DEMOGRAPHIC RESEARCH

Research Article

How the demographic transition affects kinship networks: A formal demographic approach

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Contents

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Abstract

BACKGROUND
Kinship groups can have considerable importance (e.g., generational support, inheritance, and information for key life events). During demographic transitions, kinship networks are reshaped by changes in mortality and fertility rates.

OBJECTIVE
This paper analyzes consanguineous and female kin and explores the effect on the size and structure of living kin before and after a demographic transition. We compute the kinship network of a female individual with average demographic traits (here called the Focal) at all ages but focus on only demographically dense ages (age 15 to 39).

METHODS
The analysis uses a time-invariant model (Caswell 2019) to calculate the expected number of living kin using fertility and mortality rates. We use three examples (China, India, and Japan) with fertility and mortality from World Population Prospect 2019, based on empirical data.

CONCLUSIONS
We highlight two key results. First, at a demographically dense age of the Focal, the

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maximum expected number of living aunts, sisters, or daughters is approximately the net reproductive rate R_0 (linear), while the number of living cousins is approximately $R_0{}^2$ (quadratic). Second, such effects on kinship size depend on the magnitude of fertility change and on the age-pattern of changes in mortality. And the effects of fertility and mortality on the number of kin are not additive.

CONTRIBUTION

This paper shows a simple relationship between demographic transition and kinship size, which makes it possible to estimate kinship size based on the net reproductive rate. The quadratic relationship between the number of certain kin (e.g., cousins, nieces) and the net reproductive rate is informative but not a priori obvious.

1. Introduction

Kinship networks describe consanguineous and affinal relationships among groups of people. Compared to other types of networks, a kinship network is more close-knit as kin are likely to know one another, and relationships with and among close kin are relatively permanent (Bott 1971). In modern societies, kinship groups wield considerable influence on different demographic aspects, such as inheritance (Zagheni and Wagner 2015) and intergenerational support (Jiang 1995; Wachter 1997). Moreover, in traditional societies, kinship networks act as the most substantive and reliable sources of information pertaining to an individual's life decisions – such as finding a job, a mate, or a place to live (Murray, Rankin, and Magill 1981; Bian 1997; Krackhardt, Nohria, and Eccles 2003). Analyses of kinship networks also have applications for other fields, such as medicine, psychology, and criminology. For instance, Verdery et al. (2020) examine the medical and psychological implications of kin loss during the COVID-19 pandemic. Erlich et al. (2018) investigate a technique for identifying criminal suspects by constructing an individual's kinship network based on genomic data. Furthermore, on a national level, kinship studies provide relevant insights for economic and social changes and serve as a guide to policy-making (e.g., policies regarding economic, social, and medical support for the elderly). These policies are often examined without regard to kin support (e.g., papers in Tuljapurkar, Ogawa, and Gauthier (2010)), but kinship status clearly matters. For example, Verdery and Margolis (2017) project a dramatic increase in the size of older adults with no living close kin. This population is more likely to experience health issues, which raises new challenges to related policies and should be taken into account in policy-making.

Vital rates (i.e., fertility and mortality rates), determine portions of kinship networks in contrasting ways – reduced fertility leads to fewer kin being born, whereas reduced

mortality leads to fewer kin being lost. Over the last century, the global demographic transition has thus far led to declines in both fertility and mortality rates, and this transition appears to be still ongoing (Lee 2003). Some general characteristics of the change in kinship networks have been summarized in previous studies. For example, Wachter (1997) puts forward the notion that contemporary societies – coming out of the demographic transition – are in a unique scenario with high overlap between children and grandchildren. Moreover, Bengtson (2001) uses the analogy of a beanpole to describe the kinship networks under fertility and mortality decline (i.e., a family structure in which the shape is long and thin, with more family generations alive but with fewer members in each generation). Using survey data and microsimulation, Verdery (2015) also finds that small differences in the demographic transition lead to substantial differences on kinship networks and levels of community connectivity through kinship.

Here we advance the study of kinship networks under demographic transitions, focusing on both numbers and age structure of female consanguineous kin (e.g., mother, aunts, sisters, daughters). Instead of microsimulations, we use formal demographic methods to dissect the separate contributions to kinship networks of age-pattern and levels of change in fertility and mortality. Note that in this paper, we are using the kinship terminology in the American English context as other languages and cultures may recognize kin types differently. We will use the term 'kinship size' to the number of individuals aggregating over age in some kin category (e.g., the number of daughters) or the total number of kin in a kinship network. We will try to carefully specify whether we refer to living kin at some age x of the Focal, to the sum of living and dead kin ever born up to age x, or to some other aspect of the kinship network.

Qualitatively, when only fertility changes, kinship size should be related to the total fertility rate (TFR). When both mortality and fertility change, the net reproductive rate (R_0), which is the expected number of daughters that a woman will have after considering both her fertility and survival, is the simplest measure of eventual expected numbers of kin – that is, the expected number of kin who will ever be born (Pullum 1982). For example, the eventual expected number of daughters for a female equals R_0 and the eventual expected number of granddaughters through female lines of descent equals $R_0{}^2$. When there is a decrease in R_0 from 4 to 1, the eventual expected number of daughters will decline from 4 to 1, while the number of granddaughters will decrease quadratically from 16 to 1, which is a much more dramatic change than that of daughters. Thus we expect, first that the magnitude of R_0 determines the size of the kinship network when vital rates are constant, and second that in a demographic transition the relative magnitude of changes in R_0 determines the relative magnitude of the size of kinship networks.

We examine the eventual effects of demographic transitions by comparing kinship networks before a transition with those after a transition. For a given female, if we consider only kin who are alive when she is at a certain age range, what is the relationship between changing vital rates and kinship size? Given changes in mortality and fertility,

do the two vital rates have independent impacts on kinship? How do the absolute and relative magnitudes of demographic transitions affect kinship networks?

We answer these questions by computing the kinship network under different mortality and fertility schedules. Previous studies compute kinship ties using demographic models. Goodman, Keyfitz, and Pullum (1974) calculate the expected numbers of kin of a focal individual of a specified age using a system of integral equations. Caswell (2019) takes a different approach, treating the kin of each type of a focal individual (referred to as the Focal) as a population and projecting that population using matrix operations. The latter method provides not only the numbers but also the age or age-stage distribution of the kin, and both living and dead kin. This approach has been extended to multistate, time-varying, and two-sex models (Caswell 2020; Caswell and Song 2021; Caswell 2022). Another recent paper by Coste et al. (2021) provides a general way to calculate the kinship size and structure of a focal individual. However, the method by Coste et al. (2021) is more complicated as it accommodates animals that have large litter sizes and needs further modifications to account for dead kin.

In this paper, we use Caswell (2019)'s method to calculate kinship networks under a time-invariant assumption. We use the time-invariant assumption in this study for several reasons. First, we aim to examine the effects of the magnitude of demographic transition rather than the speed. Second, our assumption allows us to examine how differences in the level of vital rates determine the nature of kinship networks: In other words, we analyze comparative statics. Third, calculations based on a time-invariant model are useful in the same way as calculations of period life expectancy, period total fertility rate, or any other period-based calculation. Period indicators provide useful insights and are among the most commonly calculated and widely reported statistics in demography. Even in a transitional context, our assumption is similar to that underlying the Keyfitz analysis of population momentum (Keyfitz 1971). We acknowledge that this time-invariant assumption also has some limitations. For example, the assumption works well for countries with a slow demographic transition but not for those with a fast transition. The effect of different speeds of demographic transitions on kinship networks can be captured using only a time-varying model.

We analyze kinship networks in Japan, India, and China as these three countries fall in different regimes of demographic transition and could serve as typical examples. From 1950 to 2020, Japan's fertility and mortality decreased to a low level. According to United Nations (2019), Japan's TFR declined from a relatively high value (2.96) to almost the lowest value in the world (1.37). With consistent survival improvement in Japan, life expectancy at birth (e_0) increased from 62.8 to 84.43 and now is among the highest level in the world. Future mortality reduction in Japan will mainly happen at old ages. During the same period, India's fertility and mortality declined moderately but still remained relatively high: TFR stayed above the replacement level (2.1) (decreased from 5.9 to 2.24), and e_0 is below 70 (increased from 36.98 to 69.27). For China, both

fertility and mortality underwent a significant decline and have reached a relatively low level. As a result of both policy intervention and socioeconomic development, China's TFR decreased from 6.11 to 1.69. Meanwhile, due to remarkable survival improvements at young ages, e_0 increased from 43.83 to 76.62.

From our model, we get the expected number of different types of living, or both living and dead, kin as a function of the age of the Focal. However, we mainly focus on kin when the Focal is at demographically dense ages (defined as age 15 to 39). The number and structure of living kin during these young adult years are of great importance as many key life cycle events (such as education, marriage, work) occur during this period (Rindfuss 1991).

We first present the size and age structure of kinship networks (only living kin) over time in China, India, and Japan. Then we examine the effect of demographic transitions on kinship size and focus on the effect for different types of kin, for different countries, and of different changing magnitudes of vital rates. Finally, we test hypotheses (stated below) on the quantitative relationship between demographic transition and kinship size.

2. Kinship model and hypotheses

2.1 Kinship model

We use Caswell (2019)'s method to compute the expected number of living and dead kin of the Focal as a function of the ages of the Focal and of its kin directly from the mortality and fertility rates. Here, we briefly describe this time-invariant kinship model in Caswell (2019). Let $\mathbf{U}$ be a matrix with age-specific survival probabilities on the subdiagonal and $\mathbf{F}$ a matrix with age-specific fertility rates on the first row and zeros elsewhere. Define $k(x)$ as a vector containing the age structure of some type of kin at age x of the Focal. As individuals survive and reproduce, the dynamics of $k(x)$ are given by

$$k(x+1) = \mathbf{U}k(x) + \beta(x), \text{and} \tag{1}$$

$$k(0) = k_0. \tag{2}$$

The first term $\mathbf{U}k(x)$ represents the survival of the kin from age x to $x+1$. The second term $\beta(x)$ accounts for the addition of new individuals. For some types of kin, no new individuals are possible and $\beta(x)$ is zero (e.g., the Focal does not accumulate any new mothers). For other types of kin, new individuals are produced by the fertility of other types of kin (e.g., new granddaughters are produced by the fertility of daughters).

An initial condition k_0 is added to specify the kin that the Focal has at her birth (e.g., the Focal has no daughters at birth but may have older sisters).

The vector $k(x)$ includes only living kin, called as $k_{\text{living}}(x)$ in the later text. This can be extended to include living and dead kin by defining a block-structured vector as

$$\tilde{k}(x) = \left(\frac{k_{\text{living}}}{k_{\text{dead}}} \right)(x), \tag{3}$$

which contains the age distribution of living kin at age x and the age distribution of accumulated dead kin up to age x. The matrix $\mathbf{U}$ is replaced by the block-structured matrix

$$\tilde{\mathbf{U}} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{I} \end{array} \right), \tag{4}$$

where $\mathbf{M}$ is a mortality matrix with probabilities of death on the diagonal and zeros elsewhere, and $\mathbf{I}$ is an identity matrix.

Equation 55 of Caswell (2019) defines the initial condition for such calculations as, in our notation here,

$$\tilde{k}(0) = \left(\frac{k_{\text{living}}}{\mathbf{0}} \right)(0) \tag{5}$$

because the calculations there were intended to describe the loss of kin actually experienced by the Focal during her lifetime. Here, we include in the initial condition the deaths of kin that happened before the Focal's birth and were thus not strictly speaking experienced by her.

As an example, consider the initial condition for older sisters, $m(0)$ in the notation of Caswell (2019), which is written there as

$$m(0) = \sum_i \pi_i a(i), \tag{6}$$

where π_i is the distribution of ages at maternity and $a(i)$ is the vector of the daughters of the Focal at age i. This is replaced in our calculations by

$$\tilde{m}(0) = \sum_i \pi_i \tilde{a}(i), \tag{7}$$

where the tildes indicate that the vectors include both the living and dead kin.

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).

Our model agrees with Goodman, Keyfitz, and Pullum (1974)'s calculation of kin ever born. We keep track of kin who died before the birth of the Focal (included in the initial condition), kin who die during the lifetime of the Focal up to age x, and the remaining living kin at age x. The sum of the three is the kin ever born in Goodman, Keyfitz, and Pullum (1974)'s paper. Defining $\mathbf{1}_n$ as a vector of length n with all elements equal to 1, the expected number of kin ever born at age x of the Focal is

$$\hat{k}(x) = \mathbf{1}_{2\omega}^{\mathsf{T}} \tilde{k}(x) = \mathbf{1}_{\omega}^{\mathsf{T}} k_{living}(x) + \mathbf{1}_{\omega}^{\mathsf{T}} k_{dead}(x), \tag{8}$$

and the expected number of living kin at age x of the Focal is

$$\hat{k}_{living}(x) = \mathbf{1}_{\omega}^{\mathsf{T}} k_{living}(x), \tag{9}$$

where superscript т indicates a transpose.

Since the model assumes time-invariant mortality and fertility rates, in our analysis, we use 'Focal's kinship network in year t' as a simple version of saying 'Focal's kinship network when we assume that all relatives experience mortality and fertility of year t through their lives'. Therefore, we do not expect our result to align with the empirical kinship network of a country in any given year.

In addition, in order to calculate the distribution of ages of the mother of the Focal when the Focal was born, we follow Goodman, Keyfitz, and Pullum (1974)'s approach and use the population structure of a stable population. Other distributions could be substituted for this stable population if desired. See Caswell (2019) for details.

2.2 Previous results on the eventual number of kin

We characterize the demographic transition in terms of net reproductive rate (R_0). In the usual notation (Coale 1972; Caswell 2001; Keyfitz and Caswell 2005) the average fertility for daughters of a woman of age x is denoted $m(x)$, and the probability of surviving to age x is denoted $l(x)$. R_0 measures the expected number of daughters that would be born to a female, calculated as $\sum_x l(x)m(x)$. The female-only total fertility rate TFR_f, calculated as $TFR_f = \sum_x m(x)$, measures the expected number of daughters of a female assuming she would survive until the end of reproduction.

Let us now focus on the total, living and dead, number of kin when the Focal's age is near the maximum possible age. So we are interested in the number

$$K_{eventual} = \max_{x \in (0,\infty)} \{\hat{k}(x)\}, \tag{10}$$

where $\hat{k}(x)$ is defined in Equation 8, and includes living and dead kin. $K_{eventual}$ is the maximum value of the expected number of kin across all ages of the Focal. Goodman, Keyfitz, and Pullum (1974) analyze this eventual expected number $K_{eventual}$. They find that $K_{eventual}$ can be easily computed if one knows the net reproduction rate (R_0) and the eventual expected number of sisters (S) (see Figure 2 in Goodman, Keyfitz, and Pullum (1974)'s paper). In their calculation, the conditional fertility function is used to calculate the eventual expected number of kin. For example, to calculate the number of sisters, the conditional fertility of the mother given that she gave birth to the Focal when she was age x is needed. Here we have only unconditional/marginal fertility, thus minor adjustments are needed. By applying marginal fertility to Goodman, Keyfitz, and Pullum (1974)'s equations, the eventual expected numbers of aunts and sisters are both S, where

$$R_0 \leq S = K_{eventual}(\text{sisters or aunts}) \leq TFR_f. \tag{11}$$

Since marginal fertility already includes the Focal herself in the calculation of sisters, S is actually the size of sisterhood. Similarly, the number of aunts includes the mother of the Focal. Therefore, if the mortality of mother is not included, S is TFR_f; otherwise, S is R_0. However, in the model, the mortality of mother is only partially considered. For example, the mortality of the Focal's mother is ignored before the Focal's birth (to ensure that the Focal can be born), and only the mortality after that has been considered. Therefore, here S is between R_0 and TFR_f.

As nieces and cousins (only first cousins in this analysis) are daughters of aunts and sisters, respectively, the eventual expected number is

$$K_{eventual}(\text{nieces or cousins}) = S \times R_0. \tag{12}$$

Similarly, the eventual expected number of the Focal's daughters is

$$K_{eventual}(\text{daughters}) = TFR_f, \tag{13}$$

as the Focal's mortality is not considered, and that of the Focal's granddaughters is

$$K_{eventual}(\text{granddaughters}) = TFR_f \times R_0. \tag{14}$$

These results are illustrated in Appendix Figure A-1 and are based on results from Caswell (2019)'s kinship model.

2.3 Our hypotheses

We already know how to calculate the expected number of living kin at different ages of the Focal, $\hat{k}_{living}(x)$, from Equation 9. To get a summary indicator for each year, we need to extract key information across different ages of the Focal. Since this paper focuses on the Focal of demographically dense ages (ages 15 to 39), we compute the maximum expected number of living kin when the Focal is at demographically dense ages, denoted as

$$K = \max_{x \in (15,39)} \{\hat{k}_{living}(x)\}. \tag{15}$$

Alternatively, we could also use the mean value of the expected number of kin across demographically dense ages of the Focal. Here we follow Goodman, Keyfitz, and Pullum (1974) and use the maximum value. As mentioned above, many key life-cycle events (such as education, marriage, and work) occur during these young adult years (Rindfuss 1991), so the kinship network during this period serves as an important source of information and support.

Considering the survival of kin and the limited age range of the Focal of interest, we hypothesize that

$$K(\text{aunts or sisters or daughters}) \approx R_0, \text{and} \tag{16}$$

$$K(\text{cousins or nieces}) \approx R_0{}^2. \tag{17}$$

The approximation will be closer when mortality is low and females complete reproduction early because the ages of the various kin differ. During the demographically dense ages of the Focal, daughters will be aged approximately 0 to 15, sisters aged 15 to 39, and aunts 39 to 75. Our hypotheses suggest that we may use R_0 to measure the magnitude of the demographic transition. Thus we expect, first, that the magnitude of R_0 determines the size of the kinship network when vital rates are constant, and second, that in a demographic transition, the relative magnitude of changes in R_0 determines the relative magnitude of the size of kinship networks.

2.4 Data sources

The vital rates we use to calculate kinship networks are from the World Population Prospects (United Nations 2019). We collect mortality and fertility rates for China, India, and Japan every five years from 1950–1955 to 2050–2055, thus including both historical data and future projections. This provides a total of 21 sets of demographic rates. For simplicity, we use the beginning years (1950, 1955, 1960, 1965, 1970, etc.) to represent time periods in the following analyses and figures. Similarly, we use the starting ages (15, 20, 25, etc.) to represent age groups (15 to 19, 20 to 24, 25 to 29, etc.) in the following figures.

## 3. Kinship size and structure in China, India, and Japan

From the kinship model, we are able to compute the expected number of living kin at each age of the Focal. To get an overview of the Focal's size of kin, we first present the maximum, over the ages of the Focal, of the expected number of living kin when the Focal is at demographically dense ages (ages 15 to 39) in China, India, and Japan across time (see Figure 1). For the Focal's living mother, this number remains the highest in Japan and the lowest in India even though the number steadily increases over time in all three countries. This increase reflects the improvement of survival, evidenced by a continuous rise in life expectancy at birth (e_0) and the probability of surviving to age 15 (l_{15}) of females (see Figure 2).

For the Focal's other living kin (aunts, sisters, daughters, cousins, and nieces), the maximum expected numbers share two similarities. First, China and India both show a peak in kinship size around 1965, while the kin size in Japan generally declines over time. Second, before the 1970s, China has the highest value for all types of kin, followed by India and Japan. After the 1970s, the number in China declines below the number in India. Japan remains the lowest for the entire interval. This difference in kinship size between the three countries reflects their different demographic transitions. The rapid decline in China's kinship size is consistent with the decline in China's R_0. Figure 2 shows that R_0 drops about 54% (from 2.6 to 1.2) in China from 1965 to 1980, while the decrease in India and Japan is only about 10% (from 2.0 to 1.8) and 10% (from 1 to 0.9), respectively. The peak of China's R_0 in 1965 is due to the fertility rebound and reduced mortality after the Great Famine (from 1959 to 1961). After 1970, the survival improvement slows down and the fertility decline accelerates as a result of economic development and family planning policy. The combined change in fertility and survival leads to a drastic decline in China's R_0, and thus in kinship size.

Figure 1: **The maximum expected number of living kin when Focal is at demographically dense ages (age 15 to 39), denoted as K, in China, India, and Japan from 1950 to 2050**
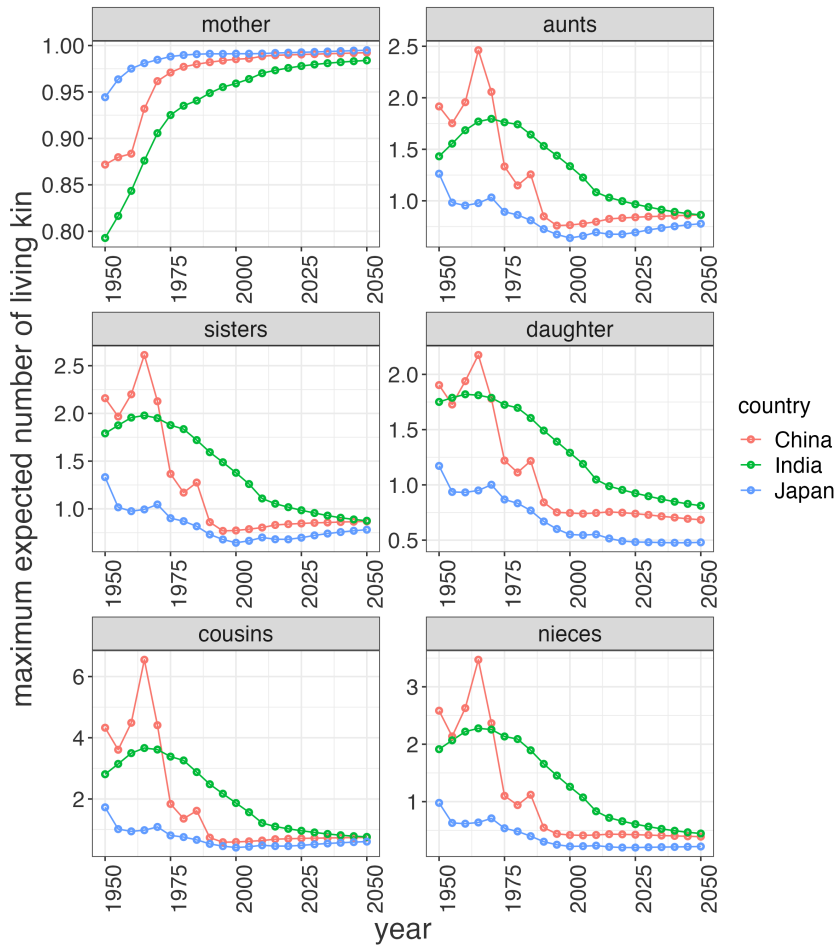
Figure 2: **Life expectancy at birth (e_0) of females, probability of surviving to age 15 (l_{15}) of females, female-only total fertility rate (TFR_f), and net reproduction rate (R_0) in China, India, and Japan from 1950 to 2050**
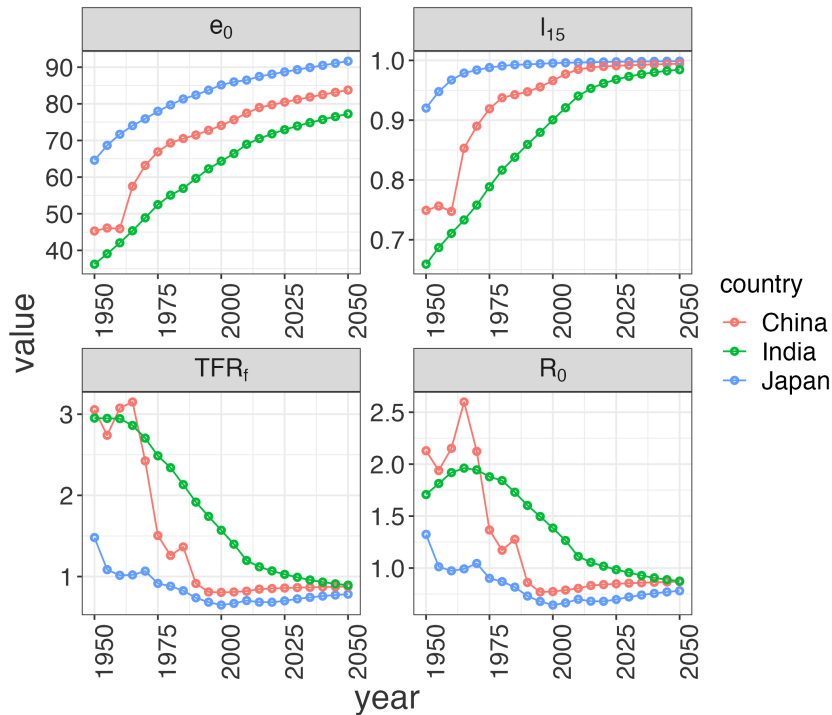
Next, we examine the age pattern of kin by analyzing the expected number of living kin at different ages of the Focal in 1950 and 2010 (see Figure 3). We find that the age pattern of each generation of kin is similar. For kin of the Focal's previous generation (mother and aunts), the expected number monotonically decreases to 0 with the Focal's age because it is less likely for the Focal to have new mothers or aunts after she was born. For kin of the Focal's own generation (sisters and cousins), the expected number first increases as new kin continue to appear after the Focal's birth and then decreases to around 0. For kin of the Focal's next generation (daughters and nieces), the increase in the expected number starts in the Focal's teen years and subsequently decreases at a much slower pace.

Figure 3 also shows that the change in the expected number of kin is much more

gradual with age in 2010 than in 1950. For example, after the Focal reaches age 20, the expected number of sisters decreases from about 1.8 to 0 in 1950, but only from about 1.1 to 0 in 2010. This difference is a result of the decline in both fertility and mortality rates. Since the Focal always has a mother when she was born, the expected number of mothers declines from 1 to 0 due to only mortality, but the decrease is at different paces between 1950 and 2010.

At the early ages of the Focal, this decrease is slower in 2010 than in 1950, and this trend reverses when the Focal is at later ages. Moreover, different countries show different changing patterns. For instance, when the Focal is at age 60 in 1950 (i.e., every kin and the Focal herself live under the fertility and mortality of 1950 throughout their whole lives), the probability that she still has a living mother is 5.6%, 5.2%, and 14.8% if she is in China, India, and Japan, respectively. This between-country difference persists over time: in 2010, the probability increases to 34%, 26%, and 51% in China, India, and Japan, respectively. This probability reflects the mortality regime.

Zooming into demographically dense ages (age 15 to 39, shown as the shaded area in Figure 3), the expected number of sisters and cousins reaches a peak during this age range, while the peak for daughters and nieces tends to appear at later ages of the Focal. These kin belong to different generations: Sisters and cousins are the contemporary kin of the Focal, and daughters and nieces are next-generation kin. Therefore, from the perspective of the Focal age, the peak for next-generation kin will come after the contemporary kin. Therefore, the Focal could theoretically get the maximum support from the peer generation without having to provide maximum support for the next generation during this age range. Besides, the odds of having a living mother increases from 1950 to 2010 but not so for aunts. If the Focal was born in China or India in 1950, there is a 50% chance that the Focal would lose her mother at demographically dense ages, while this chance is less than 25% in 2010. For aunts, compared to 2010, even though the Focal would lose more aunts in 1950, the number of living aunts still remains higher due to high fertility.

Figure 3: **Expected number of living kin with Focal's age in China, India, and Japan, 1950 and 2010. The shaded area shows demographically dense ages (ages 15 to 39)**
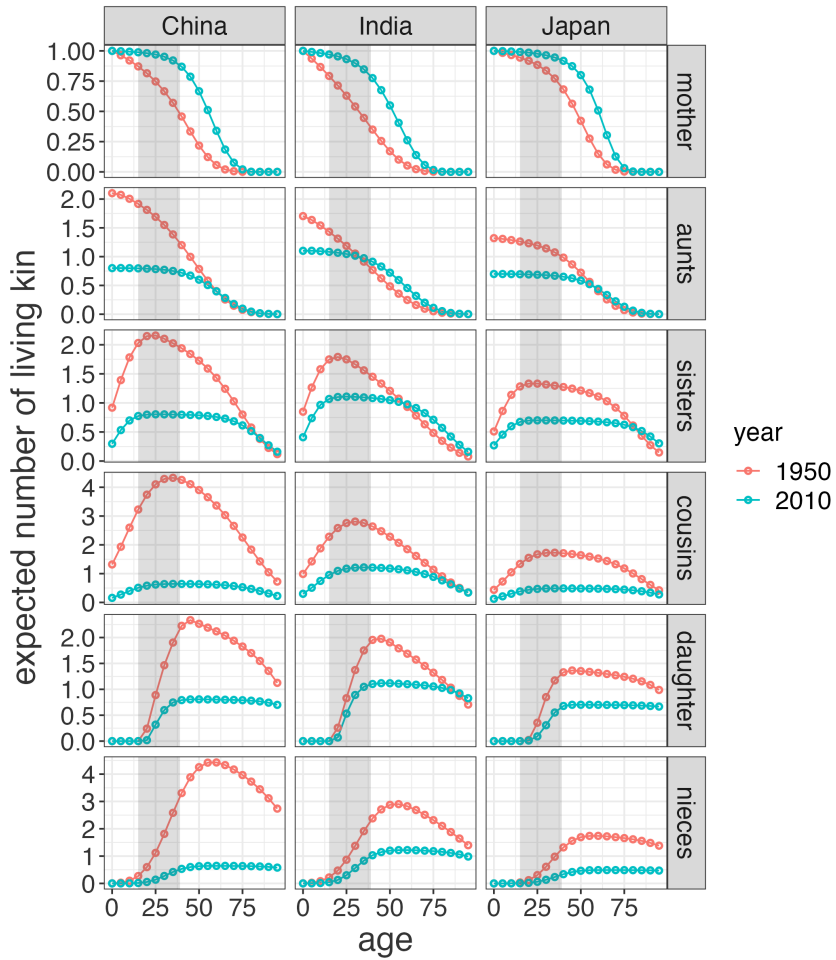
4. The effect of demographic transitions on kinship size

Since any demographic transition includes changes in both fertility and mortality rates, do the two affect kinship size separately? In other words, does the simultaneous change in vital rates have the same effect on kinship size compared to the separate change?

We construct four scenarios and present the change in kinship size under each scenario during 1970–1980 to answer the above question. We define the fertility and mortality matrices in 1970 as $\mathbf{F}_{1970}$ and $\mathbf{U}_{1970}$ and those in 1980 as $\mathbf{F}_{1980}$ and $\mathbf{U}_{1980}$. If ξ is some output from the kinship model based on a mortality–fertility combination, then each scenario captures the difference in ξ under different mortality and fertility combinations:

Scenario 1: $\xi(\mathbf{U}_{1980}, \mathbf{F}_{1970}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})$;

Scenario 2: $\xi(\mathbf{U}_{1970}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})$;

Scenario 3: $\underbrace{\xi(\mathbf{U}_{1980}, \mathbf{F}_{1970}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})}_{\text{Scenario 1}} + \underbrace{\xi(\mathbf{U}_{1970}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})}_{\text{Scenario 2}}$;

Scenario 4: $\xi(\mathbf{U}_{1980}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})$.

According to the Kitagawa–Keyfitz decomposition (Kitagawa 1955; Keyfitz 1977; Keyfitz and Caswell 2005), the difference in ξ in scenario 4 can be further decomposed as

$$
\begin{aligned}
&\xi(\mathbf{U}_{1980}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970}) \\
&= \frac{1}{2}\left[\xi(\mathbf{U}_{1980}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1980}) + \underbrace{\xi(\mathbf{U}_{1980}, \mathbf{F}_{1970}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})}_{\text{Scenario 1}} \right] \\
&+ \frac{1}{2}\left[\xi(\mathbf{U}_{1980}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1980}, \mathbf{F}_{1970}) + \underbrace{\xi(\mathbf{U}_{1970}, \mathbf{F}_{1980}) - \xi(\mathbf{U}_{1970}, \mathbf{F}_{1970})}_{\text{Scenario 2}} \right].
\end{aligned}
$$

In our analysis, ξ is the maximum expected number of kin when the Focal is at a demographically dense age. In scenario 1, fertility stays at the level in 1970 and only survival changes to the level in 1980, while in scenario 2 survival stays at the level in 1970 and only fertility changes. In scenario 3, we add the changes in kinship size from scenarios 1 and 2 to capture the effect of separate fertility and survival changes on kinship size. In scenario 4, fertility and survival change simultaneously from 1970 to 1980. After getting the maximum expected number of kin under each scenario, we compute the change in the maximum expected number of kin by subtracting the number of kin when

both mortality and fertility stay at the level in 1970. Figure 4 shows only the change for living aunts and cousins. Results for other kin can be found in the Appendix (Figure A-2).

Our results first show that survival improvement leads to an increased maximum expected number of living aunts and cousins when we focus on scenario 1 (red bars in Figure 4). Similarly, scenario 2 (green bars) suggests that fertility is positively correlated with the maximum expected number of living aunts and cousins. Interestingly, the results from scenarios 3 (blue bars) and 4 (purple bars) do not perfectly match, which suggests an interaction between fertility and mortality changes in kinship size. The difference between the two scenarios differs from one type of kin to another in terms of magnitude and direction. Take China as an example: The effect (absolute magnitude) of separate fertility decline and mortality change is smaller than the effect of simultaneous change, while both effects are larger on living cousins than on aunts. The result implies that there may be some additional effects on kinship size due to the interactions between mortality and fertility change that offsets part of the effect from separate changes.

Our results also show that both the absolute magnitude and the age pattern of demographic transition have an impact on kinship size. Figure 4 illustrates that the change in kinship size is distinct for China, India, and Japan, correlated with the different magnitudes and age patterns of change in fertility and mortality during the corresponding time period. To explain, consider Table 1 that shows the changes in age-specific mortality and the levels of overall survival and female fertility in these countries from 1970 to 1980. Using Table 1 and scenario 2 (green bars, when only fertility changes, Figure 4), we see that the magnitude of fertility change matters to the number of kin – China has the largest drop in fertility rate and thus the largest decrease in the kinship size. Using Table 1 and scenario 1 (red bars, when only survival changes, Figure 4), we see that the age pattern of mortality change matters. For example, while both China and India experienced an increase of about 6 years in e_0, China's survival improved across all age groups, whereas India's survival largely improved at the young and middle ages. As a result, India has a larger increase than China in the number of living kin. Recall that when the Focal is at a demographically dense age, her aunts and cousins are more likely to be young or middle-aged, so survival improvement at young and middle ages is important. For the same reason, the increase in kinship size in Japan is far less than half of that in China and India, even though e_0 in Japan increased about half as much as in the other two countries.

Figure 4: **Change in the maximum expected number of kin when Focal is at a demographically dense age (K), for China, India, and Japan, 1970–1980**

Table 1:   **Demographic changes from 1970 to 1980**

Country	Metric	Year 1970	Year 1980	Difference between two years
China	e_0	63.18	69.30	6.12
	l_{15}/l_0	0.89	0.94	0.05
	l_{60}/l_{15}	0.81	0.87	0.06
	l_{80}/l_{60}	0.34	0.41	0.08
	TFR_f	2.42	1.26	−1.16
	R_0	2.12	1.17	−0.95
India	e_0	48.88	55.07	6.19
	l_{15}/l_0	0.76	0.82	0.06
	l_{60}/l_{15}	0.66	0.73	0.08
	l_{80}/l_{60}	0.28	0.31	0.03
	TFR_f	2.71	2.34	−0.36
	R_0	1.94	1.84	−0.10
Japan	e_0	75.90	79.70	3.8
	l_{15}/l_0	0.98	0.99	0.01
	l_{60}/l_{15}	0.91	0.94	0.03
	l_{80}/l_{60}	0.53	0.65	0.12
	TFR_f	1.07	0.88	−0.19
	R_0	1.04	0.87	−0.17

*Source*: All data is from United Nations (2019).

Now we ask a different question: How does the relative magnitude of a demographic transition affect (1) kinship sizes among countries and (2) different types of kin within a country?

To better compare different countries, we analyze the covariation between the percent change in R_0 and the percent change in kinship size. For this calculation, we use the kinship structures and values of R_0 from the survival and fertility of 21 periods. Figure 5 shows that for a given type of kin, different countries have a similar percentage change in kinship size under the same percentage change in R_0. For instance, about a 15% decrease in R_0 results in about a 13% decline in the maximum expected number of sisters for China, India, and Japan. That is to say, the same relative change in vital rates leads to a similar percentage change in kinship size regardless of the initial value of R_0.

We also find that demographic transition exerts different impacts on different types of kin. According to Figure 5, the number of living mothers has a very weak response to the change in R_0. Other kin can be categorized into two groups: aunts, sisters, and daughters have a similar response; and cousins and nieces also have a similar response, but the response is much stronger than that of the previous group. Using the same example as before, around 15% decrease in R_0 leads to around 13% decline in the maximum

expected number of aunts, sisters, and daughters and around 20% decline in cousins and nieces. This finding is related to our hypotheses that these two groups of kin have different (linear or quadratic) relationships with R_0.

Figure 5: **Percentage change in the maximum expected number of kin when Focal is at a demographically dense age (K) versus percentage change in net reproductive rate (R_0) for China, India, and Japan from 1950 to 2050**
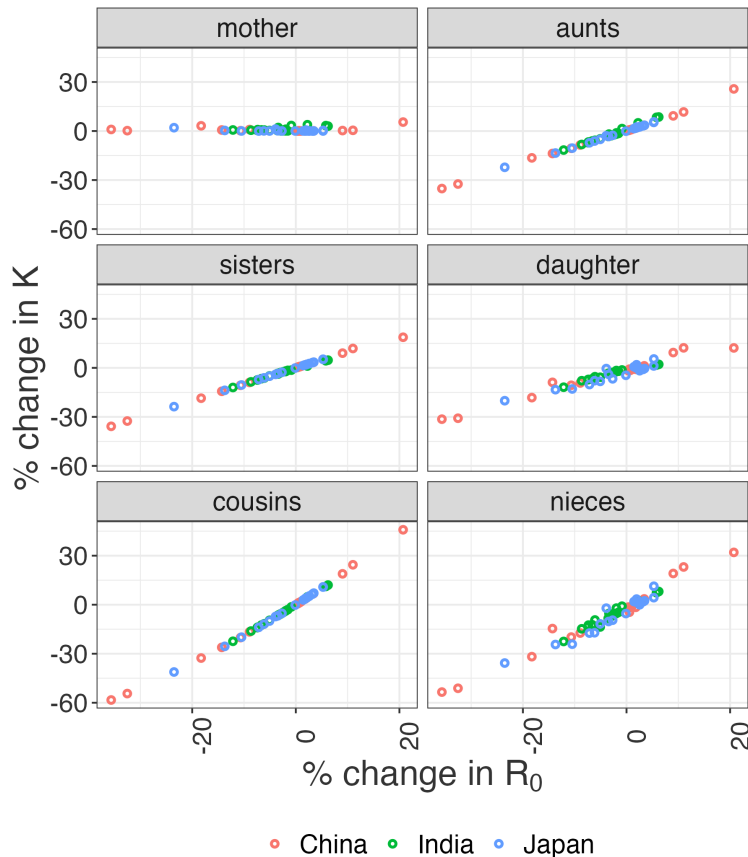
5. A simple relation between kinship size and net reproductive rate

Finally, we test our hypotheses on kinship size vis-à-vis R_0. Remember that we focus on the number of living kin when the Focal is at a demographically dense age. Figure 6 shows that the maximum expected numbers of the Focal's living aunts, sisters, and daughters are all proportional to R_0, with a slope close to 1. Similarly, the maximum expected number of the Focal's living cousins is also proportional to $R_0{}^2$ with a slope close to 1. These findings are consistent with our hypotheses and hold across countries with different demographic transitions. So a demographic transition impacts different types of kin differently: The impact is linear for some types of kin (e.g., aunts, sisters, daughters) and is quadratic for other types of kin (e.g., cousins). Using China as an example, China's R_0 for female births decreased roughly from 2 to 0.5 from 1970 to 2000, so the maximum expected numbers of the Focal's living aunts, sisters, and daughters when the Focal is at a demographically dense age also decreased from 2 to 0.5. However, the number of living cousins declined more dramatically, from 4 to 0.25.

One exception here are nieces: The maximum expected number of living nieces is consistently lower than $R_0{}^2$, and the deviation increases as R_0 increases. This could be explained by the change in the age distribution of fertility. As R_0 increases, the age distribution of fertility becomes more dispersed, thus some nieces will be born at later ages of aunts and will not show up when the Focal is at a demographically dense age. If we analyze the maximum expected number of living nieces across all ages of the Focal, this number will be much closer to $R_0{}^2$. Figure A-3 in the Appendix validates our assumption by showing a proportionality between the maximum expected number of living nieces across all ages of the Focal with $R_0{}^2$.

Figure 6: **Maximum expected number of living kin when Focal is at a demographically dense age (K) and net reproductive ratio (R_0) for China, India, and Japan. The gray line is a reference with slope 1**
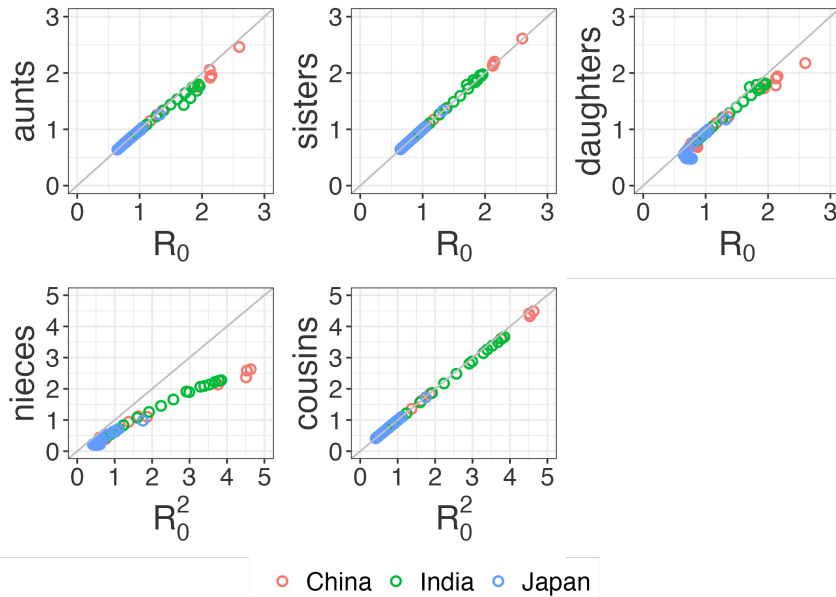
6. Discussion

In this paper, we find a simple empirical relationship between demographic transition, quantified by the net reproductive rate R_0 and the maximum size of living kin when the Focal is at a demographically dense age (ages 15 to 39). Our findings first show that as long as R_0 remains the same, change in vital rates does not affect the expected number of kin, such as aunts, sisters, daughters, cousins, and nieces. In other words, different combinations of mortality and fertility rates could lead to the same kinship network. However, when R_0 has different absolute magnitudes of change, exemplified by countries with different demographic transitions, kinship size also changes differently. Moreover, the relationship between R_0 and kinship size is different for different types of kin. We find that when the Focal is at a demographically dense age (ages 15 to 39), the maximum expected number of living aunts or sisters or daughters is approximately R_0, indicating a linear correlation between the two. However, the number of living cousins is approximately $R_0{}^2$, which is a quadratic relationship. These two results are consistent with our

hypotheses. The number of living nieces, on the other hand, is consistently lower than $R_0{}^2$, especially when R_0 is high. This is mainly due to the fact that we focus only on the kinship size when the Focal;s age is between 15 and 39. Some nieces would be born after the Focal is 39 years old and are not included.

The simple relationship we find provides a decent approximation of kinship size under the demographic transition. The quadratic relationship between the number of certain kin (e.g., cousins, nieces) and the net reproductive rate is informative but not a priori obvious. Demographic transition has been a longstanding research focus across a wide range of fields. Substantial work has studied the effects of the demographic transition on different aspects, including population dynamics (e.g., population growth rates, size, and age distribution) (Lee and Reher 2011), economic growth (e.g., "demographic dividends") (Bloom, Canning, and Sevilla 2003), and policy design (especially aiming at population aging) (Tuljapurkar, Ogawa, and Gauthier 2010). However, the demographic transition is also a kinship transition, as pointed out by Verdery (2015), and this aspect has not received enough attention. Earlier work has used microsimulations to analyze changes in numbers of kin within a single society (Murphy 2011), later extended by Verdery (2015) to examine the impact of variation in the parameters of the transition on kinship. To the best of our knowledge, none of these studies have established a clear quantitative relationship between demographic transition (quantified as R_0) and the size of living kin at demographically dense ages of an individual. Thus the linear (for aunts and sisters) and quadratic (for cousins and nieces) relationships we present here provide a crucial step in understanding the fundamental characteristics underlying kinship networks. In addition, our focus on maximum kin numbers does not say anything about the composition (age or otherwise) of the kin. The effects of R_0 on such other aspects of the kinship network is an open research question.

Second, we find that the initial value of R_0 does not matter if we consider only the percentage change (i.e., relative magnitude) in kinship size. When there is the same percentage change in R_0 (or the same relative magnitude of demographic transition), kinship size changes similarly across different countries, regardless of the characteristics of the country. This finding is consistent with our first finding – the magnitude of R_0 largely determines the size of kin, and the change in R_0 over time (relative magnitude) decides the change in the size of kin during the same period. Of course, more generally, factors such as socioeconomic development, culture, or governance are important determinants of vital rates (or R_0) and may affect kinship size.

Third, based on counterfactual analysis, we first show that there is an interaction between the effects of mortality and fertility rates on kinship size. When the two rates change independently, the effect deviates from the one when both rates change simultaneously. On reflection, it is obvious that kinship is affected by both factors and also that the effects will not be additive except in very special cases. For example, when each age group has the same proportional change in mortality and fertility, their effects can be

additive. This linkage will make possible a deeper understanding of the direct and interactive effects that changing vital rates have on an individual's kinship. Moreover, we also find that the magnitude of fertility change and the age pattern of mortality change are key to the dynamic of the number of kin. The same amount of change in life expectancy (e_0) could lead to different changes in kinship size depending on the age group that survival improvements mostly happen in. For instance, the cousins of the Focal at demographically dense ages are also likely to be at a similar age, whose survival is determined by mortality rates at young and middle ages.

Last, at demographically dense ages of the Focal, the expected number of sisters and cousins typically peaks, while a peak for daughters and nieces is likely to appear at later ages. The later peak for daughters and nieces (in terms of the age of the Focal) is largely due to the fact that they are the next-generation kin of the Focal, who arrive after the contemporary kin (e.g., sisters and cousins) from the perspective of the Focal's age. According to this result, the Focal could theoretically get the maximum support from the peer generation without having to provide maximum support for the next generation. As time goes by, the odds of having a living mother at a certain age increases from 1950 to 2010, but not so for aunts. Previous work on kinship networks has largely centered on individuals at old ages who need support or at middle ages who experience sandwiching pressures. Adolescents and young adults are relatively understudied in the realm of kinship networks. Our study seeks to fill this gap and bring attention to the kinship networks of individuals within this age group. Additionally, our results can be used to examine specific age groups of the Focal. For instance, a 15-year-old Focal has a different kinship network and experiences different important life events than a 35-year-old Focal, even though both are at demographically dense ages. According to our result, under the vital rates of India in 1950, compared to a 35-year-old Focal, the 15-year-old Focal has a higher probability of having a living mother, has more living aunts and sisters, slightly fewer living cousins, and significantly fewer living daughters and nieces. As a result, when it comes to important life events, such as choosing a high school or learning a new skill, an adolescent-aged individual may rely heavily on kin from previous and contemporary generations for support and information.

Since our analyses use a time-invariant model, there is a strict assumption here: All relatives as well as the Focal herself experience the same mortality and fertility rates of a certain year t through their lives. That is to say, a 20-year-old daughter survives and reproduces according to the vital rates in year t. When she becomes age 50, she is still living according to the vital rates in year t instead of possibly different rates in a later year (i.e., year $t + 30$). Generally speaking, demographic transitions lie between two limits. One is an instant transition when fertility and mortality fall to final values immediately. In that case, the generations after the transition will experience a new set of rates, whereas older kin will be produced at 'older' rates but die at 'newer' rates. Another is a slow transition when rates take several generations to change. In such a case, time dependency

has limited effects on kinship networks. Therefore, for a country with a slow demographic transition, the results of time-invariant and time-varying kinship models will be similar. However, if a country is going through a rapid demographic transition, the time-invariant approach will not accurately describe the real kinship network. In reality, demographic transitions happen at different speeds across time periods and countries, and the effect of such speeds on kinship networks can be captured using only a time-dependent model. However, our goal is not to calculate the most realistic/accurate kinship networks for each country but to use the time-invariant model to explore basic and important characteristics underlying kinship networks. Future work may analyze the effect on kinship networks of the speed of demographic transition, calculate a more accurate kinship network, or extend the network to male kin by employing time-varying (Caswell and Song 2021), multistate (Caswell 2020), and two-sex (Caswell 2022) kinship models.

Even though we focus on the demographically dense ages in our analysis, we compute kinship networks at all ages of the Focal, which can be easily used to analyze kinship networks of populations of other ages, such as the sandwich generation (middle-aged adults who are caring for both elderly parents and their own children) (Miller 1981) or the elderly. For example, previous work has analyzed old-age support from the perspective of kinship networks using survey data, microsimulation, and macrosimulation (Jiang 1992; Wachter 1997). Given an age range, other indicators can be used to examine the kinship network. From our model, the output is always the expected number of kin. However, this number has two dimensions as it changes with both ages of the Focal and of kin. In our analysis, we focus on the maximum value across the Focal's age while including kin of all ages. Future work could slice the output in other ways. Given a certain age of the Focal, kin at certain ages is more important to the Focal than kin at other ages. For instance, when the Focal is young (18 to 20 years old), getting information regarding college, marriage, or job from kin who are at older ages may be more important than kin who are at similar ages.

We present the number and age structure of only certain types of kin. Future work could extend it to other types, such as grandmothers and granddaughters. Moreover, our analyses use summaries of the characteristics of kin by different generations– we show that the age pattern of kin from the same generation shares similarities. It would be insightful for some readers if a future study reclassifies different types of kin to present results from another perspective. For example, Murphy (2011) divides different types of kin into two groups – primary kin (including siblings and other vertical kin, such as natural parents and children, grandparents, and grandchildren) and secondary kin (other close relatives, such as nephews and nieces, aunts and uncles, and first cousins) as they have different important functions. As time goes by, the definition of kinship networks also evolves. Previous work has extended kinship analysis by including affinal kin (Andersson and Kolk 2022), step-kin (Wachter 1997), and male kin (Caswell 2022). Our analysis could be adapted to male kin by setting the sex ratio at birth (SRB) according

to empirical data (here we simply assume the SRB as 100 boys per 100 girls). Especially under the low fertility setting, imbalanced SRB will have a considerable impact on kinship networks.

Demographic models all have some potentially counterfactual assumptions. The model we use assumes that mortality and fertility schedules apply uniformly to everyone (Caswell 2019). Therefore, we get only the expected number of kin instead of the distribution of the number. Obviously, we do not expect our model to be consistent with the results of a census or sample of a population due to factors like demographic stochasticity (random outcomes of probabilities of survival and reproduction) and environmental stochasticity (random temporal variation) (Caswell 2020). However, such comparisons may be helpful to analyze the effect of counterfactual assumptions. Previous work on kinship considered demographic stochasticity by implementing microsimulations for countries, such as the United States (Reeves 1987; Wachter 1997), China (Hammel et al. 1991; Jiang 1994), and Italy (Tomassini and Wolf 2000). Earlier work by Jiang (1994) compares microsimulations using SOCSIM with the macrosimulations of Zeng (1986) based on vital rates of China and finds a very close agreement for a wide range of kinship predictions. Therefore, our results, based on the formal kinship model (Caswell 2019), could also be compared with the result from microsimulation to examine the effect of demographic stochasticity. Moreover, when empirical data of kinship network is available (e.g. consanguineous kin by sex and birth cohort (Kolk et al. 2021) and affinal kin by socioeconomic status (Andersson and Kolk 2022) in Sweden), future studies could benefit from further comparing results from formal kinship model and from microsimulations with empirical kinship networks. For environmental stochasticity, random matrix methods (Tuljapurkar 2013) can be incorporated into the kinship model we use.

References

Andersson, L. and Kolk, M. (2022). Kinship and socioeconomic status: Social gradients in frequencies of kin across the life course in Sweden. (FLUX 6/2022 Working Papers INVEST Working Papers 53/2022.) doi:10.31235/osf.io/brcxt.

Bengtson, V.L. (2001). Beyond the nuclear family: The increasing importance of multi-generational bonds: The Burgess award lecture. *Journal of Marriage and Family* 63(1): 1–16. doi:10.1111/j.1741-3737.2001.00001.x.

Bian, Y. (1997). Bringing strong ties back in: Indirect ties, network bridges, and job searches in China. *American Sociological Review* 62(3): 366–385. doi:10.2307/2657311.

Bloom, D., Canning, D., and Sevilla, J. (2003). *The demographic dividend: A new perspective on the economic consequences of population change*. Santa Monica, CA: Rand Corporation.

Bott, E. (1971). Reconsiderations. In: Spillius, E.B. (ed.). *Family and social network. roles, norms and external relationships in ordinary urban families*. Milton Park: Routledge, vol. 2.

Caswell, H. (2001). *Matrix population models: Construction, analysis and interpretation*. Sunderland, Mass: Sinauer Associates.

Caswell, H. (2019). The formal demography of kinship. *Demographic Research* 41(24): 679–712. doi:10.4054/DemRes.2019.41.24.

Caswell, H. (2020). The formal demography of kinship ii. *Demographic Research* 42(38): 1097–1144. doi:10.4054/DemRes.2020.42.38.

Caswell, H. (2022). The formal demography of kinship iv: Two-sex models and their approximations. *Demographic Research* 47(13): 359–396. doi:10.4054/DemRes.2022.47.13.

Caswell, H. and Song, X. (2021). The formal demography of kinship iii. *Demographic Research* 45(16): 517–546. doi:10.4054/DemRes.2021.45.16.

Coale, A.J. (1972). *The growth and structure of human populations: A mathematical investigation*. Princeton: Princeton University Press.

Coste, C.F., Bienvenu, F., Ronget, V., Ramirez-Loza, J.P., Cubaynes, S., and Pavard, S. (2021). The kinship matrix: Inferring the kinship structure of a population from its demography. *Ecology Letters* 24(12): 2750–2762. doi:10.1111/ele.13854.

Erlich, Y., Shor, T., Pe'er, I., and Carmi, S. (2018). Identity inference of genomic data using long-range familial searches. *Science* 362(6415): 690–694.

doi:10.1126/science.aau4832.

Goodman, L.A., Keyfitz, N., and Pullum, T.W. (1974). Family formation and the frequency of various kinship relationships. *Theoretical Population Biology* 5(1): 1–27. doi:10.1016/0040-5809(74)90049-5.

Hammel, E.A., Mason, C., Wachter, K., Wang, F., and Yang, H. (1991). Rapid population change and kinship: The effects of unstable demographic changes on Chinese kinship networks, 1750–2250. In: *Consequences of rapid population growth in developing countries*. New York: Taylor & Francis: 243–272. doi:10.4324/9781315058979-13.

Jiang, L. (1992). *Parity and security: A simulation study of population aging, kinship network, and old age security in China*. Ph.D. thesis, University of California, Berkeley.

Jiang, L. (1994). Parity and security: a simulation study of old-age support in rural China. *Population and Development Review* 20(2): 423–448. doi:10.2307/2137526.

Jiang, L. (1995). Changing kinship structure and its implications for old-age support in urban and rural China. *Population Studies* 49(1): 127–145. doi:10.1080/0032472031000148286.

Keyfitz, N. (1971). On the momentum of population growth. *Demography* 8(1): 71–80. doi:10.2307/2060339.

Keyfitz, N. (1977). *Introduction to the mathematics of population with revisions*. Reading, Mass: Addison-Wesley Publishing Company.

Keyfitz, N. and Caswell, H. (2005). *Applied mathematical demography*, vol. 47. New York: Springer.

Kitagawa, E.M. (1955). Components of a difference between two rates. *Journal of the American Statistical Association* 50(272): 1168–1194. doi:10.1080/01621459.1955.10501299.

Kolk, M., Andersson, L., Pettersson, E., and Drefahl, S. (2021). The Swedish kinship universe: A demographic account of the number of children, parents, siblings, grandchildren, grandparents, aunts/uncles, nieces/nephews, and cousins using national population registers. (Stockholm Research Reports in Demography 2021:28). Stockholm: SUDA. doi:10.17045/sthlmuni.17704988.v1.

Krackhardt, D., Nohria, N., and Eccles, B. (2003). The strength of strong ties. In: Cross, R., Parker, A., and Sasson, L. (ed.). *Networks in the knowledge economy*. New York: Oxford University Press: 82–105. doi:10.1093/oso/9780195159509.003.0008.

Lee, R. (2003). The demographic transition: Three centuries of fundamental change. *Journal of Economic Perspectives* 17(4): 167–190.

doi:10.1257/089533003772034943.

Lee, R.D. and Reher, D.S. (2011). Introduction: The landscape of demographic transition and its aftermath. *Population and Development Review* 37(1): 1–7. doi:10.1111/j.1728-4457.2011.00375.x.

Miller, D.A. (1981). The 'sandwich' generation: Adult children of the aging. *Social Work* 26(5): 419–423. doi:10.1093/sw/26.5.419.

Murphy, M. (2011). Long-term effects of the demographic transition on family and kinship networks in Britain. *Population and Development Review* 37: 55–80. doi:10.1111/j.1728-4457.2011.00378.x.

Murray, S.O., Rankin, J.H., and Magill, D.W. (1981). Strong ties and job information. *Sociology of Work and Occupations* 8(1): 119–136. doi:10.1177/073088848100800107.

Pullum, T.W. (1982). The eventual frequencies of kin in a stable population. *Demography* 19(4): 549–565. doi:10.2307/2061018.

Reeves, J.H. (1987). Projection of number of kin. In: Bongaarts, J., Burch, T.K., and Wachter, K.W. (ed.). *Family demography: Methods and their application*. Oxford: Clarendon Press: 228–248.

Rindfuss, R.R. (1991). The young adult years: Diversity, structural change, and fertility. *Demography* 28(4): 493–512. doi:10.2307/2061419.

Tomassini, C. and Wolf, D.A. (2000). Shrinking kin networks in Italy due to sustained low fertility. *European Journal of Population/Revue européenne de Démographie* 16(4): 353–372. doi:10.1023/A:1006408331594.

Tuljapurkar, S. (2013). *Population dynamics in variable environments*, vol. 85. New York: Springer Science & Business Media. doi:10.1007/978-3-642-51652-8.

Tuljapurkar, S., Ogawa, N., and Gauthier, A.H. (2010). *Ageing in advanced industrial states: Riding the age waves-Volume 3*. New York: Springer Science & Business Media. doi:10.1007/978-90-481-3553-0.

United Nations (2019). World population prospects 2019. New York: Department of Economic and Social Affairs, Population Division, UN.

Verdery, A.M. (2015). Links between demographic and kinship transitions. *Population and Development Review* 41(3): 465–484. doi:10.1111/j.1728-4457.2015.00068.x.

Verdery, A.M. and Margolis, R. (2017). Projections of white and black older adults without living kin in the United States, 2015 to 2060. *Proceedings of the National Academy of Sciences* 114(42): 11109–11114. doi:10.1073/pnas.1710341114.

Verdery, A.M., Smith-Greenaway, E., Margolis, R., and Daw, J. (2020). Tracking the

reach of COVID-19 kin loss with a bereavement multiplier applied to the United States. *Proceedings of the National Academy of Sciences* 117(30): 17695–17701. doi:10.1073/pnas.2007476117.

Wachter, K.W., Blackwell, D., and Hammel, E.A. (1997). Testing the validity of kinship microsimulation. *Mathematical and Computer Modelling* 26(6): 89–104. doi:10.1016/S0895-7177(97)00172-6.

Wachter, K.W. (1997). Kinship resources for the elderly. *Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences* 352(1363): 1811–1817. doi:10.1098/rstb.1997.0166.

Zagheni, E. and Wagner, B. (2015). The impact of demographic change on intergenerational transfers via bequests. *Demographic Research* 33(18): 525–534. doi:10.4054/DemRes.2015.33.18.

Zeng, Y. (1986). Changes in family structure in China: A simulation study. *Population and Development Review* 12(4): 675–703. doi:10.2307/1973431.
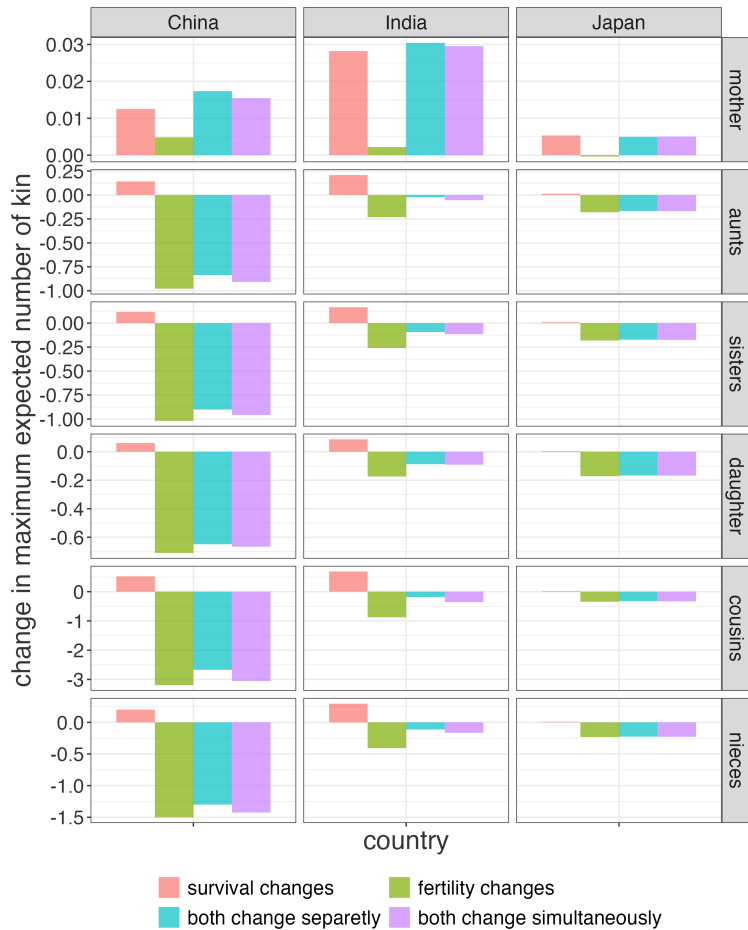
Appendix

Figure A-1: **The maximum expected number of kin ever born across all ages of Focal (i.e., the eventual expected number of kin) for China, India, and Japan from 1950 to 2050. The gray line is a reference with slope 1**
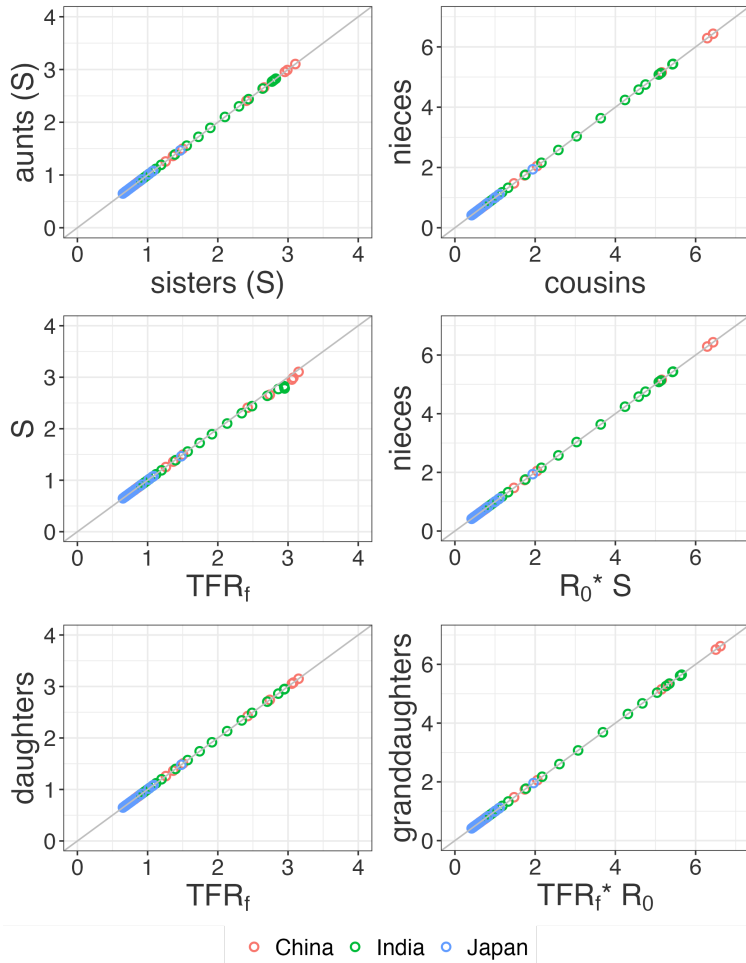
Figure A-2: **Change in the maximum expected number of kin when Focal is at a demographically dense age (ages 15 to 39) for China, India, and Japan, 1970–1980**

Figure A-3: **The maximum expected number of living kin across all ages of Focal (ages 0 to 95+) and net reproductive ratio R_0 for China, India, and Japan. The gray line is a reference with slope 1**