Changing Demographic Rates Reshape Kinship Networks

Sha Jiang, Wenyun Zuo, Zhen Guo, and Shripad Tuljapurkar

ABSTRACT The number and age of kin determine the companionship and support individuals provide or receive. Over recent decades, fertility and mortality rates have changed considerably, with varying speeds across countries. We investigate the changes in kinship networks in response to time-varying demographic rates, with a focus on the speed of change. We start with stylized demographic trajectories to determine the separate effects of fertility and mortality. First, we find that differences in the number of living kin depend strongly on the speed of fertility decline. In a fast fertility transition (as in China), a 65-year-old could have 20% fewer daughters than a 70-year-old in a specific year. However, in a slow transition (as in India), this difference is only 7%. Second, the speed of fertility decline has large effects on the mean and variability of the ages of kin. Third, a cohort perspective provides valuable insight into the changes in the number and age of kin. Fourth, we show how changes in the age pattern of mortality affect kinship for individuals at different ages. We use these conclusions to examine and understand kin dynamics based on empirical demographic data from four illustrative countries (Thailand, Indonesia, Ghana, and Nigeria).

Introduction

Kinship networks, formed by consanguineous (blood) and affinal (marriage) ties, play a vital role in shaping the lives of individuals and communities. Networks are shaped by demographic transitions, which alter the size and structure of families over time. Consider a 20-year-old individual who wants to host a party that only cousins can attend. Under a demographic transition, where both fertility and mortality are declining to a low level, the size of this party is likely to be very different for the individual, the individual's mother, and the individual's grandmother when each is at age 20. Previous work by Jiang et al. (2023) compared the size of kinship networks long before and long after demographic transition using a time-invariant model. They found a quadratic relationship between the size of kin groups and net reproductive rate. How about kinship networks during the demographic transition? Using microsimulations, Verdery (2015) analyzed the effects of the relative timing of demographic transitions in mortality versus fertility rates (i.e., the gap between the onsets of the mortality and fertility transitions) on kinship networks. In the real world,

demographic transitions also occur at different speeds across countries. For example, China's total fertility rate (TFR) halved in a decade, while the TFR in Western Europe took 75 years to fall by half, and Nigeria's fertility decline is ongoing. In this article, we explore how diverging speeds of demographic transitions affect kinship networks between populations. When the transition is fast, individuals with a small age difference will experience different sets of vital rates. On the other hand, if the transition is so slow that vital rates take several generations to change, time dependence has gradual effects on kinship networks.

The study of kinship—especially the number of types of kin—has become important in various contexts, including support and transfers across generations (Seltzer 2019; Wiemers and Park 2021; Zagheni and Wagner 2015). Generational overlap, initially studied in the context of aging (Menken 1985; Soldo 1996), now extends to the context of kinship and stepkin in the United States and other societies (Alburez-Gutierrez et al. 2021; Bengtson 2001; Jiang 1995; Park et al. 2019; Wachter 1997). Historically, kin networks were sources of important information—for example, where to find a job or spouse or a place to live (Krackhardt et al. 2003; Murray et al. 1981). In many cultures, families also transmitted knowledge, skills, and resources across generations (Schniter et al. 2023). However, these kinship functions have diminished as kin networks declined in size as a result of demographic transitions and the increasing importance of weak ties—casual, nonkin connections with acquaintances, coworkers, and social media contacts. In addition to the traditional role of resource transmission, recent studies have explored other dimensions of kinship networks, such as the number of close kin who died from the COVID-19 pandemic and its psychological implications (Snyder et al. 2022; Verdery et al. 2020), and the new approach of finding target individuals (e.g., suspects in crimes) using genetic and genealogical databases (Erlich et al. 2018).

One aspect of kinship is that it involves the individual level and so many previous findings at the population level may not be relevant. For example, while population growth may continue owing to momentum, a TFR decline can reduce the number of kin immediately under some situations, such as the number of daughters for individuals at reproductive ages. A fast TFR decline could further cause individuals only a few years apart to experience different family dynamics. Those with more kin could rely on close relatives for support, while those with fewer kin are more likely to turn to friends or online resources. Kinless individuals face reduced support overall. We also note that there is a trade-off between the size of a kinship network and the levels of support received. For instance, in large families, although older individuals may have more adult children who can potentially offer support, these adult children also bear the responsibility of caring for more young dependents. This dynamic introduces a potential trade-off between the care of parents and the care of children (Gans et al. 2013). On the other hand, fertility change determines the age structure of the total population, which also affects the age distribution of kin. For instance, a decline in fertility leads to an aging population and increases the age of mothers in the future.

Our study analyzes the change in kinship networks (specifically, female kin through female lines of descent) in response to time-varying demographic rates. We focus on how different speeds of fertility decline affect the number and age of kin when an individual is at different ages and further impact the support and resources

available to the individual. We note that there is a difference between the number of living kin and the kin availability in terms of support and resources. The former indicates only the existence of kin and does not consider factors such as health status, geographic proximity, or economic standing, which may also influence kin availability. In our subsequent analyses, we use the number of living kin as a simple proxy indicator of kin availability.

To understand the changing number and age of kin over time, we adopt a cohort perspective, linking kinship networks to cohort fertility and mortality. In demography, time is conceptualized through two perspectives: the period perspective, which focuses on chronological time, and the cohort perspective, which centers on ages of individuals born in the same year (Wachter 2014). A birth cohort, defined as a group of individuals born in the same year, shares the same experiences at the same age. In our study, the kinship network of different birth cohorts reflects distinct demographic transitions experienced by each birth cohort, which are different from the change in mortality and fertility over time. Finally, we analyze the effects of age patterns of fertility and mortality decline on the size of kin groups, providing a more comprehensive understanding of the relationship between demographic rates and kinship networks.

In terms of methodology, we use a one-sex, time-varying kinship model by Caswell and Song (2021), which is an analytical model based on the seminal work by Goodman et al. (1974) and allows us to examine the dynamics of consanguineous and female kin. We analyze kinship networks under both stylized and empirical demographic transitions. Noting that mortality typically declines before fertility in traditional models, our stylized cases expand on this model by considering a wider range of trajectories for mortality and fertility changes, including scenarios where fertility and mortality decline simultaneously, and counterfactual cases where one demographic rate remains constant. Stylized trajectories, while not directly aligned with past real-world transitions, help isolate and facilitate the study of the effects of each demographic rate distinctly in a controlled environment. Such theoretical investigation is also practically relevant because many countries recently or currently have comparatively high levels of fertility or mortality, and their transitions have followed or may follow historically unexpected patterns (Hosseini-Chavoshi and Abbasi-Shavazi 2012; Prasartkul et al. 2019). To apply these theoretical insights to real past examples, we also examine kinship networks in four illustrative countries, each with different speeds of demographic transition, using empirical fertility and mortality data. The combination of stylized and empirical data strengthens the connection between theoretical models and real-world observations, which should increase the robustness and applicability of our findings. In the final discussion, we elaborate more on our use of an analytical approach and the role of microsimulations in addressing the research question.

Kinship Model

We compute the kinship network of a specified individual Focal using the Caswell and Song (2021) one-sex, time-varying kinship model. An extension to the two-sex model is feasible if adequate time-series data for male fertility or a proper model

for mating patterns is available. Let $\mathbf{U_t}$ be a matrix with age-specific survival probabilities at time t on the subdiagonal and zeros elsewhere, and let $\mathbf{F_t}$ be a matrix with age-specific fertility rates at time t on the first row and zeros elsewhere. Define $\mathbf{k(x, t)}$ as the age distribution vector for some specified type of living kin at age x of Focal at time t. As individuals survive and reproduce, the dynamics of $\mathbf{k(x, t)}$ are given by

$$\mathbf{k(x + 1, t + 1) = U_t\,k(x, t) + \beta(x, t)}, \tag{1}$$

where

$$\mathbf{\beta(x, t)} = \begin{cases} \mathbf{0} & \text{if there are no new kin of this type} \\ \mathbf{F_t k^*(x, t)} & \text{if new kin are produced by some other type } \mathbf{k^*} \text{of kin.} \end{cases} \tag{2}$$

The first term $\mathbf{U_t\,k(x, t)}$ represents the survival of the kin from age x to $x + 1$ during time t to $t + 1$. The second term $\mathbf{\beta(x, t)}$ accounts for the addition of new individuals during time t to $t + 1$. For some types of kin, no new individuals are possible and $\mathbf{\beta(x, t)}$ is zero (e.g., Focal does not accumulate any new mothers or aunts). For other types of kin, new individuals are produced by the fertility of others, $\mathbf{k^*}$ (e.g., new granddaughters are produced by the fertility of daughters). Since survival is included, the vector $\mathbf{k(x, t)}$ includes only living kin.

An initial condition $\mathbf{k(0)}$ is added to specify the kin that Focal has at her birth. In the time-varying model, this single condition expands into two boundary conditions: the complete age vector at time $t = 0$, $\mathbf{k(x, 0)}$, and the initial age vector at each time, $\mathbf{k(0, t)}$. To calculate this time boundary $\mathbf{k(x, 0)}$, we assume that the rates $\mathbf{U_0}$ and $\mathbf{F_0}$ have been operating for a long time and generate $\mathbf{k(x, 0)}$, using a time-invariant model based on these rates. To calculate the age boundary $\mathbf{k(0, t)}$, there are two possibilities. If Focal has no kin of this type at her birth, then

$$\mathbf{k(0, t) = 0}. \tag{3}$$

Otherwise, the age boundary is calculated as

$$\mathbf{k(0, t + 1) = \sum_i \pi_i(t)k^*(0, t)}, \tag{4}$$

where $\mathbf{k^*}$ is the same as in Eq. (2) and $\pi_i(t)$ is the proportion of mothers who reproduce at age i at time t. This time-dependent distribution $\pi_i(t)$ is calculated as the age structure of the entire female population at time t multiplied by the age-specific fertility rate at time t. More details can be found in Caswell and Song (2021).

Note that, as written, the model is defined for females and thus gives expected age distributions of female kin (e.g., granddaughters) through female lines of descent (e.g., granddaughters include daughters of daughters, but not daughters of sons).

Defining $\mathbf{1_n}$ as a vector of length n with all elements equal to 1, the expected number of living kin at age x of Focal is

$$\mathbf{\hat{k}(x, t) = 1_\omega^T\,k(x, t)}, \tag{5}$$

where superscript T indicates a transpose, and ω is the length of vector $\mathbf{k(x, t)}$.

Using $\mathbf{\hat{k}(x, t)}$, we analyze the age pattern of living kin of a Focal individual at age x and time t. By employing that age pattern, we are able to calculate the mean

age and the standard deviation of ages of kin for a Focal individual of a given age at a given time.

In this article, we focus on the expected number and mean age of selected types of living kin when Focal is at selected ages while our result contains the information for Focal at each age. The calculation based on the time-varying kinship model is implemented using the R package DemoKin (Williams et al. 2021).

Stylized and Empirical Demographic Transitions

We analyze kinship networks using both stylized and empirical demographic transitions. We expect that some of the stylized transitions that result from our scenarios will not be reflected in empirical experience, but they nonetheless provide useful insight into the effects on kinship of the interactions between components of demographic change.

Scenarios for Stylized Demographic Transitions

We construct different scenarios of the change in vital rates from 1970 to 2040 and analyze the kinship network under these stylized demographic transitions. We assume TFR drops linearly from 5 to 2 children at different speeds and then stays constant. To measure the speed, we compare the time taken for fertility to fall relative to generation time, taken here to be 25 years.

1. Fast fertility change, in which TFR drops to 2 within a half generation (from 1970 to mid-1983).
2. Medium fertility change, in which TFR drops to 2 within one generation (from 1970 to 1995).
3. Slow fertility change, in which TFR drops to 2 within two generations (from 1970 to 2020).

Panel a of Figure 1 shows these patterns of change in TFR from 1970 to 2040.

To model the age pattern of fertility, we employ a specific pattern for the initial and final years to construct patterns for intermediate years. We also assume a linear change in the age patterns of fertility with only one pattern for the beginning year and two distinct patterns for the end year. In particular, we utilized China's age pattern of fertility in 1970 as the starting point, and China's early and Italy's late age patterns of fertility in 2020 as the ending point (see panel c of Figure 1). Of these, the early pattern exhibited a younger mean age at birth, implying that, on average, females tend to give birth at a later age. Combining different speeds of fertility change and different age patterns of fertility, we construct the age-specific fertility rates (see Figure A1 in the online appendix, along with all other figures designated with an "A") and mean age at birth (see panel d of Figure 1) from 1970 to 2040. Note that in our scenarios, the speed of change in TFR is the same as the speed of change in the age distribution of fertility.

For age-specific mortality rates, we consider two cases: mortality is constant at a low level, or mortality changes over time from a high level to the same low level. In
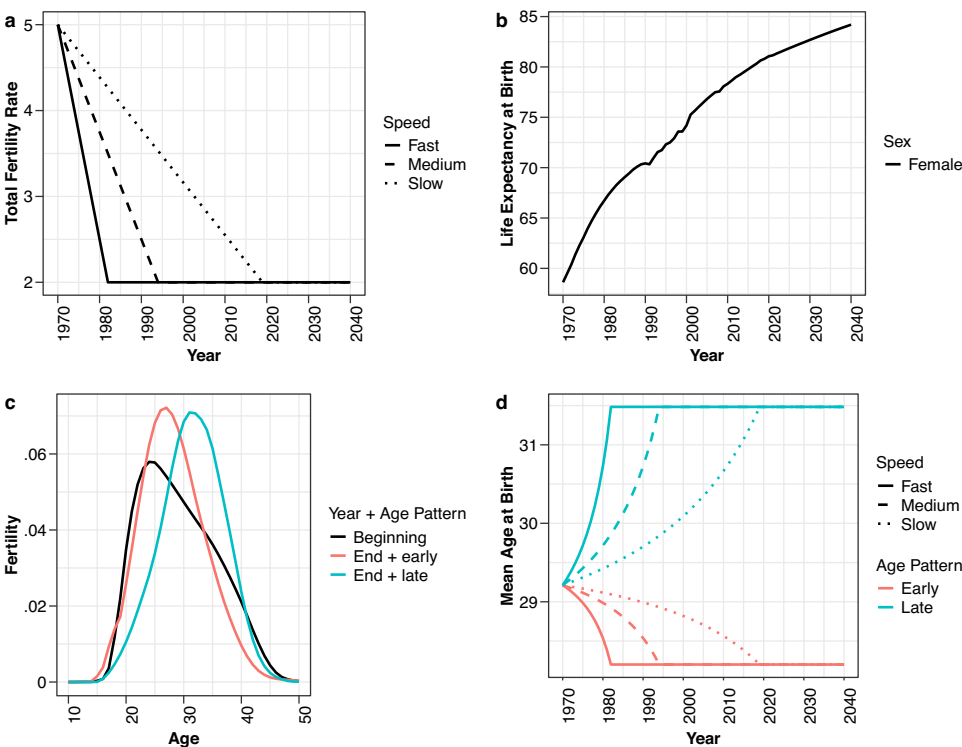
Fig. 1 Total fertility rate (TFR), life expectancy at birth (e_0), age pattern of fertility, and mean age at birth for mothers. Panel a shows the TFR over time under different speeds of fertility decline. Panel b shows the life expectancy at birth for females over time. Panel c shows the age pattern of fertility at the beginning and end years. At the beginning year, there is only one age pattern, shown in black; at the end year, there are two age patterns (early vs. late), indicated by different colors. Panel d shows the mean age at birth for mothers over time. Colors represent different types of age patterns of fertility (early vs. late). Line types represent different speeds of fertility decline.

the scenario of constant mortality, we maintain mortality at a low level, as opposed to a high level, to better reflect real-world circumstances in which countries with similar low mortality rates have varying fertility levels. For instance, sub-Saharan African countries have witnessed an increase in life expectancy at birth to approximately 60 by 2020, aligning with the levels in Europe and North America around 1950 (United Nations 2022). Yet, sub-Saharan Africa continues to have a fertility rate higher than 4.5 in 2020, while the fertility in Europe and North America was around 3 in 1950. The factors contributing to mortality decline, including advancements in health technology, public health practices, economic levels, and education, show an impact across age and gender. However, the diffusion of these factors to fertility decline is not straightforward. Consequently, a temporal disparity emerges between mortality and fertility decline, with mortality typically decreasing earlier than fertility. In this context, fixing mortality at a low level allows a meaningful exploration of the comparative impact of different fertility levels. We use China's predicted mortality in 2040 for the constant case and China's mortality decline from 1970 and 2040 for the changing case. Panel b of Figure 1 shows the dynamics of life expectancy at birth,

e_0, for females in China. Here we consider only one speed of mortality decline as we already design several speeds for fertility transition. However, our analysis could be easily extended to accommodate different speeds of mortality change.

As mentioned earlier, to calculate the time-dependent age distribution of mothers at time t, $\pi_t(t)$, we also need the age structure of the female population at time t. Therefore, we conduct population projections from 1970 to 2040 using the cohort component method, for which the input includes sex- and age-specific population at the base year, sex ratio at birth, age-specific mortality (to get the survivorship), and age-specific fertility over time. The latter two have been discussed. We set the sex ratio at birth to be constant over time as 1.04 and use the age- and gender-specific population of China in 1970 as the base population. Figure A2 in the online appendix illustrates the population age pyramids over time and under different speeds of fertility decline when mortality is constant and the age pattern of fertility converges to the early type.

We note that all vital rates that involve a particular country at a particular year are single-age and single-year data from the World Population Prospects 2022 version (United Nations 2022).

Illustrative Countries With Past Demographic Transitions

We next apply our analysis to actual past demographic transitions. We expect that such applications will provide insights into particular transition paths that have been experienced. These are, we believe, complemented by our study of stylized transition patterns. As empirical examples, we use four countries that had different speeds of demographic transition since 1950. The first is Thailand, which experienced a rapid fertility decline, with the TFR decreasing from approximately 6 to replacement level within 50 years (from 1950 to 2000). Indonesia underwent a similar transition, with TFR reaching replacement level within 75 years (from 1950 to 2025). In contrast, Nigeria and Ghana exhibited the slowest decline, maintaining a fertility rate of around 5 and 3 in 2025, respectively, predicted to reach replacement level by 2100. Likewise, the changes in survival, net reproductive rate (R_0), and mean and standard deviation of age at birth vary across these four countries at distinct rates (refer to Figure A3). We select these four countries not only because of their diverging trajectories in demographic transition but also because they shared similar economic and demographic characteristics at the onset of the transition, which improves the comparability of these countries (McNicoll 2011).

Results

Using stylized cases of demographic transition, we first examine how fertility decline impacts the number and age of kin, varying with decline speed. We then show that a cohort perspective is useful in understanding the kinship model result, and we explore how the age pattern of mortality contributes to the number of kin. Importantly, we also analyze past experiences in four countries using empirical demographic rates.

The Number of Cousins Under Demographic Transitions

We explore the kinship networks of focal individuals of different ages in different years. Panel a of Figure 2 shows the expected number of cousins over time under a slow fertility transition, with a convergence of fertility patterns to the early type and constant mortality.

There are multiple ways to interpret this figure. First, we can analyze the expected number of living cousins by fixing the age of individuals and comparing it across different time periods. This involves observing a horizontal line in panel a of Figure 2. We find a decline in the number of living cousins over time for individuals of most ages. For example, a 15-year-old individual in 2020 has fewer living cousins compared to a 15-year-old individual in 1990. However, this decline is less pronounced for older individuals, as the effects of fertility decline take longer to manifest in the older age groups, and the improvements in survival at old ages can offset some of the loss caused by fertility decline.

Second, we can maintain a fixed year and compare the number of living cousins among individuals of different ages, represented by vertical lines in panel a of Figure 2. Within a given year, the number of cousins initially increases and then decreases with age. For individuals below the age of 60, where fertility has the greatest impact on the number of cousins, younger individuals have fewer living cousins compared with their older counterparts. However, this pattern is reversed for older individuals, as female survival significantly decreases with age. This perspective allows comparison within and between generations. For instance, individuals who are 25 years old and 50 years old in the same year belong to different generations, while a 25-year-old and a 15-year-old are considered peers.

Furthermore, we can also examine individuals in the same birth cohort, represented by oblique lines in panel a of Figure 2. The number of cousins initially increases and then decreases as individuals age, with later birth cohorts generally having fewer cousins. Comparing different birth cohorts helps answer the question posed at the beginning of the article regarding the differences in the size of the cousin-only party for individuals, their mothers, their grandmothers, and even their peers when fertility patterns change over time.

Next, we investigate how different speeds of fertility decline affect the number of cousins (see panel b of Figure 2). As we might expect, the number of cousins under the slow fertility transition is consistently larger than or equal to the number under the fast transition. The effect gradually extends to higher ages over time, but not linearly. For instance, the maximum difference is observed around age 18 in 2000, age 31 in 2020, and age 50 in 2040 (shown as the red circles in panel b of Figure 2). In a linear progression, peaks would be at age 18 in 2000, age 28 in 2020, and age 48 in 2040. In other words, these peaks are associated with different birth cohorts.

The Speed of Fertility Decline and Peer Difference in the Number of Kin

We keep the focus on the speed of fertility decline and explore how the speed affects the number of kin among individuals within the same generation. We examine the percentage difference in the number of living cousins among peers (individuals with
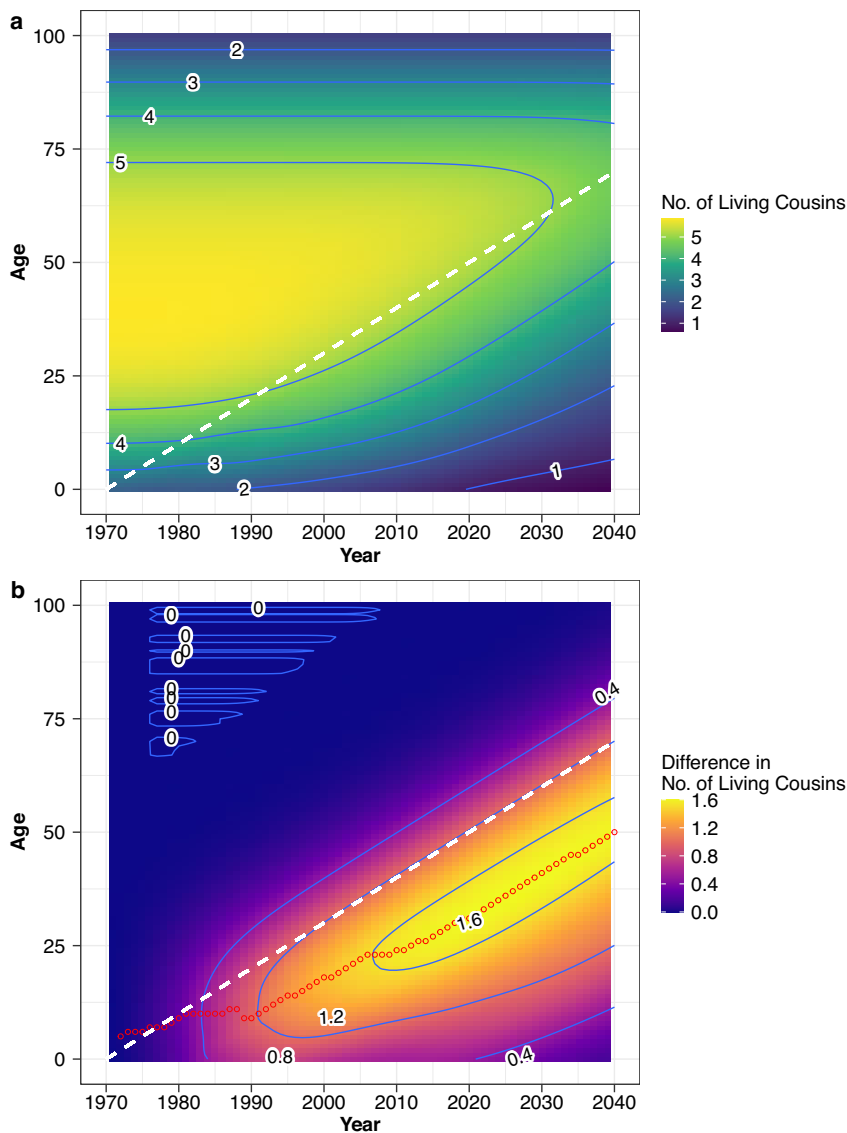
Fig. 2 Expected number of living cousins. Panel a shows the expected number of living cousins for individuals of different ages in different years under a slow fertility transition. Panel b shows the difference in the expected number of living cousins between fast and slow fertility transitions (slow minus fast). In both panels, the age pattern is the early type, mortality is constant over time, and the dashed line is a reference line that shows the life trajectory of a cohort born in 1970. In panel b, the red circles represent the maximum absolute differences across ages at different years.

similar ages) within a given year, referred to as peer difference. To capture different life stages, we select high school students (aged 15), recent college graduates (aged 25), individuals who have recently started families with young children (aged 35), and those with relatively older children (aged 45). Despite the mere 10-year age difference between these adjacent groups, they encounter different opportunities and
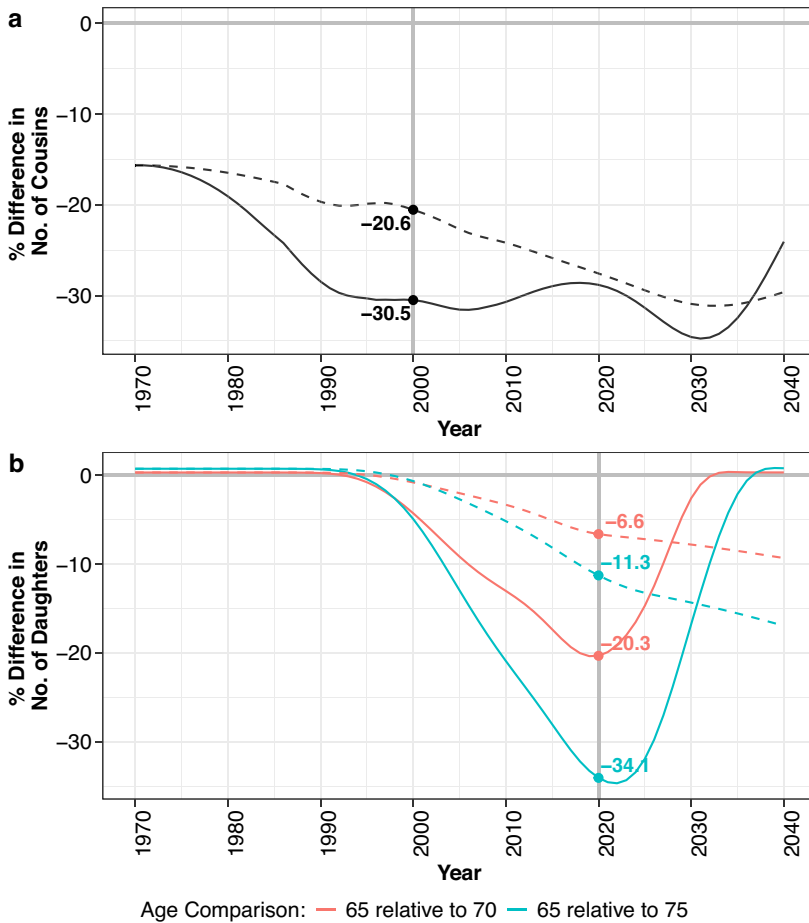
Fig. 3 Percentage difference in the expected number of living kin. Panel a shows the percentage difference in the expected number of living cousins between 15- and 25-year-old focal individuals, while panel b illustrates the difference in the expected number of living daughters between 65- and 70-year-old (shown as red lines) and between 65- and 75-year-old focal individuals (shown as blue lines). Solid and dashed lines represent fast and slow demographic transitions, respectively. These differences are calculated as $(E_{young} - E_{old}) / E_{old} \times 100\%$, where E_{young} and E_{old} denote the expected number of kin for younger and older focal individuals, respectively. The numbers in the figure, highlighted by the gray vertical lines, represent percentage differences in 2000 and 2020. The gray horizontal line at 0% marks the threshold for more or fewer kin for younger focal individuals.

challenges in their lives. The peer difference in the expected number of living cousins shows a declining trend over time, with some fluctuations. Compared with a fast fertility decline, a slow decline results in a smaller peer difference. For instance, in 2000, a 15-year-old under a slow transition would have 20% fewer living cousins than a 25-year-old, compared with more than 30% under a fast transition (see panel a of Figure 3). This percentage difference also holds when comparing other age groups (see Figure A4). Our results show that family support or family needs (indicated by the number of living kin) may depend on the speed of the fertility transition.

Furthermore, the difference in kin size between individuals of these characteristic ages will increase under a faster transition. However, such an effect will diminish as fertility eventually converges regardless of the speed. By 2000, fertility has already declined to 2 under a fast transition with a large peer difference in the number of cousins between 15- and 25-year-olds (approximately 30% vs. 20%). After 2020, even with a slow speed, the fertility decline has been completed, which reduces the impact of transition speed on kin differences.

We present the percentage difference instead of the absolute difference because the absolute difference is influenced by our choice of TFR. For interested readers, the absolute differences are shown in the appendix (Figure A5).

Another informative example is the peer difference in living daughters among old-age Focals. Older individuals with more adult daughters may have better emotional and instrumental support, which is crucial for their well-being and quality of life. As with cousins, a rapid shift in fertility rates also impacts the number of adult daughters for an older Focal. In 2020, a 65-year-old Focal under a slow transition has approximately 7% fewer daughters than a 70-year-old, while this peer difference is about 20% under a fast transition (red lines in panel b of Figure 3). This divergence is even greater with a 10-year age gap: a 75-year-old relative to a 65-year-old has about 11% fewer daughters under slow transition and 34% fewer under fast transition. This peer discrepancy is expected to vanish around 2040 under a rapid fertility decline. For a 75-year-old Focal in 2040, her daughters would have been born between 1980 and 2015 (if she gave birth between ages 15–50). Recall that under the fast-speed scenario, fertility declines to 2 around 1982 and stays constant until 2040, so the daughters of such an old Focal are not impacted by the fertility transition. Similar reasoning applies to a 65- and a 70-year-old Focal in 2040.

Our analysis of the expected number of living daughters reveals the transient effect of fertility decline on the dependence of older individuals on those of working age. Under the assumption that only the number of daughters influences the degree of support, the more living daughters an older individual has, the lower the average support per living daughter, and the lower the dependence of the older individual on each living daughter. In the long run, as fertility declines to the same low level regardless of the speed of decline, the degree of dependence and support will increase and stabilize, showing the diminishment and disappearance of the impact of different speeds of fertility decline.

The Speed of Fertility Decline and the Age of Kin

The age of kin, much like the number of kin, is also impacted by fertility decline. The age distribution of kin is a factor in determining the type of support and information available. For a middle-aged Focal, similar-aged cousins may provide emotional support and share resources as they might face similar life challenges. If cousins are much younger, instead of receiving support from cousins, the Focal may need to provide support to and share knowledge with them. However, as the Focal gets older, such younger cousins can provide physical support.

When examining the age distribution of cousins of a 50-year-old Focal, we found that the mean age of living cousins increases over time (left panel of Figure 4)
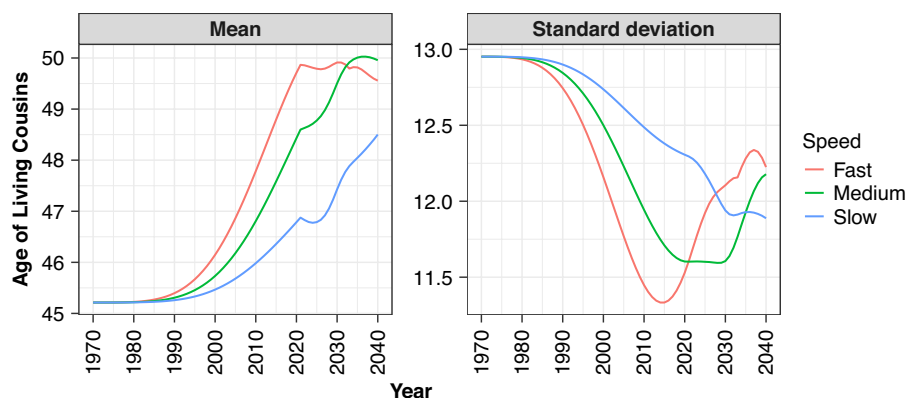
Fig. 4 Mean ages (left panel) and standard deviations in ages (right panel) of living cousins when Focal is at age 50. For each panel, the mortality is constant, the age pattern of fertility is the early type, and different speeds of fertility transition are shown by different colors.

followed by a plateau or even a slight decrease, while the standard deviation initially decreases and then increases (right panel of Figure 4). These changes are more pronounced under a faster fertility transition. This suggests that with fast fertility transitions, Focal individuals can more easily find similar-aged cousins for support and resource sharing. To better understand the age distribution of kin, we adopt a cohort perspective in the next section.

Moreover, we find that the mean age of Focal's cousins tends to be lower than her own, owing to fertility age patterns. In our scenarios, the age distribution of fertility is always right-skewed under the early type (see Figure A1 for details), resulting in the mean age of mothers being higher than their median age and, in turn, the mean age of daughters being lower than their median age. Thus, a Focal's mother likely has more younger than older siblings. This means that the Focal is more likely to have younger aunts, leading to more younger cousins.

Using a Cohort Perspective to Understand the Number and Age of Kin

The kin of Focal at a certain year are accumulated from previous years. For example, for Focal aged 50 in 2000, a 10-year-old daughter was born in 1990; a 30-year-old daughter born in 1970. However, all these daughters are the offspring of the 1950 cohort. That is to say, the kinship network of a given age Focal at a given year is also the kinship network of a corresponding birth cohort, which requires a complemented view from a cohort perspective. By reshaping the period fertility data from 1970 to 2040 and assuming constant fertility before 1970, we can obtain the cohort fertility rates by age of mother for birth cohorts from 1920 to 1990 (see Figure A6).

Figure A6 and Figure A1 highlight the difference between cohort and period perspectives. Using period age-specific fertility rates, we calculate the TFR for both period and cohort. In our scenarios, period TFR declines at different speeds from 1970 to 2040 with no effect from the age pattern of fertility (panel b of Figure 5).
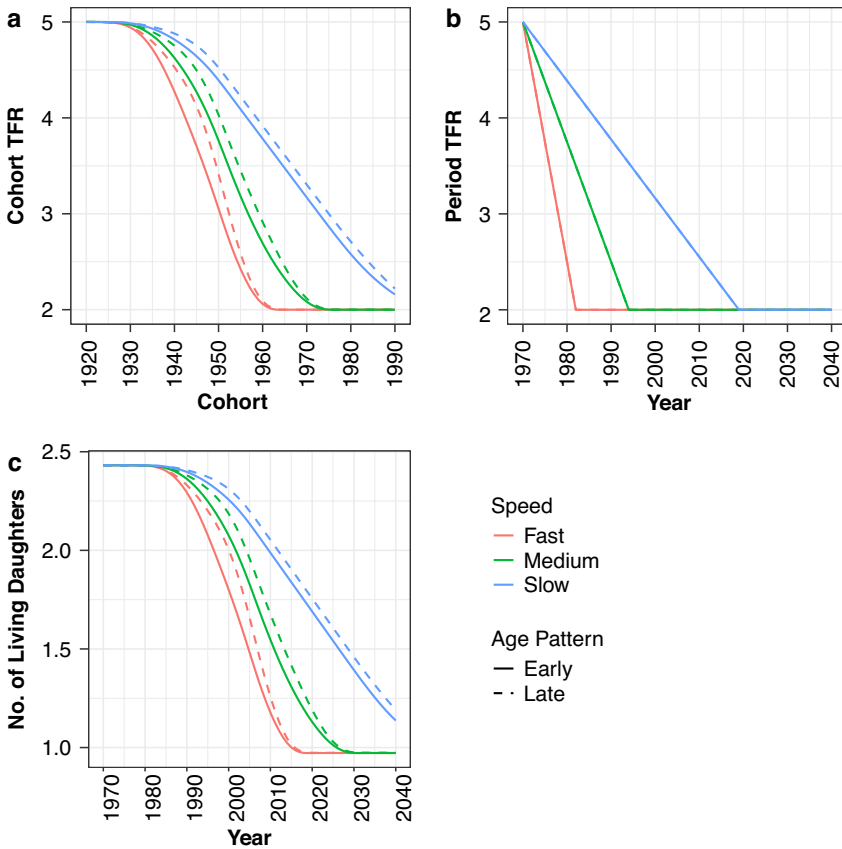
Fig. 5 Cohort and period total fertility rate for different birth cohorts and the expected number of living daughters when Focal is at age 50. Panels a and b show the cohort and period TFR, respectively, and panel c shows the expected number of living daughters when Focal is at age 50, which is calculated from the kinship model. For each panel, the mortality is constant and different speeds of fertility transition are shown by different colors. Solid lines show results under an early age pattern of fertility, and dashed lines show results under a late age pattern.

Cohort TFR also declines over birth cohorts at different speeds, but a late fertility age pattern (with a large mean age at birth) always leads to a higher cohort TFR compared with an early pattern of fertility (panel a of Figure 5).

As Ni Bhrolcháin (1992) noted, changes in the timing of cohort fertility distort period measures of the quantum, or level, of fertility. A large mean age at birth means that women are delaying reproduction instead of stopping, therefore, TFR observed from a period perspective is lower than that from a cohort perspective. The tempo effect can be especially pronounced in countries where women have children at increasingly older ages. By looking at the expected number of living daughters when Focal is at age 50, we can observe a similar effect of fertility age pattern on the number of kin (panel c of Figure 5): a late age pattern of fertility leads to more living daughters compared with an early age pattern. (Remember that we consider only living daughters.)
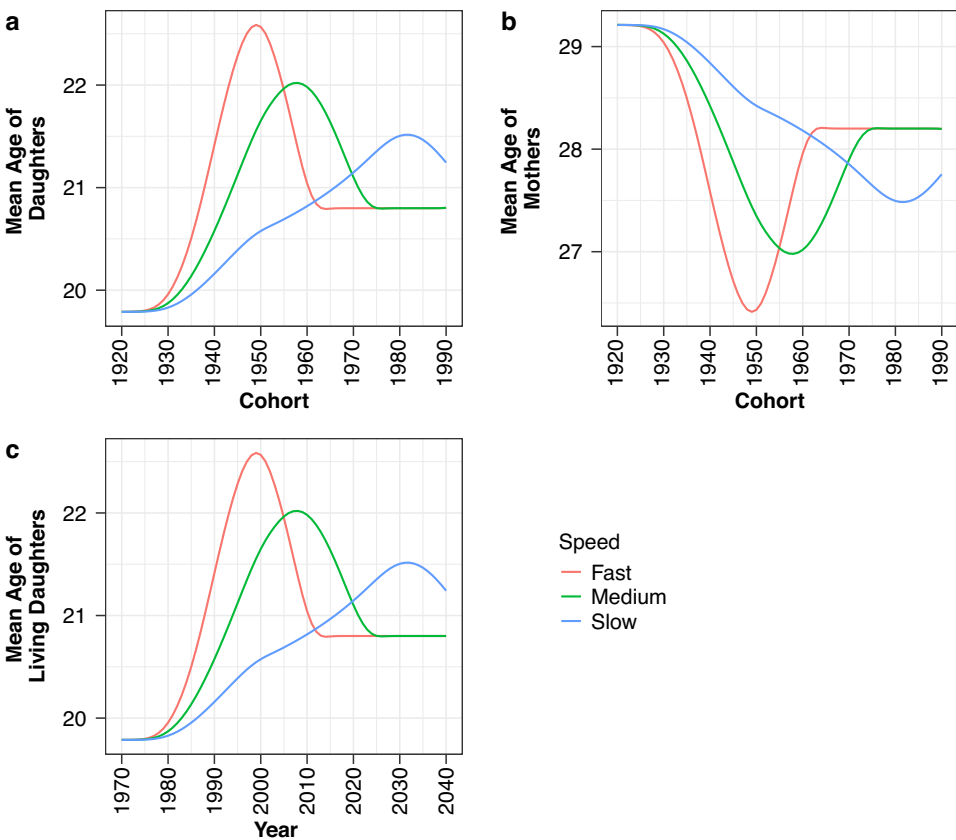
Fig. 6 Mean age of daughters and mothers calculated from cohort fertility rates, and the mean age of living daughters when Focal is at age 50 calculated using the kinship model. Panels a and b show the mean age of daughters and mothers when the mother is at age 50 by birth cohorts on the basis of cohort fertility rates. Panel c shows the mean age of living daughters when Focal is at age 50, which is calculated from the kinship model. For each panel, the mortality is constant, the age pattern of fertility is the early type, and different speeds of fertility transition are shown by different colors.

Next, we use a cohort perspective to understand the age of kin. We calculate the age of daughters when Focal is at age 50 as

$$\text{Age}_{\text{daughter}} = 51 - \text{Age}_{\text{mother}}. \tag{6}$$

Here we use age 51 instead of 50 as we assume the birth event happens at the beginning of the age interval. The cohort mean age of mothers (i.e., cohort mean age at birth) is calculated as the weighted arithmetic mean of ages of mothers, where the weights are cohort age-specific fertility rates. Equation (6) gives the cohort mean age of daughters when the mother is age 50. Panels a and b of Figure 6 present the mean age of daughters and mothers, assuming an early age pattern of fertility and constant mortality.

Our analysis shows that while the period mean age at birth increases, the cohort mean age at birth does not increase in a linear fashion. In any cohort, the age of daughters is negatively correlated with the reproductive age of mothers, resulting in opposite trends between daughters' age and mothers' age at birth. Furthermore,

the cohort mean age of daughters follows a trend similar to the mean age of living daughters in Figure 6, which is calculated from the kinship model. The difference is due to the survivorship of daughters, which is negligible given our assumption of low mortality rates at young ages. Similarly, cohort fertility can also help in understanding the age variation among kin, as shown in Figure A7 for an example of daughters.

Overall, this example of daughters shows the connection between period and cohort perspective and underscores the utility of a cohort perspective for understanding the number and age of kin. The comparison between the result from cohort data and the result from the kinship model clarifies the mechanism underlying the model. Nevertheless, comprehending the dynamics of other types of kin is more complicated. For daughters of Focal, we can trace the mother's birth cohort (i.e., Focal herself) for Focal of a certain age at a certain year. However, for other types of kin, the procedure is more intricate as their mothers are a mixture of different birth cohorts with different fertility rates and age structures.

Changes in the Age Pattern of Mortality and the Number of Kin

In contrast to the preceding analyses, the expected number of living mothers (i.e., the average probability of having a living mother) is largely determined by mortality. We find that as mortality rates decrease, the probability of having a living mother increases for both 15- and 55-year-old Focal individuals (as shown by the solid lines in panel a of Figure 7). In contrast, under a constant mortality schedule (as shown by the dashed lines in panel a of Figure 7), the probability of having a living mother remains relatively constant over time. The difference between the two scenarios is the effect of survivorship improvement on the number of kin. We further observe that this effect of survivorship improvement is different for a 15-year-old Focal individual than for a 55-year-old Focal individual. Specifically, around 2020, survivorship improvement has little effect on the average probability of having a living mother for a 15-year-old Focal, while it still has an impact on a 55-year-old Focal. This contrast can be explained by changes in the age pattern of mortality.

While survivorship rates for both the 0–55 and 50–90 age intervals increase over time, the age pattern of mortality/survivorship is also changing (panel b of Figure 7). Survivorship improvement for the 0–55 age interval almost stops around 2020, while it continues for the 55–90 age interval. Since a 15-year-old Focal individual is very likely to have a mother who is younger than 55 years old, around 2020 we also observe the disappearance of the effect of survivorship improvement on the probability of having a living mother for a 15-year-old Focal.

The expected number of living mothers for a young individual has significant implications for the economic and familial assistance that the individual may receive. Similarly, the probability of having a living mother for a person of working age is relevant to the support that the individual may need to provide.

From Stylized Demographic Transition to Empirical Cases

Our previous analyses are based on stylized demographic transitions, a simplified representation of real-world scenarios. To connect the stylized transitions
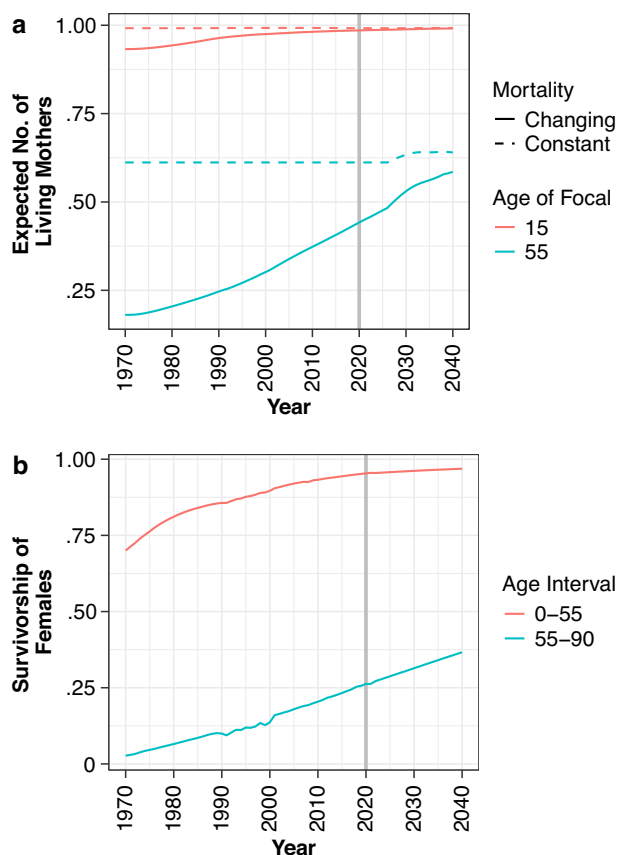
Fig. 7 Average probability of having a living mother when Focal is at age 15 and 55 and survivorship for age intervals 0–55 and 55–90. Panel a shows the average probability of having a living mother when Focal is at age 15 and 55 (shown as different colors); line types indicate different mortality schedules. The change in fertility is fast and the fertility age pattern is the early type. Panel b shows the female survivorship for age intervals 0–55 and 55–90 (shown as different colors).

with empirical cases, we examine kinship networks in four illustrative countries with different speeds of demographic transition—Thailand, Indonesia, Ghana, and Nigeria.

We first show the variations in the expected number of living kin across individuals of different ages and countries in 1950, 2000, 2050, and 2100 (see Figure A8). Generally, the probability of having a living mother diminishes with increasing age owing to increased mortality (first row in Figure A8). The expected number of living cousins and daughters initially rises and then declines, influenced by both fertility and mortality patterns (second and third rows in Figure A8). Compared with the other three nations, Thailand experiences a more rapid decline in mortality, leading to a faster increase in the probability of individuals of all ages having a living mother. Similarly, the number of cousins and daughters for individuals in Thailand initially decreases more swiftly owing to a rapid decline in fertility rates. For instance, in the
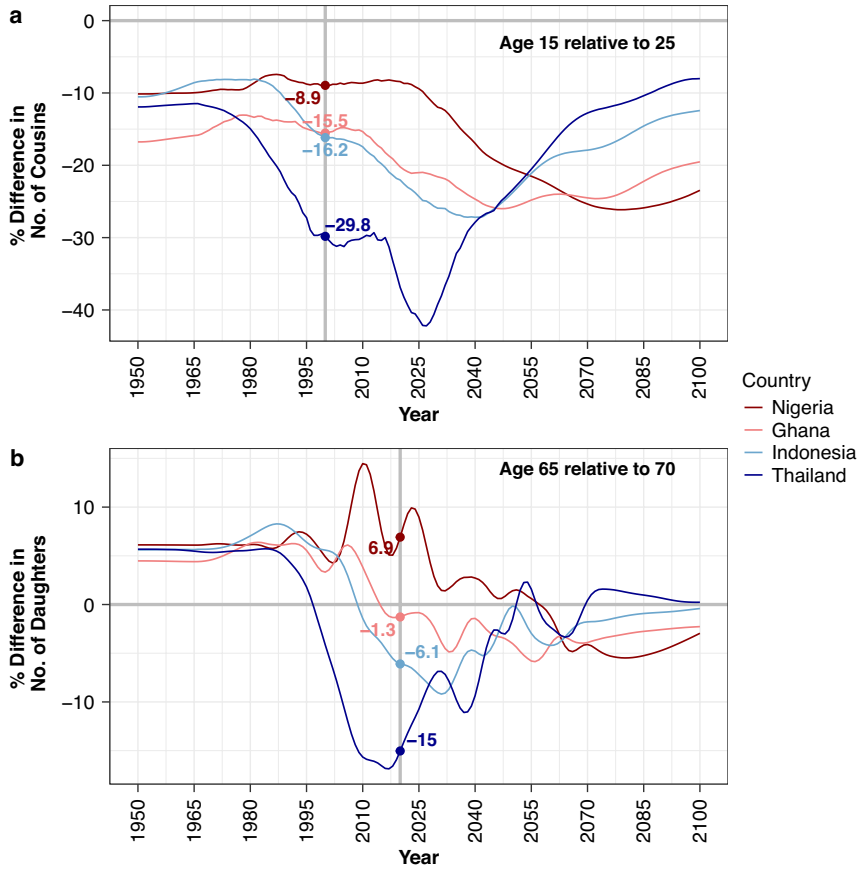
Fig. 8 Percentage difference in the expected number of living kin. Panel a shows the percentage difference in the expected number of living cousins between 15- and 25-year-old focal individuals, and panel b illustrates the percentage difference in the expected number of living daughters between 65- and 70-year-old focal individuals. Different colors represent different countries. These differences are calculated as (E_{young} − E_{old}) / E_{old} × 100%, where E_{young} and E_{old} denote the expected number of kin for younger and older focal individuals, respectively. The numbers in the figure, highlighted by the gray vertical lines, represent percentage differences in 2000 and 2020. The gray horizontal line at 0% marks the threshold for more or fewer kin for younger focal individuals.

year 2000, individuals aged 20–60 in Thailand, who were likely to have children between 1960 and 2000, had the fewest living daughters among the countries studied. This result is attributable to the rapid fertility decline in Thailand from 1960 to 2000.

Next, we analyze the peer difference in the number of kin. We use the example of cousins to understand the support and information potentially received from or provided by kin of the same generation. A 15-year-old, on average, has fewer living cousins than a 25-year-old (see panel a of Figure 8). In 2000, this peer difference was as much as 30% in Thailand, similar to the fast-fertility-decline scenario in our stylized transitions (refer to panel a of Figure 3). For old-age support, we examine the expected number of living daughters for older individuals. We find that the peer

difference manifests in two stages (see panel b of Figure 8). In stage 1, a 65-year-old has more living daughters than a 70-year-old owing to similar fertility levels (before the fertility transition begins) and higher daughter survival for a 65-year-old. In stage 2, when their reproduction is influenced by fertility decline—with its impact surpassing that of mortality decline—a 65-year-old begins to have fewer daughters than a 70-year-old. The onset of stage 2 varies by country, occurring earlier in rapid-fertility-decline countries like Thailand and Indonesia (around 2000–2010) and later in Nigeria and Ghana (around 2060 and 2020, respectively). This timing difference creates divergent peer differences. For instance, in 2020, a 65-year-old in Thailand has 15% fewer daughters than a 70-year-old, while in Nigeria, a 65-year-old has 7% more daughters than a 70-year-old. When fertility continues to be stable and mortality remains low, as in Thailand and Indonesia in 2100, the peer difference gradually diminishes.

When comparing the findings from the stylized cases to the empirical results, we observe both similarities and more pronounced variations in the empirical cases. For instance, the trends observed in Thailand closely align with the fast transition scenario in the stylized cases, where the percentage peer differences in the number of cousins and daughters initially increase and then decrease. This pattern suggests that rapid demographic transitions result in significant initial differences, which eventually disappear over time. In contrast, Ghana's results resemble the slow transition scenario from the stylized cases. In Ghana, changes in the number of kin progress more gradually. The impact of demographic shifts is less pronounced at the beginning but becomes more apparent over an extended period. This gradual change reflects a slower pace of demographic transition, where the effects of changes in fertility and mortality rates take longer to manifest.

In addition, we examined the age distribution of cousins of a 50-year-old focal individual. We found that the mean age of living cousins typically follows a pattern where it increases, reaches a plateau, and then decreases over time, shown as the left panel of Figure A9. Meanwhile, the standard deviation of age shows a more complex pattern: in Thailand and Indonesia, it initially decreases and then increases, whereas in Nigeria and Ghana, the change is less pronounced and more gradual (right panel of Figure A9). Similar to the results based on stylized cases, the changes are more pronounced in countries with rapid demographic transitions, such as Thailand and Indonesia, where the entire process is more compressed. In these countries, the age distribution of a focal individual's cousins becomes more uniform initially (shown as smaller standard deviations) before diversifying again. Over a longer timescale, countries with slower demographic transitions, such as Nigeria and Ghana, may also experience a turnaround in these trends, transitioning from an increase to a decrease or vice versa in the mean age and standard deviation in ages of living cousins.

Conclusion and Discussion

Conclusions Based on Stylized and Empirical Cases

The effect of demographic transitions on kinship networks has been of considerable general interest. In this article, we explore how demographic transition, especially

the speed of transition, affects the number and age of kin. In our stylized cases, a fast fertility decline is completed in only half a generation, a medium one in a generation, and a slow one in two generations.

We first find that the dynamics of the number of living kin depend on the speed of a fertility transition: so at any time, a fast fertility decline results in fewer living kin than a slow decline for most types of kin, with the exception of direct ancestors (such as mothers and grandmothers), whose numbers are mostly affected by survival. The difference in the number of kin among peers (individuals who are only a few years apart in age) is also larger in a fast fertility decline. For example, from our stylized demographic transitions, a 65-year-old individual on average has about 20% fewer daughters than a 70-year-old individual in a given year under a fast fertility decline, while the difference is only 7% under a slow decline. This disparity means that old individuals who are only 5 or 10 years apart in age may experience different lives. In many cultures, daughters provide instrumental and emotional support to their old parents even after marriage, thereby maintaining the economic and social stability of the household (Lei 2013). Moreover, from a biological standpoint, daughters are one of the primary means by which an individual's genes are transmitted to future generations, making them crucial for maintaining a family lineage. Although daughters are frequently primary caregivers in many contexts, we also acknowledge that caregiving responsibilities can be shared among family members or supplemented by external sources.

While the number of kin is undoubtedly important, the age distribution of kin is also crucial in determining the kind of support and information that individuals can obtain from their kin. We find that the speed of fertility decline has a dramatic effect on the mean and on the variability of the ages of kin. For instance, for a 50-year-old Focal, the mean age of Focal's cousins increases with time but remains lower than Focal's own age, while the variability in cousins' ages initially decreases and then increases. Faster fertility transitions also lead to greater changes in both the mean age and age variability among cousins. Our results show that a faster fertility transition enlarges the prospects for a middle-aged individual to find a similar-aged cousin. Such cousins may provide emotional support and share resources during crises or major life changes, as they often face similar challenges and share generational experiences. However, the anthropology literature suggests that age dispersion within kin networks may also be beneficial, offering access to diverse perspectives, skills, and resources. Future research could explore the balance between the advantages of age similarity and age dispersion in kin support networks.

We show that a cohort perspective is valuable for understanding the changes in the number and age of kin under different fertility levels, as well as the effect of the age pattern of fertility. Essentially, the kinship network of a given age Focal is an accumulation of demographic events that may be best understood from a cohort perspective. Using cohort fertility rates, we calculate the expected number as well as the mean and standard deviation of ages of daughters. These results are of course consistent with those from the time-varying kinship model. Even with the same changes in period TFR, different age patterns of fertility (e.g., early or late mean age at birth) lead to different numbers of kin. This finding can be understood from a cohort perspective as the quantum of period fertility tends to have large fluctuations and provides a distorted view when there is change in the timing of cohort fertility (Ni Bhrolcháin

1992; Schoen 2022). Indicators have been developed to address the fluctuation of period measurements, such as the "tempo-adjusted total fertility rate" (Bongaarts and Feeney 1998). While we do not claim that the cohort perspective is more satisfactory in demographic research, as some have advocated (Ryder 1980, 1986), we emphasize that the cohort perspective is valuable for our understanding of kinship dynamics. The above cohort analyses as well as the kinship model center around the Focal, who serves as the reference point for all timelines involved. Therefore, the convenience of using the daughter as an example is that we can track the birth cohort of the mother of daughters (which is the birth cohort of Focal herself) when we fix Focal's age at a certain year. This allows us to make a straightforward comparison between the results obtained from the fertility rates of different birth cohorts and the results derived from the kinship model. However, for other types of kin, the procedure is more complex because their mothers belong to different birth cohorts and have different fertility rates and age structures.

Finally, because mortality decline varies by age, changes in the age pattern of mortality also affect the number of kin. Using Focal's mother as an example, survivorship improvement impacts the probability of having a living mother differently for 15- and 55-year-old Focal individuals, because their mothers are at different ages and experience different survivorship improvements. Historically, survivorship improved first among infants and young children, which led to an increase in life expectancy at birth (Cutler et al. 2006). Advances in medical technology then extended these improvements to other age groups. In the last few decades, increases in human longevity have been driven by reductions in mortality at older ages (Lee and Tuljapurkar 1997). These survivorship improvements not only pose individual and social challenges, such as pension system sustainability (Bongaarts 2004; Lee and Skinner 1999), but also cause changes in kinship networks. For example, the increase in the probability of having a living mother stops earlier in time for a young Focal individual than for an old Focal individual. A living mother is fundamental to the support individuals receive from and provide to her. Health status, economic status, and geographic proximity are also important and can be captured by a multistate kinship model (Caswell 2020). The presence or absence of a living mother also affects the level of bereavement that individuals may experience, which has significant implications for their physical and mental health (Ott 2003). The loss of a mother can also have effects on individuals' social, economic, and relationship well-being (Ellis et al. 2013; Finkelstein 1988; Mack 2004). Because our analysis includes only living kin, future work could focus on the effect of demographic transition, especially the speed of transition, on the number and age of deceased kin.

In addition, we conduct similar analyses using empirical data from four illustrative countries and find that the results align well with the patterns from stylized cases. In countries with rapid demographic transitions, such as Thailand and Indonesia, the changes in the number and age of kin are more pronounced, which matches the fast transition scenario in our stylized demographic transition. Conversely, in countries with slower demographic transitions, such as Nigeria and Ghana, the changes in kinship networks are more gradual, consistent with the slow transition scenario in the stylized cases. These findings indicate that, despite their simplicity, stylized cases can help one understand kinship dynamics in real-world contexts. By holding one factor constant (such as fertility or mortality), we can further isolate and analyze the effects

of the other factor on kinship dynamics using stylized cases. However, stylized cases cannot fully capture the complexities of actual demographic transitions. Therefore, the integration of stylized and empirical cases, as used in this article, offers a more comprehensive understanding.

Discussions on Formal Demographic Method

We use a formal demographic method instead of microsimulation to analyze the changes in kinship networks. Formal demographic methods are based on well-established mathematical relations that are straightforward and transparent (Coale and Trussell 1996). Their simplicity and reproducibility are valuable for macro-level analyses, where standardized comparisons across different studies and populations are essential. Such simplicity also encourages researchers to focus on key determinants of outcomes, which increases the clarity of the analysis by eliminating unnecessary complexity. By utilizing this analytical approach, our study offers a broad view of how demographic transitions impact kinship networks and can serve as a reference point for future research incorporating microsimulations or empirical data of kinship networks.

Despite these advantages, formal demographic methods have significant limitations. They often assume a static framework with constant rates over time and linear relationships, which may not reflect the complexities of real-world demographic processes (Keyfitz and Caswell 2005). They also typically do not account for individual-level heterogeneity or clustering within populations. In the context of kinship networks, although the model we use accounts for temporal variations in demographic rates, it still falls short in providing detailed information on the distribution of the number of kin to capture the individual heterogeneity. For instance, consider two societies where, on average, a 70-year-old woman has two living daughters. However, there is a significant distinction, both socially and economically, between a society with an equal distribution (where every woman aged 70 has two living daughters) and one with a more skewed distribution (where 50% of such women have no living daughters while the other 50% have four living daughters). Empirical data suggest that such variability in kin numbers is not trivial (Kolk et al. 2023), but formal demographic models struggle to capture the detail. Multistate kinship models (Caswell 2020) can address some issues of heterogeneity by incorporating various individual states, such as education, marital, and health status. However, as more individual characteristics and complex interactions are included, formal demographic methods become insufficient.

In contrast, microsimulation models offer greater flexibility and detail. These models simulate individuals, generating synthetic populations with realistic genealogical structures and enabling evaluations of kin-dependent processes (Wachter 1997). Microsimulations complement and extend formal methods by allowing the examination of individual heterogeneity (van Imhoff and Post 1998) and providing the distribution of the number of kin, which is essential to capture the variations and disparities within a population. Microsimulation can also simulate interactions within families, which can be challenging in formal demographic methods (Caswell 2001; Caswell and John 2018). However, the accuracy of microsimulation models requires detailed

and extensive input data, which are challenging to obtain and validate. For instance, to model individual behaviors and interactions, microsimulations require a wide array of input variables, which include not only standard demographic rates (e.g., birth, death, marriage) but also socioeconomic factors, health variables, and more. Such high-dimensional spaces of inputs lead to equally complex outputs, which makes the calibration process computationally intensive (Ruggles 1993; Zagheni 2015).

When considering the preferred contexts for each method, formal demographic methods are ideal for standardized, macro-level analyses where clarity and stability are important. They offer a reliable framework for comparing different studies and populations. On the other hand, microsimulation models are advantageous for detailed, individual-level analyses that require an understanding of population heterogeneity and interactions, especially when there are a large number of variables and numerous possible attributes for these variables (Spielauer 2011; van Imhoff and Post 1998). Recent advancements in computational power and the availability of large-scale data have also made microsimulation models more feasible for demographic research (Zagheni 2015). In fact, both approaches are valuable and provide complementary insights into demographic processes (Billari 2015; Bongaarts et al. 1987). ∎

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Sha Jiang (corresponding author)
jiangsha@stanford.edu

Jiang • Department of Biology, Stanford University, Stanford, CA, USA; Max Planck Institute for Demographic Research, Rostock, Germany; https://orcid.org/0000-0002-8230-4264

Zuo • Department of Biology, Stanford University, Stanford, CA, USA; https://orcid.org/0000-0002 -7623-0481

Guo • Sociology School, and Social Investigation and Research Center, Huazhong University of Science and Technology, Wuhan, China

Tuljapurkar • Department of Biology, Stanford University, Stanford, CA, USA; https://orcid.org/0000 -0001-5549-4245