Measuring the Overlap with Ancestors Throughout the Life Course of the Swedish Cohorts 1751–2000

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Abstract

Measuring generational overlap — the extent to which individuals share their lives with relatives from other generations — is essential for examining how demographic changes affect family structures and intergenerational relationships over time. This research uses the SOCSIM demographic microsimulation programme and Swedish fertility and mortality data from 1751 to 2100 to estimate the probability of having living parents, grandparents and great-grandparents throughout the life course of cohorts born between 1751 and 2000. Three key measures are calculated: the mean number of living ancestors at birth, the distribution of living generations at birth and at age 20, and lifetime overlap with each ancestor, operationalised as years with at least one living ancestor, aggregate person-years of overlap, and mean overlap per ancestor. The results show increasing lifetime overlap with ancestors over time, particularly with parents and grandparents and among cohorts born after 1850. The analysis also reveals greater overlap with female ancestors, particularly grandmothers and great-grandmothers, than with their male counterparts. By examining ancestral availability by age and cohort, the study highlights how demographic change has shaped opportunities for intergenerational relationships, support and caregiving in ageing societies. These insights deepen understanding of changing family dynamics and opportunities for intergenerational relationships in ageing societies.

Keywords: Demographic microsimulation, Generational overlap, Historical Demography, Kin availability, Sweden

Introduction

How common has it been to have living parents, grandparents and great-grandparents throughout one's life course over time? As kinship networks are shaped by demographic behaviour (Caswell and Song, 2021; Alburez-Gutierrez et al., 2023; Kolk et al., 2023; Jiang et al., 2023, 2025), long-term patterns and changes in ancestral availability should be examined alongside historical changes in fertility and mortality. In earlier centuries, shorter lifespans meant that elderly ancestors were rarely alive throughout one's lifetime. However, since the 20^{th} century, changes in mortality and increased longevity have created more opportunities for family interactions across more than two generations (Uhlenberg, 1980, 1996; Bengtson, 2001; Murphy, 2010a, 2011). Understanding how demographic changes have enabled the coexistence of multiple generations requires long-term analysis of the availability of living ancestors throughout the life course. This may contribute to a better understanding of the potential for intergenerational relationships, support, and caregiving arising from long-term changes in demographic and kinship dynamics.

The historical transition from high to low fertility and mortality rates, known as the 'Demographic Transition', has had a profound impact on population dynamics, which has been widely studied in the literature. Besides their effect on population size and age structure, demographic changes have been associated with other transitions, including the 'epidemiological' (Omran, 1971, 1998), the 'health' (Frenk et al., 1991; Vallin and Meslé, 2004) and the 'mobility' (Zelinsky, 1971) transitions. Otherwise, recent changes in family dynamics, roles and behaviours have been described as the 'Second Demographic Transition' (Lesthaeghe, 2014, 2020), while long-term changes in family structures and kinship networks (Murphy, 2011) have led to describing the 'Demographic Transition' as a 'kinship transition' (Verdery, 2015).

In terms of kinship, increasing longevity and declining fertility have resulted in the emergence of the 'beanpole' family structure. As vertical kin become more prevalent and horizontal kin less so, this process is also referred to as the 'verticalisation' of the family.

This is characterised by an increase in the number of living generations, including children, parents, grandchildren, grandparents, great-grandchildren, and great-grandparents, and a decrease in the number of individuals within each generation (Bengtson et al., 1990). Declines in mortality have increased the survival of parents and grandparents, thereby enhancing the potential for relationships across multiple generations (Jiang, 1995; Uhlenberg, 1996; Bengtson, 2001; Murphy, 2010a, 2011). However, declining fertility has reduced the number of living grandchildren for the elderly (Murphy, 2010a, 2011), while postponing fertility has widened the intergenerational gap, counteracting the rise in the number of living generations (Lundholm and Malmberg, 2009).

Cross-national comparisons have shown considerable variation in the timing of grandparenthood across Europe and the United States, whereas its duration appears to depend on the timing of fertility (Leopold and Skopek, 2015). Other studies have identified trends towards delayed grandparenthood in Canada (Margolis, 2016); a high prevalence of three generations of living kin (parents, children and grandchildren) among adults in the United States (US), particularly those in their fifties and with low level of education (Margolis and Wright, 2016); longer periods of healthy grandparenthood with substantial differences by race/ethnicity and education in the US (Margolis and Wright, 2017), and educational differences in the transition to grandparenthood in West Germany (Skopek and Leopold, 2017). The above patterns illustrate how demographic change affects the number and structure of living generations, raising questions about the number of ancestors available throughout individuals' life courses, the duration of their coexistence, and how this has changed over time. Furthermore, despite the growing interest in multigenerational dynamics, the availability of ancestral kin, including not only parents and grandparents, but also great-grandparents, remains underexplored in demographic literature.

Such an analysis requires a long historical perspective, which is challenging given the scarcity of demographic data, including information on family relationships. Researchers have therefore turned to demographic modelling techniques, notably analytical methods and microsimulation, to reconstruct and project kinship networks. These models have been used to study various phenomena, including long-term changes in kin availability and the coexistence of multiple generations, also referred to as 'generational overlap' (Jiang (1995); Perrenoud (1998); Margolis and Wright (2017); Alburez-Gutierrez et al. (2021, 2023)).

Analytical approaches have been used, for example, to estimate how much of the potential created by mortality decline for spending more years as a child, parent, or spouse, and combinations of these statuses, has been realised in the US (Watkins et al., 1987). Another study estimated the overlapping years between grandparents and grandchildren (so-called 'multigenerational exposure') to assess the effect of twentieth-century fertility and mortality trends on increasing shared lifetimes in the US (Song and Mare, 2019). Using formal demographic kinship models (Caswell, 2019; Caswell and Song, 2021), researchers examined how the demographic transition affects the size and structure of living kin in China, India, and Japan (Jiang et al., 2023) and analysed changes in the number and ages of female kin throughout the demographic transitions in Thailand, Indonesia, Ghana, and Nigeria (Jiang et al., 2025). The formal demography of kinship has recently been extended to calculate the mean and variance of the overlap with kin of any type over a lifetime of a focal individual ('lifetime kin overlap') (Caswell and Vries, 2025). This measure combines the time-invariant matrix kinship model with a Markov Chain with Rewards model to capture lifetime overlap. However, the model has not yet been developed for time-varying rates, which the authors consider to be an open research question.

Microsimulation methods have also been used to study kinship dynamics over long periods using time-varying rates. Murphy (2004) employed the SOCSIM microsimulation model to examine patterns of descent over five centuries, considering pre-transitional (1250-1850) and post-transitional (1750-2350) demographic regimes. In subsequent work, he investigated changes in the mean numbers of different kin types and in the percentages of the population with those kin, by age group, for selected years (Murphy, 2010a,b) and birth cohorts (Murphy, 2011), across the First and Second Demographic Transitions in Britain. These analyses have highlighted substantial changes in kin availability by age, the extent and direction of which depend on the type of kin. They also revealed an ageing of generational relationships, including the postponement of life course events such as parental death, and a rising importance of multigenerational relationships following an increase in the proportions of individuals with living parents and grandparents. Furthermore, Verdery (2019) examined the effects of current and future demographic rates on family and kinship structures in China, particularly changes in the numbers of living kin by sex and age and in the proportions of the kinless.

Some SOCSIM-based analyses have more directly measured generational overlap. Researchers have estimated the numbers and proportions of elderly individuals who have living children and grandchildren during their lifetime in the US (Wachter, 1997; Margolis and Verdery, 2019), and the effect of changing demographic rates on the family support available for the elderly in China (Jiang, 1995). A global study estimated trends in parental and grandparental 'sandwichness', defined as being squeezed between dependent (grand)children and frail older parents, at the global, regional, and country levels (Alburez-Gutierrez et al., 2021).

Whilst prior research has used demographic models to examine kinship structures and generational overlap, a systematic account of the availability of ancestors throughout the life course over extended periods remains underdeveloped. In particular, there is limited evidence of long-term trends in the number of parents, grandparents, and great-grandparents alive at different ages, and the lifetime shared with them, across different demographic regimes. Furthermore, despite the well-documented differences in male and female mortality, existing studies rarely disaggregate ancestor availability by sex. The inclusion of great-grandparents and a life-course perspective tracking long-term cohort-level changes from birth to death also remains largely absent from the literature.

Adopting a long-term historical perspective is essential for identifying continuities and changes in lifetime overlap with ancestors throughout the demographic transition. However, this requires a context in which such extensive demographic data is available, as well as methods capable of reconstructing kinship networks and measuring lifetime overlap under time-varying demographic rates. Sweden's comprehensive national population statistics, which date back to the mid-eighteenth century and include detailed records of births and deaths, make it an ideal case study for simulation.

This study uses demographic microsimulation (1751–2100) to reconstruct and project patterns of ancestor availability for cohorts born between 1751 and 2000, measuring the mean number of living ancestors at birth, the distribution of living generations at birth and at age 20, and the years shared with them across the cohorts' life course (0–100). By analysing age and cohort patterns and changes in the lifetime overlap with ancestors, the study sheds light on how long-term demographic changes have increased opportunities for intergenerational relationships, support and caregiving. While the analysis is based on the Swedish context, the approach can be applied to other settings and is relevant to wider discussions about ageing populations and family change.

Data and Methods

To examine the availability of living ancestors at different ages of individuals' life courses, a large synthetic population was simulated using the SOCSIM demographic microsimulation programme and Swedish fertility and mortality data from 1751 to 2100. The model provides a complete record of every synthetic individual who has ever been alive during the simulated period, including details of vital events such as births and deaths, as well as kinship relationships. This enabled the reconstruction of the kinship networks of all individuals in the synthetic cohorts born from 1751 to 2000, and the estimation of their lifetime overlap with ancestors.

SOCSIM is an open-source microsimulation programme, originally developed at the University of California, Berkeley, and written in C programming language (Hammel et al., 1976), which has been used for decades in demographic research. The simulator requires two inputs: an initial population file containing information on the synthetic individuals' sex and date of birth, and monthly age-specific fertility rates and age-specific probabilities of death that apply to individuals of a given sex, and optionally marital status and group[1], over the simulated period. If parity-specific fertility rates are available, they can be included using conditional age-specific rates by birth order. If only sex- and age-specific rates are available, the same set of demographic rates can be applied regardless of marital status, group or parity, using SOCSIM's default rules. In such cases, individuals are not differentiated by group or marital status and parity does not affect the stochastic exposure to sex- and age-specific rates. During the simulation, SOCSIM schedules and executes demographic events (births, marriages and deaths) for each synthetic individual in the initial population and their descendants.

The operation of the microsimulator is described in Socsim Oversimplified (Mason, 2016) and is summarised below. At the beginning of each simulation segment (i.e. when demographic rates or societal constants change) or month, SOCSIM schedules a future event for each synthetic individual. Only one event can be scheduled for each individual at any one time. Following the execution of an individual's event (excluding deaths) or a change in marital status or parity, a new event is scheduled for that individual. The next event to be scheduled is determined by generating random waiting times based on sex- and age-specific rates, and, optionally, group and marital status. Once waiting times have been randomly generated for all potential events, the event with the shortest waiting time is selected and scheduled. Event competition thus follows a competing-risks framework, whereby the probability of an individual experiencing each event for which they are at risk, given their sex, age, and marital status, is independent of the probabilities of the

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[1] In SOCSIM, individuals are considered to belong to a single 'group' by default. However, the simulator has the option of creating 'groups' within the synthetic population and defining different rates for their members based on characteristics such as ethnicity, location, health status, wealth, and education. This option, nevertheless, requires highly disaggregated data, which are rarely available.

others. All scheduled events are executed sequentially in a random order. Subsequently, SOCSIM increments the month and repeats the event-execution process. At the end of the simulation, SOCSIM creates an output population file containing information about every synthetic individual who has ever lived, and a marriage file containing information about each simulated marriage. The output population file contains one row for each individual, including their personal identification number ('pid'), sex, dates of birth and death, the pid of some of their close kin, and other variables. Using the pid of individuals and their parents, it is possible to reconstruct each individual's kinship network.

One large simulation was run using the 'rsocsim' R-package (Theile et al., 2023), with an initial population of 50,000 synthetic individuals and age-specific rates obtained from the Human Fertility Collection (HFC), the Human Fertility Database (HFD) and the Human Mortality Database (HMD) over 1751–2023 and the World Population Prospects (WPP) 2024 Revision (United Nations, 2024) over 2024–2100. HFD and HMD data were retrieved via the 'HMDHFDplus' R-package (Riffe, 2015). To ensure consistency between historical and projected mortality data, the HMD life tables were closed at age 100, with the final age interval limited to one year to align with the WPP life tables. For fertility rates, the open-ended age intervals were also limited to one year, while retaining the age ranges provided by each source: HFC [14–50], HFD [12–55], and WPP [14–50]. While the estimates differ slightly between sources, the variation appears minimal when comparing the datasets from 1950 to 2023, for which HMD, HFD and WPP data are all available (see figure A1 in the Appendix).

In the absence of age-specific marriage rates by sex for the entire period, the rsocsim 'marriage after childbirth' directive was used to define lifelong partnerships and select living, single partners whenever a previously single woman gave birth. Despite its name, this directive corresponds to lifelong partnerships rather than to actual marriages in a sociological sense. Following Alburez-Gutierrez et al. (2021), partners for each woman were selected from all living single men to minimise the squared difference between the observed distribution of 'man's age - woman's age' and a normal distribution with a mean of two and a standard deviation of three. This lifelong partnership is formed when a previously single woman becomes a mother for the first time. Candidates are limited to single men selected according to the desired distribution of age differences, without considering other characteristics. The partnership formed at the time of the first birth is used to assign paternity to subsequent births while both partners are alive. In terms of the event schedule and execution, individuals remain independent: women are exposed to fertility rates, and both sexes are exposed to sex-specific mortality rates. If a partner dies, a new partner can be assigned for subsequent births. Otherwise, the same partner is assigned as the father. Further information on this directive can be found in the supplemental material of Alburez-Gutierrez et al. (2021).

Following the standard procedures of previous SOCSIM studies, the simulator was initially run for 100 years using the first available set of age-specific rates (1751) to produce a stable age structure. After a century of demographic stability, the population had tripled to 150,000 individuals by the beginning of 1751. These individuals were then exposed to the corresponding annual rates for the period 1751–2100. The size of the synthetic population reached approximately one million individuals in the 1970s. After this, it decreased slightly, reaching around 650,000 by the end of the simulation in 2100. The accuracy of the microsimulation output was assessed by comparing the age-specific fertility and mortality rates and the summary measures (total fertility rate and life expectancy at birth) derived from the simulation inputs (i.e., HFC, HFD, HMD and WPP 2024) and outputs. Figure A2 in the Appendix shows that the output estimates are broadly consistent with the inputs.

From SOCSIM outputs, three types of measures were computed for Swedish synthetic cohorts born between 1751 and 2000: the mean number of parents, grandparents, and great-grandparents alive at birth; the number of living generations at birth and at age 20, and the mean number of overlapping years with each type of ancestor throughout the life course. Great-great-grandparents were also included in the calculations to ascertain their relevance to the analysis. However, their numbers are negligible for most cohorts and are shown only when they exceed zero or are meaningful.

Following Song and Mare (2019) and Caswell and Vries (2025), lifetime overlap with ancestors was measured in three complementary ways. *Overlap with any ancestor* refers to the sum of the years throughout the individuals' lives during which they have at least one living parent, grandparent or great-grandparent of each sex. This lifetime *overlap with any ancestor* considers both the mean total number of years of overlap with at least one living ancestor of each generation and sex and the proportion of individuals in each cohort who at each age have at least one living ancestor of each generation and sex. The former indicates the potential for interaction with ancestors throughout life, whereas the latter shows how this potential changes with age.

Overlap with all ancestors corresponds to the sum of the person-years of overlap with all living ancestors of each generation and sex throughout each individual's life. Lifetime *overlap with all ancestors* considers both the total person-years of overlap with all living ancestors of each generation and sex, and the mean number of ancestors of the same generation and sex who are alive at each individual's age. The former indicates the extent of lifetime opportunities for intergenerational interaction, while the latter shows how the number of coexisting ancestors within the same generation changes with age. Finally, *overlap per ancestor* considers the above *overlap with all ancestors* of a given generation and sex, divided by the expected number of such ancestors. This provides a more intuitive measure by limiting the years of overlap to an individual's lifetime and accounting for differences among ancestors of the same generation and sex.

Results

Using the SOCSIM output, the lifetime overlap between the Swedish synthetic cohorts born between 1751 and 2000 and their ancestors was measured, considering the number of living ancestors, the years of overlap with them across the cohorts' life courses, and the cohorts' distribution of the number of living generations.

The number of ancestors available to individuals in each cohort at birth is an appropriate starting point for the analysis. Figure 1 shows the mean number of ancestors alive at birth, disaggregated by the ancestors' generation and sex. As expected under the setup, the number of living mothers and fathers in the same month of ego's birth is exactly 1 for all cohorts. The number of grandparents and great-grandparents alive at birth has increased relatively steadily for cohorts born after 1850, with higher numbers for female than male ancestors (solid and dashed lines, respectively). Individuals born before 1850 had around 0.2 more grandmothers than grandfathers alive at birth, with a slightly smaller sex difference for the earliest cohorts. They also had around 0.05 more great-grandmothers than great-grandfathers alive at birth. The sex gap in the number of living grandmothers and grandfathers at birth has decreased slightly for cohorts born after 1850, with fewer than 0.2 more grandmothers than grandfathers among those born after 1900. However, the sex gap in the number of great-grandparents has substantially increased across post-1850 cohorts, reaching more than 0.6 great-grandmothers than great-grandfathers among those born in 2000. The mean number of great-great-grandparents is negligible for most cohorts, except for those born after 1960, for whom there has been a slight increase, particularly in the number of great-great-grandmothers.

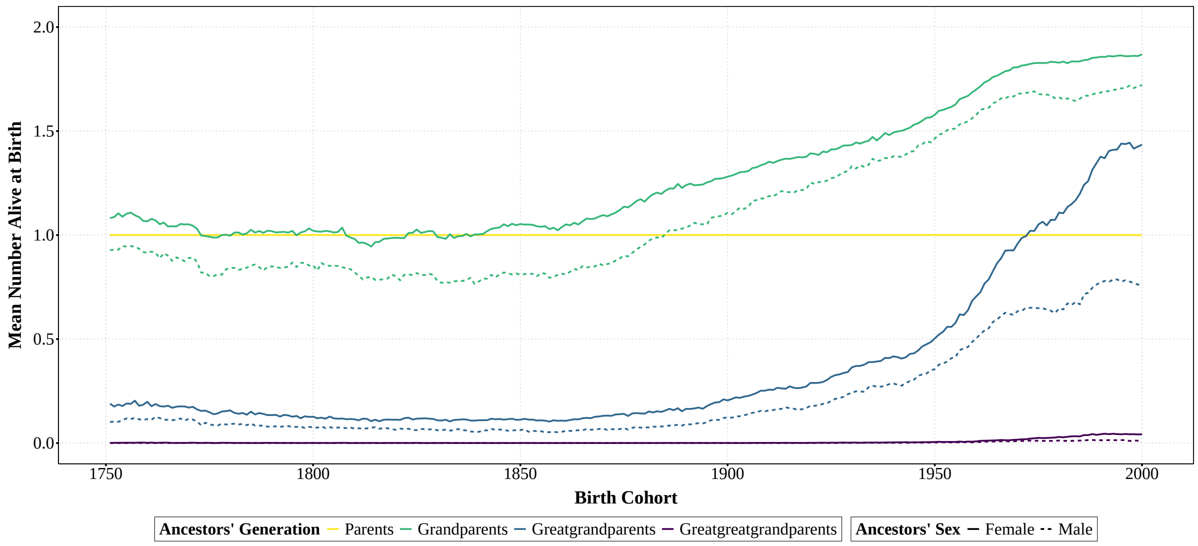

Figure 1: Mean number of ancestors alive at birth, by ancestors' generation and sex, for Swedish synthetic cohorts born 1751—2000

Alongside changes in the mean number of living ancestors at birth, the distribution of living generations at birth has varied across cohorts (see the 'Age 0' panel at the top of Figure 2). The majority of individuals in the eighteenth- and nineteenth-century cohorts were born into three-generation families (with at least one parent and one grandparent alive), exceeding the proportions born into two-generation families (with only one parent alive) or four-generation families (with at least one great-grandparent alive). Among twentieth-century cohorts, the proportion of individuals born into two- or three-generation families decreased, whereas the proportion born into four-generation families increased substantially, with the largest share (around 75%) among those born in 2000. The proportion of individuals born into five-generation families (with at least one great-great-grandparent) also shows a slight increase among post-1950 cohorts.

As the population ages, the distribution of the number of living generations changes (see the 'Age 20' panel at the bottom of Figure 2). Considering an age threshold of 20, approximately one quarter of people born before 1850 had at least one living grandparent (three generations), over half had at least one living parent (two generations), and the rest had no living ancestors (one generation). Conversely, the proportion of individuals who had at least one parent and one grandparent alive by the age of 20 (three generations) has increased for people born after 1850, while the proportion who had only one parent (two generations) or none (one generation) has decreased. This suggests that both parents and grandparents of the post-1850 cohorts experienced greater longevity. The proportion of individuals with at least one great-grandparent alive by the age of 20 (four generations) has also increased slightly among post-1950 cohorts.

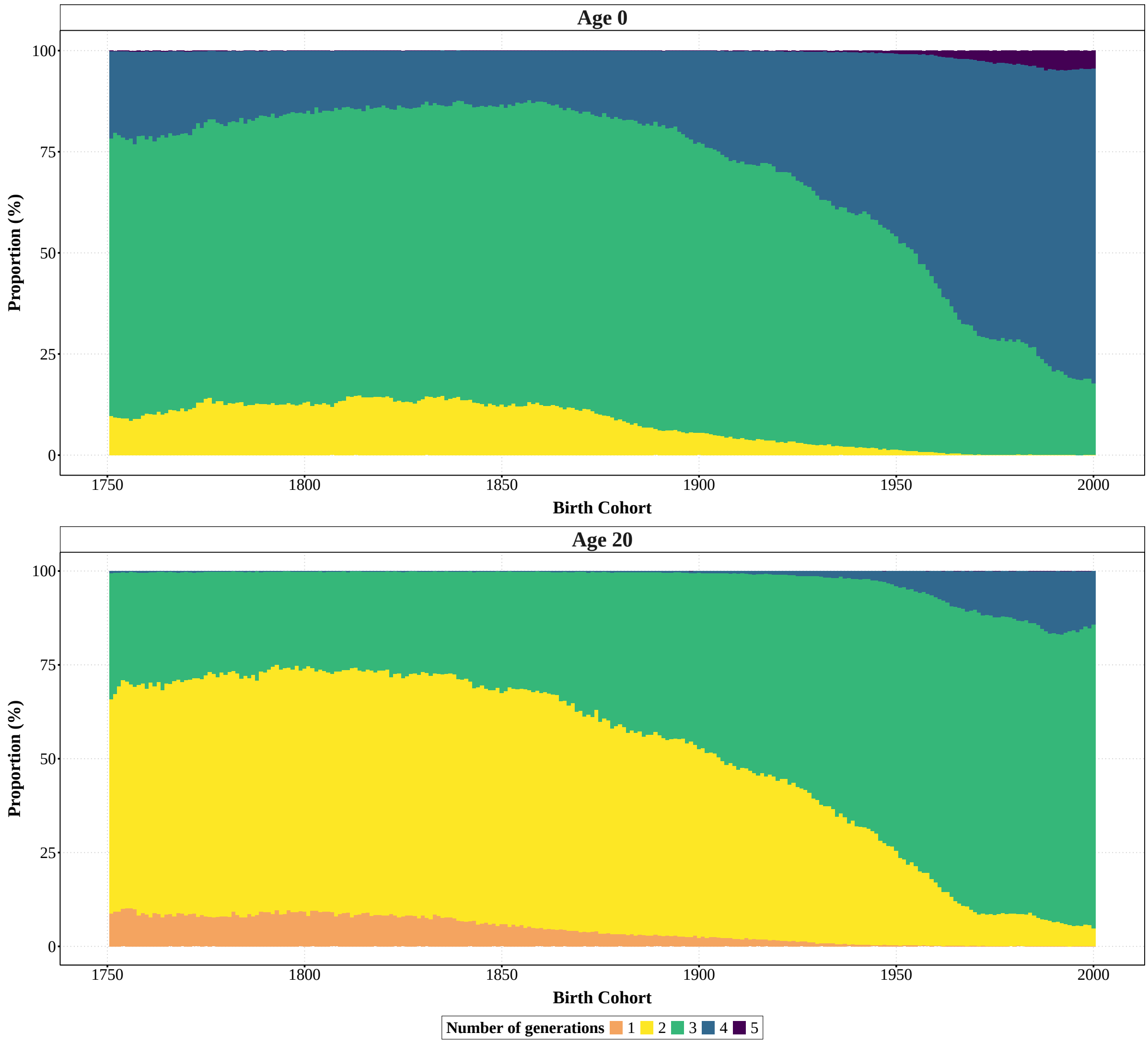

Figure 2: Distribution of the number of generations (ego and ancestors) alive at ego's birth and age 20 for the Swedish synthetic cohorts born 1751–2000

The increasing lifetime overlap with multiple generations of ancestors can be better understood by examining the average years of overlap with at least one living ancestor of each generation and sex throughout the life course (0-100 years) of the synthetic cohorts. Figure 3 shows that there is an overall increase in lifetime overlap with most ancestors, but the starting point and extent of this improvement vary between generations. The lifetime individuals share with their parents, grandparents, and great-grandparents increases substantially among the post-1800, post-1850, and post-1900 cohorts, respectively. The most substantial increase in lifetime overlap is observed with parents, followed by grandparents and, to a lesser extent, great-grandparents. However, this overlap appears to be greater for female ancestors than for male ones, and it has increased more for the former. Considering cohorts born in the mid-eighteenth and late-twentieth centuries, the increases in lifetime overlap are approximately 40 years with mothers, 36 years with fathers, 27 years with grandmothers, 23 years with grandfathers, 9 years with great-grandmothers, and 5 years with great-grandfathers. The increase is negligible for great-great-grandparents, but it is still slightly greater for great-great-grandmothers.

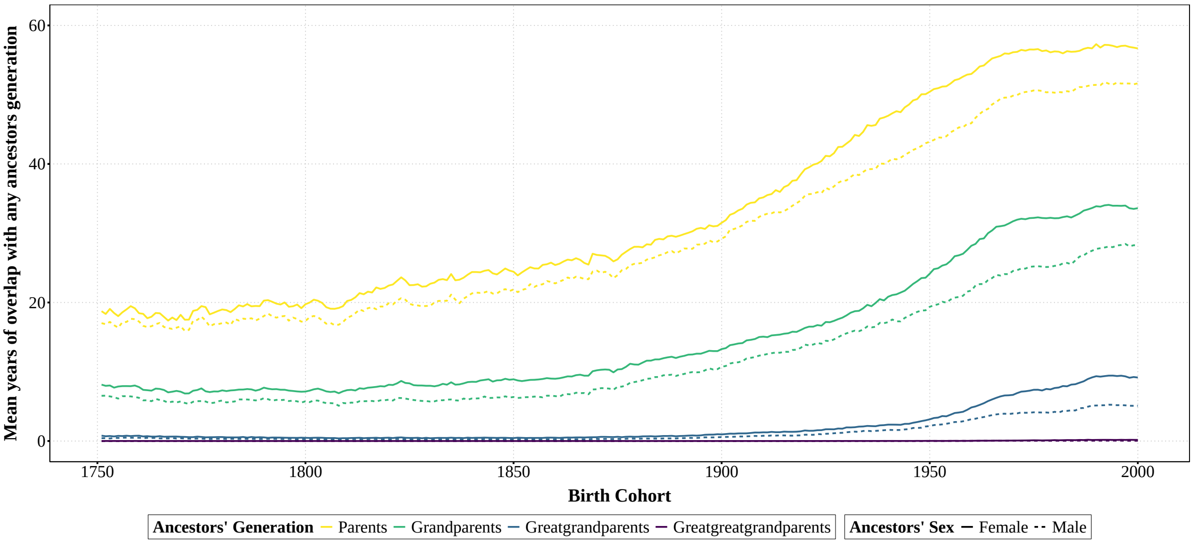

Figure 3: Mean overlapping years with at least one living ancestor, by ancestors' generation and sex, for Swedish synthetic cohorts born 1751—2000

Beyond the total years of overlap, the proportion of living individuals in each cohort who, at each age (0–100), have at least one parent, grandparent or great-grandparent of each sex alive shows the changes in potential overlap with each ancestral generation over the life course of these synthetic cohorts (1751–2000). Figure 4 shows a consistent increase in the proportion of the population who have at least one living ancestor of each generation across all birth cohorts (the darker the colour, the greater the percentage), as well as in the maximum age until which the overlap is experienced (changes on the y-axis). The proportion of the population that has experienced generational overlap with parents and grandparents is substantial across all cohorts, whereas overlap with great-grandparents is relevant only to individuals born in the twentieth century.

The majority of individuals across all birth cohorts spend their early years of life with their parents alive. However, as both individuals and their parents age, the proportion of people who overlap with them decreases, whereas the duration of overlap increases across cohorts. In the pre-1800 cohorts, the age-specific proportions of individuals who experienced overlap remained relatively stable, and only a minimal proportion (less than 5%) overlapped with their mothers after age 56 and with their fathers after age 53. In the nineteenth-century cohorts, there was a slight increase in the length of overlap, but only a small proportion of individuals (5%) had both their mother and father alive at ages 60 and 57, respectively. However, the proportion of individuals who overlap at each age increased gradually. In the case of the twentieth-century cohorts, a greater proportion of individuals experience overlap with their parents into older ages, as the age-specific proportions increased with age across cohorts (see the rise in the 50% threshold in Figure 4). Nevertheless, no more than 5% of the 2000 cohort are likely to experience overlap with their mothers after the age of 73 or with their fathers after the age of 70.

The proportion of individuals who overlapped with at least one of their grandmothers or grandfathers throughout their lifetime remained relatively stable for cohorts born before 1850, increasing slightly for those born in the late nineteenth century. Among the pre-1850 cohorts, fewer than 5% of individuals had overlap with any of their grandmothers or grandfathers after ages 30 and 27, respectively. Among the late nineteenth-century cohorts, there was a slight increase in the proportion of individuals who overlapped with any of their grandmothers or grandfathers in their early years (see changes in the 50% threshold), as well as in the maximum length of overlap (see 5%), albeit to a lesser extent. The twentieth-century cohorts experienced the largest increase in lifetime overlap with any grandmother or grandfather, in terms of both the proportion of individuals sharing their lifetimes (see changes in the 95% and 50% thresholds) and the maximum length of life shared with their ancestors (see 5% threshold). However, there have been only negligible changes in the lifetime overlap with any great-grandmother or great-grandfather, which becomes only noticeable among twentieth-century cohorts, particularly those born after 1950.

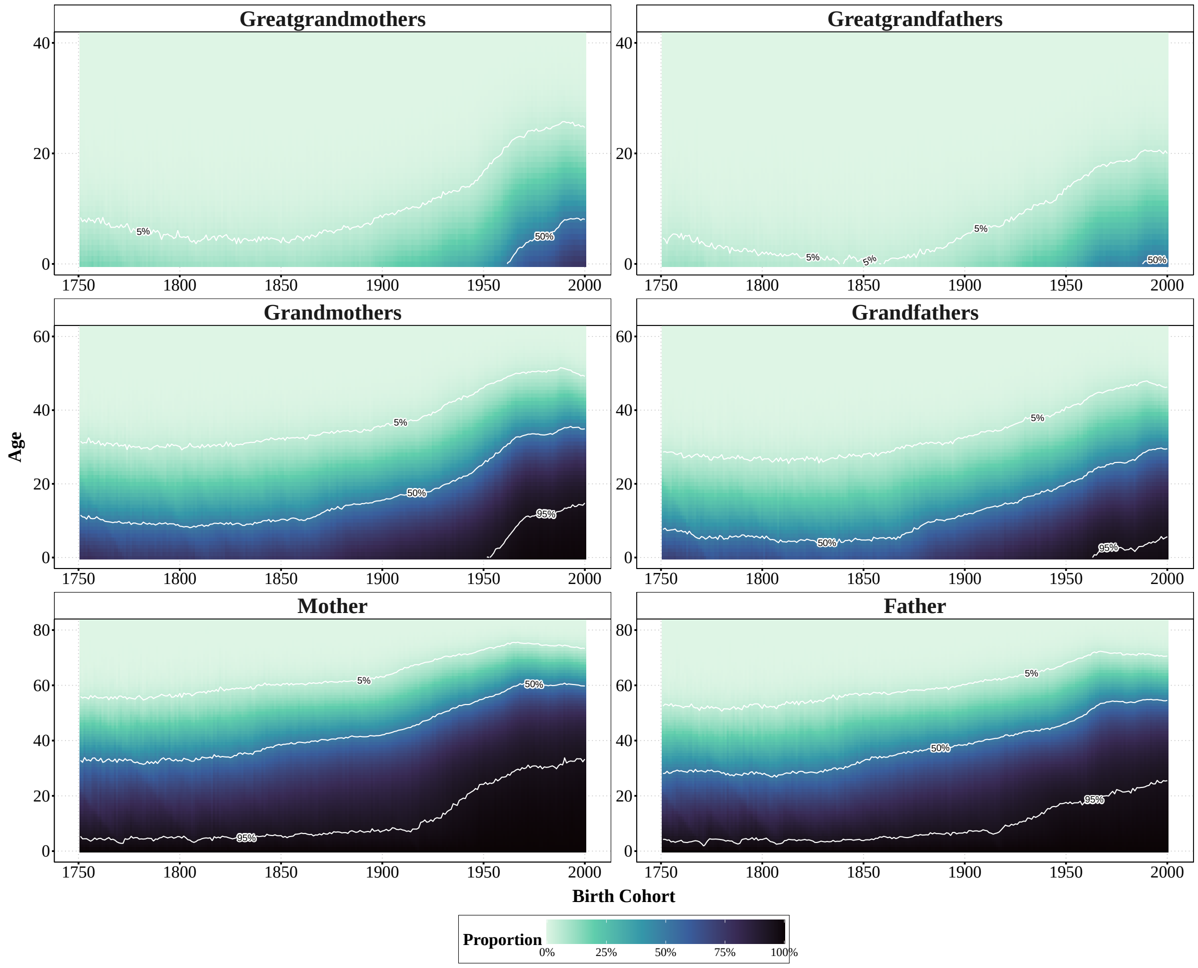

Figure 4: Proportion of individuals in the Swedish synthetic cohorts born 1751—2000, with at least one ancestor alive at each age, by ancestors' sex and generation

While the existence of at least one living ancestor of a given generation indicates the potential for interaction with each generation, the total number of years that an individual overlaps with all their ancestors of a given generation indicates the extent of the opportunities available to them for such intergenerational interaction. Figure 5 illustrates the aggregate person-years of *overlap with all living ancestors* over the life course of the synthetic cohorts (1751–2000), disaggregated by the sex and generation of the ancestors. To represent the accumulation of person-years, the estimates for each type of ancestor within each generation and sex (e.g., maternal and paternal grandmothers) are stacked on top of each other. Within each generation, the overlap with each maternal ancestor is displayed in lighter colours stacked at the top (e.g. maternal grandmother in beige), and the overlap with each paternal ancestor is displayed in darker colours stacked at the bottom (e.g. paternal grandmother in fuchsia). The *overlap with all ancestors* shows analogous trends to those delineated for the *overlap with any ancestors* (see Figure 3). However, it reveals slight differences among ancestors of the same generation (e.g., maternal and paternal grandmothers), notably that the overlap is slightly longer with maternal ancestors (lighter colours) than with paternal ancestors (darker colours).

The *overlap per ancestor* provides an additional measure that limits the years of overlap to an individual's lifetime, by averaging the *overlap with all ancestors* (Figure 5) across the expected number of ancestors in each generation and sex (e.g., two grandmothers). The *overlap per ancestor* is consistent with the figures previously outlined for *overlap with any ancestors* (see Figure 3). However, it shows slightly lower values (see Figure A3 in the Appendix) because certain ancestors, with shorter lifetimes, may reduce the average overlap. These individuals are likely male or from the paternal side.

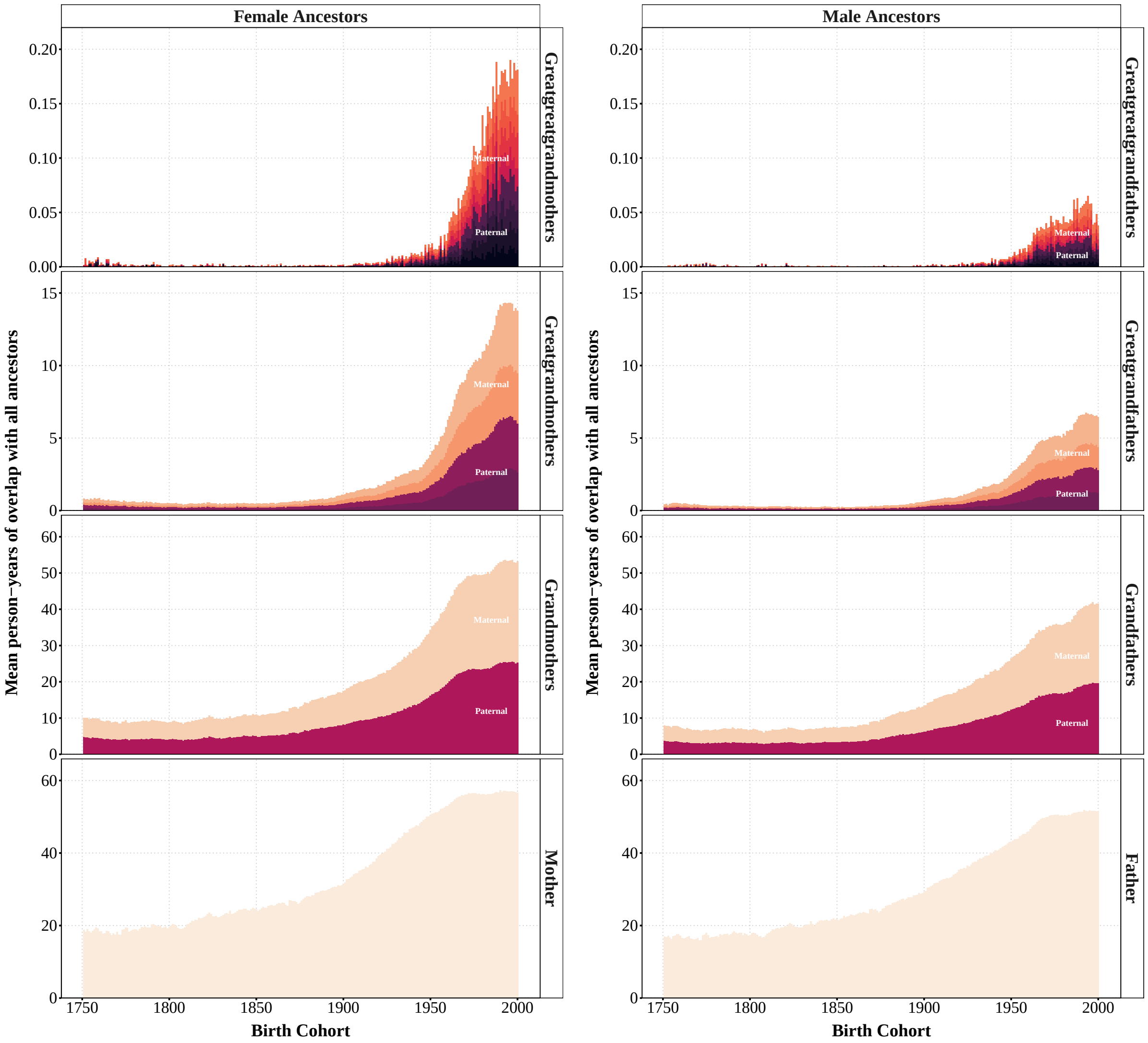

Figure 5: Mean overlapping person-years with all living ancestors, by ancestors' sex and generation, for Swedish synthetic cohorts born 1751—2000. The years of overlap are displayed in lighter colours for maternal ancestors, stacked at the top of each panel, and in darker colours for paternal ancestors, stacked at the bottom.

The mean number of same-generation ancestors alive at each age of the synthetic individuals provides a final perspective on their lifetime overlap with ancestors (see Figure 6). In all synthetic cohorts, individuals are born with one living mother and one living father, but this ratio declines with age as some individuals begin to lose their parents. However, the age at which almost all individuals still have a living mother and a living father (see area below the 0.99 threshold) increases across cohorts, particularly for those born in the twentieth century. The mean number of grandmothers and grandfathers in the early years of life is nearly one for individuals born before 1850, but it increases for those born thereafter, approaching two grandparents of each sex among late-twentieth-century cohorts. Moreover, the age at which individuals still have more than one living grandmother or grandfather increases across cohorts, particularly for post-1950 cohorts, reaching nearly 1.5 grandmothers at age 20 for individuals born in 2000. Otherwise, the mean number of living great-grandparents is almost negligible, even in early life, for cohorts from the eighteenth and nineteenth centuries. However, the number increases for twentieth-century cohorts, particularly for those born in the final two decades, who overlap with one great-grandmother, or even more, in their infancy.

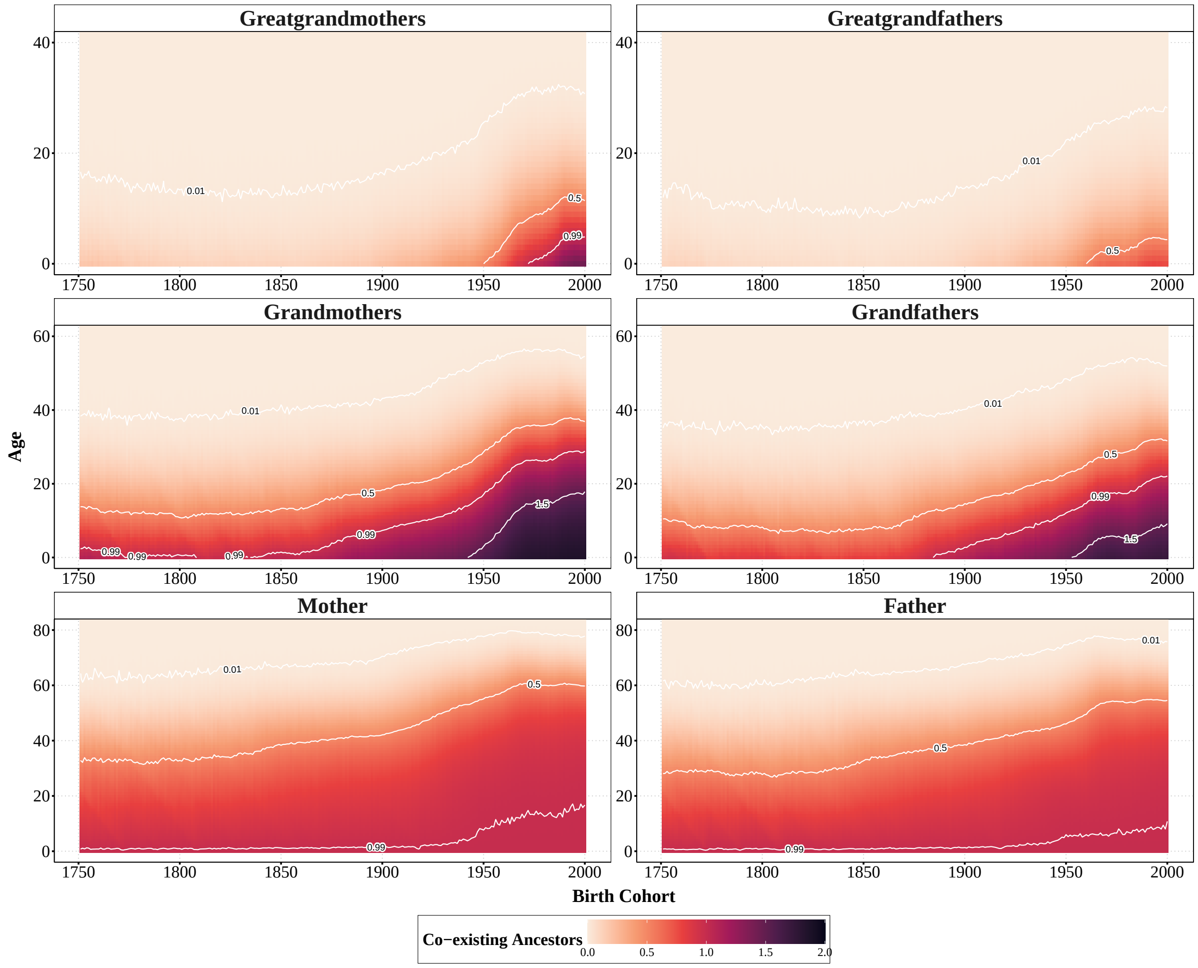

Figure 6: Mean number of co-existing ancestors alive at each age for the Swedish synthetic cohorts born 1751—2000

Discussion

Long-term demographic changes, particularly declining mortality rates and increasing life expectancy, have expanded opportunities for different generations to share lifetimes and interact. However, our understanding of the availability of parents, grandparents and great-grandparents throughout the life course, and of the years of life shared with them, remains limited, especially when considering extended historical and projected periods. This study used SOCSIM demographic microsimulation and Swedish fertility and mortality data (1751—2100) to estimate patterns of ancestor availability throughout the life course (0–100) of Swedish synthetic cohorts born between 1751 and 2000. The analysis focused on the mean number of ancestors alive at birth in each cohort, the distribution of living generations at birth and at age 20, and the mean number of years they overlapped with their ancestors throughout their life courses.

The results show an overall increase in the lifetime overlap between individuals and their ancestors across cohorts. However, the starting point and extent of this improvement vary across ancestral generations. The overlap is more substantial with parents and grandparents than with great-grandparents, while its duration increases across cohorts born after 1850, due to an increase in the maximum age of overlap. The results also reveal a consistent sex gap in the number of living ancestors. Individuals are more likely to have lifetime overlap with female ancestors, especially grandmothers and great-grandmothers, than with their male ancestors.

The observed increase in the number of living ancestors, particularly among the post-1850 cohorts, reflects broader demographic and kinship changes. Although the rise in life expectancy may have begun before the eighteenth century and the collection of national statistics in Sweden, it has become more consistent since the mid-nineteenth century (Wilmoth, 2000), likely due to improvements in health and mortality. At that time (1840), Swedish women exhibited the highest recorded life expectancy among the countries examined by Oeppen and Vaupel (2002). Further improvements in mortality over the twentieth century have resulted in a greater number of ancestors surviving into advanced ages and sharing a longer lifetime with their descendants, although the number of descendants has decreased due to a decline in fertility (Jiang, 1995; Uhlenberg, 1996; Bengtson, 2001; Murphy, 2010a, 2011). This phenomenon is associated with the process of 'verticalisation' of the family, reflected in the increased lifetime overlap with ancestors and the growing number of living generations observed in this study.

Otherwise, the consistent sex difference in the availability of ancestors may be associated with the emergence of the female longevity advantage. In pre-industrial times, women's health was considered more fragile due to high maternal mortality rates and diseases that only affected women. However, reductions in fertility and maternal mortality, especially in the burden of infectious diseases, have resulted in a significant increase in life expectancy over the past few centuries (Goldin and Lleras-Muney, 2019). The greater number of survivors in early life led to healthier cohorts who were less susceptible to health disorders or chronic diseases later in life. As the burden of infectious disease fell, both sexes lived longer, but women were impacted more greatly. The female longevity advantage first emerged in Europe in the early nineteenth century and in the US in the late nineteenth century. However, it seems to have emerged even earlier in Sweden, likely due to a less severe infectious disease environment (Goldin and Lleras-Muney, 2019). This could explain why the greater availability of female ancestors is evident across all cohorts in this study.

Previous studies using SOCSIM have examined the long-term changes in the availability of different kin types, including parents and grandparents, in Britain (Murphy, 2010a,b, 2011) and in China Verdery (2019). These analyses have also demonstrated a significant increase in the number of living parents and grandparents, as well as in the proportion of individuals with these ancestors alive at various ages, over several centuries. However, these studies have focused on mean numbers and proportions of individuals with these kin, rather than measuring lifetime overlap. In contrast, SOCSIM studies that have measured generational overlap have focused either on kin available to the elderly (Jiang, 1995; Wachter, 1997; Margolis and Verdery, 2019) or on trends in parental and grandparental ‘sandwichness’ (Alburez-Gutierrez et al., 2021), but have not measured availability throughout the life course. The present analysis provides a complementary perspective by estimating the mean number of living ancestors at birth, the distribution of living generations and the mean number of years of overlap with ancestors throughout the life course of birth cohorts born over two and a half centuries.

The microsimulation model used in this study has certain limitations that must be acknowledged. As highlighted by (Ruggles, 1993), microsimulation models do not consider the similarity in demographic behaviour between members of the same family. This could result in a more homogeneous distribution of kin compared to real populations and fewer extreme cases, particularly of exceptionally long-lived individuals. However, the number of parents and grandparents estimated from a SOCSIM microsimulation for Sweden using a similar setup was found to be consistent overall with the estimates derived from Swedish administrative registers for the cohorts born between 1915 and 2017. Future research could also compare the microsimulation estimates of the life course availability of parents and grandparents with those derived from Swedish administrative register data.

Otherwise, the analysis measures the potential for individuals to share years of life with their ancestors across different cohorts. However, it does not examine the realisation of such generational overlap, nor does it consider the dynamics of intergenerational contact, exchange or care provision. Furthermore, the nature of intergenerational relationships and transfers is likely to have evolved significantly between the eighteenth century and the most recent cohorts. While these issues are beyond the scope of this study, they could be avenues for further investigation.

By analysing patterns of ancestral availability by cohort and age over the last centuries, this study highlights how demographic changes have shaped opportunities for intergenerational relationships, support and caregiving. Sharing a lifetime with more living ancestors for longer is likely to impact family dynamics, particularly in later life, and create opportunities for intergenerational transfers and care provision, which are essential in an ageing society.

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Data and code availability statement

The code to retrieve the data, run the microsimulations and reproduce the results is available online: `https://github.com/liliana-calderon/SOCSIM_Living_Ancestors`

Appendix

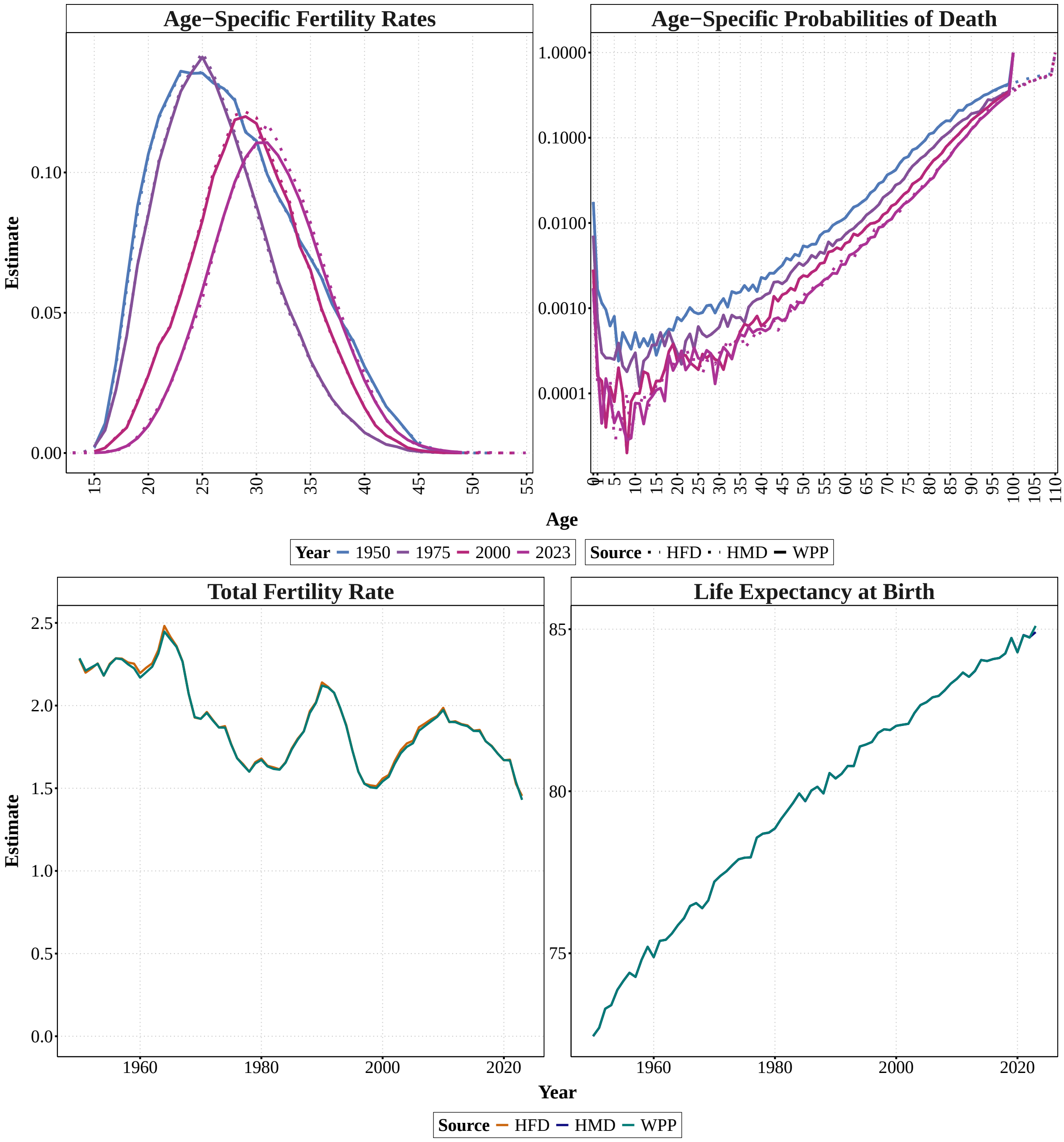

Figure A1: Age-specific and summary demographic measures for women in Sweden, retrieved from the Human Fertility Collection (HFC), the Human Fertility Database (HFD), the Human Mortality Database (HMD) and the World Population Prospects (qx in log-scale excluding NA)

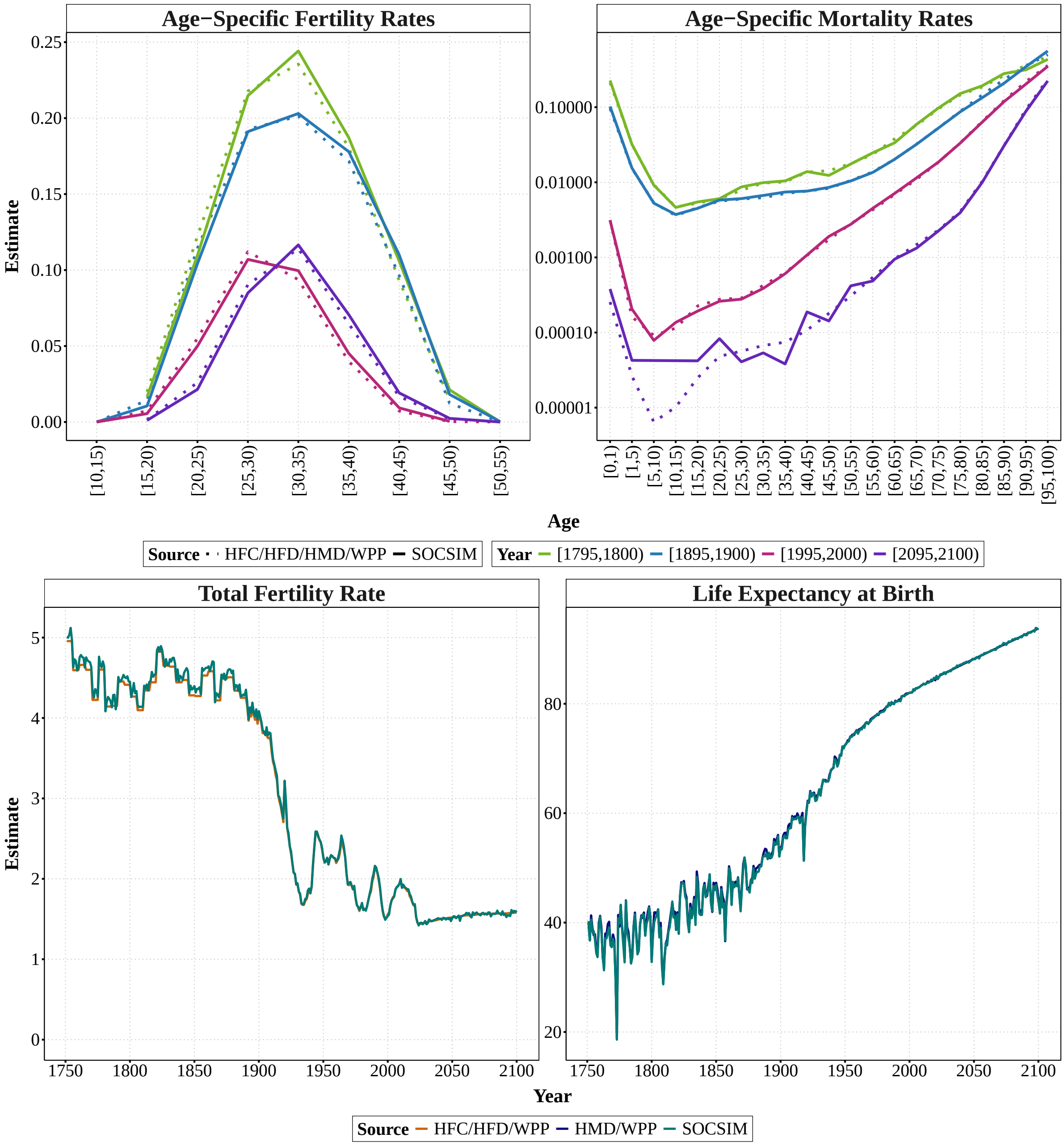

Figure A2: Age-specific and summary demographic measures for women in Sweden, retrieved from the input databases – Human Fertility Collection (HFC), the Human Fertility Database (HFD), the Human Mortality Database (HMD) and the World Population Prospects (WPP) – and SOCSIM output (ASMR in log-scale excluding NA)

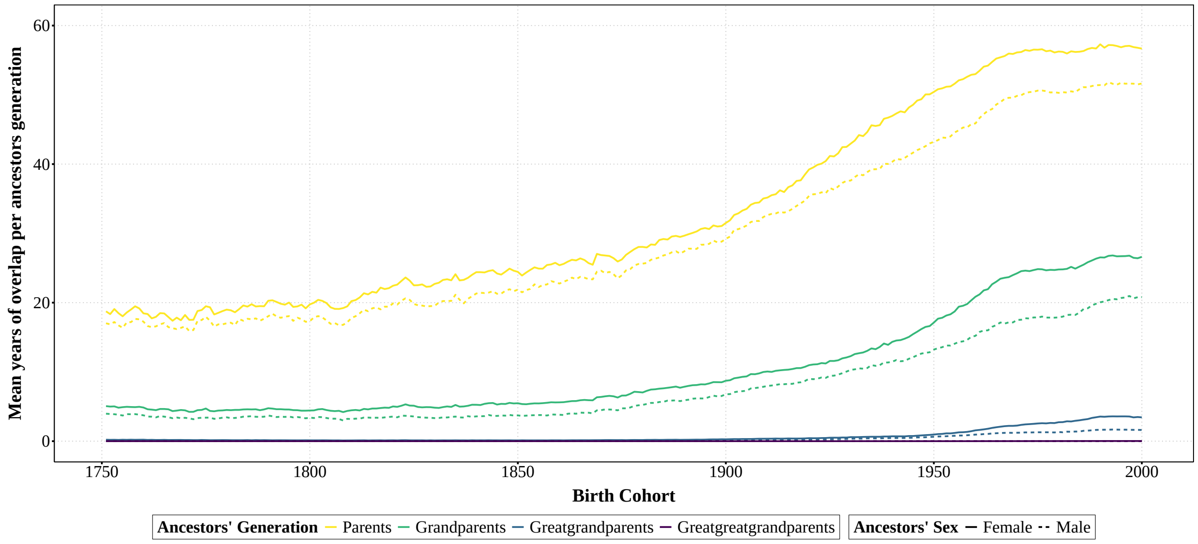

Figure A3: Mean overlapping years per each ancestor's generation, by ancestors' generation and sex, for Swedish synthetic cohorts born 1751—2000.

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