuals who die before they can migrate, artificially decreasing the average age of death for non-migrants relative to migrants (Kasakoff & Adams, 1995; Ruggles, 1992). However, studies still find a mortality advantage even after accounting for many of these potential biases (Abraído-Lanza et al., 1999).

Non-migrants in the origin country are more likely to share early-life conditions and other characteristics that may be associated with their survival outcomes. Comparing migrants to their stayer peers in the origin country also permits the examination of alternative mechanisms that may shape the migrant mortality advantage, such as the role of unobserved factors shared between

siblings (e.g., early-life environment or parental resources) which may contribute to similarities in mortality between migrants and their non-migrant siblings. Table 1 shows two common approaches of studies investigating the migrant mortality advantage, including data requirements and interpretations for these approaches. The first, more common approach is to compare migrants to non-migrants in the destination country, and the second approach is to compare migrants to non-migrants from the same origin country.

Table 1 Migrant mortality comparison approaches

Comparison	Data required	Interpretation	Example studies
Migrants and origin country non-migrants	Data from both the origin country and the destination country	There is a mortality advantage for migrants over their peers in their origin country; migrants deviate from the baseline mortality in their home countries	Migrants tend to live longer than their stayer relatives (Mourits & Puschmann, 2023); Norwegian migrants were negatively selected from urban areas and experienced low returns to migration (Abramitzky et al., 2012)
Migrants and destination country non-migrants	Data from the destination country	There is a mortality advantage for migrants over individuals in the destination country, though it is not clear if this is due to migration or selection	The mortality advantage is less certain when considering early 20th century white migrants from Southern and Eastern Europe (Bakhtiari, 2022); the Latino mortality paradox 11/21/2023 11:48:00 AM

Though migrants may be healthier than their counterparts in the destination country, it is less clear how much healthier they are than those who do not migrate, i.e., the family and neighbors they leave behind. Migrants are not drawn from the population at random and could have lived longer regardless of whether they migrated. On one hand, emigrants may be positively selected on a host of factors that are typically associated with a longer life: socioeconomic status, health status, or survival to migration age, for example. On the other hand, emigrants may have moved due to a lack of economic and social opportunities in their home country, and thus benefitted from better conditions in their destination which increased their lifespan.

Scholars have argued that mortality differences that emerge due to migration are driven by conditions in the destination rather than the origin country (Hatton, 2021). Recent research confirms this argument; immigrants to the United States in the early 20th century saw a mortality

*dis*advantage compared to non-migrants because of higher infectious disease exposure in U.S cities (Bakhtiari, 2022). As such, the mechanisms behind the migrant mortality advantage are not certain. It may be that migrants are healthier and otherwise more positively selected compared to their peers, or, alternatively, migrating allows individuals to avoid poor conditions in their home countries that would have negative effects on their mortality.

Migrant mortality advantages and family effects

Individuals are not randomly selected into migration. Rather, selection into migration occurs at both the population level, where some individuals are more or less likely to migrate based on their socioeconomic circumstances, and within families, as siblings may have different abilities, economic opportunities, or familial responsibilities (Abramitzky et al., 2012; Mourits & Puschmann, 2023). For example, individuals who do not expect to inherit their family's land, by virtue of gender or birth order, may have an increased propensity to migrate .

If migrant siblings possess mortality advantages because they are positively selected from the population, their non-migrant siblings may be similarly advantaged, as health-protective factors are correlated within families (Mourits & Puschmann, 2023). Siblings are more similar to each other than they are to random members of the population, likely because of shared genetic and environmental factors (Piraino et al., 2014), though evidence regarding whether the socio-environmental or genetic component is more influential for mortality is mixed (Cournil & Kirkwood, 2001; Gudmundsson et al., 2000; Piraino et al., 2014). Families may select the healthiest member to migrate as a risk diversification strategy (Stark & Bloom, 1985). Yet, siblings compete for scarce resources amongst themselves (Donrovich et al., 2014; Lam & Marteleto, 2008), which could diminish the magnitude of shared mortality advantages between siblings. Evidence for the effect of sibling size on mortality is mixed (Baranowska-Rataj et al., 2017; Sonneveldt et al., 2013), though overcrowding due to having many siblings may be a key mechanism driving poor outcomes, especially for higher parity siblings (Hatton & Martin, 2008). In light of these findings, it is important to consider both the role of unobserved factors shared between siblings and individual characteristics when considering the relationship between migration and mortality during this time period.

Historic emigration from the United Kingdom and Ireland

Scholars have argued that the Demographic Transition together with the Industrial Revolution set the stage for mass migration (Hatton & Williamson, 1994; Richards, 2018). In the United Kingdom, mortality decreased sharply, combined with stable fertility until the mid-nineteenth century and declining fertility thereafter, resulting in a large population increase as the country moved through the second and third stages of the Demographic Transition (Friedlander & Okun, 2022). This population growth exceeded agricultural labor demands, especially during a time of increasing agricultural productivity (Richards, 2018). Coupled with rapid urbanization during the Industrial Revolution from 1750–1850, urban areas were subject to overcrowding, poor sanitation, and poor health conditions, resulting in decreased lifespan, particularly for low socioeconomic status individuals (Taylor, 1988).

Emigrants moved for a variety of reasons. Economic circumstances worsened for many, with higher rent and declining access to land (Hatton & Williamson, 1994; Horn, 1998; Richards, 2018). Emigration acted as a "safety valve" in the face of overcrowding and few economic opportunities, relieving the pressure caused by higher populations due to the Demographic Transition (Hatton & Williamson, 1994). Migrants' social networks also encouraged further migration: as one family member migrated, many followed behind. The emigrants themselves were among a group most poised to benefit from migration: typically young, single, unskilled men or young couples with small children (Hatton & Williamson, 1994; Horn, 1998; Thompson, 2009; Tomlins, 2001). Yet, it is important to note that many migrants were coerced to move, including convicts and indentured servants (Richards, 2018; Tomlins, 2001).

From the late 18th to the early 20th century, millions of Europeans emigrated, largely unencumbered by the restrictive immigration policies that exist today. Colonial relationships with overseas territories facilitated mass migration for Europeans to colonies in North America, Australasia, and Africa. Emigrants from the United Kingdom accounted for a large percentage of this flow, with the vast majority settling in the United States, Canada, Australia, and New Zealand. The sheer size of this flow, combined with the lack of legal restrictions on their immigration to these countries, makes it well-suited to studying differences between migrants and non-migrants (Hatton, 2021). The varied destinations of the flow also make it possible to test the migrant mortality advantage in different contexts.

Current study

We focus on the flow of migrants from the United Kingdom and Ireland to Canada, the United States of America, South Africa, Australia, and New Zealand for several reasons. Migrants moving from the United Kingdom and Ireland made up a large percentage of the flows of this time period (Hatton, 2021). This period is also unique because the U.K.'s colonial relationship with its territories facilitated virtually free international movement for European migrants on a scale that is no longer possible due to legal and immigration restrictions. Population growth during the Demographic Transition combined with the increased urbanization and scarcity of land due to the Industrial Revolution also incentivized mass migration during this period (Hatton & Williamson, 1994; Richards, 2018). As such, this period is an ideal case study for studying mortality differences between migrants and non-migrants as there was less selection of migrants on characteristics such as socioeconomic status and education level (Hatton, 2004, 2021).

We contribute to the continued debate on the migrant mortality advantage by using a novel genealogical dataset that can identify historic migration flows and transnational kin ties. We explicitly account for unobserved similarities between siblings that may shape the magnitude of the migrant mortality advantage. Our modelling strategy allows us to identify whether the migrant mortality advantage is heterogeneous by destination. Where other studies are constrained by data challenges, Familinx allows us to compare migrants to non-migrants in the sending country rather than the destination country. Finally, by analyzing historical data, we can measure the migrant mortality advantage across time rather than cross-sectionally.

Data & Methods

Data & Sample

Data for the current study come from Familinx, a novel genealogical dataset with information on the timing and location of vital events such as birth and death for over 86 million individuals (Kaplanis et al., 2018). These data are crowdsourced in the sense that they represent the work of amateur genealogists to reconstruct family lineages across several centuries and world regions. Genealogical data have been used to investigate a variety of demographic outcomes (Chong et al., 2022; Cozzani et al., 2023; Gavrilov et al., 2002; Piraino et al., 2014), and represent an opportunity for demographers to answer long-discussed questions about the nature of inter- and intragenerational demographic processes (Alburez-Gutierrez et al., 2019). Individuals born in the U.K. and Ireland are well-represented in Familinx, and the data's genealogical structure is better

suited for studying migration than similar family reconstructions using parish records which suffer from migration censorship (Ruggles, 1992). This genealogical structure also allows us to identify transnational ties between kin and thereby account for unobserved similarities between siblings.

Though these data were scraped from Geni.com, there were several instances of reporting errors and other issues which necessitated extensive data cleaning and treatment before analysis. For example, some profiles in the dataset have missing information for country of birth or death; some records have implausible values for variables such as age at death; and some birth and death location names varied by language and changed over time. We outline in detail our data preparation procedure, including our treatment of missingness in key variables, in Appendix A of the Online Supplement. For transparency and reproducibility, we provide replication materials for the entire data cleaning process at https://osf.io/b87t6/. Despite the biases inherent in crowdsourced genealogies (Calderón Bernal et al., 2023; Stelter & Alburez-Gutierrez, 2022), and the messiness of the raw data, we took steps to ensure transparency in data processing and in the reliability of our data and results.

The initial sample consisted of over 86 million individuals, with parent-child ties for 43 million individuals. Because our interest is only in individuals who were born in the United Kingdom and Ireland between 1735-1895, we reduced our analytic sample to 98,057 profiles (see Figure A1 in the Online Supplement for a visualization of the data cutting process). We identify all individuals with complete information (year of birth and death, location of birth and death, and gender) who were born in the United Kingdom and Ireland between 1735-1895. We impute missing date and location information for birth and death using baptism and burial information, respectively. Due to data limitations, we consider return migrants as non-migrants; however, given the period and destinations we analyze, there are likely few such cases. We limit the maximum age at death to 110 to avoid including profiles with implausibly long lifespans whose information was likely entered erroneously. The sample consists of individuals who died either within the U.K. and Ireland (N = 62,076) or in Canada (N = 5,068), the United States (N = 18,381), South Africa (N = 1,185), Australia (N = 8,600), and New Zealand (N = 2,747). The data cleaning and imputation process is further detailed in Appendix A of the Online Supplement. Our final sample consists of N = 98,057 individuals (N = 35,981 migrants) who lived to at least age 15.

Measures

We measure the outcome of age at death by subtracting one's birth year from their death year. While the data does not allow us to measure migration directly, individuals whose birth is recorded in the United Kingdom or Ireland and death is recorded in Australia, New Zealand, South Africa, the United States, or Canada are considered migrants for the purposes of this study, as we infer that they would have migrated to their eventual death location. Individuals whose birth and death are recorded in the United Kingdom or Ireland are considered non-migrants, as we infer that they died in the same country where they were born and thus did not migrate.

To account for potential confounding between age at death and migration status, we control for gender and birth cohort, the latter measured as a categorical variable in 10-year intervals. We also include controls for the number of siblings, coded as a categorical variable (0, 1, 2, 3-5, 6+). To account for sibling effects, we construct a family ID for each profile using the unique ID of one's mother, or father's ID if mother's is missing. Siblings are defined as individuals who share one or more parent ties, and we link individuals with their siblings. Individuals without recorded siblings are given an individual ID. Table 2 shows descriptive statistics of selected variables.

Table 2 Sample descriptive statistics

Variable	Mean/Prop.	SD	Min	Max
Number of siblings	1.604	2.324	0	21
Age at death	65.870	18.272	15	109
Migrant	0.367	–	–	–
Proportion male	0.606	–	–	–

Note: N = 98,057

The migration and mortality literatures recognize the influence of socioeconomic status on one's propensity to migrate and age at death, respectively (Clouston & Link, 2021; Lindstrom & Lauster, 2001; Link & Phelan, 1995). However, as our data consists of only demographic variables such as date and location of birth, date and location of death we cannot explicitly control for socioeconomic factors. This is a limitation of our study that we discuss in further detail below.

Analytic Strategy

To examine the migrant mortality advantage for those born in the United Kingdom and Ireland between 1735-1895, we estimate age at death using mixed effect models that incorporate random effects to capture unobserved similarities between siblings. We first examine mortality differences between migrants and non-migrants (Model A; migrant effects), and then estimate differences by one's country of death (Model B; destination country effects), as we infer this to be their migration destination. We interact these variables (migrant and country of death, separately) with birth cohort to account for different propensities to migrate across time. The family random effects account for unobserved factors within families that are shared by siblings which may be associated with the possibility of the effect varying over time (Abramitzky et al., 2012). Family random effects have been used similarly in other studies of the migrant mortality advantage (Abramitzky et al., 2012; Cozzani et al., 2023; Mourits & Puschmann, 2023). Though survival models are common in mortality research, we did not implement them due to concerns about how the quality of our data would affect the assumptions of hazard models. In addition, since hazard models are designed for incomplete data with right censoring issues, they were not necessary for our analyses as all observations within our dataset are deceased individuals who have completed the life course. As such, we use linear regression models which we found to provide a better fit to our data.

Results

A migrant effect?

We estimate the relationship between migration and age at death using mixed effect regression models. Results are presented as average marginal effects (AME) in figures, which allows us to interpret our findings as the effect of being a migrant (versus a non-migrant) on average in our sample, and predictions are based on the observed values of the predictor and control variables for each individual (Mize, 2019). Additionally, because the average age at death in our sample is likely higher than the true average age at death for this population, AMEs are more appropriate than regression coefficients or marginal estimates.

Figure 1 demonstrates the AME of being a migrant versus a non-migrant (Model A1) across birth cohort. We include the full regression estimates in Table B1 of the Online Supplement. While there is fluctuation in the size of the AME, it remains positive and significant for every

cohort in our sample, indicating that migrants had a mortality advantage over their non-migrant peers across cohort.

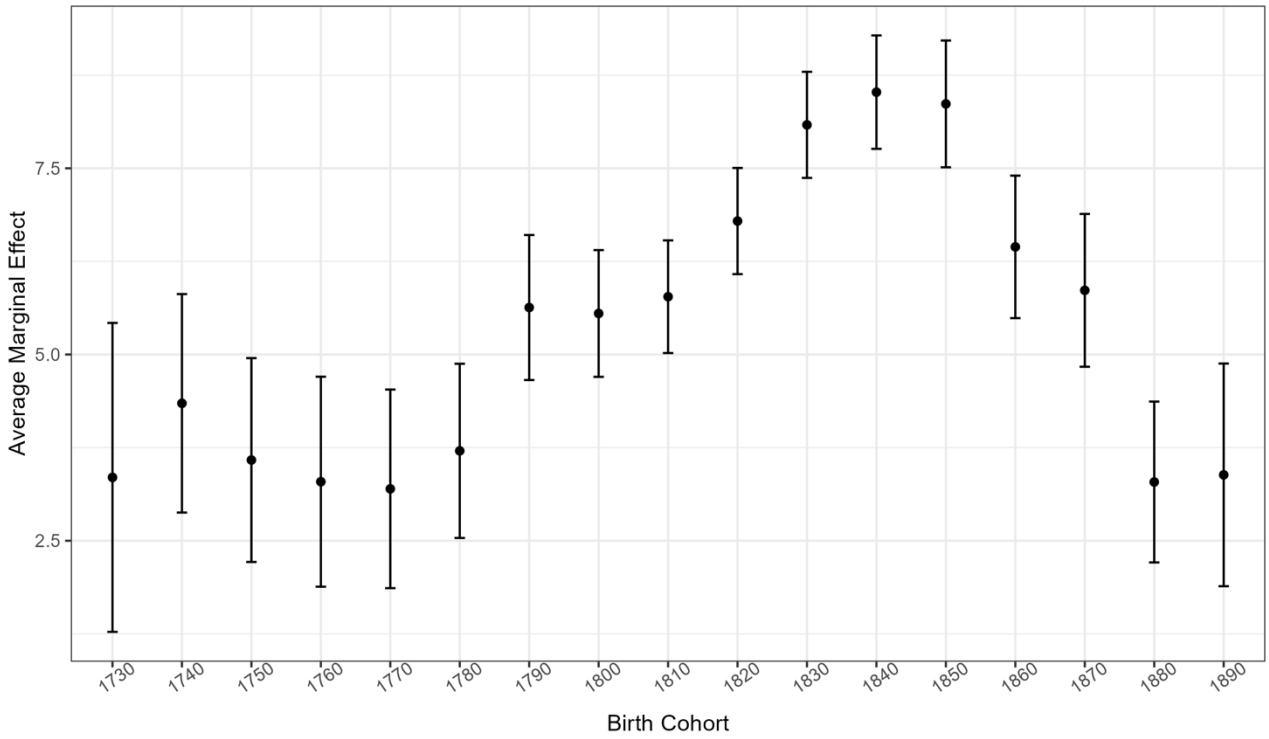


Figure 1 Average marginal effect of migration on age at death, across birth cohort (Model A1).

Next, we turn to the predicted contrasts by destination country (Model B1; see Figure 2). Here, the AMEs can be interpreted as the effect of migrating to a specific country versus not migrating at all. We include the AME from Model A1 as a solid grey line and 95% confidence intervals as dotted grey lines to demonstrate the contrasts between the main migrant effect and individual country effects. When comparing migrants to non-migrants overall in model A1, we find an AME of 5.9 years, 95% CI [5.7, 6.2] for individuals who migrate. However, this model masks heterogeneity by destination country. When disaggregating by destination country in model B1, we find that the AME of migrating ranges from 2.6 years, 95% CI [1.1, 4.0] in South Africa to 8.7 years, CI [6.3, 11.2] in New Zealand. The AMEs for all destinations are positive and highly statistically significant ($p < 0.001$), suggesting a clear mortality advantage for individuals who migrate. Comparing Models A1 and B1 shows that while Australia and the United States of America have similar estimates to the overall migrant AME, Canada and New Zealand have AMEs

higher than the overall AME, and South Africa's is lower. We return to these findings in the discussion.

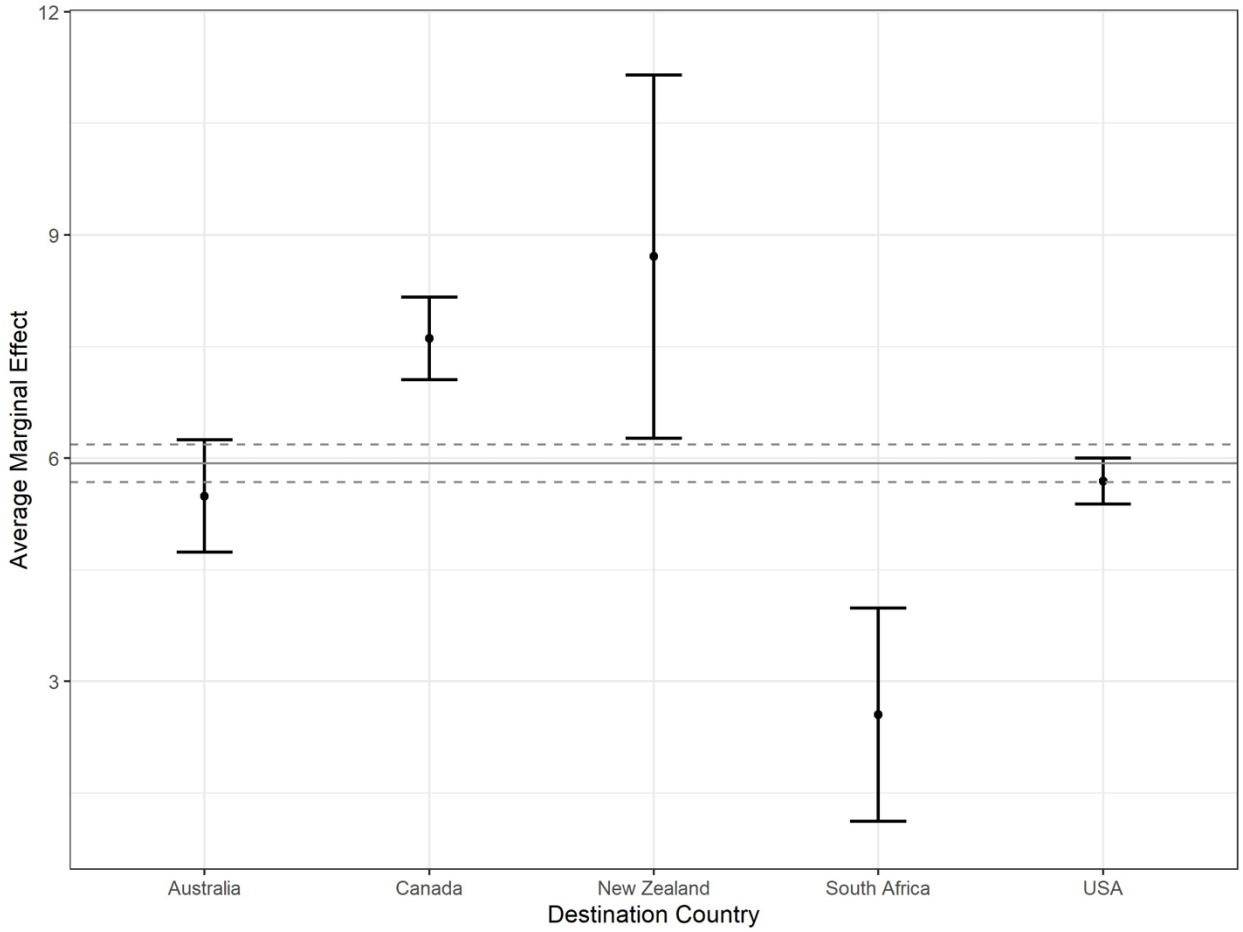


Figure 2 AME of migrating on age at death by destination country (Model B1) in black with 95% CIs. AME for Model A1 (migrant versus non-migrant) is shown by the solid grey line, with 95% CIs as dashed grey lines.

Supplementary models

We estimate several supplementary models to be sure of the robustness of our results. We first limit our sample to only individuals with at least one sibling in the data (N = 49,263). Figure 3 indicates substantively similar results as in the previous models (see Table B2 in the Online Supplement for regression estimates). The AMEs from Model A1 are shown in light grey. We interpret the similarities between the set of models as an indication of model robustness, as well as that the migrant mortality effect is generally stronger when looking at those with siblings,

including sibling groups with mixed migration statuses. Table B3 in the Online Supplement shows AMEs for Models A1, A2, B1, and B2.

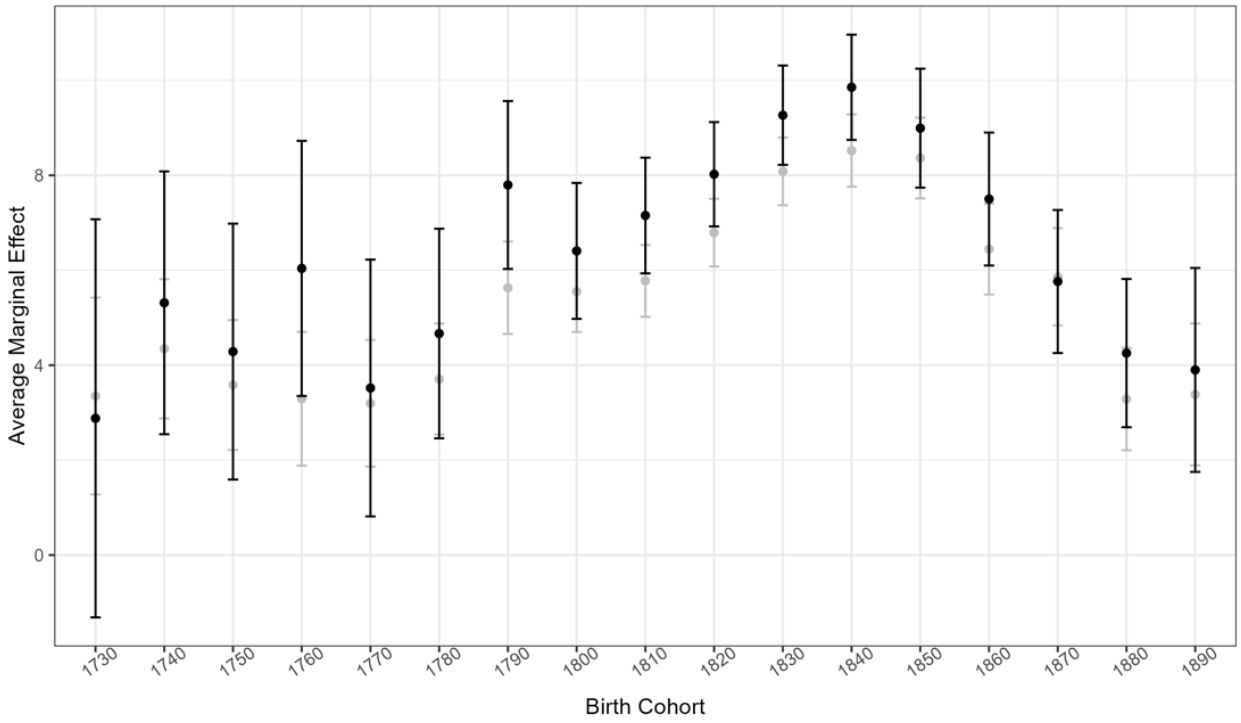


Figure 3 Average marginal effect of migration on age at death, across birth cohort (Model A2) shown in black. AMEs for full sample (Model A1) in grey.

The AMEs for each destination country in the siblings-only sample can be seen below (Model B2; see Figure 4). We again include the AME from Model A2 as a solid grey line and 95% CIs as dotted grey lines. We note that the findings are substantively similar to the main models, though the AMEs are larger.

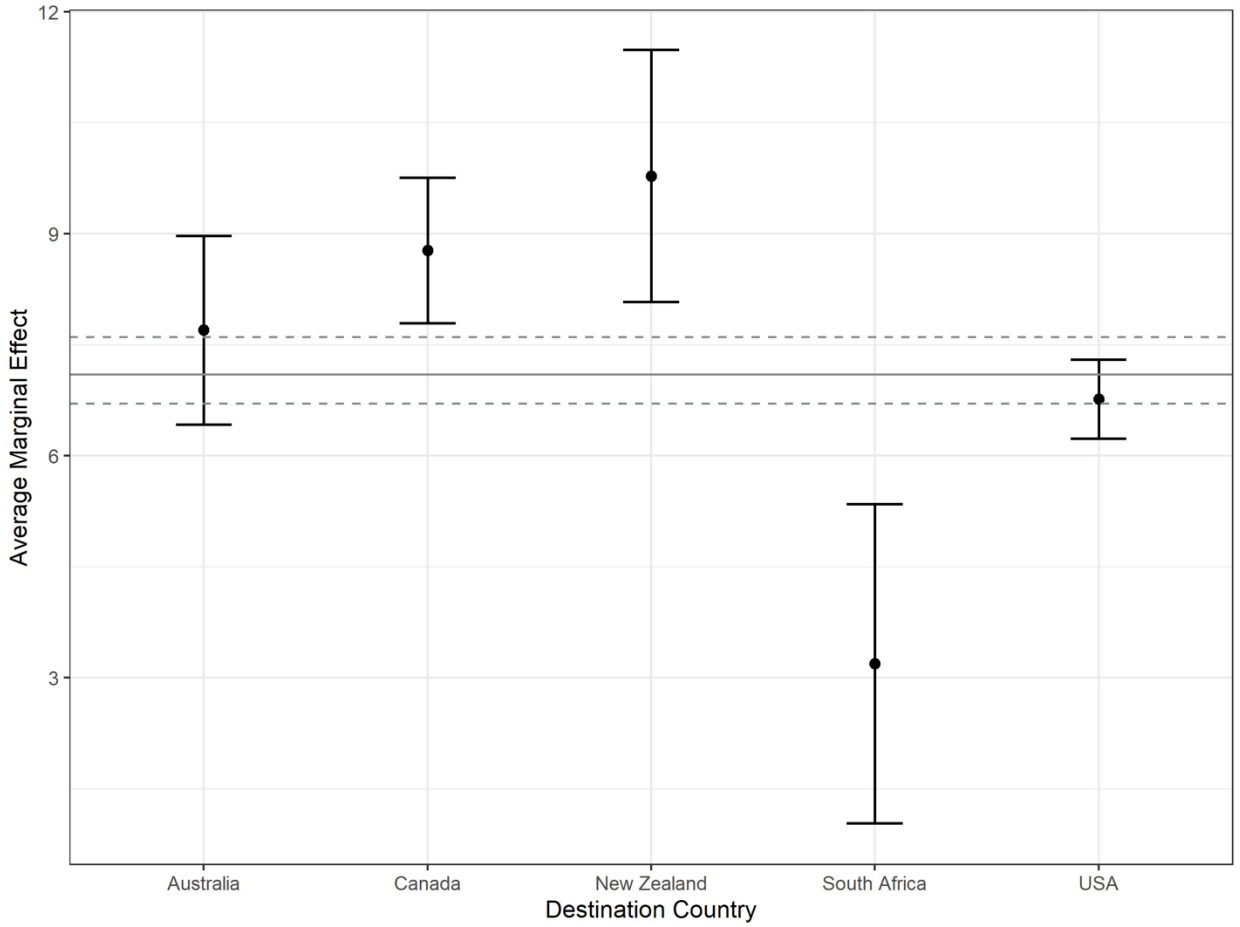


Figure 4 AME of migrating on age at death by destination country (Model B2) in black with 95% CIs. AME for Model A2 (migrant versus non-migrant) is shown by the solid grey line, with 95% CIs as dashed grey lines.

In the next set of supplementary models we repeat our analyses, conditioning on survival to alternate ages, i.e., 0, 5, 10, 20, 25, …, 50. In doing so, we attempt to correct for the fact that the migrant mortality advantage may vary across age (Guillot et al., 2018). Full regression estimates are available upon request. In the migrant effect models (Model A3; see Figure 5), we find that the AME of being a migrant is consistent for ages below 15. The AMEs decrease as the age cut-off increases, though they are all positive and statistically significantly different from zero, indicating that the migrant mortality advantage is robust across sample specification.

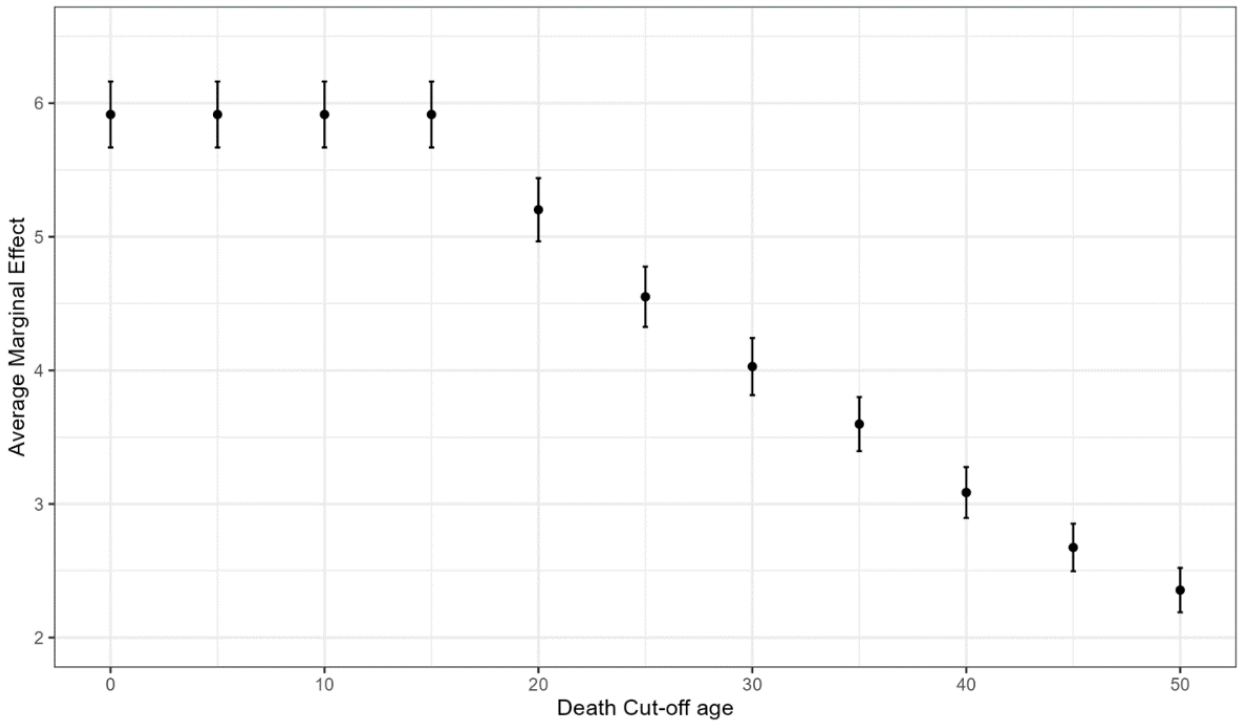


Figure 5 AMEs of migration on age at death across alternate age cutoffs (Model A3).

Similarly, when looking at differences by migrants' destination country (Model B3; see Figure 6) we find a similar pattern: consistent AMEs of migrating under the age of 15 that decrease as the age cut-off increases. These AMEs are positive and significantly different from zero (save for age cut-offs above age 25 among South African migrants), indicating that our findings are robust across age cut-off, though the estimated extent of the migrant mortality advantage does vary.

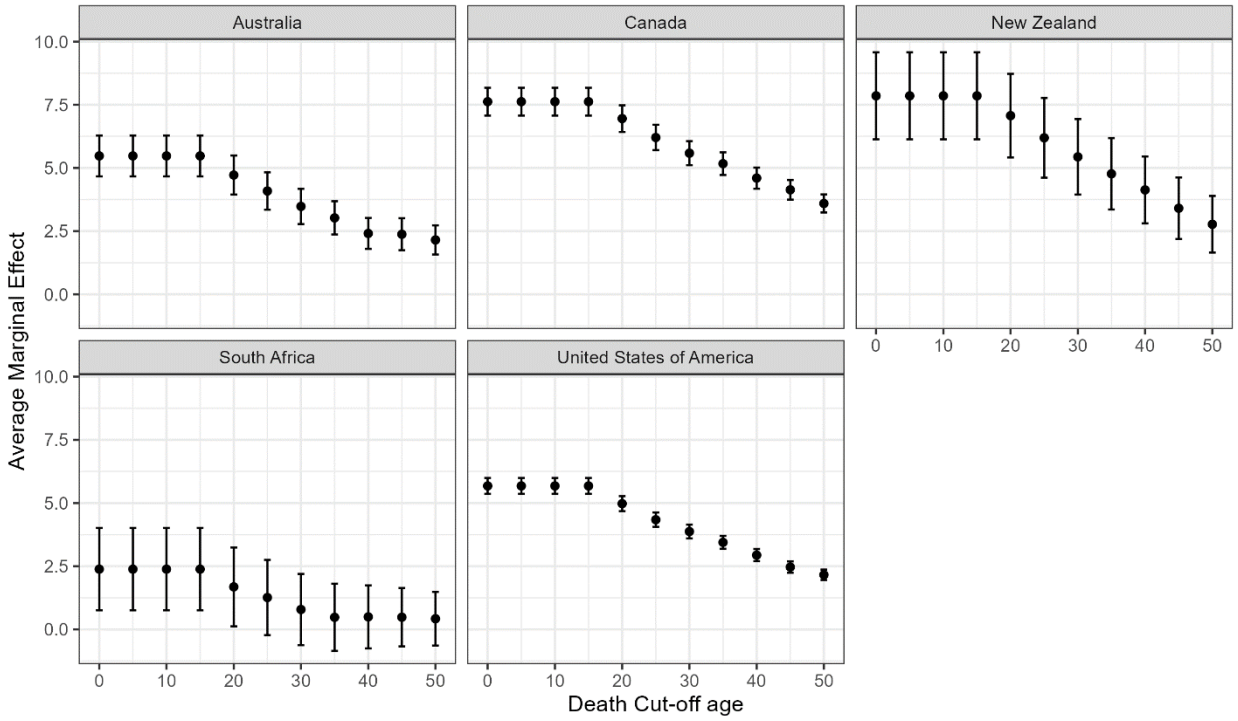


Figure 6 AMEs of migration on age at death across alternate age cutoffs and disaggregated by destination country (Model B3).

Discussion

Using the case of emigration from the United Kingdom and Ireland to the United States, Australia, New Zealand, Canada and South Africa during the 18th and 19th centuries, we test the migrant mortality advantage hypothesis in historical migration flows. Using mixed effect regression models, we find that migrants live 5.9 years, 95% CI [5.7, 6.2] longer on average than non-migrants. The gap is heterogeneous by destination country, ranging from 2.6 years, 95% CI [1.1, 4.0] in South Africa to 8.7 years [6.3, 11.2] of difference in New Zealand. These findings are robust to alternate age cut offs and sample specifications. Taken together, this suggests that the migrant mortality advantage is robust across birth cohort, even after accounting for unobserved similarities within families and comparing migrants to non-migrants in the United Kingdom and Ireland. We also highlight the possibility for online crowdsourced genealogical data to contribute to demographic research.

Our findings build on a long tradition of literature focused on understanding the existence and extent of the migrant mortality advantage across contexts. While the literature originally focused on the paradoxical mortality advantages found among Hispanic migrants living in the

United States (Abraído-Lanza et al., 1999; Pablos-Méndez, 1994; Palloni & Arias, 2004), over time it has come to describe a range of the experiences of migrant groups in various destination countries, ranging from historical flows (Mourits & Puschmann, 2023; Puschmann et al., 2016) to more recent ones (Andersson & Drefahl, 2017; Guillot et al., 2023; Helgesson et al., 2019; Mehta et al., 2016). These studies have tended to focus on non-migrants in the destination as their comparison group. We argue that it is necessary to understand the extent to which migrants hold a mortality advantage over their compatriots left behind – especially so as many of the ones left behind are family members such as siblings who provide a stronger counterfactual group for the existence and extent of the migrant mortality advantage.

Like much of the literature (Feliciano, 2020), we confirm the existence of a migrant mortality advantage for migrants from the United Kingdom and Ireland during the 18th and 19th centuries. We also find that this advantage ranges between migrants' country of destination. This variation may be evidence of positive selection *among* migrants. For example, some destination countries such as Australia and New Zealand saw more highly skilled immigration while migrants to the United States and Canada tended to be more unskilled (Haines, 1997; Hatton, 2021; Murdoch, 2004). Yet, relative to the native-born, migrants from the U.K. and Ireland to the United States tended to earn more even soon after arrival (Abramitzky et al., 2014). Reasons to migrate changed across time as well: what was originally the forced migration of convicts to Australia later became a flow of migrants seeking land and wealth in the Gold Rush (Murdoch, 2004). Another interpretation is that distance played a role in shaping the extent of the mortality advantage. Migrant survival advantages are stronger the further they move (Puschmann et al., 2016, 2017), which may be because the journey from the U.K. and Ireland to Australia and New Zealand was much longer than the journey to the United States and Canada. Alternatively, the discrepancy may be a result of varying conditions across destination countries that would have differential effects on mortality. The smaller sample size of some destinations in our sample, especially that of South Africa compared to the United States, likely also plays a role in this variation.

An underexplored potential mechanism driving the migrant mortality advantage may be that time spent in either the origin or destination country (i.e., one's exposure to potentially unfavorable conditions in the origin country) may contribute towards a "weathering" effect on one's health. For example, Bakhtari (2022) notes the *absence* of a mortality advantage for many European immigrant groups living in 20th century United States. In our application, exposure to

diseases such as smallpox, in combination with persistent poverty and overcrowding throughout the United Kingdom and Ireland may have shortened non-migrants' lifespans, while migrants were able to avoid such conditions. This framing runs contrary to the typical narrative of the migrant mortality advantage because it posits that mortality advantages are due to poorer conditions experienced by non-migrants which depress their mortality. Yet, this line of analysis is outside the scope of our paper as the nature of the data prevents us from being able to confidently identify when individuals migrated. Future studies should further investigate exposure to poor conditions in the origin country as a potential mechanism of the migrant mortality advantage.

Limitations

Our study suffers from a few key limitations. Several biases are inherent to crowdsourced genealogical datasets (Calderón Bernal et al., 2023): recorded people may only be those who had children, family trees may be incompletely reconstructed, and there is unequal access to information about relatives. For example, these biases may lead to childless women being less likely to be recorded or the underreporting of infant and child mortality. While we attempt to ameliorate the latter bias by conditioning our sample on survival to age 15, we do identify a gender bias in the recording of women, leading to an overrepresentation of men in the sample.

Additionally, we classify individuals who moved between Ireland and the United Kingdom as "non-migrants" rather than "migrants" because our interest was primarily in migration to Canada, the United States of America, South Africa, New Zealand, and Australia. As such, we do not investigate the possibility of a migrant mortality advantage between the United Kingdom and Ireland. We also do not capture migration between countries within the United Kingdom nor domestic rural-urban migration during this period. These limitations are in part due to the ambiguous usage of "United Kingdom" to describe locations within the dataset and the difficulty in extracting more granular location data from free text entries. Future work should certainly investigate this possibility, as migration within the United Kingdom and Ireland occurred at non-trivial levels, often driven by many of the same factors that encouraged migration to the countries in this study (Nicholas & Shergold, 1987).

Finally, though Familinx is rich in terms of the overall size of the data, it suffers from a lack of detail at the individual level. As a result, we are unable to control for socioeconomic status (i.e., literacy, financial resources, etc.) directly, which may influence not only one's propensity to

migrate but also their mortality. We are also unable to determine when an individual migrated or account for multiple moves within one's life, although future work could attempt to account for this using the birth location of children as a proxy for timing of migration. Migrant outcomes may be partially determined by one's country of residence during early life (Alexander & Ward, 2018), yet we are unable to capture one's "exposure" to different epidemiological or socioeconomic conditions at specific points in their lifespan. Though we are able to identify some "salmon" migrants who migrated abroad but returned to die in their home country using the birthplace of their children, we are unable to do so for childless individuals. Future studies should investigate the impact of exposure to poor conditions in the origin country as a mechanism depressing non-migrants' mortality.

Though our setting is historical, our findings are relevant for present-day migration flows. The migrant mortality advantage literature has focused on the paradox of immigrants outliving the native-born even when of a lower socioeconomic status (Abraído-Lanza et al., 1999; Boen & Hummer, 2019; Palloni & Arias, 2004). Less work recognizes how emigration may depress mortality estimates in the origin country, though Hendi and Ho (2021) note that immigrants increase life expectancy in the United States. Future work on the mechanisms driving this mortality advantage are necessary to help ascertain whether it is an associational or causal relationship, i.e., whether migrants would have always outlived their non-migrant peers, or whether migration *causes* a longer life.

References

Abraído-Lanza, A. F., Dohrenwend, B. P., Ng-Mak, D. S., & Turner, J. B. (1999). The Latino mortality paradox: A test of the "salmon bias" and healthy migrant hypotheses. *American Journal of Public Health*, *89*(10), 1543–1548. https://doi.org/10.2105/AJPH.89.10.1543

Abramitzky, R., Boustan, L. P., & Eriksson, K. (2012). Europe's Tired, Poor, Huddled Masses: Self-Selection and Economic Outcomes in the Age of Mass Migration. *American Economic Review*, *102*(5), 1832–1856. https://doi.org/10.1257/aer.102.5.1832

Abramitzky, R., Boustan, L. P., & Eriksson, K. (2014). A Nation of Immigrants: Assimilation and Economic Outcomes in the Age of Mass Migration. *Journal of Political Economy*, *122*(3), 467–506. https://doi.org/10.1086/675805

Alburez-Gutierrez, D., Aref, S., Gil-Clavel, B. S., Grow, A., Negraia, D. V., & Zagheni, E. (2019). Demography in the digital era: New data sources for population research. In *Smart statistics for smart applications: Book of short papers SIS2019* (pp. 23–30). Pearson. https://doi.org/10.31235/osf.io/24jp7

Aldridge, R. W., Nellums, L. B., Bartlett, S., Barr, A. L., Patel, P., Burns, R., Hargreaves, S., Miranda, J. J., Tollman, S., Friedland, J. S., & Abubakar, I. (2018). Global patterns of mortality in international migrants: A systematic review and meta-analysis. *The Lancet*, *392*(10164), 2553–2566. https://doi.org/10.1016/S0140-6736(18)32781-8

Alexander, R., & Ward, Z. (2018). Age at Arrival and Assimilation During the Age of Mass Migration. *The Journal of Economic History*, *78*(3), 904–937. https://doi.org/10.1017/S0022050718000335

Andersson, G., & Drefahl, S. (2017). Long-Distance Migration and Mortality in Sweden: Testing the Salmon Bias and Healthy Migrant Hypotheses. *Population, Space and Place*, *23*(4), e2032. https://doi.org/10.1002/psp.2032

Bakhtiari, E. (2022). The Missing Mortality Advantage for European Immigrants to the United States in the Early Twentieth Century. *Demography*, *59*(4), 1517–1539. https://doi.org/10.1215/00703370-10111916

Baranowska-Rataj, A., Barclay, K., & Kolk, M. (2017). The effect of number of siblings on adult mortality: Evidence from Swedish registers for cohorts born between 1938 and 1972. *Population Studies*, *71*(1), 43–63. https://doi.org/10.1080/00324728.2016.1260755

Boen, C. E., & Hummer, R. A. (2019). Longer—But Harder—Lives?: The Hispanic Health Paradox and the Social Determinants of Racial, Ethnic, and Immigrant–Native Health Disparities from Midlife through Late Life. *Journal of Health and Social Behavior*, *60*(4), 434–452. https://doi.org/10.1177/0022146519884538

Calderón Bernal, L., Alburez-Gutierrez, D., & Zagheni, E. (2023). *Analyzing biases in genealogies using demographic microsimulation*. MPIDR Working Paper. https://dx.doi.org/10.4054/MPIDR-WP-2023-034

Chong, M., Alburez-Gutierrez, D., Del Fava, E., Alexander, M., & Zagheni, E. (2022). *Identifying and correcting bias in big crowd-sourced online genealogies* (WP-2022-005; 0 ed., p. WP-2022-005). Max Planck Institute for Demographic Research. https://doi.org/10.4054/MPIDR-WP-2022-005

Clouston, S. A. P., & Link, B. G. (2021). A retrospective on fundamental cause theory: State of the literature, and goals for the future. *Annual Review of Sociology*, *47*(1), 131–156. https://doi.org/10.1146/annurev-soc-090320-094912

Cournil, A., & Kirkwood, T. B. L. (2001). If you would live long, choose your parents well. *Trends in Genetics*, *17*(5), 233–235. https://doi.org/10.1016/S0168-9525(01)02306-X

Cozzani, M., Minardi, S., Corti, G., & Barban, N. (2023). Birth month and adult lifespan: A within-family, cohort, and spatial examination using FamiLinx data in the United States (1700–1899). *Demographic Research*, *49*, 201–218. https://doi.org/10.4054/DemRes.2023.49.9

Donrovich, R., Puschmann, P., & Matthijs, K. (2014). Rivalry, solidarity, and longevity among siblings: A life course approach to the impact of sibship composition and birth order on later life mortality risk, Antwerp (1846-1920). *Demographic Research*, *31*, 1167–1198. https://doi.org/10.4054/DemRes.2014.31.38

Feliciano, C. (2020). Immigrant Selectivity Effects on Health, Labor Market, and Educational Outcomes. *Annual Review of Sociology*, *46*(1), 315–334. https://doi.org/10.1146/annurev-soc-121919-054639

Friedlander, D., & Okun, B. S. (2022). Demographic Transition and the Industrial Revolution in England: Inverse Rural and Urban Processes. *Journal of Family History*, *47*(4), 401–412. https://doi.org/10.1177/03631990221114065

Gavrilov, L. A., Gavrilova, N. S., Olshansky, S. J., & Carnes, B. A. (2002). Genealogical data and the biodemography of human longevity. *Biodemography and Social Biology*, *49*(3–4), 160–173. https://doi.org/10.1080/19485565.2002.9989056

Gudmundsson, H., Gudbjartsson, D. F., Kong, A., Gudbjartsson, H., Frigge, M., Gulcher, J. R., & Stefánsson, K. (2000). Inheritance of human longevity in Iceland. *European Journal of Human Genetics*, *8*(10), Article 10. https://doi.org/10.1038/sj.ejhg.5200527

Guillot, M., Khlat, M., Elo, I., Solignac, M., & Wallace, M. (2018). Understanding age variations in the migrant mortality advantage: An international comparative perspective. *PLOS ONE*, *13*(6), e0199669. https://doi.org/10.1371/journal.pone.0199669

Guillot, M., Khlat, M., Gansey, R., Solignac, M., & Elo, I. (2023). Return Migration Selection and Its Impact on the Migrant Mortality Advantage: New Evidence Using French Pension Data. *Demography*, 10938784. https://doi.org/10.1215/00703370-10938784

Haines, R. (1997). 'The idle and the drunken won't do there': Poverty, the new poor law and nineteenth-century government-assisted emigration to Australia from the United Kingdom∗. *Australian Historical Studies*, *27*(108), 1–21. https://doi.org/10.1080/10314619708596025

Hatton, T. J. (2004). Emigration from the UK, 1870-1913 and 1950-1998. *European Review of Economic History*, *8*(2), 149–171. https://doi.org/10.1017/S1361491604001121

Hatton, T. J. (2021). Emigration from the United Kingdom to the United States, Canada and Australia/New Zealand, 1870–1913: Quantity and quality. *Australian Economic History Review*, *61*(2), 136–158. https://doi.org/10.1111/aehr.12218

Hatton, T. J., & Martin, R. M. (2008). *The Effects on Stature of Poverty, Family Size and Birth Order: British Children in the 1930s* (3314; IZA Discussion Paper Series). IZA. https://docs.iza.org/dp3314.pdf

Hatton, T. J., & Williamson, J. G. (1994). What Drove the Mass Migrations from Europe in the Late Nineteenth Century? *Population and Development Review*, *20*(3), 533. https://doi.org/10.2307/2137600

Helgesson, M., Johansson, B., Nordquist, T., Vingård, E., & Svartengren, M. (2019). Healthy migrant effect in the Swedish context: A register-based, longitudinal cohort study. *BMJ Open*, *9*(3), e026972. https://doi.org/10.1136/bmjopen-2018-026972

Hendi, A. S., & Ho, J. Y. (2021). Immigration and improvements in American life expectancy. *SSM - Population Health*, *15*, 100914. https://doi.org/10.1016/j.ssmph.2021.100914

Horn, J. (1998). British Diaspora: Emigration from Britain, 1680–1815. In P. J. Marshall, A. Low, & Wm. R. Louis (Eds.), *The Oxford History of the British Empire: Volume II: The Eighteenth Century* (p. 0). Oxford University Press. https://doi.org/10.1093/acprof:oso/9780198205630.003.0002

Kaplanis, J., Gordon, A., Shor, T., Weissbrod, O., Geiger, D., Wahl, M., Gershovits, M., Markus, B., Sheikh, M., Gymrek, M., Bhatia, G., MacArthur, D. G., Price, A. L., & Erlich, Y. (2018). Quantitative analysis of population-scale family trees with millions of relatives. *Science*, *360*(6385), 171–175. https://doi.org/10.1126/science.aam9309

Kasakoff, A. B., & Adams, J. W. (1995). The Effect of Migration on Ages at Vital Events: A Critique of Family Reconstitution in Historical Demography. *European Journal of Population*, *11*(3), 199–242.

Lam, D., & Marteleto, L. (2008). Stages of the Demographic Transition from a Child's Perspective: Family Size, Cohort Size, and Children's Resources. *Population and Development Review*, *34*(2), 225–252. https://doi.org/10.1111/j.1728-4457.2008.00218.x

Lindstrom, D. P., & Lauster, N. (2001). Local Economic Opportunity and the Competing Risks of Internal and U.S. Migration in Zacatecas, Mexico. *International Migration Review*, *35*(4), 1232–1256. https://doi.org/10.1111/j.1747-7379.2001.tb00059.x

Link, B. G., & Phelan, J. (1995). Social Conditions As Fundamental Causes of Disease. *Journal of Health and Social Behavior*, *35*, 80. https://doi.org/10.2307/2626958

Mehta, N. K., Elo, I. T., Engelman, M., Lauderdale, D. S., & Kestenbaum, B. M. (2016). Life Expectancy Among U.S.-born and Foreign-born Older Adults in the United States: Estimates From Linked Social Security and Medicare Data. *Demography*, *53*(4), 1109–1134. https://doi.org/10.1007/s13524-016-0488-4

Mize, T. (2019). Best Practices for Estimating, Interpreting, and Presenting Nonlinear Interaction Effects. *Sociological Science*, *6*, 81–117. https://doi.org/10.15195/v6.a4

Mourits, R. J., & Puschmann, P. (2023). Exploring familial factors in the migrant mortality advantage among domestic migrants in later life: Zeeland, the Netherlands, 1812–1962. *SSM - Population Health*, *22*, 101359. https://doi.org/10.1016/j.ssmph.2023.101359

Murdoch, A. (2004). *British emigration, 1603-1914*. Palgrave Macmillan.

Nicholas, S., & Shergold, P. R. (1987). Internal migration in England, 1818–1839. *Journal of Historical Geography*, *13*(2), 155–168. https://doi.org/10.1016/S0305-7488(87)80144-5

Pablos-Méndez, A. (1994). Mortality Among Hispanics. *JAMA: The Journal of the American Medical Association*, *271*(16), 1237. https://doi.org/10.1001/jama.1994.03510400023017

Palloni, A., & Arias, E. (2004). Paradox lost: Explaining the Hispanic adult mortality advantage. *Demography*, *41*(3), 385–415. https://doi.org/10.1353/dem.2004.0024

Piraino, P., Muller, S., Cilliers, J., & Fourie, J. (2014). The transmission of longevity across generations: The case of the settler Cape Colony. *Research in Social Stratification and Mobility*, *35*, 105–119. https://doi.org/10.1016/j.rssm.2013.08.005

Puschmann, P., Donrovich, R., Grönberg, P.-O., Dekeyser, G., & Matthijs, K. (2016). Disfavored in Life, Favored in Death? Later-Life Mortality Differences (Ages 30+) between Migrants and Natives in Antwerp, Rotterdam and Stockholm, 1850-1930. *Historical Social Research*, *41*(4). https://doi.org/10.12759/HSR.41.2016.4.257-290

Puschmann, P., Donrovich, R., & Matthijs, K. (2017). Salmon Bias or Red Herring?: Comparing Adult Mortality Risks (Ages 30–90) between Natives and Internal Migrants: Stayers, Returnees and Movers in Rotterdam, the Netherlands, 1850–1940. *Human Nature*, *28*(4), 481–499. https://doi.org/10.1007/s12110-017-9303-1

Razum, O. (2008). Migrant Mortality, Healthy Migrant Effect. In W. Kirch (Ed.), *Encyclopedia of Public Health* (pp. 932–935). Springer Netherlands. https://doi.org/10.1007/978-1-4020-5614-7_2188

Richards, E. (2018). *The genesis of international mass migration: The British case, 1750-1900*. Manchester University Press.

Ruggles, S. (1992). Migration, Marriage, and Mortality: Correcting Sources of Bias in English Family Reconstitutions. *Population Studies*, *46*(3), 507–522. https://doi.org/10.1080/0032472031000146486

Sonneveldt, E., DeCormier Plosky, W., & Stover, J. (2013). Linking high parity and maternal and child mortality: What is the impact of lower health services coverage among higher order births? *BMC Public Health*, *13*(Suppl 3), S7. https://doi.org/10.1186/1471-2458-13-S3-S7

Stark, O., & Bloom, D. E. (1985). The New Economics of Labor Migration. *The American Economic Review*, *75*(2), 173–178.

Stelter, R., & Alburez-Gutierrez, D. (2022). Representativeness is crucial for inferring demographic processes from online genealogies: Evidence from lifespan dynamics. *Proceedings of the National Academy of Sciences*, *119*(10), e2120455119. https://doi.org/10.1073/pnas.2120455119

Swerdlow, A. J. (1991). Mortality and Cancer Incidence in Vietnamese Refugees in England and Wales: A Follow-Up Study. *International Journal of Epidemiology*, *20*(1), 13–19. https://doi.org/10.1093/ije/20.1.13

Taylor, D. (1988). Public Health in Britain 1750–1900. In D. Taylor, *Mastering Economic and Social History* (pp. 301–331). Macmillan Education UK. https://doi.org/10.1007/978-1-349-19377-6_19

Thompson, R. (2009). *Mobility and Migration: East Anglian Founders of New England, 1629-1640* (Reprint edition). University of Massachusetts Press.

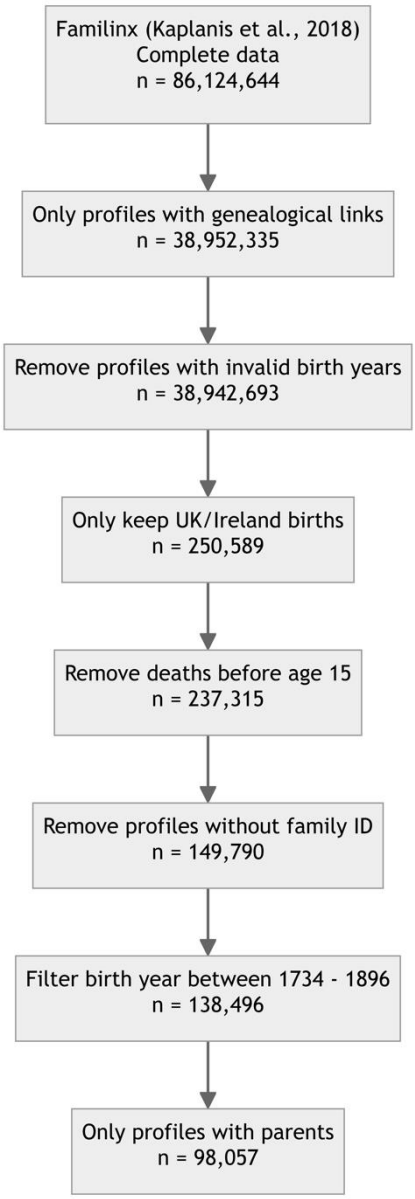
Tomlins, C. (2001). Reconsidering Indentured Servitude: European Migration and the Early American Labor Force, 1600–1775. *Labor History*, *42*(1), 5–43. https://doi.org/10.1080/00236560123269

Supplementary Material

Appendix A. Data Cleaning & Imputation

We began with a dataset of over 86 million individuals, many of whom had missing values across most variables. In preparing the data for imputations, only individuals with observed kinship ties were kept from the full data set. To address the high degree of missingness in key variables among the remaining observations, we imputed several types of missingness: (1) missingness in the birth and death year, (2) missingness in the birth and death location, and (3) missing gender. Figure A1 offers a visual representation of our data cleaning process.

Figure A1. Flow of data cutting process



For type (1), we imputed missing birth and death years with birth and baptism years, which are included in the Familinx dataset. Similarly for type (2), we used coordinate information on birth, death, baptism, and burial to extract countries of interest for each event. Missing birth and death locations were imputed using baptism and burial locations, respectively. This included baptism and burial locations that were derived from coordinate information. Finally, entries containing abnormal birth years (negative years and years occurring after 2020) that likely contained errors were removed.

The coordinate information matching process was conducted as follows. Using the *countrycode* package (Arel-Bundock et al., 2018), columns containing country code information were then used to fill in entries that were still missing in these four columns, with imputed baptism and burial information from their respective country codes being used to fill in country level information. The *countrycode* package was also used to fill in birth and death countries with "USA" from the state-based location columns if they matched names or abbreviations of U.S. states. Finally, the free text columns were used to extract country level information through regex for rows that were still missing country information. This was repeated on the baptism and burial free text columns which were then used to impute birth and death country information that was still missing.

To fill in type (3) information for individuals with a missing gender, kinship ties were used. When two individuals were both parents of another individual in the data set and the gender information for one parent was known, this was used to fill in the gender information for the parent missing gender information.

To create the final country categories, a combination of term matching and regex approaches were used. For Ireland and Northern Ireland, regex was used to detect references to Ireland or "eire". For England, Scotland, Wales, a term matching approach was adopted to match various spellings, languages and cities referenced. Finally, for the USA, Australia, South Africa, New Zealand and Canada, terms matching in the country column included references to territories, regions, states (that had not already been picked up previously), alternate spellings and names in other languages. The full list of terms used for term matching is presented in T11/21/2023 11:48:00 AMable A1.

Table A1. Term matching

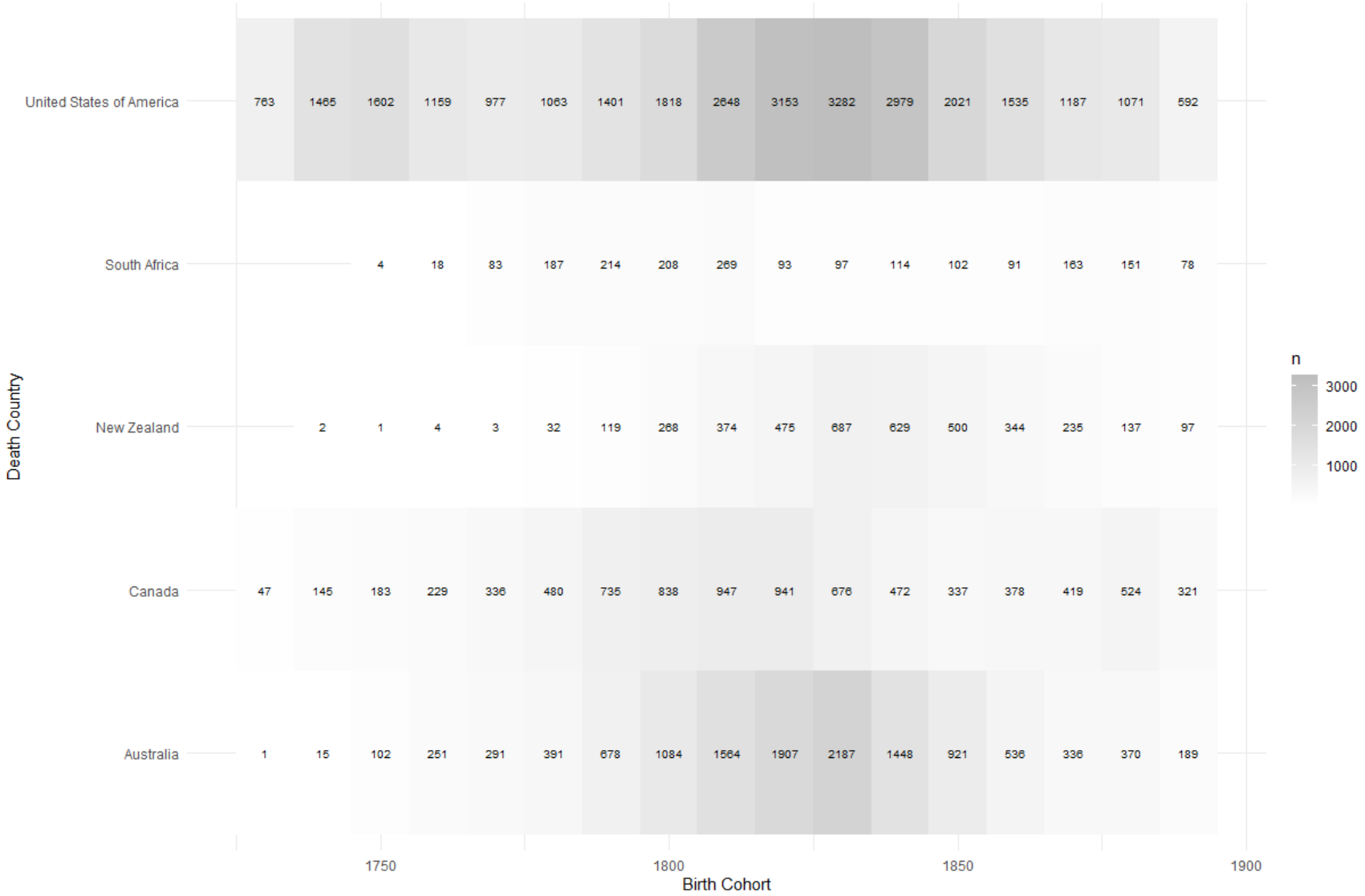
Country	**Term**
United Kindgom	'united kingdom', 'x-england', 'england', 'x-scotland', 'x-united-kingdom', 'scotland', '(present uk)', 'x-great-britain', 'x-wales', 'gb', 'x-northern-ireland', 'uk', 'northern ireland', 'england, uk', 'u.k.', 'wales', 'england, united kingdom', 'great britain', 'england uk', 'uk:great britain', 'uk:northern ireland', 'england (present uk)', 'scotland, united kingdom', 'uk:northern ireland', 'uk.', 'scotland, uk', 'uk:isle of wight', 'ireland (present northern ireland)', 'north ireland', 'scotland, uk', 'scotland, united kingdom', 'scotland uk', 'south wales', 'britain', 'england/ uk', 'n.ireland', 'engand', 'englnd', 'northern ireland, uk', 'middlesex', 'n. ireland', 'huntingdonshire', 'lancashire', 'london', 'uk:scotland:shetland islands:mainland', 'u k', 'united kingdom of great britain and ireland', 'northern-ireland', 'nothern ireland, uk',

	'ireland (northern)', 'n. ireland', 'ireland or scotland', 'scotland or ireland', 'enfland', 'storbritannia', 'bonhill, dunbartonshire, scotland', 'cambridgeshire', 'chatham', 'crickdale, wiltshire, uk', 'eicester, leicestershire, uk', 'endgland', 'england.', 'englanmd', 'englnad', 'enland', 'essex', 'fifeshire', 'gloucester', 'great briatin', 'great britai', 'herfordshire', 'lower bebington', 'newcastle upon tyne', 'north wales', 'reino unido', 'royaume uni', 'scotlans', 'swindon, wiltshire, england', 'tyrone', 'uk /england', 'uk/wales', 'uk:wales:anglesey', 'umited kingdom', 'united kinbgdom', 'united kinbgdom', 'winwick', 'woolwich, kent, uk', 'yorkshire', 'xengland', "yhdistynyt kuningaskunta", "(present u.k.)", "(present day united kingdom)", "-england", "(now united kingdom)", "present united kingdom)", "המלכה המאוחדת", "aberdeen city", "englang", "england,uk", "england or pa", "wales or england", "verenigd koninkrijk", "unitedkingdom", "united-kingdom", "uk:scotland:barra", "uk, england", "u. k.", "heathfield, sussex, england"
Ireland	'ireland', 'ie', 'republic of ireland', 'eire', 'bydoney,tyrone ,ireland', 'ireland, uk', 'uk (ireland)', 'ireland ???', 'ireland (eire)', 'ireland.', 'or ireland', 'kilkenny', 'tipperary', 'waterford', 'ulster', 'galway', 'down', 'carlow'
United Stats of America	us", 'usa', 'united states', 'united states of america', 'america', '(present usa)', 'colonial america', 'province of new york', 'new netherland colony', 'new england colonies', 'new england', 'present united states', 'american colonies', "british america", "new netherlands", 'new york', 'american colonies [present united states]', 'british north america', 'u.s.a.', 'new netherlands (usa)', 'nieuw netherlands', 'british colonies', 'nouvelle france', "british colonies of north america", 'american colonies (present usa)', 'usa:new york:long island', 'usa:49', 'usa:massachusettes:nantucket island', 'usa:massachusettes:martha\'s vineyard', 'usa:44', 'the united states of america', 'massachusetts colony', 'british amercia', 'now usa', 'martin county, indiana, usa', 'richland county', 'u,s.a.', 'u.sa.', 'united sates', 'unitet states', 'usa.', 'usa:hawaii:kauai', "ee.uu.", "(currently) united states", "(present usa)", "(present (usa)", "(present) usa", "amerikas forente stater", "cleveland", "estados unidos", "usa:california:santa catalina island", "usa (all present day)", "us virgin islands", "kittery, york, maine", "in what will be america"
Australia	'australia', 'au', 'australien', 'australia:tasmania', 'new south wales', 'australia [green slopes hospital]', 'aust', 'western australia', 'austrailia', 'australis', 'nsw', 'port melbourne', 'portsea', 'sydney nsw', 'tasmania'
New Zealand	'new zealand', 'nz', 'new zealand:north island', 'new zealand:south island', 'new zealand.', ', new zealand', 'christchurch', 'king street, sydenham, christchurch, nz', 'new zeaand', 'new zealand of senile decay', 'new, zealand',

	'tennyson street, sydenham, christchurch, nz', "king street, sydenham, christchurch, nz"
Canada	'canada', 'ca', 'kanadas', 'canada:27', 'united province of canada', 'british north america (present canada)', 'canada:cape breton island', 'province of canada', 'canada:11', 'canada:newfoundland', 'upper canada', '(present canada)', 'acadie', 'canad', 'can", 'canadá', 'canada:15', 'canada:vancouver island'
South Africa	'za', 'south africa', 'suid afrika', 'cape of good hope', 'cape colony', 's africa', 'cape colony (south africa)', 'rep south africa', 'south africa', 'south afica', 'south africa.', 'union of south africa'

To produce the final data set, only rows that were complete (i.e: had no missing information regarding birth/death year, gender and birth/death location) were kept. All individuals born in the UK/Ireland and dying in the UK/Ireland, USA, Australia, Canada, New Zealand, and South Africa were kept. Figure A2 shows the counts of migrants by destination country and birth cohort.

Figure A2. Counts of Migrants by Birth Cohort



Examining patterns of missingness among migrants and non-migrants

To ensure that the samples of migrants and non-migrants are reasonably similar, we examine patterns of missingness in birth month, a variable that is not used in the analysis but should help point to accuracy in reporting. Table A2 shows the number and proportion missing birth month between migrants and non-migrants, while Table A3 looks within the migrants to examine patterns of missingness. Tables A4 and A5 repeat the analyses found in A2 and A3 respectively, but focusing instead on the subset of individuals who are reported to have siblings.

Table A2. Missingness of Birth Month

	N	Number Missing Birth Month	Proportion Missing Birth Month
Migrants	54,774	21,472	.392
Non-Migrants	83,722	45,750	.546

$$\chi^2(1,\ N = 138{,}496) = 3163.9,\ p < .01$$

Table A3. Missingness of Birth Month Among Migrants by Destination Country

Destination	N	Number Missing Birth Month	Proportion Missing Birth Month
USA	28,716	9,672	.336
Canada	8,008	3,557	.444
Australia	12,271	6,239	.508
New Zealand	3,907	1,466	.375
South Africa	1,872	538	.287

$$\chi^2(4,\ N = 138{,}496) = 1246.5,\ p < .01$$

Table A4. Missingness of Birth Month (Siblings)

	N	Number Missing Birth Month	Proportion Missing Birth Month
Migrants	16,123	4,855	.301
Non-Migrants	33,140	16,231	.489

$$\chi^2(1,\ N = 49{,}263)\ =\ 1{,}576.6,\ p\ <\ .01$$

Table A5. Missingness of Birth Month Among Migrants by Destination Country (Siblings)

Destination	N	Number Missing Birth Month	Proportion Missing Birth Month
USA	7,763	1,802	.232
Canada	2,355	824	.349
Australia	4,081	1,712	.419
New Zealand	1,310	386	.294
South Africa	614	131	.213

$$\chi^2(4,\ N = 16{,}123)\ =\ 496.72,\ p\ <\ .01$$

Appendix B. Results and Robustness Checks

This section is organized as follows. We first present regression estimates from the main models in Table B1. Next, we present regression estimates from supplementary models that were estimated on the reduced sample of individuals with at least one sibling in Table B2. Finally, we show that our models are robust to alternate minimum age cutoffs in Figure B1 and B2.

Table B1. Results from Main Models

	Dependent variable: Age at Death	
	Model A: Migrant	Model B: Country of Death
Migrant (*reference: Non-Migrant)*	3.350***	
	(1.058)	
Destination country *(reference: United Kingdom/Ireland)*		
Canada		1.242
		(4.637)
South Africa		1.992
		(2.716)
Australia		23.950
		(17.595)
New Zealand		4.728**
		(2.276)
United States of America		3.377***
		(1.071)
Birth cohort (*reference: 1730)*		
1740	-0.743	-0.744
	(0.718)	(0.718)
1750	-0.744	-0.744
	(0.710)	(0.709)
1760	0.957	0.956
	(0.698)	(0.697)
1770	2.068***	2.067***
	(0.680)	(0.679)
1780	1.413**	1.411**
	(0.669)	(0.668)
1790	0.042	0.039
	(0.660)	(0.659)

1800	-0.667	-0.666
	(0.655)	(0.654)
1810	-1.556**	-1.560**
	(0.654)	(0.653)
1820	-2.908***	-2.914***
	(0.650)	(0.649)
1830	-4.918***	-4.919***
	(0.653)	(0.653)
1840	-5.655***	-5.657***
	(0.656)	(0.656)
1850	-5.831***	-5.832***
	(0.660)	(0.660)
1860	-4.315***	-4.320***
	(0.665)	(0.665)
1870	-1.971***	-1.974***
	(0.668)	(0.667)
1880	1.414**	1.414**
	(0.675)	(0.674)
1890	3.220***	3.219***
	(0.733)	(0.732)
Male *(reference: female)*	0.0003	0.0002
	(0.117)	(0.117)
Number of siblings *(reference: none)*		
1	-1.860***	-1.861***
	(0.177)	(0.177)
2	-2.927***	-2.926***
	(0.213)	(0.213)
3-5	-2.894***	-2.889***
	(0.179)	(0.179)
6+	-2.468***	-2.439***
	(0.281)	(0.281)
Migrant X Birth cohort interaction *(reference: 1730)*		
1740	0.995	
	(1.286)	
1750	0.233	

	(1.266)
1760	-0.058
	(1.278)
1770	-0.154
	(1.258)
1780	0.356
	(1.214)
1790	2.281*
	(1.168)
1800	2.201*
	(1.143)
1810	2.426**
	(1.126)
1820	3.442***
	(1.119)
1830	4.733***
	(1.119)
1840	5.172***
	(1.127)
1850	5.014***
	(1.144)
1860	3.095***
	(1.165)
1870	2.511**
	(1.180)
1880	-0.062
	(1.193)
1890	0.034
	(1.304)
Destination country X Birth cohort interaction *(reference: UK/Ireland & 1730)*	
Canada:1740	6.812
	(5.071)
Australia:1740	-27.468
	(18.693)
New Zealand:1740	-19.768

	(12.822)
United States of America:1740	0.717 (1.314)
Canada:1750	3.462 (4.989)
South Africa:1750	-9.603 (12.907)
Australia:1750	-20.242 (17.823)
New Zealand:1750	21.868 (17.844)
United States of America:1750	0.051 (1.300)
Canada:1760	4.672 (4.918)
South Africa:1760	8.050 (6.256)
Australia:1760	-20.349 (17.718)
New Zealand:1760	3.531 (17.984)
United States of America:1760	-0.785 (1.340)
Canada:1770	6.418 (4.826)
South Africa:1770	-1.007 (3.788)
Australia:1770	-20.676 (17.669)
New Zealand:1770	12.420 (17.983)
United States of America:1770	-1.663 (1.365)
Canada:1780	5.180

	(4.765)
South Africa:1780	0.523 (3.429)
Australia:1780	-19.386 (17.642)
New Zealand:1780	6.123 (4.295)
United States of America:1780	-1.398 (1.329)
Canada:1790	7.663 (4.726)
South Africa:1790	0.373 (3.257)
Australia:1790	-18.345 (17.619)
New Zealand:1790	3.631 (3.076)
United States of America:1790	0.767 (1.267)
Canada:1800	5.398 (4.713)
South Africa:1800	-0.017 (3.117)
Australia:1800	-19.143 (17.610)
New Zealand:1800	2.873 (2.663)
United States of America:1800	2.302* (1.224)
Canada:1810	6.842 (4.701)
South Africa:1810	-0.009 (3.025)
Australia:1810	-19.261 (17.606)

New Zealand:1810	3.639
	(2.545)
United States of America:1810	2.309*
	(1.183)
Canada:1820	7.709
	(4.701)
South Africa:1820	2.711
	(3.572)
Australia:1820	-18.470
	(17.604)
New Zealand:1820	3.913
	(2.494)
United States of America:1820	3.431***
	(1.165)
Canada:1830	9.520**
	(4.723)
South Africa:1830	1.410
	(3.663)
Australia:1830	-17.703
	(17.603)
New Zealand:1830	2.965
	(2.429)
United States of America:1830	5.660***
	(1.164)
Canada:1840	7.929*
	(4.752)
South Africa:1840	1.880
	(3.418)
Australia:1840	-16.297
	(17.606)
New Zealand:1840	4.338*
	(2.454)
United States of America:1840	5.563***
	(1.171)

Canada:1850	7.069
	(4.785)
South Africa:1850	0.987
	(3.452)
Australia:1850	-15.637
	(17.610)
New Zealand:1850	6.153**
	(2.485)
United States of America:1850	4.700***
	(1.202)
Canada:1860	4.712
	(4.774)
South Africa:1860	-2.004
	(3.473)
Australia:1860	-17.647
	(17.620)
New Zealand:1860	5.006**
	(2.550)
United States of America:1860	2.890**
	(1.240)
Canada:1870	6.444
	(4.759)
South Africa:1870	-1.099
	(3.193)
Australia:1870	-18.831
	(17.632)
New Zealand:1870	3.600
	(2.659)
United States of America:1870	2.254*
	(1.271)
Canada:1880	2.450
	(4.745)
South Africa:1880	2.230
	(3.247)

Australia:1880		-20.162 (17.632)
New Zealand:1880		0.615 (2.894)
United States of America:1880		-0.864 (1.299)
Canada:1890		2.156 (4.831)
Australia:1890		-19.513 (17.674)
United States of America:1890		-0.415 (1.484)
Constant	66.785***	66.784***
	(0.608)	(0.607)
Sibling random effects	Yes	Yes
Observations	98,057	98,057
Note:	*p<0.1 **p<0.05 ***p<0.01	

Next, we present results from the supplementary models. This table corresponds to the AMEs presented in Figure 2 in the main article.

Table B2. Results from Supplementary Models, Only Individuals with Siblings

	Dependent variable: Age at Death	
	Migrant	Country of Death
Migrant (*reference: Non-Migrant)*	2.881	
	(2.139)	
Destination country *(reference: United Kingdom/Ireland)*		
Canada		12.404
		(18.608)
South Africa		2.810
		(4.025)
Australia		24.674
		(18.820)
New Zealand		8.164**
		(3.182)
United States of America		2.553
		(2.153)
Male *(reference: female)*	0.221	0.231
	(0.177)	(0.177)
Number of siblings *(reference: 1)*		
2	-1.076***	-1.072***
	(0.271)	(0.272)
3-5	-1.046***	-1.030***
	(0.242)	(0.242)
6+	-0.699**	-0.662*
	(0.341)	(0.341)
Constant	63.838***	63.822***
	(1.029)	(1.029)
Sibling random effects	Yes	Yes
Interaction effects	Yes	Yes
Observations	49,263	49,263

Note: we suppress coefficients for all interactions for space. *p<0.1, **p<0.05, ***p<0.01

Table B3. AMEs of Models A1, B1, A2, B2

Dependent Variable: Age at Death

	Full Sample		Profiles with siblings	
Model:	A1	B1	A2	B2
Migrant	5.9**		7.1**	
	(0.12)		(0.2)	
Australia		5.5**		7.7**
		(0.38)		(0.65)
Canada		7.6**		8.8**
		(0.28)		(0.5)
New Zealand		8.7**		9.8**
		(1.24)		(0.87)
South Africa		2.6**		3.2**
		(0.73)		(1.1)
USA		5.7**		6.8**
		(0.16)		(0.27)
Observations	98,057	98,057	49,263	49,263

Notes: For model A2 and B2 the sample is limited to only individuals with at least one sibling

$^{**}p < .01$

References

Arel-Bundock, V., Enevoldsen, N., & Yetman, C. (2018). countrycode: An R package to convert country names and country codes. *Journal of Open Source Software*, *3*(28), 848. https://doi.org/10.21105/joss.00848