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Research Note: Estimating Kinship Size of Older Adults in Europe With Models and Surveys

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ABSTRACT Measures of kinship size are increasingly common in sociodemographic studies. The size and structure of older adults' kinship networks can be ascertained via direct observation in a social survey or modeled using demographic techniques. Each approach has advantages and disadvantages, but whether the two provide comparable estimates of kinship size is an open question. In this research note, we answer this question using social survey data and demographic models to estimate the size of older adults' kinship networks in 22 European countries. We find an impressively high association between the two approaches, with important variations by the kin type considered. We discuss the reasons for the divergence in the estimates and provide guidance for researchers interested in using either approach to quantify kinship size.

KEYWORDS Accordance • Cross-national comparison • Measurement • Kinship size

Introduction

Studies in family sociology and demography have increasingly recognized the importance of kin beyond the nuclear and coresident family (Caswell and Song 2021; Furstenberg 2020; Madhavan et al. 2017). Kinship size matters in studies on social cohesion, stratification, and modernization, and research using kinship measures has expanded with increasing data availability and computer power (Alburez-Gutierrez et al. 2022; Furstenberg 2020). The importance of kinship for demographic and sociological questions cannot be overlooked. Examples are questions regarding kin solidarity, such as the functioning of families and support for a focal individual (Murphy 2011); kin inequalities, such as intergenerational mobilities and transfers, be it two-generational or multigenerational (Mare 2011); and the mutual impact between kin and societal modernization processes (Murphy 2008). In the aging societies of Europe, the question of the kin solidarity of older adults is of particular importance. More specifically, issues regarding the kin that might care for older adults are central in this respect.

Data on extended and non-coresident kin are relatively sparse. For this research note, we distinguish two main methods of quantifying kinship size at the country

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level: (1) direct observation via a survey and (2) demographic models using aggregate fertility and mortality data as input. First, we describe the research design of these two methods of conducting cross-national comparisons of kinship size in Europe. Second, we examine the extent to which these two methods produce overlapping calculations. We end this research note with a short discussion of the implications of this exercise for future research and recommendations for further research.

We pose two research questions. First, to what extent do direct observation using survey data and model-based estimates produce comparable country-level mean kinship sizes for older adults in Europe? Second, what explains the differences in the calculations between these methodological approaches? We define kinship size as the total number of biological relatives, including parents, children, siblings, and grandchildren.

Research Design

We produce estimates of kinship size using two independent analytical approaches, each of which relies on a different methodology and data source. In this section, we outline the estimation methods. We also point the interested reader to specialized literature with further technical information that we omit here to save space.

Direct Observation via Survey Data

Data

We use survey data from the Survey of Health, Aging, and Retirement (SHARE; Waves 1, 2, and 4–6). The data contain nationally representative samples of the population aged 50+ between 2004 and 2015. We considered these waves reliable, in contrast to the data collected in 2017 and 2019/2020 (Waves 7 and 8). Because the latter two waves seem to be more biased concerning the target populations of the countries under scrutiny (see the online appendix), we decided to discard these waves from our analyses. We selected SHARE respondents who were aged 50–64 or 65–79 at the time of the interview. From our initial sample of 170,672 respondents aged 50–64 and 65–79 in 22 countries, we excluded 18,957 because they lacked information on at least one kin category—upward (parents), downward (children or grandchildren), or lateral (siblings). The final analytical sample therefore consisted of 151,715 respondents.

Measures

We focus on survey questions about the number of living parents, children, siblings, and grandchildren. These data are directly comparable to kin estimates from the demographic models, with some exceptions. The exact wording of the questions can be found in the online appendix. Note that children include biological, step-, adopted, and foster children. Data from Waves 1 and 2 show that roughly 7% of the total number of children are nonbiological. Comparative figures from Waves 4 and 5 (where the question on biological children is asked for each child) are 9% and 11%, respectively. Because the demographic models focus on only biological kin, the two data sources might not perfectly correspond. To assess the potential size of error in concordance between SHARE and the formal kinship models, we performed a sensitivity analysis using only biological children for Waves 4 and 5 (conducted in 2011 and 2013, respectively). The results were similar; see the online appendix.

Analytical Strategy

We generate the variable *kinship size*, calculating the sum of each interviewed individual's living biological parents, siblings (both nonbiological and biological), children, and grandchildren. We calculate this sum only for those who answered all these questions, and we assume that listwise deletion does not lead to a selective deletion of respondents. Furthermore, there might be sampling errors because SHARE is based on probability samples. We account for sampling bias in region, sex, and age by weighting the mean kinship sizes per country using the cross-sectional calibrated weights provided by SHARE (see the online appendix for details). SHARE researchers express little concern about low response rates and moderate attrition levels because relative to other European and U.S. surveys, the overall response rate of SHARE is high (Börsch-Supan et al. 2013). Of course, even after the correction of sample selection bias by using weights, the survey might not be representative of or generalizable to the entire country populations of interest. Bias according to sex and age appears to be minimal, however (Bergmann et al. 2019). In addition to using sample selection weights, we also correct the standard errors for the clustered, stratified sampling strategies in each country. To do so, we use the primary sampling unit and strata information.

The Matrix Kinship Model Approaches

Our approach to modeling kinship size is based on the principle outlined by Goodman et al. (1974) that every population with a known set of age-specific fertility and mortality rates has an implicit kinship structure. In this context, kinship structure refers to the expected number of siblings, parents, cousins, and so on for an average member of the population. The initial implementation of this model, known as the Goodman–Keyfitz–Pullum kinship equations (GKP), relies on a series of recursive integrals operating in a theoretical one-sex population with stable vital rates. Our implementation of the kinship models follows from a recent development of the GKP equations proposed by Caswell (2019). Here, we refer to these equations as our *demographic models* because they use aggregate demographic rate data as input. Unlike the original GKP models, they rely on demographic projection techniques to produce kinship estimates using linear algebra. This implementation is more efficient and flexible than the original GKP approach. In particular, we rely on an extension of the demographic models that allows for two-sex populations (Caswell 2022) with time-variant demographic rates (Caswell and Song 2021).

Our models take age-specific mortality and fertility rates as input and return the kin counts for an average member of the population as output (referred to here as *Focal*). Thus, the models return the average number of living kin for Focal by country, year, kin type, age and sex of kin, and age and sex of Focal. The models allow us to determine, for example, the expected number of grandchildren for a 55-year-old man in Germany in 2016. We rely on a model implementation similar to that of Alburez-Gutierrez et al. (2023) and use data from the 2022 United Nations World Population Prospects (United Nations 2022). We use age-specific survival probabilities (for women and men) and age-specific fertility rates (only for women) for 1950–2016. These data are historical estimates compiled by the United Nations Population Division and contain no demographic projections. We implement the demographic models in the R language package *DemoKin* (Williams et al. 2023).

We face two limitations regarding data availability. First, our two-sex models require male and female fertility rates, which are not available for all countries we study. To overcome this limitation, we rely on an androgynous fertility approximation (Caswell 2022), which assumes that males reproduce similarly to females. A recent multicountry study found that the androgynous fertility approximation results in a slight overestimation of male ancestors (Alburez-Gutierrez et al. 2023). For Sweden in 2017, where quality baseline data are available (Kolk et al. 2023), the largest overestimation was for great-grandfathers (the model projected 0.037 more great-grandfathers for a focal individual aged 0 relative to the baseline estimate). To reduce the magnitude of this bias, we average across male and female kin in this study—for example, presenting estimates for grandchildren without distinguishing between grandsons and granddaughters.

The second limitation derives from the 1950 start of our time series of demographic rates. Following Caswell and Song (2021), we take 1950 as the reference year for the model's time boundary condition. Thus, we assume that the 1950 demographic conditions were in effect for a very long time and use the resulting kinship structure to determine the initial conditions of our kinship projections. Assuming demographic stability before 1950 might introduce a slight bias in the data because it ignores the previous demographic history of a population, including the post–World War II baby boom. Nevertheless, several multicountry studies have found that the magnitude of the bias is small and decreases rapidly with time (Alburez-Gutierrez et al. 2021; Alburez-Gutierrez et al. 2023; Snyder et al. 2022). An empirical analysis using Swedish data found that the resulting bias was virtually undetectable after 2015 (Alburez-Gutierrez et al. 2021).

Results

The left panel in Figure 1 compares the country-level mean and 95% confidence intervals for kinship size obtained using SHARE data (x-axis) and the demographic models (y-axis). Colors differentiate the kinship type, and black circles indicate estimates with unexpectedly low coefficients of variation (CV = standard error / estimate × 100). The legend displays the fraction of the matrix kinship model estimates within the SHARE's 95% confidence intervals. The right panel of the figure plots the SHARE estimates against the relative difference between the two estimates.

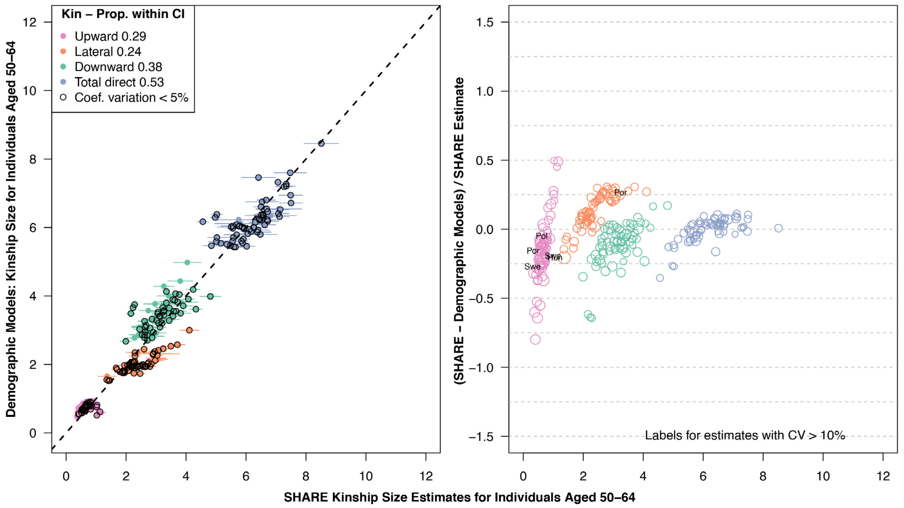

Fig. 1 Country-level mean kinship sizes according to direct observation using SHARE data and model-based estimates (left panel) and differences between the two estimates (right panel) for adults aged 50–64 in selected European countries, 2004–2016. Each point is one country-wave, and labeled circles indicate CVs above 10%.

Markers' sizes are proportional to the CV of the country-level estimates of the SHARE data, with larger labeled circles indicating CVs above 10%.

Overall, these panels suggest consistency in the mean kinship size estimated via direct observation and demographic models. Most points hover around the diagonal line in the left panel and within –0.25 and 0.25 along the *y*-axis in the right panel, indicating that the estimates are similar and that most relative differences are less than 25%. The most significant relative discrepancies between these methods are in upward kinship estimates. As a result, the country-wave correlations between the matrix kinship model and SHARE estimates are .76 for total kinship, .69 for downward kinship, .85 for lateral kinship, and .32 for upward kinship.

Despite this consistency, two systematic discrepancies are worth noting. First, less than 50% of the matrix model estimates lie within the SHARE's 95% confidence intervals, meaning that SHARE estimates are potentially statistically different from matrix model estimates. Some of these cases stem from unrealistically short confidence intervals (i.e., estimates with a CV of less than 5%), particularly for upward and lateral kinship, where the fraction of matrix model estimates within SHARE's confidence intervals is only .25 (not presented in the figure).

Second, most SHARE estimates of lateral kin surpass matrix model estimates: individuals tend to report more lateral relatives than demographic models project. Notably, more than one in four matrix model estimates of lateral kinship lie within SHARE's confidence intervals (.24, as reported in the legend). The reverse is true for downward and upward kinship: on average, individuals tend to report fewer children, grandchildren, and parents than matrix models project. The two methods show higher correspondence for downward kinship, with 38% of the matrix model estimates lying within SHARE's 95% confidence intervals.

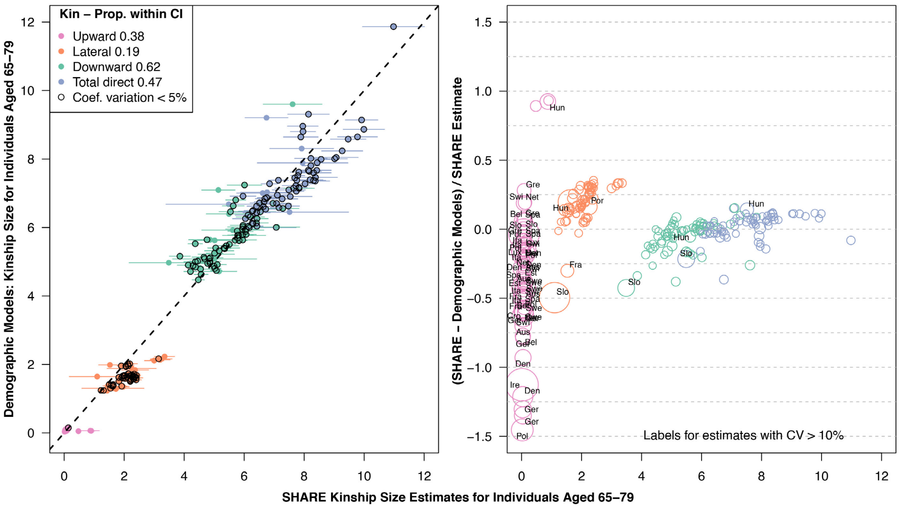

Fig. 2 Country-level mean kinship sizes according to direct observation using SHARE data and model-based estimates (left panel) and differences between the two estimates (right panel) for adults aged 65–79 in selected European countries, 2004–2016. Each point is one country-wave, and labeled circles indicate CVs above 10%.

Moving on to the relative size of these discrepancies, displayed in the right panel of Figure 1, the disparity between the estimates of upward kinship is between –0.5 and 0.5 for most country years, signaling substantial differences between the sources. Matrix models yield higher projected upward kinship. These estimates also display more significant CVs with large circles, indicating high standard errors relative to their mean in the SHARE data. Overall, relative differences for downward, lateral, and total kin are between –0.25 and 0.25 on the *y*-axis, indicating that the magnitude of the discrepancy between the estimates does not surpass 25% of the SHARE estimates (i.e., the denominator of the *y*-axis metric). This result indicates strong correspondence between matrix models and SHARE's reports.

Figure 2 compares the SHARE and the matrix model estimates of kinship size for an older age group, 65–79. The consistency between the two methods is similar to that observed in the younger group (in Figure 1), with most points close to the diagonal. The country-level correlations between the two estimates are above .72 for all kinship types except upward, which displays a negative correlation (–.09). Note that the population born before 1950 has been assumed to have the same mortality rates as those born in 1950. This assumption could explain higher survival rates for parents of the focal individual in the demographic models, which is in line with the overestimation of demographic models' upward kin we find here. As for the younger age group, most differences between the two methods favor SHARE estimates for lateral kin and formal demographic models for downward kin.

Regarding the patterns in the right panel, the relative differences cluster between –0.25 and 0.25, except for upward kinship, where the differences between SHARE and kinship models tend to be larger. In addition, estimates for this older group display more significant uncertainty than those for the younger group, with several estimates displaying a CV above 10% (indicated by large circles).

Three patterns in Figure 2 relative to Figure 1 are consistent with individuals' age differences (i.e., older vs. younger individuals). First, estimates in Figure 2 display more significant CVs, indicating that the kin estimates are more uncertain among older individuals than among younger ones owing to smaller numbers of surviving kin, particularly upward and lateral. Second, the absolute value of the average downward kin is more prominent among older individuals, reflecting their more prolonged exposure to becoming (in this case) grandparents. In other words, children of older individuals have had, on average, more time to have children than children of younger individuals. Third, estimates of upward kinship are very close to zero, reflecting the higher mortality of parents of individuals aged 65–79 relative to parents of those aged 50–64.

Discussion

Summary

In this research note, we compare direct observation via survey data and demographic models for calculating the sizes of different kinship types: downward, lateral, upward, and total. Although the two approaches use different methods and rely on different assumptions, we find a relatively high association between them. This correspondence raises our confidence in relying on direct observation via the SHARE survey or using demographic models based on fertility and mortality schedules. Also, we found a higher estimation of downward kin when using the demographic model and a higher estimation of lateral kin when using the SHARE survey. The SHARE estimates of upward kin seem more unreliable owing to the low number of living parents, especially for the older group.

Comparing the Two Approaches

What could explain the observed differences between demographic models and empirically based survey estimates? The models are demographic projections that rely on a series of simplifying assumptions. They underestimate the complexity of the real world, whereas surveys might better reflect reality. Probabilistic surveys allow for the calculation of standard errors, which in turn serve to assess estimates' uncertainty. By relying on population averages, kinship models ignore within-population variability and do not allow for uncertainty assessment, for the time being. Migration is another limitation. The period rates used in formal models ignore premigration contexts, potentially leading to an underestimation or overestimation of kin, depending on the kin type considered, the current age of the focal individual, country of origin, and age at migration. These limitations are significant when the kinship sizes of older adults are quantified, particularly for relatively uncommon kin types (e.g., parents of individuals aged 65–79).

In contrast, surveys are appropriate tools to quantify within-country heterogeneities in kinship size across, for example, subnational areas, socioeconomic status, education, income, wealth, propinquity, and health status (provided sufficient sample sizes and cross-national comparability in question wording). Studying these heterogeneities might enable researchers to examine mechanisms, answering research questions about kinship size. However, survey data might suffer from sampling and nonsampling errors, leading to difficulties in generalizing to entire country populations. Sampling error is considered by calculating standard errors, using a correction for complex sampling designs. Nonsampling errors (e.g., coverage, measurement, processing, nonresponse, and specification errors) are more difficult to address. Also, the longitudinal nature of SHARE amplifies potential errors due to attrition, which might increase sample bias for the target population if the dropout is selective. We tried to correct such nonresponse issues by using a mixture of scaling and proportional weights (i.e., reciprocal sampling ratio per stratum in the case of a clustered stratified random sample). The consistency in our weighted SHARE estimates over time gives us confidence that sample bias due to attrition plays a minor role.

Recommendations and Future Research

Our analysis suggests that surveys and formal models can effectively estimate kin counts for older adults in Europe, which should be reassuring for survey researchers and modelers. Our analysis also points toward the usefulness of empirical data for benchmarking and improving demographic models of kinship. Scholars and policymakers alike can thus use both approaches, which are likely to be reliable proxies of kinship size in the various European populations. Yet, which approach is recommended for estimating kinship size? The answer depends on whether one focuses on explanation or projection.

On the one hand, for scholars interested in the mechanisms explaining country differences in kinship size by macro-indicators proxying kinship regimes or in relating explanatory individual-level factors to kinship sizes, such as socioeconomic indicators or variables describing the circumstances and well-being of the focal individual and its kin, we recommend using the SHARE data. Note that we discarded Waves 7 and 8 (covering 2017–2020) from the SHARE data because these country-years are unreliable.

On the other hand, we recommend using kinship models in the following situations. First, they can be combined with demographic projection data to forecast the future development of kinship size. Second, demographic models have the advantage that all second- and third-degree kin members can be included. Finally, kinship models can estimate kinship size in settings where no empirical kinship observations exist. Yet, it is important to remember that the quality of these estimates will depend on the quality of the demographic data used as input. Ultimately, we foresee that model- and survey-based estimates can be combined to produce a clearer and more complex picture of kinship dynamics. This coordinated approach will likely be more useful for studying kinship in regions of the Global South, where older adults are projected to have ever-smaller networks of kinship support on which to rely (Alburez-Gutierrez et al. 2023) and where data are particularly scarce. Although we cannot determine the exact nature of the bias that models and surveys might introduce for other world regions, we can draw lessons from our findings. This research note shows that model and survey estimates diverge more (in relative terms) when kin counts are small. This concern might be more relevant for some countries in East Asia, which have experienced prolonged periods of low fertility and, as a result, have small family sizes (Alburez-Gutierrez et al. 2023). It can also affect estimates of siblings, cousins, and parents of older adults in regions such as sub-Saharan Africa, where low life expectancy results in fewer horizontal kin among older adults. Future work in kinship demography should examine these topics in more detail. ■

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