

Projecting Generational Placement Trajectories: Empirical and Simulated Populations in Norway

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Author contributions

B.H. and D.A.-G. conceived the study and designed the research. B.H. ran the simulations and conducted the analyses. B.H. led the writing of the manuscript, with support from D.A.-G. B.H. produced the visualizations. B.H. and D.A.-G. read and approved the final version of the manuscript.

Keywords

Intergenerational family; kinship; projections; shared lifetime; population heterogeneity; demographic change; population ageing; cohort change; mortality; fertility

Abstract

Much existing research in the demography of kinship focuses on quantifying the number and characteristics of living kin, such as age and sex. We know less about how individuals transition through different ‘generational placements’ over their life—for example, when and how long they are parents, children or experience overlap of multiple family generations. We use simulated micro-level data to project generational placement trajectories for life courses of the complete population of Norway born 1960 and 2000. Our microsimulations use age-specific fertility and mortality rates from 1846 to 2100. First, we benchmark projected trajectories for the 1960 cohort against observed trajectories from empirical register data from 1960 to 2019. Second, we project full life-course trajectories, from age 0 to 100, for the 1960 and 2000 cohorts. Results from sequence analysis show that generational placement trajectories efficiently capture individual-level heterogeneity in intergenerational kin availability and that results based on our simulated populations largely match those from empirical data. Over cohorts, typical generational placement trajectories will likely become more stable but “thinner”, with later (and shorter) demographic “(double) sandwiching” and increasingly frequent “fading family lines.” The analysis paves the path toward results on a global level and including projections for the future.

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Introduction

The (intergenerational) family structure is often understood as a product of socially stratified demographic behavior (L. Andersson and Kolk 2024). However, it constitutes an important component of social inequality in itself, structuring and affecting various aspects of individuals' lives. First, members of the intergenerational family (i.e., children, parents, and grandparents) are among the main providers and receivers of informal support of different kinds, ranging from emotional to instrumental (care). Second, intergenerational family transitions (i.e., the birth of children and grandchildren as well as parental death) are crucial life events that signify the start or end of holding some of the most fundamental social roles in life (e.g., being a parent or being a child). Third, (not) holding such roles was shown to be connected to an individual's emotional, physical, psychological (Hünteler and Hank 2025; Nomaguchi and Milkie 2020) as well as financial well-being (Benton and Keister 2017; Lersch et al. 2017). Thus, (not) having kin constitutes a correlate of various dimensions of social inequality and may even be understood as a dimension of social inequality itself, in the form of social capital or a 'relational reserve' (Cullati et al. 2018; Hünteler and Hank 2025).

Consequently, an increasing body of research is interested in the structural availability of intergenerational kin to individuals (Alburez-Gutierrez et al. 2022, 2023; Bel et al. 2025; Hünteler 2022; Kolk et al. 2023; Leopold and Skopek 2015a; Margolis and Verdery 2019; Song and Mare 2019), that is the number and kind of kin alive at a given age, for the past, present, and future. Also, lack of or ageing with limited intergenerational kin and its correlates have increasingly been investigated (e.g., Brown et al. 2022; Verdery et al. 2019), where the absence of descendants has been described as 'fading family lines' (Kolk and Skirbekk 2022), thus,

adding an extended view on the longer-standing tradition on childlessness studies (e.g., Kravdal 2021; Kreyenfeld and Konietzka 2017; Mynarska et al. 2015).

Family structures are dynamic, that is, changing over time, and the processes by which they evolve are central to understanding social inequality from a life course perspective. The timing, sequencing, and order in which family events happen (sequencing)—and consequently, the resulting family structures—vary between individuals, over historical time, and also across an individual’s life course. Such family life courses can be more or less standardized, that is, different between individuals, and differentiated, that is, variable or predictable across an individual’s life course (e.g., Brückner and Mayer 2005; Van Winkle 2018). Thus, the family structure, and thereby the availability and demand for support differs across life stages, between subgroups of the population, and by period (L. Andersson and Kolk 2024; Daw et al. 2016; Hünteler 2022). Moreover, the life stage and order in which family transitions occur can modify their impact on individuals’ lives (e.g., Hagestad 1988; Hünteler et al. 2025). For instance, experiencing parental death has been shown to be linked to declining levels of life satisfaction, but the decline was particularly strong for individuals who lost their parents relatively early in life (Leopold and Lechner 2015). Similarly, individuals who became grandparents relatively late in their life and only after their own parents had died were wealthier than individuals who became grandparents before they lost their own parents (Hünteler et al. 2025). Therefore, it is crucial to move beyond estimations of average family size in order to capture the full picture of available support networks over the life course, how they evolve dynamically, and the heterogeneity of individual family experiences (Daw et al. 2016; Zimmermann et al. 2024).

Previous research has introduced *generational placement trajectories* (GPT) as a framework to empirically examine such intergenerational life-course family structures (Hünteler 2022). These trajectories depict a person’s relative position within their intergenerational family and describe if, when, and for how long they are a child, parent, or

grandparent. At the same time, GPT also define life-course intergenerational family structures because they highlight which family members are alive at a given time, thereby indicating generational overlap between multiple family generations¹. Being embedded in the sequence analysis tradition, GPT also depict the standardization and differentiation of intergenerational family life courses.

The analysis of GPT requires extensive individual-level demographic data in which members of various generations can be linked. Surveys can be used to study GPT, but they face limitations given lower data quality, reporting bias, a focus on a narrow range of kin, and selective participation. Moreover, survey data are usually right-censored by the respondent's last participation in the survey, resulting in an underestimation of the prevalence of and age at grandparenthood as one crucial role in the intergenerational family system (Leopold and Skopek 2015a; Margolis and Verdery 2019). Administrative population registers can be used to overcome some of these limitations but they are only available for a few countries and periods although taking a long-term cross-country perspective in analyzing (intergenerational) family life-courses would be important (Van Winkle and Fasang 2021). Lastly, register data are also right-censored to the date of data extraction, so it is not possible to study later-life kinship dynamics for younger cohorts.

Given these data limitations, a separate stream of research has used demographic microsimulation to model kin availability for a range of kin and geographical contexts (Alburez-Gutierrez et al. 2023; Margolis and Verdery 2019; Murphy 2011). These models rely on macro-level input data on fertility and mortality that are available for most world countries. Simulations can be used to study historical periods and to glimpse into the future by relying on

¹ The term 'generation' in this context refers to the genealogical position one occupies in relation to their direct line of ancestors or descendants.

the demographic projections that national and international statistical agencies routinely produce. The approach is limited because it ignores individual- and group-level heterogeneity and relies on a series of simplifying assumptions. Nevertheless, studies have consistently shown that model-based estimates of kinship are able to reproduce average patterns of kin availability (Wachter et al. 1997). It is not known whether demographic microsimulation can be used to study the individual-level GPT that are the focus of this study.

Here, we integrate empirical, that is, register-based, and simulated, that is, microsimulation-derived, data to examine typical kinship availability across individual life courses and ask: Can microsimulation be used to validly estimate generational placement trajectories (RQ1)? Which typical patterns emerge when considering the full life course (ages 0–100) for the 1960 and 2000 birth cohorts (RQ2)? How do these patterns compare between the cohorts regarding the timing of transitions as well as occurrence and duration of states (RQ3)? We focus on Norway as it has high-quality register data to benchmark our microsimulation (RQ1). The investigation of ‘future’ GPT in Norway serves as a first empirical application of using microsimulation to study intergenerational family life course heterogeneities (RQ2 and RQ3).

We proceed in two steps: *First*, to answer RQ1, we analyze GPT based on empirical register data from Norway using sequence and cluster analysis for the 1960 birth cohort and apply the same methods to a SOCSIM-generated simulated population for the period in which both sources overlap (1960–2019). This corresponds to ages 0–59 of the 1960 birth cohort. Afterwards, we compare the results of the two data sources and discuss the degree to which the simulated data captures the individual-level trajectories in the benchmark empirical data. *Second*, to answer RQ2 and RQ3, we use the microsimulations to project the GPT for the ages 0–100 of the 1960 and the 2000 birth cohorts in order to provide an outlook on future structural

availability of kin in Norway across the entire life course (RQ2) and compare the typical patterns and their specifics between the two cohorts (RQ3).

The current examination contributes to existing research on the analysis and projection of kinship structures from a cohort perspective (Margolis and Verdery 2019) by emphasizing their variation across and between life courses and, thus, moves beyond the investigation of average kin counts (Daw et al. 2016). Moreover, it provides a first test of the performance of applying the concept of GPT with sequence and cluster analyses to microsimulated data for this field. The study generates novel evidence on the past, present, and future structural availability of kin in Norway as a first empirical example. We present crucial life-course measures for the availability of intergenerational kin, namely, the timing and duration of generational overlap with different combinations of family generations alive. In this way, our approach combines insights from kinship demography, the demography of grandparenthood and the literature on standardization and differentiation of life courses.

Availability of Kin Across the Life Course

Generational Placement Trajectories (GPT) and Social Inequality

Generational placements display the relative position of a person in their intergenerational family network—depending on whether parents, children and/or grandchildren are alive—and describe a person’s current social roles as well as their intergenerational kin availability. Generational placement *trajectories* (GPT) capture the placements across the life course (Hünteler 2022). GPT reflect a specific form of social capital, describing a person’s intergenerational kinship reservoir (or reserve) in which existing family members can function as a safety net, potentially making individuals more resilient in time of crises (Cullati et al. 2018; Hünteler and Hank 2025). Thus, GPT may be considered a dimension of social inequality in themselves because some people have larger relational reserves than others. However,

having multiple family roles may also lead to role strain and increased potential for conflict (e.g., Grundy and Henretta 2006).

Building on the life-course and sequence analysis tradition (Aisenbrey and Fasang 2010), GPT contain various dimensions that are relevant to individuals lives: (1) they capture which family *transitions* an individual experiences (e.g., birth of first child) and (2) when, that is, at which age these transitions happen (*timing*). The order of transitions (*sequencing*) directly results in (3) the *occurrence* of the *generational placement* itself, i.e. the role individuals hold within their intergenerational family system at each given age. Lastly, (4) the *duration* spent in each of the generational placements depends on both the timing and order of transitions (Hünteler 2022).

Each of these GPT components have been shown to be associated with various dimensions of individual life outcomes, such as well-being, health, and wealth, that represent different aspects of social inequality. *First*, the family transitions contained in GPT, particularly the birth of the first child and parental death, but also the birth of grandchildren, are often considered as turning points in individuals' lives with major implications for overall well-being and happiness (Hansen 2012; Leopold and Lechner 2015; Nomaguchi and Milkie 2020), income and wealth trajectories (Bergsvik et al. 2020; Hünteler et al. 2025), or health and mortality (Ellwardt et al. 2021; Grundy and Kravdal 2008; Kravdal and Grundy 2016). *Second*, aligning with the life-course paradigm, when individuals experience these life events was shown to matter. For example, declines in mental well-being differed by the age at parental death (Leopold and Lechner 2015) as did wealth accumulation depending on the age at parenthood (Lersch et al. 2017). *Third*, the relevance of the occurrence of states can most easily be exemplified with parenthood: Parents and non-parents—individuals never becoming parents—differ in the generational placements they experience because non-parents will never enter states involving having children. Both groups have been shown to differ in various life

domains, such as income, wealth, or mortality (Grundy and Kravdal 2008; Hünteler et al. 2025; Lersch et al. 2017). Additionally, research investigating phenomena such as ‘sandwich generations’ addresses the occurrence of states in line with the GPT-logic, as they examine generational overlap and its potential challenges, such as a double care burden (e.g., Alburez-Gutierrez et al. 2021; Daatland et al. 2010). *Fourth*, the importance of the duration of states for social inequality has been explicitly addressed in research investigating, for instance, the grandparent-grandchild exposure and its influence on the transmission of educational attainment (Song and Mare 2019).

Previous research based directly on GPT, thus including all the above features simultaneously, indicated that the prevalence of typical GPT changes across historical time, that is, between cohorts (Hünteler 2022) and found associations between typical GPT with later-life health and well-being (Hünteler and Hank 2025) as well as differential wealth accumulation (Hünteler et al. 2025).

Demographic Forces

The availability of kin across the life course, captured as GPT, is a function of an individual’s, their ancestors’, and their descendants’ fertility and mortality (see also Hünteler 2022). Demographic events determine if and when a person (a) becomes a parent, (b) experiences parental death, and (c) becomes a grandparent. Parenthood is simply defined by one’s own fertility (timing). The age at which parental death occurs is influenced by the parent’s fertility timing and their life expectancy, with earlier parental fertility and higher parental life expectancy resulting in a ‘later’ parental death experience and longer generational overlap, from the perspective of the focal individual. Grandparenthood is the most complex function of these events as it depends on the fertility and mortality not only of an individual but also their children, and is, therefore, also called a ‘countertransition’ (Hagestad 1988). Parenthood is a prerequisite for grandparenthood. Shorter life expectancy lowers both the likelihood of

reaching grandparenthood and the years spent in it. Higher parity and earlier childbearing increase the probability and duration of grandparenthood, whereas later childbearing by either the individual or their children reduces these chances and postpones its onset (see Margolis and Verdery 2019).

Understanding population change over time is essential because the demographic processes that shape GPTs span multiple generations. Norway experienced a prolonged post-WWII baby boom, peaking in the 1960s with up to 3.0 children per woman and remaining above 2.5 until the early 1970s. Fertility then declined, stabilizing at a record-low of 1.6–1.7 in the 1980s (G. Andersson et al. 2009; Rønsen 2004). In line with the ‘Nordic fertility regime’ and unlike most European countries (G. Andersson et al. 2009), Norway saw a fertility rebound, maintaining a relatively high TFR of around 1.9 throughout the 1990s and early 2000s. After peaking at nearly 2.0 in 2009, TFR declined sharply, breaking with the promise of sustained high fertility in the Nordic countries (Hellstrand et al. 2021). These shifts reflect tempo and quantum effects: the median age at first birth rose from 23 (women born 1935–1955) to nearly 27 (1970 cohort), reaching period-specific mean ages of 29 by 2023 (G. Andersson et al. 2009; Hellstrand et al. 2021). The share of women never becoming mothers also rose, from under 10% (1935–1949 cohorts) to about 14% (1975 cohort) (G. Andersson et al. 2009; Hellstrand et al. 2021). Conversely, cohort TFR dropped from 2.5 (1935 cohort) to just over 2.0 (post-1953) (G. Andersson et al. 2009) and is expected to fall for women born after the 1970s, to below 1.75 for those born in 1990 (Hellstrand et al. 2021).

Life expectancy in Norway increased notably and almost linearly over the past century across all age groups, most strongly at birth (from 57 (54) to 85 (81) years from 1905 to 2020 for women (men)). Gender differences in life expectancy were exceptionally high during the years of World War II (5.3 years at birth) and have been increasing since the 1950s (from 3.4

years at birth), peaking in the 1980s (up to 6.7 years at birth), with a decline thereafter (Statistics Norway 2021).

Despite Norway's egalitarian welfare regime including near-universal healthcare, both fertility and mortality remain socially stratified. For instance, the median childbearing age has been consistently higher among women with higher compared to those with lower education (difference of 5.4 years in 1945-1949 cohort to 7.1 years in 1965-1969 cohort) (G. Andersson et al. 2009). Also, the share of women not becoming mothers used to be higher among highly educated women, though this association reversed for more recent cohorts, resulting in declining educational differences in women's cohort TFR (Jalovaara et al. 2019). Moreover, older-age mortality rates have persistently been lower among higher educated individuals (Moe et al. 2012) and gains in life expectancy have been higher for those with higher incomes (Brønnum-Hansen et al. 2021).

Studies have proposed that demographic change triggers "kinship transitions" in the sense of demographic transitions, in which macro-level shifts alter the family configurations individuals experience across the life course (Jiang et al. 2023, 2025; Verdery 2015). Early work in sociology hypothesized that longer lifespans and lower and later fertility would lead to a verticalization of kin networks, comprising more vertical, that is, intergenerational family members, and fewer horizontal kin, such as siblings or cousins (Bengtson 2001; Hagestad 1988). Recent work projecting kinship structure using methods from mathematical demography has come to similar conclusions (Alburez-Gutierrez et al. 2023). Changes in the availability or lack of kin that derive from these kinship transitions can leave clear marks in individuals' life-courses (Brown et al. 2022; Hünteler 2022; Verdery et al. 2019). For example, it can be expected that the share of individuals without intergenerational kin will become increasingly larger over time, as the number of individuals without children and without grandchildren continues to increase (Verdery et al. 2019). This, coupled with increasing shared

lifetime between members of different family generations (Hünteler 2022; Leopold and Skopek 2015b), may lead to growing intergenerational transmission of (dis)advantage—as there is more time for influencing each other (‘multigenerational exposure’ (Song and Mare 2019)) and more intensively as time is shared with fewer individuals—and care burden becomes more concentrated in a smaller number of individuals (Lersch 2019; Song and Mare 2019)

Research Design

We start by providing an overview of our research design, which is also summarized in Figure 1. *First*, to answer RQ1, we benchmarked microsimulated GPT (Figure 1, panel B) against GPT from empirical register data for the period in which both data sources overlap—namely, the 1960 birth cohort from ages 0–59 (Figure 1, panel A). For this benchmarking, we compared aggregate measures of the two registers, life-course-specific characteristics based on the generated GPT, and the characteristics of the identified clusters (Figure 1, panel C). *Second*, to answer RQ2 and RQ3, we compared GPT from the 1960 and 2000 simulated birth cohorts—based on the microsimulated data—over their entire life course (ages 0–100), using the same comparisons as in the previous step (Figure 1, panels A and D). We explain all of these steps in more detail in the following sections.

Data Sources

Norwegian Register Data

For the ‘empirical’ part of the analysis, we used data from the Norwegian Population Register that was provided by Statistics Norway. This contained information on individuals’ registration status (alive, dead, emigrated) and demographic information (dates of birth and death, sex) for the population of Norway in a given year. The most recent data was available for 2019. The Norwegian Population Register was established in 1964, based on the census conducted in

1960, and was updated ever since. Also, included individuals' parents, children, and grandchildren can reliably be identified. Thus, we used the 1960 birth cohort as the basis for our analyses as these individuals had the longest-recorded life courses, allowing us to quantify

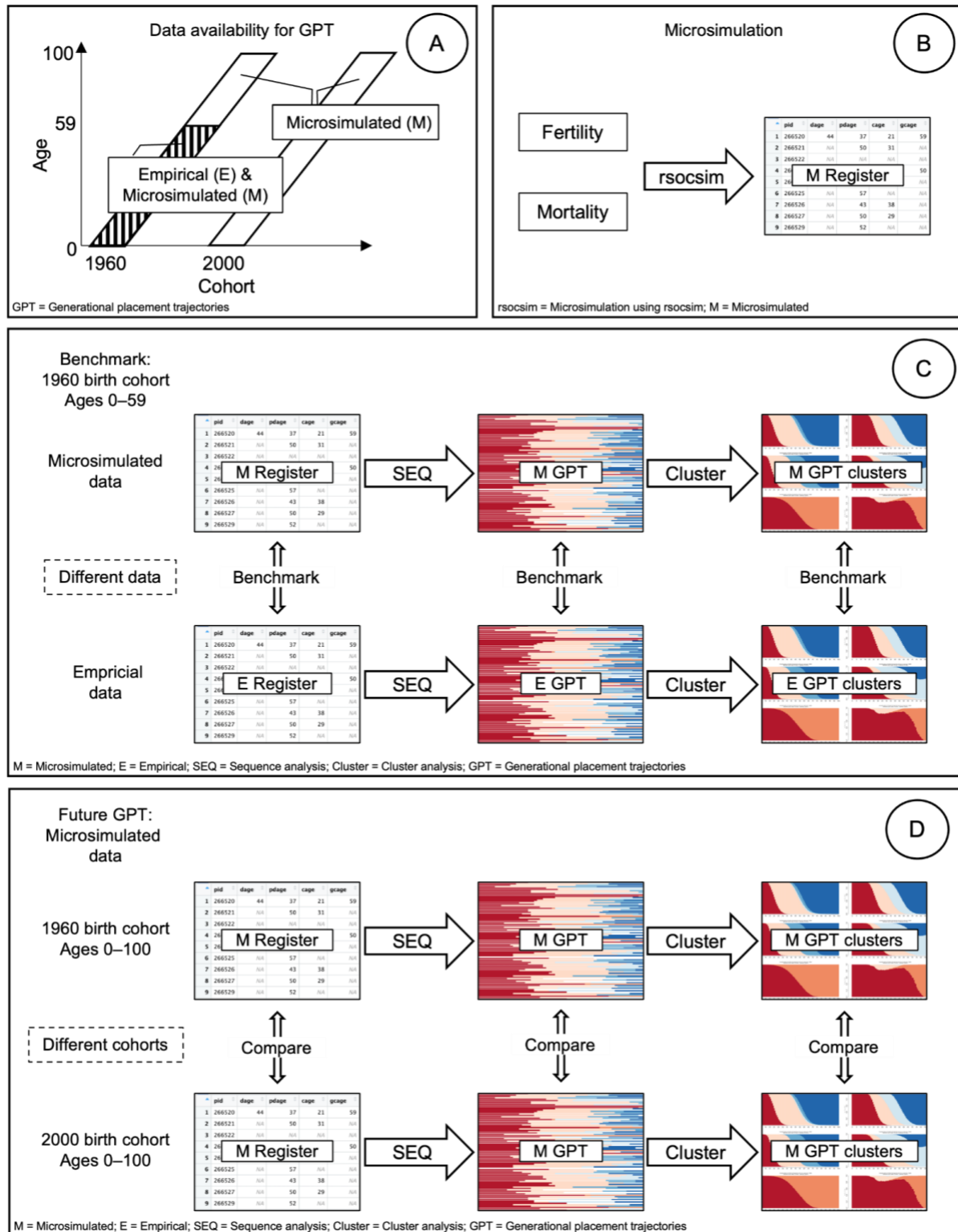


Figure 1 Research design flow chart

generational placements between birth and age 59, observed between 1960 and 2019 (see Figure 1, panel A).

To identify and reliably track the generational placements over the life course (see more information on the operationalization below), individuals and their parents had to be registered residents in Norway over the entire observation period. Thus, from all registered individuals born in 1960 ($N = 78,396$), we excluded those who were not born in Norway ($N = 17,295$ excluded), who had ever emigrated from Norway ($N = 4,555$ excluded), for whom we could not identify at least one parent ($N = 1,455$ excluded), and whose parents were not born in Norway ($N = 1,904$ excluded). Lastly, because this can produce inconsistencies in the sequence analysis, we also excluded individuals who died before their first birthday ($N = 9$), resulting in a final analytical sample size of $N_E = 53,178$. This data and a similar sample have previously been used to successfully identify GPT clusters (Hünteler et al. 2025).

Demographic Microsimulation

The second data source for analysis was based on simulated registers generated using the SOCSIM microsimulator as implemented in the R package *rsocsim* (Theile et al. 2023). SOCSIM takes population-level age-specific fertility and mortality rates to generate simulated micro-data with plausible demographic and generational structures (see Figure 1, panel B). We followed the simulation setup of Alburez-Gutierrez et al. (2021), in which the simulator stochastically determines whether and when individuals within a simulated population experience specific demographic transitions, such as death or childbirth. The likelihood of experiencing such transitions is provided on a monthly basis according to macro-level input rates. These input rates are age- and sex-specific so that individuals are subject to varying risks of experiencing the transitions while they are alive, depending on their age and sex at different time periods. The simulator identifies two individuals as being in a “union” only when a child is born to them. Because the model omits rates of union formation and dissolution, such unions

can end only when one partner dies. They are therefore not unions in the strict demographic sense, and we do not treat them as such. This simplification did not affect our results, as partners and affinal relatives are outside the scope of the present study. For more details, see Albrez-Gutierrez et al. (2021) and our replication files (<https://github.com/huentelb/simGPT>).

Although the Norwegian context provided detailed demographic information, we deliberately chose to not add any complexity to the simulation setup, such as explicitly modelling male fertility or accounting for socially stratified demographic rates. We did this because our intention was to evaluate whether a relatively ‘naive’ simulation could capture within- and between-family life-course heterogeneity. We are aware that more complex simulation setups are possible but we are not interested in implementing them. This is because, if successful, this naive setup could be applied to other contexts, for which only basic demographic information exists.

The final output of the microsimulations was an individual-level roster of all individuals that have ever lived in the population, including their vital information. We restructured the SOCSIM-generated populations to match the format of the Norwegian registers. The data included a column to identify the parents of each simulated individual. This allowed us to identify parents, children and grandchildren, and determine the GPT across the ages 0–100 for any individual in the population born until 2000 with the input data we can use (see below). Because the microsimulation was based on stochastic models, we ran ten microsimulations with a starting population of 10,000 individuals each with random age-sex-distributions. For the main analysis, we merged all ten simulations to increase the population size and account for stochastic variability from the simulator.

With the aim of generating a simulated version of the Norwegian population registers, we used historical mortality rates for the 1846–2023 period from male and female life tables generated by the Human Mortality Database (HMD 2023). We relied on historical female

fertility rates provided by the Human Fertility Collection (HFC 2023) that were generated by Brunborg and Mamelund (1994) for 1946–1992 and the Human Fertility Database (2023) for 1993–2022. Historical fertility rates for the year 2023 were derived from the United Nations World Population Prospects (United Nations 2024). In order to simulate the future 2024–2100 Norwegian population, we used the projection scenarios of demographic rates produced by the United Nations World Population Prospects (United Nations 2024). The current version of the UNWPP contained one scenario for future mortality (‘medium’) and three scenarios (‘low’ = declining, ‘medium’ = stable, and ‘momentum’ = increasing rates) for future fertility. Our main analyses were based on the medium-medium combination.

Male fertility was not directly included as an input in the simulations, so men did not have an independent risk of becoming fathers, but they had two options to enter into parenthood. First, a man became a father when he was in a union and his partner transitioned into motherhood based on her age-specific risk to become a mother. Second, when a woman transitioned into motherhood while she was not in a union, she was assigned a partner. This partner was selected based on the general rules of the marriage market, i.e., an adequate age of the woman’s partner, for instance. Her new partner became the father of her child. Details on the marriage market used in this simulation can be found in the Appendix of Alburez-Gutierrez et al. (2021).

For the main analyses, we relied on $N_{M60} = 19,630$ individuals ‘born’ in 1960 and $N_{M00} = 17,441$ individuals ‘born’ in 2000. Each of these samples stemmed from the 10 separate microsimulation runs combined. A comparison of the aggregated (simulated) demographic rates and the (empirical) input rates showed that our models were able to reproduce the target population structure (see Figure A 1 & Figure A 2).

Sequence Analysis to Identify Generational Placement Trajectories

We applied sequence and cluster analysis to identify typical generational placement patterns (see Hünteler 2022). We considered six potential ‘states’ reflecting the generational placements, ranging from not having any intergenerational kin alive to having parents (G1), children (G3), and grandchildren (G4) alive at the same time: “*None* (G2)”, “*Child* (G1, G2)”, “*Child & parent* (G1, G2, G3)”, “*Parent* (G2, G3)”, “*Child, parent, grandparent* (G1, G2, G3, G4)”, and “*Parent & grandparent* (G2, G3, G4)” (see also legend of Figure 2). Three life events (‘transitions’) determined entry and exit into each of these states: the death of the last remaining parent, the birth of a first child, and the birth of the first grandchild. Individuals could transition through any of these states on an annual basis and we generated one trajectory for each individual. For example, a given person born in 1960 was a *child* from ages 0–25. At age 25, their first child was born, so they were a *child and a parent* in the 26–40 age range. At age 40, both of their parents died, so that they were *parent* from ages 40–70. At age 70, their child gave birth so that they were *parent and grandparent* over the 71–80 age range. The given person died at age 81, so the trajectory was censored from age 81–100.

As a next step, we clustered the trajectories based on their similarity to one another. We used the timing-sensitive Chi-square distance measure (Studer and Ritschard 2016) to estimate the pairwise similarities. This distance measure, in contrast to other available measures, emphasizes differences between trajectories based on the timing of events—which was particularly important in the given context—and has been shown to separate GPT meaningfully and empirically well (Hünteler 2022; Hünteler et al. 2025). Moreover, Chi-square can be applied to sequences of different length whereas other timing-sensitive distance measures, such as Hamming and related ones, cannot (Studer and Ritschard 2016). Consecutively, we applied the Partitioning Around Medoids cluster algorithm (Studer 2013), to group the trajectories into distinct clusters, that comprised trajectories that were similar to one another within the same

cluster and different from trajectories in other clusters. This combination of methods has produced stable and reasonable cluster results in previous research (Hünteler 2022; Hünteler et al. 2025). We used the GPT clusters to characterize the typical GPT in the population.

According to our research questions, we ran these steps on different data sources and based on different birth cohorts with varying age ranges (Figure 1, panel A): First, we used observed empirical register data for the birth cohort 1960 (age range 0–59) to use it as a benchmark for examining the quality of using microsimulation to investigate GPT (Figure 1, panel C). The 1960 birth cohort was the first cohort whose own vital information as well as their parents’ have reliably been documented in the Norwegian register. Thus, trajectories with the longest age range we could construct based on the empirical register data stemmed from this cohort. We used the same birth cohort and age range but from the simulated dataset for this benchmarking (RQ1). Second, we extended the observed age range to 0–100 years and analyzed the GPT for the birth cohorts 1960 and 2000 using the simulated dataset (RQ2 and RQ3, Figure 1, panel D). All analyses were based on individuals who survived at least until their first birthday to avoid potential inconsistencies in the sequence analysis due to sequences of the length zero.

Comparisons of GPT Across Data Sources and Cohorts

We took the same analytical steps for benchmarking (RQ1) and comparing future GPT (RQ2 and RQ3). We applied these to (a) the 1960 empirical and ‘simulated’ cohorts across ages 0–59 for benchmarking (Figure 1, panels A and C) and (b) the 1960 and 2000 ‘simulated’ cohorts across ages 0–100 for comparing future GPT (Figure 1, panels A and D).

First, we compared *average aggregate indicators* of the GPT, that is the average age at each transition and their variation as well as the proportion of individuals having experienced the events. Second, we accounted for the *sequences as a whole* and compared different descriptive indicators of the sequences following Ritschard (2023) and using the function

seqindic from the *TraMineR*-package (Gabadinho et al. 2011). We assessed the average mean time spent in each state, that is, the length of the sequences ℓ , the proportion of visited states vp , the proportion of transitions tp , longitudinal entropy as a measure of the diversity of visited states that depicts its unpredictability h_{norm} (entropy is zero when a same state is observed all along the sequence; entropy is one when no state is more probable than any other state), as well as the mean $\underline{d}$ and standard deviation s^2_d of the spell durations. We also described and compared the within-sequence variability—or “the arrangement within sequences” (Ritschard 2023, p. 2045)—between the data sources through the composite measure of the ‘sequence complexity’, $c(x)$. It takes into account the variation in the number of different states and unpredictability of these states within life courses, that is, longitudinal entropy (Gabadinho et al. 2010, 2011).

Additionally, we compared the sequences based on pairwise calculated distances regarding the (a) occurrence of states, (b) timing of transitions, and (c) duration spent in states using the Bayesian Information Criterion (BIC) and the Likelihood-Ratio Test (LRT). These measures have the advantage of quantifying the substantive and statistical significance of the differences. We followed the procedure and measures as proposed by Liao and Fasang (2021) using the *seqCompare* program available in the *TraMineRextras* package (Ritschard et al. 2024). The comparisons based on ‘numbers’ were accompanied by comparisons based on visualization of the results, following the sequence-and-cluster-analysis tradition.

In a last step, we identified the optimal *cluster solutions* for both data sources and compared the resulting clusters following previous research that conducted cluster-comparisons using other clustering techniques (Morin et al. 2016). We accounted for configural (number of clusters), distributional (size of the clusters), structural (within-cluster means), and dispersion (within-cluster variability) similarity. Additionally, we compared the cluster-specific complexity indeces.

Results

Empirical vs. Microsimulated GPT (RQ1)

To answer our first research question, we assessed the quality of using microsimulated data for analyzing GPT by benchmarking the results against GPT based on empirical register data. The following results were based on comparisons of aggregate indicators, GPT characteristics, and GPT cluster characteristics for the 1960 cohorts from both the Norwegian empirical register data and the microsimulated data (i.e., the simulated register) as described above. We compared each cohort's GPT from birth to age 59, as well as their typical GPT clusters as generated using sequence and cluster analysis following Hünteler (2022) and Hünteler et al. (2025) (Figure 1, panels A and C).

Comparison of Average Sample Indicators

Overall, there is a high consistency between sources in the demographic characteristics related to parenthood and parental loss (Table 1). However, the share of grandparents was higher in the microsimulated data than in the registers, while the number of grandchildren was slightly lower than in the register data. The cohort's average age at death until the end of the observation period (age 59) was substantially lower in the microsimulated data. We cannot rule out that mortality at younger ages in the register was underreported because we found fewer cases of death within the first two years than would be expected based on the age-specific mortality rates. Thus, the deviation in age at death seems plausible.

Table 1 Comparisons of sequences between data sources and cohorts

Measure	<i>Benchmarking GPT</i>		<i>Comparison of Future GPT</i>	
	Birth cohort 1960 (ages 0–59) ¹		Microsimulated data (ages 0–100)	
	Data source		Birth cohort	
	Empirical register	Micro- simulation	1960	2000
<i>Aggregate indicators</i>				
Age at individual's death ¹				
Mean	42.4	35.65	81.78	90.16
SD	13.43	19.83	19.05	12.24
Median	46	41	88	93
Both parents dead ¹	.47	.62	1.00	1.00
Age at 2 nd parent's death ¹				
Mean	48.85	47.27	55.00	62.03
SD	7.92	9.09	12.57	8.98
Median	51	49	56	63
Share of parents ¹	.84	.86	.86	.76
Number of children ¹				
Mean	2.38	2.01	2.01	1.43
SD	0.97	1.38	1.38	1.16
Median	2	2	2	1
Age at parenthood ¹				
Mean	26.81	26.74	26.74	30.79
SD	5.61	5.6	5.60	5.25
Median	26	26	26	30
Share of grandparents ¹	.39	.56	.80	.67
Number of grandchildren ¹				
Mean	1.89	1.37	3.21	2.09
SD	0.81	1.74	2.81	2.21
Median	2	1	3	2
Age at grandparenthood ¹				
Mean	50.56	51.14	55.53	61.56
SD	5.16	5.1	8.41	7.24
Median	51	52	55	61
<i>Mean time spent in states^{1, 2}</i>				
G1-G2	28.66	30.42	28.92	37.76
G2	0.99	0.85	3.42	6.85
G1-G2-G3	19.02	20.97	19.47	20.42
G2-G3	4.20	2.96	6.63	5.34
G1-G2-G3-G4	2.59	2.48	4.31	3.10
G2-G3-G4	2.11	1.16	19.54	16.69
<i>Overall sequence indicators</i>				
Mean length of sequences	58.85	57.56	82.30	90.16
Proportion of visited states	.45	.49	.58	.56

Measure	<i>Benchmarking GPT</i>		<i>Comparison of Future GPT</i>	
	Birth cohort 1960 (ages 0–59) ¹		Microsimulated data (ages 0–100)	
	Data source		Birth cohort	
	Empirical register	Micro- simulation	1960	2000
Proportion of transitions	.03	.03	.03	.03
Entropy	.45	.48	.61	.58
Mean spell duration	24.90	21.47	24.48	29.24
SD of spell duration	7.83	8.50	9.52	11.15
Complexity	0.11	0.13	0.13	0.12
<i>BIC difference</i>				
Occurrence	-1.42 *		5.65 **	
Timing	-1.41 *		0.83 **	
Duration	-1.23 *		4.49 **	
N	53,178	19,630	19,630	17,441

Notes: ¹Observations of the 1960 cohorts are right-censored at age 59, resulting in an underestimation of the age at parental death, grandparenthood and the share of grandparents.

²See labels of Fig 2. BIC = Bayesian information criterion. P-values for likelihood-ratio-test of difference: ** p<0.05, * p<0.1

Comparison of the Sequences

The comparison of sequence-related characteristics revealed a high consistency between the data sources (except for mean duration in states and its variance), with the microsimulated sequences showing shorter durations and slightly smaller predictability (i.e., higher entropy) and larger complexity. While we did find some variation between the data sources, these overall sequence differences in occurrence of states, timing of transitions, and duration spent in states, was neither substantial nor significant, as the BIC values were below 2, which represents a critical threshold (Liao and Fasang 2021). The benchmarking analysis increased our confidence in the ability of microsimulated data to capture heterogeneity in the life-course availability of intergenerational family members (RQ1).

Comparison of the Clusters

Taking a closer look at the identified clusters of GPT, we, first, found high *configural* similarity, that is, the same number of clusters, between the two sources, with both samples suggesting a 6-cluster solution being optimal (Figure A 3). We based the decision on the number of clusters on the standard measures of the quality of partition, like the average silhouette width (Studer 2013), as well as a qualitative assessment through interpretability. These cluster solutions also indicated, secondly, a comparable *distributional* similarity (size of the clusters). More specifically, we identified the following six typical GPT (Table 2; also see Figure A 4 and Figure A 5): For both data sources and similar to previous findings, two clusters were characterized by a pattern in which individuals were sandwiched in a three-generation family. Individuals in one cluster experienced parenthood relatively late and many had not yet experienced parental death nor grandparenthood at age 59, resulting in a stable three-generation-family consisting of their parents (G1), themselves (G2), and their children (G3) (microsimulated 32%, empirical 40%, Cluster 1). For individuals in the other cluster, parenthood happened earlier in their lives and parental death occurred at a similar age as the birth of the first grandchild, so they also lived in a 3-generation family but with experiencing a transition from the G1-G2-G3-family to a G2-G3-G4-family (microsimulated 15%, empirical 9%, Cluster 5). The differences in the size of these two clusters—overestimation of the ‘early 3-generation’ and underestimation of the ‘later 3-generation family’ in the microsimulated data—is likely driven by the overestimation of the share of individuals who had become grandparents by age 59, the end of our observation for the benchmarking, as the average age at parenthood did not differ substantially between the two data sources. One cluster showed a relatively early parent- and grandparenthood paired with a late parental death. This brought about a four-generation family, or “double-sandwich” position (Manor 2020),

Table 2 Cluster characteristics comparing the same clusters between the two data sources for the 1960 birth cohort (censored at age 59)

	Cluster 1		Cluster 2		Cluster 3		Cluster 4		Cluster 5		Cluster 6	
	Late 3-gen family		4-gen family		2-gen family		Non-parents late		Early 3-gen family		Non-parents early	
	E	M	E	M	E	M	E	M	E	M	E	M
Age at i's death												
Mean	48.37	47.89	54.09	55.37	51.06	53.56	34.52	19.26	55.06	56.38	51.65	53.43
SD	7.14	7.96	3.61	3.1	6.04	4.98	14.25	16.22	3.09	2.78	6.85	5.63
Median	49	49	55	56	53	55	34	19	56	57	54	56
Both parents dead	.27	.44	.16	.27	1	1	.33	.47	1	1	1	1
Age at 2 nd parent's death												
Mean	55.59	54.78	56.21	56.25	44.33	39.47	53.47	51.71	47.04	46.21	43.78	40.89
SD	2.42	3.37	1.65	2.31	7.33	7.75	5.67	7.2	6.43	6.2	8.35	9.75
Median	56	55	57	57	46	41	55	54	49	47	46	43
Share of parents	1	1	1	1	1	1	.08	.09	1	1	.03	.06
Number of children												
Mean	2.3	2.05	2.63	2.77	2.23	2.05	1.41	0.12	2.58	2.75	1.73	0.11
SD	0.93	1.08	1.01	1.24	0.92	1.08	0.59	0.4	0.98	1.23	0.81	0.51
Median	2	2	3	3	2	2	1	0	2	3	2	0
Age at parenthood												
Mean	28.33	29.12	22.71	22.94	29.05	29.45	39.14	31.93	23.09	23.5	38.59	35.25
SD	5.04	5.12	3.15	3.7	5.51	5.34	10.2	8.57	3.29	3.66	8.63	6.69
Median	28	29	22	23	29	29	43	30	23	23	37	34.5
Share of grandparents	.22	.39	1	1	.16	.40	.00	.04	1	1	.00	.01
Number of grandchildren												
Mean	1.35	0.61	2.16	2.98	1.37	0.67	1.75	0.07	2.07	2.84	1.83	0.03
SD	0.55	0.99	0.8	1.79	0.55	1.07	0.7	0.42	0.79	1.71	0.94	0.28
Median	1	0	2	3	1	0	2	0	2	2	2	0
Age at grandparenthood												
Mean	55.62	56.01	48	48.27	55.48	55.12	51.34	51.91	48.96	49.31	49.17	53.31
SD	2.66	3.02	4.33	4.24	2.44	3.23	4.67	4.69	4.41	4.11	5.41	6.12
Median	56	57	49	49	56	56	52	52	50	50	50.5	56
Complexity	0.10	0.11	0.15	0.15	0.14	0.15	0.02	0.02	0.18	0.18	0.07	0.08
N	21,301	6,229	9,775	4,123	8,325	3,334	6,303	2,049	4,889	2,973	2,585	922
Cluster size (%)	40	32	18	21	16	17	12	10	9	15	5	5

Notes: E = Empirical register data; M = Microsimulated data, i = individual/focal. Corresponds to analytical step described in panel C of Figure 1 and describes clusters as plotted in Figure A 4 and Figure A 5 in the Appendix.

in which great-grandparenthood (G1-G4) existed (microsimulated 21%, empirical 18%, Cluster 2). For another cluster, the pattern was the opposite: the birth of children and grandchildren occurred relatively late whereas parental death happened earlier. This patterning resulted in a two-generation family consisting of the sample individuals (G2) and their children (G3) (microsimulated 17%, empirical 16%, Cluster 3). Lastly, two of the six clusters comprised individuals who never became parents. Individuals in one cluster lost their own parents relatively early in their life course (5% each, Cluster 6). Individuals in the other cluster held a stable position of being a child only (G2) because they either experienced parental death late in life or their own lives were censored through a relatively early own death (microsimulated 10%, empirical 12%, Cluster 4).

Third, *structural* similarity (within-cluster means) was also high—as assessed by the proportions of those experiencing parent- and grandparenthood and parental death, as well as the average in timing of transitions and number of (grand)children—although we did identify some discrepancies (Table 2). These discrepancies resembled those identified on the aggregate level, for example in the overestimation of grandparents in the microsimulated data, although they were not present in all the clusters equally.

Fourth, *dispersion* similarity (within-cluster variability) was assessed through comparing the sequence complexity index (Gabadinho et al. 2010, 2011; Ritschard et al. 2024). The clusters did virtually not differ at all in their complexity between the two data sources (Table 2).

Future trajectories (RQ2)

As a next step, we projected the life-course intergenerational family structure into the future to investigate how the GPT evolved over a 100-year lifespan for two birth cohorts (1960 and 2000). Please keep in mind that these are not actual but simulated cohorts.

Comparison of Average Sample Indicators

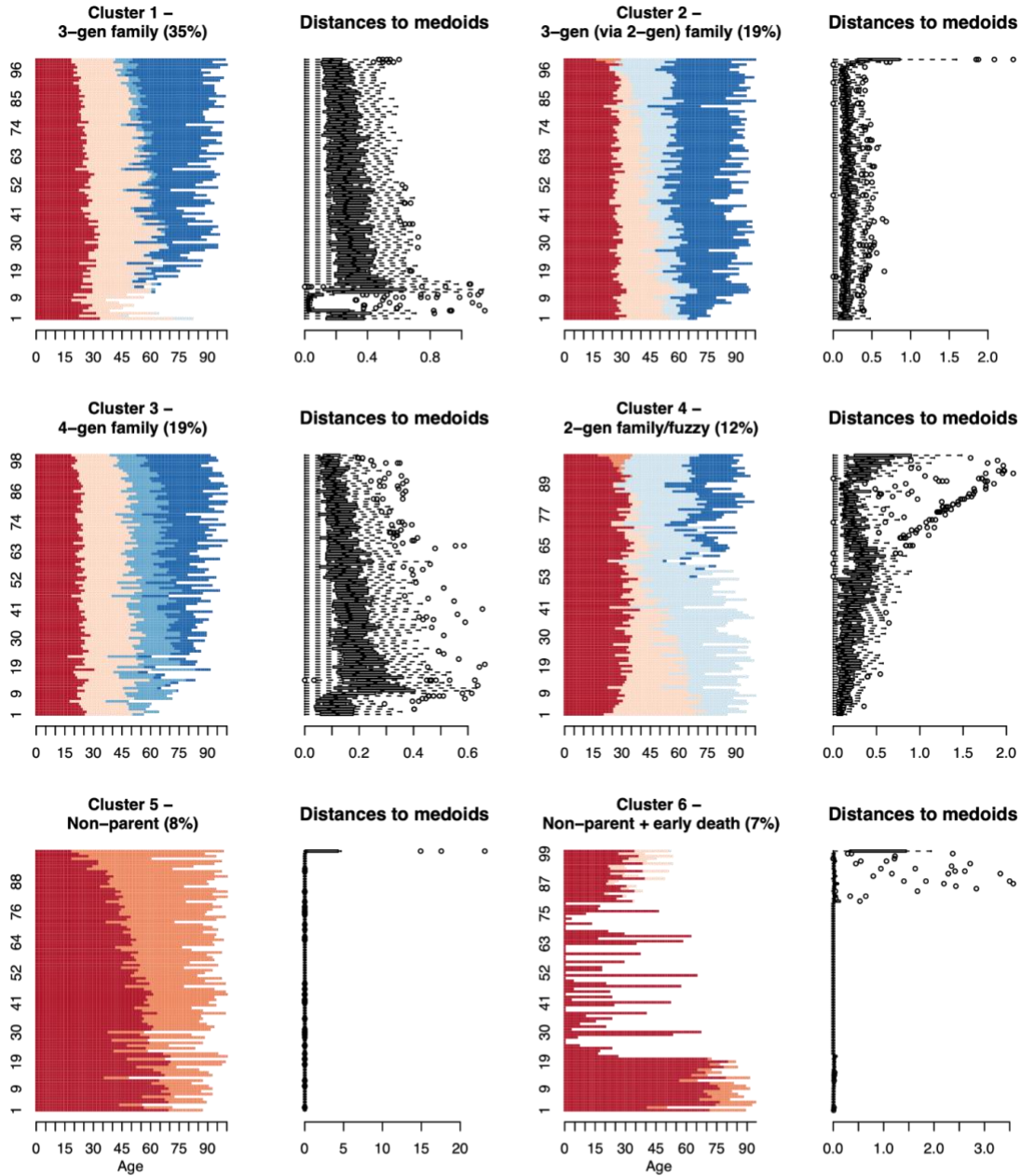
The average age at death for individuals and their parents increased by around 8 years between the two cohorts (Table 1), reflecting population aging. As expected, the share of parents and grandparents decreased notably over time by 12% and 16%, respectively. This was associated with an increased average age at the transitions (4 and 6 years, respectively) as well as a lower number of descendants, on average (2.01 vs 1.43 children and 3.21 vs 2.09 grandchildren).

Comparison of the Sequences

Living longer and experiencing the family events later in life resulted in a larger mean time spent in the states shared with the parents (including the G1-G2-link) and parents only (G1-G2) or without any intergenerational kin (G2), but shorter generational overlap with one's children (including the G2-G3 link) and grandchildren (including the G2-G4 link) for the 2000 birth cohort, on average. The overall sequence indicators were largely comparable, except that the mean spell duration was, on average, 5 years larger and showed a higher variability for the later-born birth cohort. With BIC values of 2 to 6 and significance levels of the LRT below .05, the two cohorts differed significantly positive in their occurrence of states as well as the duration spent in the states but not in the timing of experiencing family transitions (Liao and Fasang 2021). To learn more about the details of these differences, as a next step, we compared the optimal cluster solutions for the two cohorts.

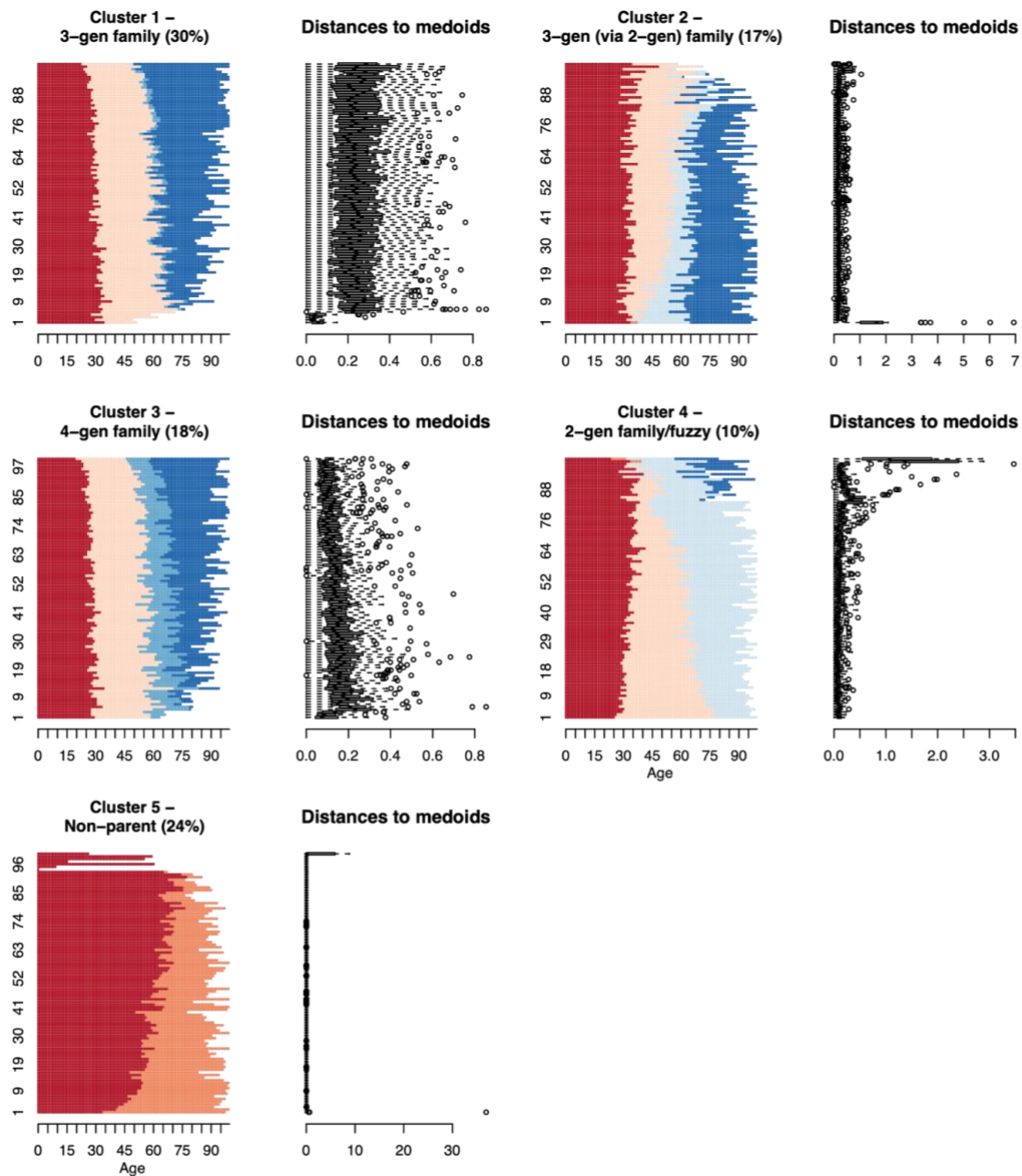
Comparison of the Clusters

According to the formal quality of partition (Figure A 6) as well as interpretability of the results, we identified a 6-cluster solution to be optimal for the GPT covering ages 0 to 100 for the simulated 1960 birth cohort and a 5-cluster solution to be optimal for the simulated 2000 birth cohort. Figure 2 and Figure 3 show the clusters represented through the most



Existing intergenerational family members		Corresponding generational placement
Individual only	G2	None
Individual and parent(s)	G1 G2	Child
Individual, parent(s) and child(ren)	G1 G2 G3	Child & parent
Individual and child(ren)	G2 G3	Parent
Individual, parent(s), child(ren) and grandchild(ren)	G1 G2 G3 G4	Child, parent & grandparent
Individual, child(ren) and grandchild(ren)	G2 G3 G4	Parent & grandparent

Figure 2 Relative frequency sequence plots by cluster showing the 100 most representative sequences (medoids) per cluster (left panels) and their representation quality as dissimilarity-to-medoid plots (right panels) for the 1960 simulated birth cohort from microsimulated data. The right panels show box plots of the pairwise distance between each medoid (shown on the left) to the trajectories they represent (not shown). Better representation is indicated by lower average distances between medoids and the represented trajectories.



Existing intergenerational family members		Corresponding generational placement
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Individual, parent(s) and child(ren)	G1 G2 G3	Child & parent
Individual and child(ren)	G2 G3	Parent
Individual, parent(s), child(ren) and grandchild(ren)	G1 G2 G3 G4	Child, parent & grandparent
Individual, child(ren) and grandchild(ren)	G2 G3 G4	Parent & grandparent

Figure 3 Relative frequency sequence plots by cluster showing the 100 most representative sequences per cluster (medoids; left panels) and their representation quality as dissimilarity-to-medoid plots (right panels) for the 2000 simulated birth cohort from microsimulated data. The right panels show box plots of the pairwise distance between each medoid (shown on the left) to the trajectories they represent (not shown). Better representation is indicated by lower average distances between medoids and the represented trajectories.

typical 100 sequences per cluster (left panels), including their representation quality as dissimilarity-to-medoid plots (right panels), with more information to be found in Table 3. Considering the different number of optimal clusters, *configural* similarity was not perfect when comparing the two cohorts, suggesting potentially more standardized life-course family structures for the younger cohort. Yet, most of the GPT clusters matched in terms of the family types they represented. The largest share of GPT in both cohorts was characterized by a *3-generation family* structure (35% for the 1960 and 30% for the 2000 cohort, Cluster 1), with individuals direct transitioning from a G1-G2-G3 to a G2-G3-G4-family, occurring due to grandparenthood and parental death happening at virtually the same age. Two clusters in each cohort were characterized by comparatively long spells in the two-generation family consisting of themselves (G2) and their children only (G3): In one of these patterns (*3-gen (via 2-gen) family*, Cluster 2), individuals eventually ended up transitioning from the G1-G2-G3 to the G2-G3-G4-family after spending more than 10 years, on average, in the 2-generation structure (19% in 1960s and 17% in 2000s). The other cluster (*2-gen family/fuzzy*, Cluster 4) showed a more fuzzy pattern, in which many individuals remained in this 2-generation family without ever becoming grandparents, while the rest eventually transitioned into the 3-generation family (G2-G3-G4). This transition happened notably later than for individuals in the other 2-generation family pattern, thereby showing an extended period of around 30 years with only G2-G3 alive (12% in 1960s and 10% in 2000s). The share of individuals with a notable time spent in the *4-generation family* or “double sandwich” position—due to early fertility and late parental death—was similarly large in the two cohorts (19% in 1960s and 20% in 2000s, Cluster 3). Lastly, we identified two patterns without parenthood over the 100-year lifespan for the 1960s birth cohort but only one non-parent-pattern for the 2000 birth cohort (24%, Cluster 5). The two non-parent clusters for the 1960s clearly distinguished between individuals remaining non-parents over their entire (long) life-span (8%, Cluster 5) and those not becoming

parents or not being parents for long because they died relatively early (7%, Cluster 6). Thus, although we identified one cluster less in the 2000 cohort, most of the clusters were comparable in the typical life-course family patterns they represented.

Regarding the *distributional* similarity between comparable clusters in the two cohorts, we observed some stability but also notable change: *first*, although the two types of 3-generation families (either with direct transitioning from G1-G2-G3 to G2-G3-G4 (35% vs 30%) but also via the 2-generation family (19% vs 17%)) were the most prevalent patterns in both cohorts, their total share declined by 13% over time. *Second*, the cluster sizes for the 2- and 4-generation family patterns were robust over time. *Third*, the total share of individuals in the non-parent patterns increased by 60%, from 15% in the 1960 cohort (summing Cluster 5 and 6) to 25% in the 2000 cohort (Cluster 5).

Even if many of the clusters were comparable in their overall family type, we identified noteworthy differences in the within-cluster means (*structural* similarity, Table 3), also affecting average sequence lengths within the clusters, similar to what we sketched out in the sequence comparison above. For instance, within the *3-generation family* patterns (Cluster 1), the average age at the transition from the G1-G2-G3 to the G2-G3-G4-family and own death were delayed by about 7 years, resulting in more family stability and increased generational overlap between the G1-G2 and G2-G3 parent-child links (+7 and +2 years, respectively). Moreover, within the *2-generation via 3-generation* clusters (Cluster 2), the average time spent with children (G2-G3 links) or grandchildren (G2-G4 links) decreased by 4 and 7 years, respectively, while the average time spent in the 4-generation “double sandwichness” declined from 18 to 13 years within the *4-generation* clusters (Cluster 3) across cohorts. This is the result from delayed parent- and particularly grandparenthood (+4 years and +7 years, respectively) setting off increased longevity of the cohort members’ parents (G1) (+2 years). Additionally,

Table 3 Cluster characteristics comparing different clusters between the two simulated birth cohorts

	Cluster 1 - 3-gen family		Cluster 2 - 3-gen (via 2-gen) family		Cluster 3 - 4-gen family		Cluster 4 - 2-gen family/fuzzy		Cluster 5 & 6- Non-parent		
	1960	2000	1960	2000	1960	2000	1960	2000	1960 (Cluster 5)	1960 (Cluster 6)	2000 (Cluster 5)
Age at i's death											
Mean	83.77	90.83	89.18	90.67	85.09	90.76	82.72	91.55	88.13	34.76	87.91
SD	14.26	10.52	7.81	10.29	10.71	8.57	12.64	8.12	9.53	28.41	17.77
Median	88	94	91	93	88	93	86	94	90	28	93
Both parents dead	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Age at 2 nd parent's death											
Mean	57.62	62.88	43.53	54.91	67.90	69.65	45.36	58.33	51.34	59.00	61.90
SD	7.64	5.82	8.90	8.36	6.57	5.21	13.13	11.06	11.90	12.26	9.11
Median	57	63	44	55	68	70	45	60	52	59	63
Share of parents	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	.00	.21	.00
Number of children											
Mean	2.45	1.97	2.31	1.75	2.66	2.18	1.65	1.29	0.00	0.31	0.00
SD	1.20	0.97	1.17	0.87	1.24	1.04	0.91	0.55	0.05	0.69	0.08
Median	2	2	2	2	3	2	1	1	0	0	0
Age at parenthood											
Mean	26.18	30.35	27.88	33.38	23.82	27.80	30.81	33.01	36.40	29.69	32.74
SD	5.09	4.50	5.32	5.25	4.40	4.35	6.02	5.59	4.10	6.34	7.79
Median	26	30	28	33	23	28	31	33	39	29	33
Share of grandparents	0.98	0.99	1.00	0.98	1.00	1.00	0.55	0.19	0.00	0.18	0.00
Number of grandchildren											
Mean	3.97	3.08	3.75	2.57	4.81	3.71	1.43	0.39	0.01	0.49	0.01
SD	2.57	1.99	2.46	1.78	2.71	2.20	1.91	1.01	0.10	1.30	0.11
Median	3.00	3.00	3.00	2.00	4.00	3.00	1.00	0.00	0.00	0.00	0.00
Age at grandparenthood											
Mean	55.37	61.51	57.71	66.22	49.72	56.03	66.12	73.64	65.40	58.89	62.20
SD	7.39	5.61	7.68	6.55	5.93	5.37	8.10	7.52	5.73	9.19	10.29
Median	55.00	61.00	57.00	66.00	49.00	56.00	66.00	74.00	68.00	58.00	61.00
Complexity	0.15	0.14	0.16	0.06	0.16	0.16	0.15	0.15	0.06	0.03	0.12
N	6,915	5,251	3,693	3,052	3,675	3,184	2,335	1,733	1,653	1,359	4,221
Cluster size (%)	35	30	19	17	19	18	12	10	8	7	24

Notes: i = individual/focal. Corresponds to analytical step described in panel D of Figure 1 and describes clusters as plotted in Figure 2 and 3.

the average number of children and grandchildren declined from 2.45 to 1.97 and 3.97 to 3.08, respectively. Lastly, comparing the two 2-generation families (Cluster 4), the share of grandparents within the clusters decreased notably, from 55% to 19%, while the age at grandparenthood increased from age 66 to 73. Thus, although we summarized the patterns as largely reflecting a similar family type, the within-cluster characteristics revealed substantial differences, pointing to an increased share of individuals without grandchildren in the 2000 cohort overall, despite an almost constant cluster size.

Lastly, although the measures of cluster complexity did not differ much, we observed reduced variation in the timing of transition across most clusters across cohorts (*dispersion* similarity). This further supports our conclusion of higher standardization of intergenerational family life courses in the later-born cohort.

Discussion

We set out to answer the question of whether demographic microsimulation can reproduce individual-level generational placement trajectories (GPT) recorded in high-quality register data and, once validated, what such a tool can tell us about the past, present, and likely future of intergenerational family life courses in Norway. For this, we benchmarked a SOCSIM-generated simulated register against the empirically observed 1960 Norwegian birth cohort, then projected and compared full life-course GPT for the 1960 and 2000 cohorts.

Our benchmarking analysis found high concordance between simulated and empirical GPT. Aggregate demographic indicators aligned closely, and sequence-level statistics differed only marginally. Using cluster analysis, we showed that the simulation was able to replicate the number, size, and internal structure of “typical” trajectories for the empirical 1960 cohort, confirming that a naive demographic microsimulation can capture not only averages but also heterogeneity in timing and sequencing of life events (RQ1).

As a second step, we produced simulated individual-level life courses up until age 100 for individuals born in 1960 and 2000 in Norway. We found that the share of trajectories with no descendants—our operationalization of “fading family lines”—rose substantively over the cohorts. This was driven by a 60% increase in non-parent clusters and a decline in the share of grandparents within the 2-generation family cluster from 55% to 19%. At the same time, we found evidence of a standardization of intergenerational life courses, signaled by a decline in the number of distinct GPT clusters, a concentration of the ages at first births, and a reduction in the variability of the ages at death. We project that individuals will spend more years with parents alive but without descendants and sandwiched between multiple generations. The three-generation family pattern will continue being dominant but is expected to decline by roughly 14% across birth cohorts. The net effect is a “thinner” but more stable intergenerational kinship reservoir, with fewer potential supporters but more predictable kin availability across the life course.

We identify several contributions to our work. Initially, we provided an empirical population-level characterization of GPT in Norway for the 1960 cohort. Our results show when and for how long individuals are children, parents, and grandparents, and how those roles co-occur over the life course. Second, we provide the first systematic comparison of life course trajectories using sequence analysis in real and simulated populations. Third, we propose a reproducible pipeline for studying GPT using simulated populations with credible kinship structures using the SOCSIM microsimulator. We provide reproducible code that can be applied to other settings. Because the projection step relies only on age-specific fertility and mortality rates, after calibration, the approach can be applied in data-scarce settings. As such, it lays the groundwork for truly global, comparative studies of the intergenerational family that includes countries in the global South that are often ignored given data limitations.

Our empirical findings have implications for social policy. We project that family structures in Norway will both be thinner and more homogeneous, signaling a diminished but more predictable “reservoir” of intergenerational support for members of more recent birth cohorts. Policymakers should expect a rising share of adults who reach mid-life with living parents but no descendants. At the same time, simultaneous demands on care time coming from members of different generations (e.g., the “sandwich” and “double sandwich” generations) will be experienced at older ages and for shorter time periods.

Identifying groups with different care needs in advance will be crucial for adjusting welfare systems as families become smaller and more vertical and informal support from (biological) kin becomes even scarcer than it currently is. Nonetheless, it is possible that declining kin availability (measured as the number and ages of living kin) is complemented by rising non-kin ties in individuals’ social networks. We do not consider these in this study as friendship networks are very difficult to model and project with our methodology, but this is an exciting area of work for future research. In any case, timely investments in young- and old-age support are essential to anticipate these shifts in lifecourse trajectories that will place a greater burden on individuals and on the state.

Limitations

We identify a number of limitations. *First*, our modelling strategy presumes relatively standardized life courses. As a result, our simulations may fail to reproduce ‘real-world’ heterogeneity in contexts where life-courses are more complex. *Second*, we ignore socio-economic stratification by assuming the same rate set for all members of the population. This may be less problematic in the case of Norway, even though a recent Swedish study shows evidence of SES gradients in kin availability (Andersson & Kolk 2024). However, it may matter more for contexts where demographic behaviour varies significantly across

socioeconomic groups. *Third*, we do not model union formation or dissolution. While this does not affect our estimates directly, it does mean that we are unable to consider in-laws. *Fourth*, we do not include parity-specific fertility and only consider female fertility rates. Whereas, this does not affect age-specific fertility, it may introduce deviations from empirical fertility trends, in particular in high-fertility settings where male and female fertility are very different (Schoumaker 2019). *Fifth*, we treat fertility and mortality as independent processes, which is a common assumption in studies that use SOCSIM simulations (Ruggles 1993). However, in reality they can be interrelated. For example, experiencing kin loss can affect subsequent fertility behavior. *Sixth*, despite a high level of agreement between sources, microsimulation produces simulated populations that are unlikely to capture the complexity of the real world. Simulated populations remain model artefacts. *Lastly*, our analyses focus on vertical biological kin only, thereby not accounting for collateral or horizontal kin, such as siblings or aunts, or non-biological family, such as partners or step-relations. Future work can extend our analyses beyond intergenerational family networks.

Conclusions

We showed that a relatively “naive” microsimulation setup (based on population-level fertility and mortality rates only) can recover the complexity of empirically observed generational placement trajectories (GPT) in Norway. Projecting those GPTs forward in time indicates that, for individuals born in 2000, the proportion of “fading family lines” (individuals who age without direct biological descendants) will rise to roughly one-third of their birth cohort, while three-generation constellation will shrink by about 13% and overlap with own parents will lengthen considerably, while demographic “sandwiching” between multiple generations will happen later and be—regarding the “double sandwich”—shorter. Together these shifts point to a thinner but more predictable reservoir of intergenerational support, sharpening the need to

support individuals with no kin or in a position of later-life “sandwichness.” Beyond the empirical analyses, we show that a combination of microsimulation and lifecourse analysis can be used in contexts that lack linked micro-data and provide the necessary analytical code to do this, thereby opening new comparative horizons for kinship demography and inequality research.

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Appendix

Figures

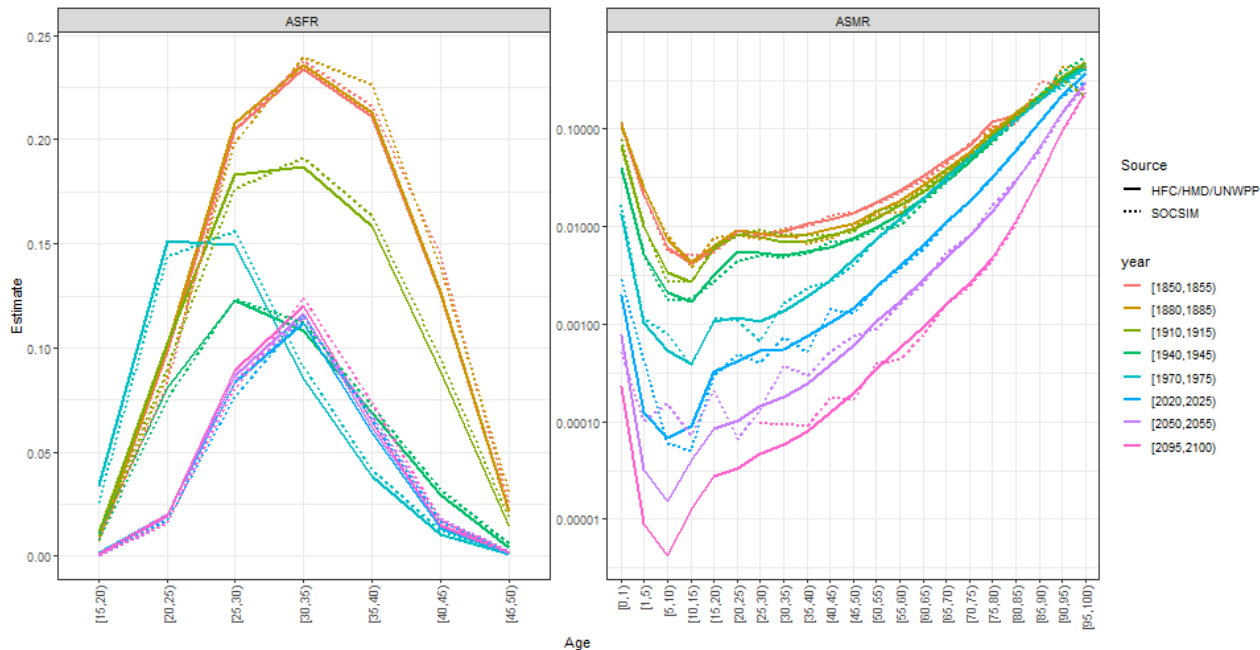


Figure A 1 Comparison of women's aggregate age-specific fertility and mortality rates between empirical and simulated populations for one simulation

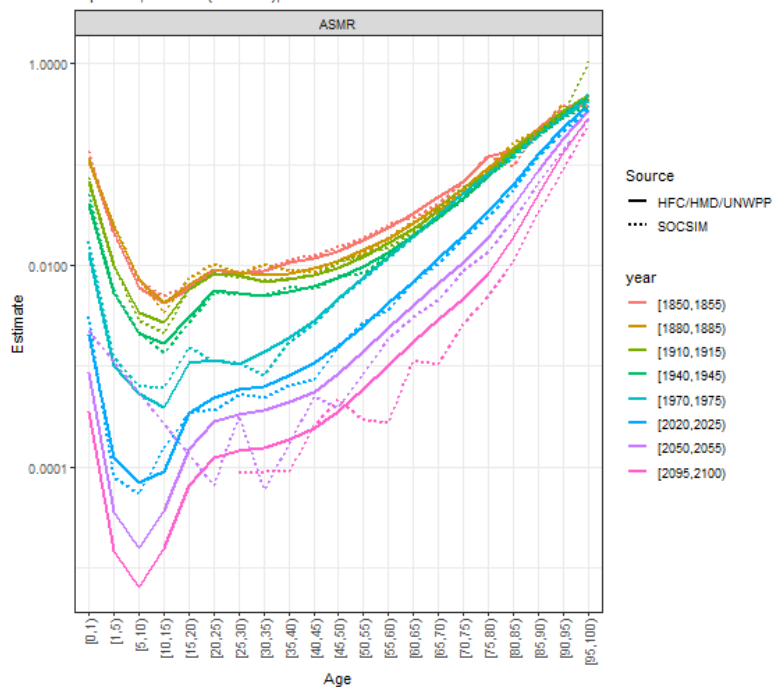


Figure A 2 Comparison of men's aggregate age-specific fertility and mortality rates between empirical and simulated populations for one simulation

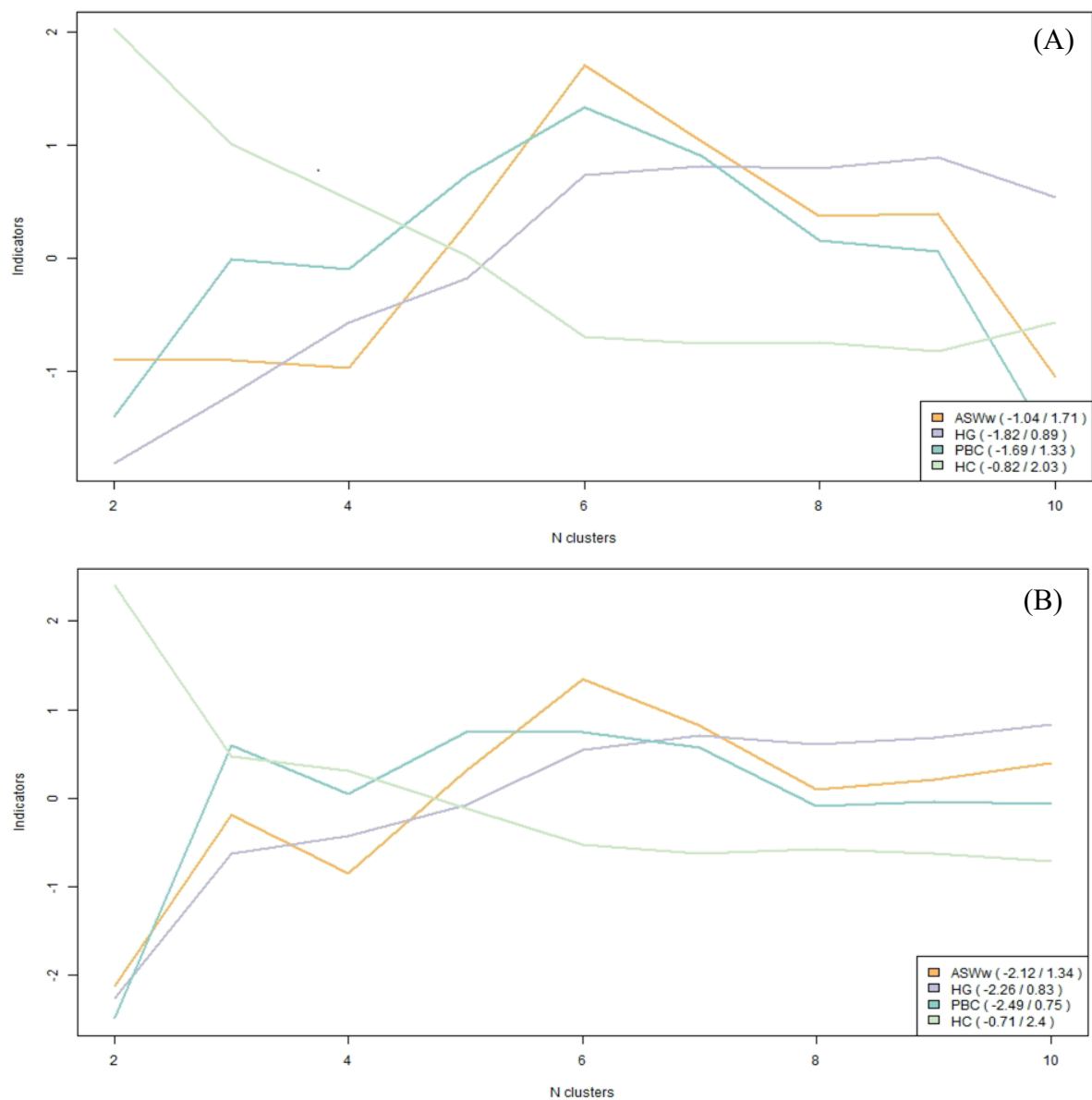
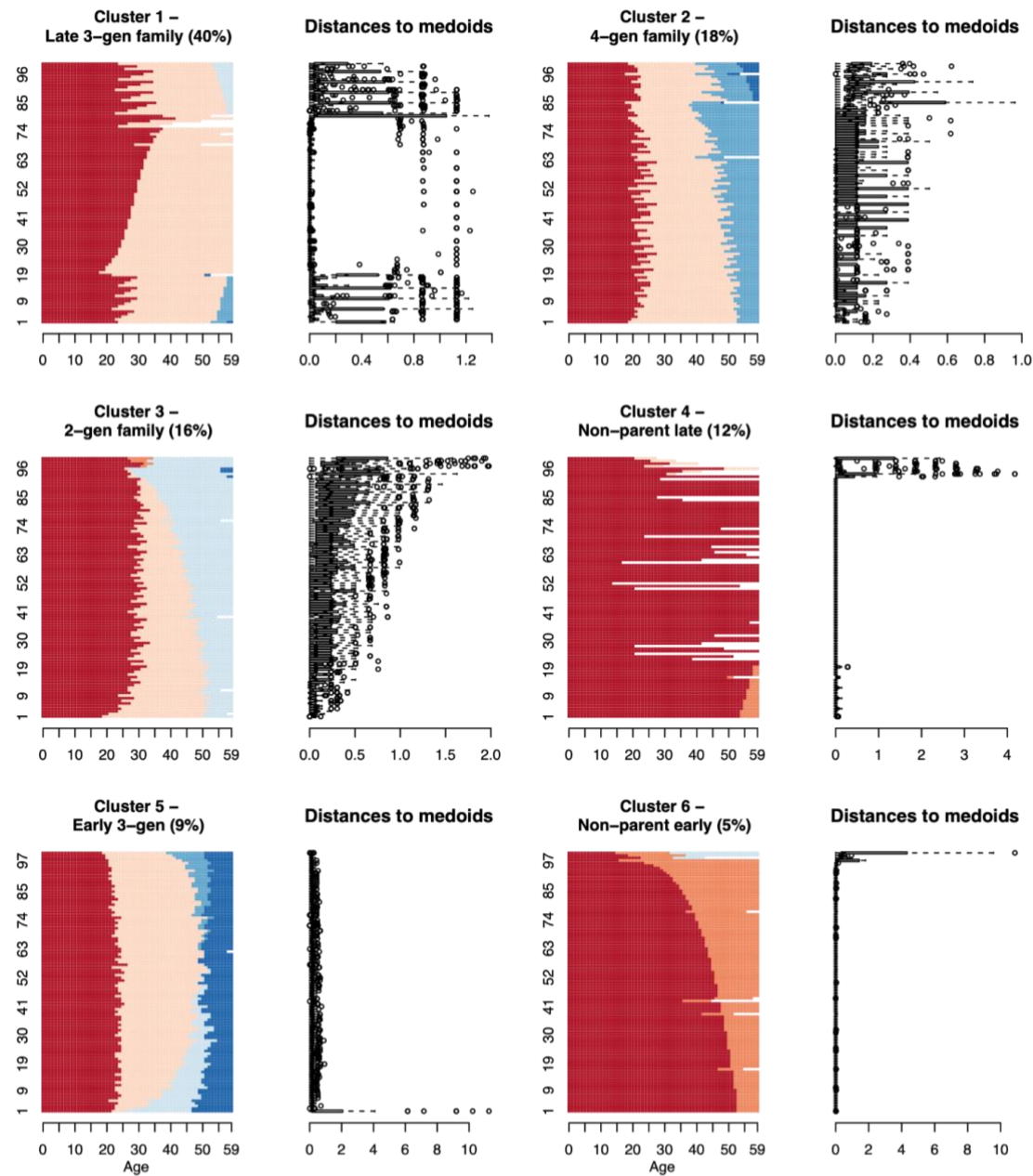
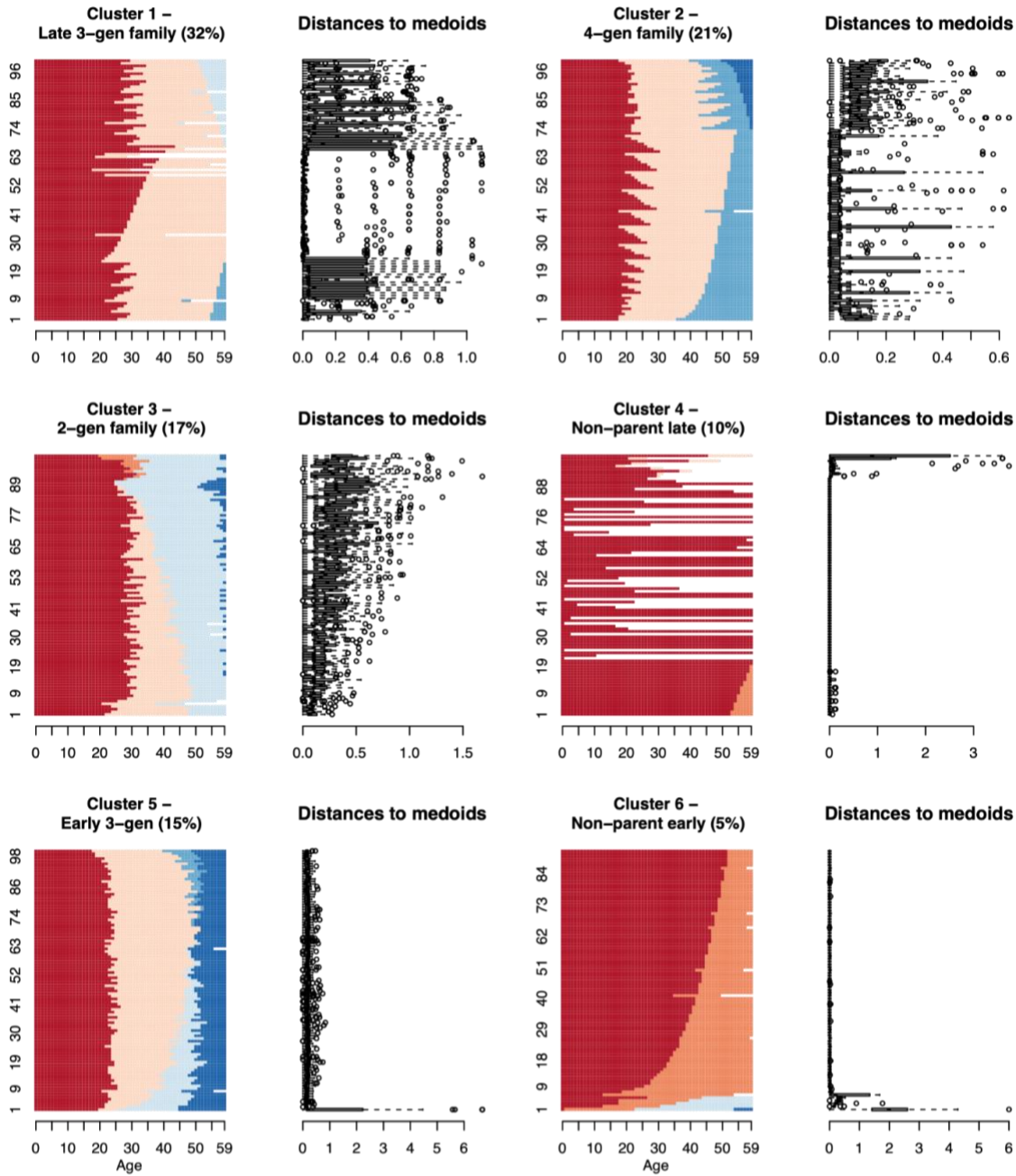


Figure A 3 Standardized cluster quality indicators for (A) empirical register data and (B) microsimulated data over different numbers of clusters for the 1960 birth cohort (aged 0–59).



Existing intergenerational family members		Corresponding generational placement	
Individual only	G2		<i>None</i>
Individual and parent(s)	G1 G2		<i>Child</i>
Individual, parent(s) and child(ren)	G1 G2 G3		<i>Child & parent</i>
Individual and child(ren)	G2 G3		<i>Parent</i>
Individual, parent(s), child(ren) and grandchild(ren)	G1 G2 G3 G4		<i>Child, parent & grandparent</i>
Individual, child(ren) and grandchild(ren)	G2 G3 G4		<i>Parent & grandparent</i>

Figure A 4 Relative frequency sequence plots by cluster showing the 100 most representative sequences per cluster (medoids; left panels) and their representation quality as dissimilarity-to-medoid plots (right panels) for the 1960 birth cohort from *empirical* register data. The right panels show box plots of the pairwise distance between each medoid (shown on the left) to the trajectories they represent (not shown). Better representation is indicated by lower average distances between medoids and the represented trajectories.



Existing intergenerational family members		Corresponding generational placement	
Individual only	G2	None	
Individual and parent(s)	G1 G2	Child	
Individual, parent(s) and child(ren)	G1 G2 G3	Child & parent	
Individual and child(ren)	G2 G3	Parent	
Individual, parent(s), child(ren) and grandchild(ren)	G1 G2 G3 G4	Child, parent & grandparent	
Individual, child(ren) and grandchild(ren)	G2 G3 G4	Parent & grandparent	

Figure A 5 Relative frequency sequence plots by cluster showing the 100 most representative sequences per cluster (medoids; left panels) and their representation quality as dissimilarity-to-medoid plots (right panels) for the 1960 simulated birth cohort from *microsimulated* data. The right panels show box plots of the pairwise distance between each medoid (shown on the left) to the trajectories they represent (not shown). Better representation is indicated by lower average distances between medoids and the represented trajectories.

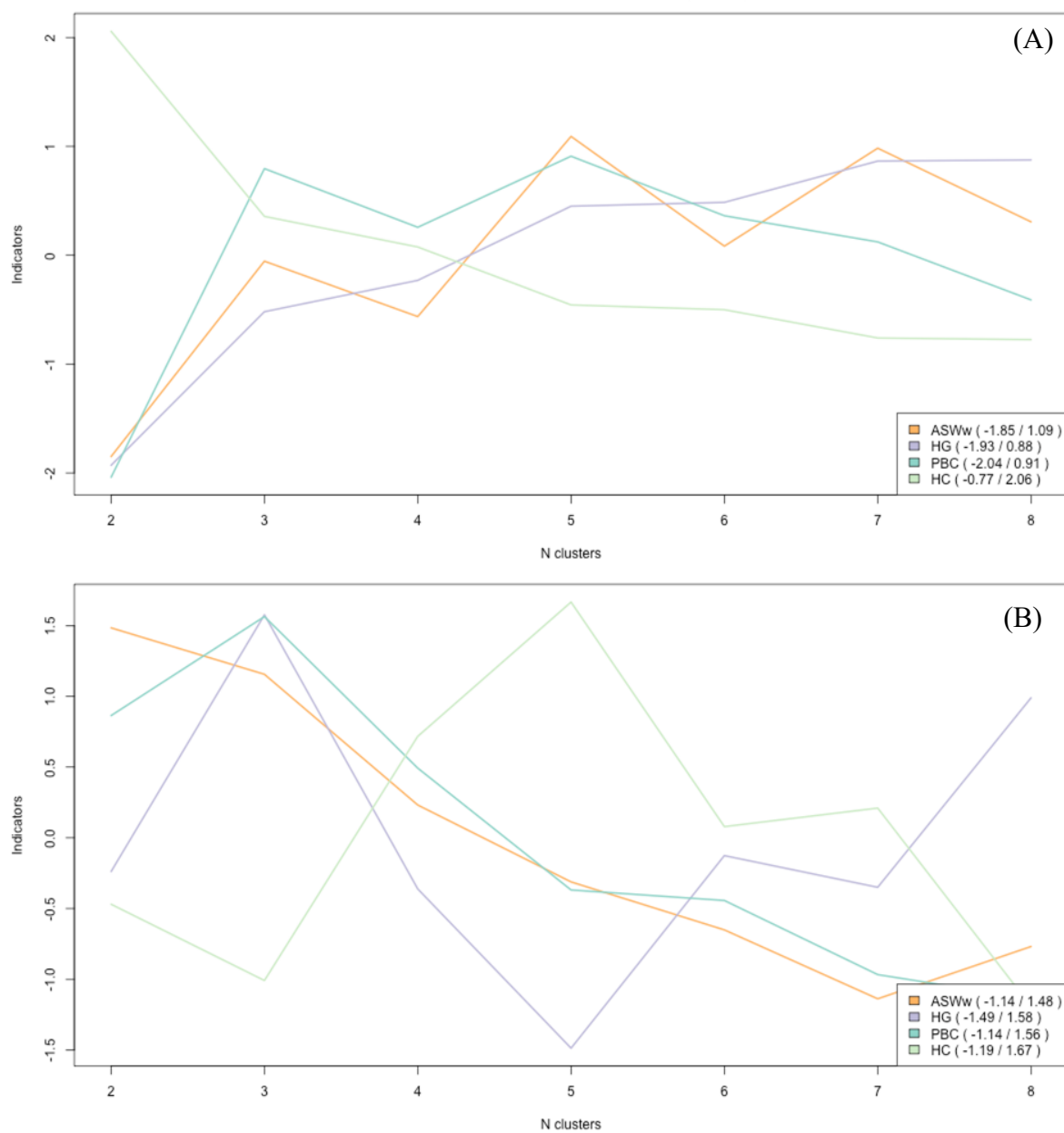


Figure A 6 Standardized cluster quality indicators for microsimulated register data for (A) the 1960 birth cohort and (B) the 2000 birth cohort (aged 0–100).